

# The HEM User's Guide

## Version 5.0

Instructions for using the Human Exposure Model for Single and Multiple Facility Exposure and Risk Modeling

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# 1. Introduction

The Human Exposure Model Open-Source Version 5 (“HEM”) is a streamlined, but rigorous tool you can use for estimating ambient concentrations, population exposures, and health risks that result from air pollutant emissions from complex industrial facilities. HEM can be used to model impacts from a single facility or from multiple facilities located across the United States (U.S.) and its territories, as well as outside the U.S. anywhere in the world. HEM is designed for use by the U.S. Environmental Protection Agency (EPA), state agencies, local agencies, industry, and other stakeholders, and is used in the Risk & Technology Review (RTR) assessments by EPA of regulated source categories. HEM includes the dispersion model AERMOD as a compiled executable program used to model emissions and the resulting ambient concentrations from hundreds of facilities, whether located within close proximity or thousands of miles away from each other. HEM then predicts the potential exposures and inhalation health risks posed by these emissions, including in zones with combined impacts from multiple nearby facilities. The model incorporates risk summary reports that summarize the cancer risk and noncancer health hazards from the modeled emissions. HEM also incorporates browser-based graphical viewing and analysis tools including contours of cancer and noncancer risk around modeled facilities, and demographic assessments to evaluate potential impacts to the surrounding populations. Air concentrations, risk, and health impacts can be modeled at U.S. Census block receptors as well as at alternate and user-defined receptors inside or outside the U.S. In lieu of HEM-AERMOD modeling, HEM can calculate risks based on user-supplied air concentrations for a gridded or random set of receptor locations. HEM is available for download as a zipped executable file on EPA’s [Download Human Exposure Model \(HEM\) website](#).

## 1.1. Organization of the HEM User’s Guide

This User’s Guide is organized into 11 sections plus two appendices:

Section 1	Overview of HEM’s operations, features, requirements, and limitations
Section 2	Installing HEM and its data libraries
Section 3	Preparing input files for a HEM run
Section 4	Step-by-step instructions for running HEM
Section 5	Calculations performed by HEM for each modeled facility
Section 6	Description of HEM’s facility-specific outputs
Section 7	Description of HEM’s risk summary outputs
Section 8	Description of HEM’s demographic assessment
Section 9	Understanding HEM’s modeled risk results
Section 10	Quality assurance remodeling
Section 11	References
Appendix A	Sample HEM output files
Appendix B	Demographic assessment calculations

## 1.2. Overview of HEM's Operations and Features

In a typical model run, HEM performs four main operations: (1) dispersion modeling of emissions using AERMOD, (2) estimation of population exposure, (3) characterization of the associated human health risks, and (4) demographic assessment of the exposed population (if the run is based on U.S. Census blocks). Alternatively, in lieu of dispersion modeling, HEM includes an option that allows the user to enter pollutant concentration data, from which HEM will estimate population exposure and human health risks. An overview of HEM's main modeling operations and this alternative feature is discussed below in this section.

### 1.2.1. Dispersion Modeling

For dispersion modeling, the American Meteorological Society - U.S. EPA Regulatory Model (AERMOD) is run by HEM as a compiled executable program. AERMOD is a state-of-the-science Gaussian plume dispersion model that EPA prefers for most industrial source modeling applications for air toxics applications (USEPA, 2005, 2017). AERMOD was developed under the auspices of the American Meteorological Society - Environmental Protection Agency Regulatory Model Improvement Committee (AERMIC) as summarized on EPA's [AERMOD website](#), which contains the AERMOD model documentation as well as links to AERMOD's preprocessors, AERMET, AERMAP, AERSCREEN, AERSURFACE and BPIP PRIM and post-processor, LEADPOST (USEPA, 2025). HEM5 incorporates **AERMOD version 24142**, which was originally made available to the public in November 2024 (USEPA, 2024a, 2024b, 2024c, 2024d, 2024e).

AERMOD can model dispersion of emissions from a wide range of different source types that may be associated with an industrial source complex (or "facility") including stack sources, area sources, and volume sources. Additionally, AERMOD is capable of modeling polygon, line, and buoyant line source types. AERMOD can also model emissions that vary in time or with wind speed, deposition with or without plume depletion, and other complex plume processes such as building downwash.

HEM supplies AERMOD with meteorological data pre-processed by AERMET (USEPA, 2024d) and required for AERMOD's dispersion calculations. HEM's Meteorology Library contains meteorological ("met") data from over 800 observation stations across the continental U.S., Alaska, Hawaii, and Puerto Rico. Section 2.4 provides information on how to download the met data used by HEM, discusses how the met files were processed and the data contained in each, and includes a national map of the locations for all met stations. HEM runs AERMOD as many times as is necessary to address the gaseous and particulate pollutants emitted from each modeled facility. AERMOD outputs average ambient concentrations at discretely modeled receptor locations, through the simulation of hour-by-hour dispersions from the emission sources into the surrounding atmosphere. These average concentrations are based on a year's worth of hourly met data by default or based on the specific period of data you specify, as discussed more in Section 3.2.2.

### 1.2.2. Population Exposure

For U.S. emission sources, after running AERMOD for dispersion modeling, HEM estimates population exposure and human health risks by drawing on additional data libraries that are provided with the model, including U.S. Census Files and Toxicity Value Files available from EPA's [Download Human Exposure Model \(HEM\)](#) webpage. The Census Files library of census block internal point ("centroid") locations and populations provides the basis of human exposure

calculations for HEM runs based on the U.S. Census. HEM draws upon the Census Files library to identify all census block locations within the study domain, as defined by the default modeling radius around each facility or a radius that you specify. The Census Files library includes locations and populations, elevations, and controlling hill heights for all the approximately 5.8 million populated blocks tabulated in the 2020 U.S. Census (US Census Bureau, 2022b, 2023a). Section 2.3 provides information on how to download the census data and discusses the data contained in HEM's Census Files library. Alternatively, HEM can model population exposures without the U.S. Census Files by using population values associated with locations you provide in an Alternate Receptors file, for modeling within the U.S. or anywhere in the world, as described in Section 3.5.8.

### 1.2.3. Estimation of Human Health Risks

HEM uses its [Toxicity Value Files](#) library of pollutant unit risk estimates (UREs) and reference concentrations (RfCs) to calculate population cancer risks and noncancer health hazards, respectively. These UREs and RfCs are based on values recommended by the EPA for hazardous air pollutants (HAP) and other toxic air pollutants. For cancer, HEM's URE-based computed cancer risk estimates reflect the risk of developing cancer for an individual breathing the ambient air at a given receptor site 24 hours per day over a 70-year lifetime. For noncancer, HEM estimates health hazards or "risks" using hazard quotients (HQs) and hazard indices for 14 target organs and systems. The HQ for a given pollutant and receptor site is the ratio of the ambient concentration of the pollutant to the RfC at which (and below which) no adverse noncancer health effects are expected. The chronic hazard index (HI) for a given target organ is the sum of HQs for substances that affect that organ. HEM computes target organ-specific hazard indices (TOSHIs) for the following 14 organ systems: respiratory, liver, neurological, developmental, reproductive, kidney, ocular, endocrine, hematological, immunological, skeletal, spleen, thyroid, and whole-body. Section 2.2.1 discusses the terms URE, RfC, HQ, HI and TOSHI in more detail. More information on how EPA uses dose-response values in risk assessments, including the source for these values, is also provided on EPA's Dose-Response Assessment webpage (USEPA, 2024f).

Using the air concentration results from AERMOD, in combination with the data supplied by HEM's Census Files (or your Alternate Receptors file) and the Toxicity Value Files, HEM estimates cancer risks and noncancer health hazards resulting from inhalation exposure at the modeled receptor locations. The predicted cancer and noncancer risk estimates are generally conservative with respect to the modeled emissions because they are not adjusted for attenuating exposure factors such as indoor/outdoor concentration ratios, daily hours spent away from the residential receptor site, and years of lifetime spent living elsewhere than the current residential receptor site.

Optionally, HEM can estimate acute (short-term, such as hourly) concentrations for each pollutant and receptor site, including the location of the maximum acute concentration for each pollutant emitted from the facility. In addition, the model outputs a listing of the associated acute benchmarks for each pollutant at or below which certain acute adverse effects are not expected. From these acute concentrations and benchmarks, the ratio of the maximum acute concentration to the associated benchmark is computed to determine the maximum acute HQ for each pollutant of concern. Acute noncancer HQs, like chronic noncancer TOSHIs and cancer risk, are conservative estimates in HEM.

HEM provides the average ambient air concentration, predicted lifetime cancer risk, chronic noncancer TOSHIs, and (optionally) acute concentration at every receptor location and identifies

receptor locations where the impact is highest. For these locations, the model gives the concentrations of the modeled pollutants emitted from each emission source driving the overall cancer risks, chronic TOSHIs, and (optionally) acute impacts. The locations of maximum cancer risk and maximum noncancer TOSHIs are located by the model off of facility property, as determined by source locations plus a small buffer around these sources. The model also estimates the number of people exposed to various cancer risk levels and TOSHI levels as a result of the modeled emissions.

HEM outputs these results for each individual modeled facility and also consolidates facility-specific results into output files that provide results for all modeled facilities as a group. HEM's post-processors, the risk summary programs, produce additional outputs of combined and summarized results that are useful in capturing the risk and health hazards, as well as the pollutant and emission source drivers of these impacts, for a group of modeled facilities as a whole (e.g., an entire source category of facilities modeled under the EPA's RTR program). HEM provides a browser-based option of viewing all the summarized results in graphical form, including an interactive map of the facilities modeled, pie and bar charts of overall cancer incidence, population risks, and pollutant and source risk drivers, and risk contour maps surrounding each facility.

#### **1.2.4. Demographic Assessment**

When modeling with U.S. Census receptors, HEM's Demographic Assessment module can be used to link the modeled population in each facility domain – including cancer and noncancer risk estimates for that population – to demographic information from the Census' American Community Survey (ACS) that describe aspects of the modeled population. HEM reports demographics based on race and ethnicity, age, poverty status, lack of high school education, limited English speaking household, and disabilities (US Census Bureau, 2023b, 2024a, 2024b). HEM also provides these demographic data at the county, state, and nationwide levels for comparison. The Demographic Assessment module thereby allows for the identification of cancer and noncancer risks posed by the modeled emissions to various groups within the modeled population. HEM also provides an interactive browser-based option for viewing each modeled facility's demographic results in comparison to other modeled facilities, and in comparison to the county, state, and nationwide demographic breakdowns. Section 8 discusses the methodology used for HEM's demographic assessment.

#### **1.2.5. Alternative Option: User-Supplied Pollutant Concentrations**

Although HEM is typically run using AERMOD for dispersion modeling of pollutant emissions to predict concentrations, you can bypass this modeling step by inputting air pollutant concentration data for a gridded or random set of geographic locations. HEM will then interpolate concentrations from those locations to the census block centroids (or to alternate receptors). HEM processes the interpolated air concentrations in the same way as those generated by AERMOD to estimate cancer risks and noncancer health hazard indices due to inhalation exposure. There may be several reasons you would want to estimate risks but not run AERMOD in HEM, including the use of an [alternative dispersion model](#). You may also wish to use the results of an existing AERMOD model run that included modeling options not currently available in HEM, such as an atypical source type or pollutant decay. It is also possible to use air monitoring results as the pollutant concentration inputs under this option; however, you should ensure that you have adequate data to properly characterize the area of interest. Section 3.6 discusses the User-Supplied Concentration file associated with this feature.

### 1.3. HEM5 Improvements Compared to Previous Versions

HEM was originally developed as a screening tool for exposure assessment in the 1980s (USEPA, 1986). The original model was upgraded to run in a Windows™ environment, eventually called HEM-3, and regularly improved and re-released by EPA in several HEM-3 versions over the years, including in 2007, 2014, 2017 and 2019. HEM-3 was written in the FoxPro® language, last published by Microsoft® in 2007 and now unsupported. HEM is now written in the open-source software language Python™. HEM version 4.1, the first Python version, was originally released to the public in September 2021 and includes census data from the 2010 Decennial Census and 2015-2019 ACS demographic data. Next, HEM version 4.2 was released to the public in January 2023. HEM4.2 includes the same capabilities and features as version 4.1 but updated 2020 Decennial Census data, 2016-2020 ACS demographic data, and AERMOD version 22112 released in June 2022.

The HEM4.1 and HEM4.2 User's Guides include a description of the enhancements incorporated in the progression from HEM-3 to HEM4.1 to HEM4.2 and are available on EPA's [FERA website](#). To enable modeling with different Decennial Census data and different ACS demographic data, HEM4.1 and HEM4.2 models are still available for download from the FERA website on the [HEM download page](#). Compared to HEM-3, HEM4.1 and HEM4.2 include additional modeling and analysis capabilities, improved and streamlined user interfaces, and enhanced graphical output capabilities.

HEM5 builds on these improvements, including additional features and enhanced capabilities, an updated AERMOD version, updated Census data, and updated ACS demographic data. The list below encapsulates HEM5's improvements compared to previous versions.

#### HEM (version 5):

- Incorporates [AERMOD version 24142](#) (released November 2024).
- Uses U.S. Geological Survey (USGS) web services, by default when you choose to model with elevations, to retrieve elevation data for sources and receptors and to calculate hill heights.
- Allows an alternative “offline” method when you choose to model with elevations, but the USGS service is inaccessible or unavailable, which interpolates receptor data to estimate elevations and hill heights.
- Allows you to create contour maps of cancer risk or noncancer hazard index surrounding each facility.
- Allows the use of AERMOD's flagpole feature to model concentrations and risk at user-specified heights above ground level.
- Includes an enhanced integrated processor to change the Census by adding block receptors, in addition to moving, deleting, and zeroing out receptors.
- Uses a single nationwide Census file, rather than individual state files.
- Incorporates American Community Survey (ACS) 2018-2022 five-year Census demographic data (released December 2023) and includes two additional demographic categories: Asian race and People with One or More Disabilities. The demographic outputs also contain updated terminology and more detailed footnotes describing the demographic methodology and source of the population data.

- Allows you to bypass AERMOD if you input air pollutant User-Supplied Concentrations data for a gridded or random set of geographic locations, which HEM interpolates and uses to calculate risks.
- Includes a more efficient All Outer Receptor module, with a vectorized interpolation function.
- Includes a more efficient Alternate Receptor module, with a Python library used to rapidly read this potentially large input file.
- Includes an improved generic “catch-all” error handler as a backstop to specific error handling and also includes additional more specific pop-up and log error messages.

#### **HEM (versions 5 and 4.2):**

- Includes the 2020 Decennial Census population data. The previous versions (including version 4.1) were based on the 2010 Decennial Census.
- Includes a more precise determination of the dispersion environment, rural or urban, based on the Census 2020 population density surrounding each facility. The previous method was based on coarser Census 2010 urbanized areas.

#### **HEM (versions 5, 4.2 and 4.1):**

- Bases model selection options primarily on the data in your input files, rather than on responses to user interface questions, which is less prone to user error.
- Performs consistency checks on your input files and includes more specific and instructive error messages, to aid you in rectifying any errors or inconsistencies in your input files before the model run begins.
- Can model impacts anywhere in the world with user-provided Alternate Receptors, in addition to U.S. Census block receptors.
- Includes meteorological data based primarily on 2019 observations.
- Will default to using the full year of selected met data, but you may instead model with a specified period of met data by indicating a start and end date and even hour.
- Allows you to specify the exact location of the facility center or use the center location calculated by the model.
- Allows you to specify polar ring distances or use the polar ring locations calculated by the model.
- Allows you to choose Method 1 or Method 2 for particle deposition. Method 2 requires less knowledge of the particle size distribution of your emissions compared to Method 1, which requires a detailed particle size input file.
- Allows you to choose a different acute high value for each facility (e.g., maximum, 99th percentile, 98th percentile), rather than modeling each facility with the same maximum acute value.
- Incorporates buoyant line updates including modeling of multiple buoyant line source groups, each with different parameters, for a given facility.
- Includes the Risk Summary Report programs (previously called the RTR Summary Programs) integrated into the model itself, rather than as an add-on suite of programs.
- Includes enhanced Risk Summary Reports. The HI Histogram output accounts for all 14 TOSHIs (not just three). The Incidence Drivers output is now sorted in descending order of pollutant-specific incidence and includes the pollutant’s percentage contribution to

total incidence. The Source Type Risk Histogram output includes the maximum overall risk histogram and incidence for all modeled facilities in your run group, in addition to the histogram and incidence specific to each source type.

- Includes enhanced capabilities for visualization and analysis of outputs, including browser-based interactive tables, graphs, and mapping options.
- Includes an integrated Demographic Assessment module, which allows you to assess the demographics of the people within user-specified proximities to modeled emissions and the demographics of the people at risk from the modeled emissions.
- In addition to the improvements listed above, HEM versions 5, 4.2 and 4.1 has maintained all the capabilities of the 2019 HEM-3 version, which included numerous enhancements compared to the previous versions.

These HEM enhancements, along with HEM's basic functions and features, are described in detail in this User's Guide.

## 1.4. Strengths, Limitations and Uncertainties of HEM

HEM is designed to perform detailed and rigorous analyses of chronic and acute air pollution risks for populations located near industrial emission sources. The model was previously updated with the goal of simplifying the running of AERMOD without sacrificing any of AERMOD's strengths. In keeping with this goal, you can specify complex emission source configurations, including point sources for stacks, area and volume sources for fugitive emissions, obliquely oriented area sources for roadways, line sources for airport runways, buoyant line sources for roof vents, and polygon sources for a variety of area source shapes including entire census blocks and tracts. HEM also analyzes multiple pollutants concurrently, with the capability of including particulate and gaseous pollutants in the same model run. The model identifies all receptors located near each facility, including U.S. census blocks or alternate receptors. You can also specify the locations of individual houses, schools, facility boundaries, monitors, or other user-defined receptors to model. HEM-AERMOD can account for impacts of terrain (elevation and hill height effects), building downwash effects, pollutant deposition and plume depletion, temporally varying emissions, and can predict receptor concentrations at ground level or at user-specified "flagpole" heights above ground level.

However, HEM's framework has some limitations and incorporated uncertainties. HEM's concentrations are estimated using AERMOD and are subject to AERMOD's uncertainties and limitations. While AERMOD is considered state-of-the-science for Gaussian plume dispersion (not considering secondary air pollutant formation), like all air pollutant dispersion models, AERMOD is subject to uncertainties as described more on EPA's AERMOD webpage. (Refer to the studies and support documents listed under "Model Supporting Documents" on the [Air Quality Dispersion Modeling - Preferred and Recommended Models website](#).)

HEM also incorporates the uncertainties associated with its dose response estimates. Pollutant UREs for cancer, RfCs for noncancer HI, and benchmarks for acute health effects are subject to uncertainties as described more on EPA's Dose-Response Assessment webpage (USEPA, 2024f). Another limitation of HEM is that when modeling with U.S. census block receptors the model estimates pollutant concentrations and risks for the block centroid, as defined by the U.S. Census Bureau. Values calculated for this internal point are not representative of the range of values over the entire block and may not represent where most people reside within a block. Furthermore, these values do not account for the movement of people from their home census

blocks to other census blocks, due to commuting or other daily activities. In addition, as previously noted, HEM calculates ambient outdoor concentrations of air pollutants. These concentrations do not account for indoor sources of pollution, or the reduction of outdoor pollution in conditioned indoor air.

HEM performs several tests on user input data—including ensuring consistency of input files and some parameters—before using AERMOD to calculate air pollution impacts. However, there are some potential problems users may introduce to their input files that HEM may not detect in these initial tests (e.g., using numerical values for inputs that correspond to units other than what HEM-AERMOD expects, such as feet instead of meters). To avoid this, carefully review the model input guidelines to make sure that the contents and format of your input files meet these guidelines before initiating a HEM run.

#### **1.4.1. Limitations and Uncertainties of User-Supplied Concentration Runs**

If you bypass AERMOD in HEM and instead provide your own air pollutant User-Supplied Concentration file for a gridded or random set of geographic locations, then you should be aware of the model uncertainties associated with whichever model was used to generate the air concentrations. Also, with this option there is the additional uncertainty associated with interpolation from your geographic locations to the census blocks or alternate receptors of interest. If your input data are sparse, then the interpolated values would be more uncertain. This uncertainty could be reduced if you use an adequate number of locations in a regular grid that provides good coverage of your area of interest. This uncertainty could also be minimized if you are using an alternative model (or AERMOD outside of HEM) but use the census blocks (or alternate receptors) as the model receptors, in which case the interpolated values would be nearly identical to those generated by the model.

The user-supplied concentrations option is capable of processing input files that cover large areas (e.g., an input file for an entire state with several million rows) but you should be aware that the output files can exceed 1GB. Also, this option will interpolate to all census blocks (or alternate receptors) within the “envelope” or convex hull of the input data points. For input points over an entire state, and where the points do not cover the boundary areas well, the convex hull can extend into unexpected areas and interpolate receptors outside the area of interest.

### **1.5. Requirements for Running HEM**

You can use HEM on any Windows™ based personal computer running Windows XP™ or later. The HEM executable package is approximately 1.7 GB in size once it has been uncompressed from the zip file. Disk space requirements for running HEM will depend on the number of census and meteorological files that you use. To model an individual facility, the model requires, at minimum, 10 megabytes (MB) of disk space for a small facility and 1 to 2 gigabytes (GB) for a large, complex facility. Furthermore, disk space requirements can be 10 to 20 times larger (than 2 GB) for complex facilities located in densely populated urban areas (i.e., with many receptors), depending on the modeling options you choose. The full census and meteorological libraries that you can download in addition to the model require about 2 GB of space. The HEM model also will need a minimum of 8 GB of random-access memory (RAM). Once installed, you can use HEM to model risks and exposures for any location in the U.S. or around the world, and for a wide range of emission source configurations.

For each model analysis, you should provide emission rates for all HAP and emission source locations in the form of Excel™ spreadsheet files. Detailed instructions are provided in Section 3, *Preparing HEM Input Files*. HEM requires separate estimates of emission rates for each pollutant, from each emission source, at each facility to be modeled. The model also requires detailed information on each emission source, including location, release height, emission velocity and temperature for point (stack) sources, and the configuration of non-point emission sources (e.g., area sources which emit with negligible velocity at ambient temperature). You will be able to design the model receptor network around each facility to be modeled via an input spreadsheet file. You can also use an optional spreadsheet file to provide the dimensions of buildings near emission sources, for use in computing building downwash effects. When modeling particulate emissions, you can use an optional spreadsheet file to provide particle size information and deposition parameters. If you opt to model dry deposition of gaseous emissions, you will need to provide additional spreadsheet input files describing the land use and vegetation surrounding the facility. You will be prompted to indicate the location of your input spreadsheet files through user input screens, which are discussed in more detail in Section 4, *Step-by-Step Instructions for Running HEM*.

This user's guide is designed to provide all the information you will need to run HEM. However, some of the options for running HEM draw on advanced features of AERMOD. If you are unfamiliar with the AERMOD dispersion model, you may need to refer to EPA's AERMOD documentation (available on the [AERMOD Modeling System page](#)) in order to develop some of the inputs needed for HEM (USEPA, 2024a, 2024e). This is particularly true for some of the more complex modeling options, such as plume deposition and depletion, building downwash, temporal and wind speed emission variations, and complex source configurations.

## 2. Installing HEM

This section provides instructions for downloading and installing the HEM model and required data libraries from the EPA's HEM Download Page.

### 2.1. Downloading the HEM Model and Libraries

The HEM model is available from EPA's [HEM Download webpage](#). This site includes general installation instructions, including hardware and software requirements, as well as links to download and install HEM and its associated data libraries. Download the HEM zip install package under "Software available for download." HEM can be installed anywhere on your PC and the root folder is not required to be named HEM. However, **for the purposes of this User's Guide, it is assumed the root folder will be named "HEM"**. HEM is started by running the executable file ending in ".exe". Note: The HEM version 5 source code is available at <https://github.com/USEPA/HEM5>.

In addition to user-supplied inputs describing the nature and location of the emissions (discussed in Section 3), HEM relies upon several data libraries that supply other required inputs for a modeling run. To complete the installation of HEM, download the following data libraries:

- the [Toxicity Value Files](#) containing each HAP's specific dose response values and benchmark values for affected organs. Upon installation, HEM's *resources* folder will include a Dose Response Library and Target Organ Endpoints table, but check the [HEM Download webpage](#) for EPA updates to these files;
- the [Census Files](#) nationwide zip file containing the population numbers and terrain elevation data for census blocks across the nation (based on the 2020 Census); and
- the [Meteorological Files](#) containing met station files (a surface and profile file for each station) with data for over 800 stations nationwide.

You will find links to these three HEM data libraries on the [HEM Download page](#). The following sections provide instructions for downloading these files, along with a brief description of each of these data libraries.

### 2.2. Toxicity Value Files Library

HEM uses a Toxicity Value Files library of pollutant-specific unit risk estimates (UREs) and reference concentrations (RfCs) to calculate risks for cancer and noncancer health hazards, respectively. To download these values, click on the "HEM Toxicity Value files (zip)" link on EPA's [HEM Download page](#). Before initiating a modeling run, check for EPA-updated versions of these files on the HEM Download Page. When updated files become available, copy these into the *resources* folder under the HEM directory that you selected during installation. Be sure to unzip the files and verify they are located in the specified folder when finished. The folder containing HEM's Toxicity Value Files is "HEM\resources."

#### 2.2.1. Description of Toxicity Value Files

For each pollutant or HAP, the Toxicity Value Files include one or more of the following parameters, if applicable and available based on the chemical health effects data for the HAP:

- URE for cancer risk;
- RfC for chronic noncancer health effects;
- reference benchmark concentrations for acute health effects; and
- target organs affected by the pollutant (for chronic noncancer effects), in a separate file.

These parameters are based on the EPA's database of recommended dose response values for HAP (USEPA, 2024f), which is updated periodically, consistent with continued research on these parameters. The URE represents the upper-bound excess lifetime cancer risk estimated to result from continuous exposure to an agent (HAP) at a concentration of 1 microgram per cubic meter ( $\mu\text{g}/\text{m}^3$ ) in air. For example, if the URE is  $1.5 \times 10^{-6}$  per  $\mu\text{g}/\text{m}^3$ , then 1.5 excess cancer cases are expected per 1 million people, if all 1 million people were exposed daily for a lifetime to 1 microgram of the pollutant in 1 cubic meter of air. UREs are considered plausible upper limits to the true value; the true risk is likely to be less but could be greater (USEPA, 2024g).

The RfC is a concentration estimate of a continuous inhalation exposure to the human population that is likely to be without an appreciable "risk" of deleterious noncancer health effects during a lifetime, including to sensitive subgroups such as children, asthmatics, and the elderly. No adverse effects are expected to result from exposure if the ratio of the potential exposure concentration to the RfC, defined as the hazard quotient (HQ), is less than or equal to one (1). The uncertainty of the RfC estimates can span an order of magnitude (USEPA, 2024g). Target organs are those organs (e.g., liver) or organ systems (e.g., reproductive) which may be impacted by chronic noncancer health effects from exposure to the pollutant in question. The hazard index (HI) is the sum of hazard quotients for substances that affect the same target organ or organ system, also known as the target organ specific hazard index (TOSHI). HEM's Toxicity Value Files library includes the following target organs and organ systems for estimating 14 TOSHIs:

- Respiratory HI,
- Liver HI,
- Neurological HI,
- Developmental HI,
- Reproductive HI,
- Kidney HI,
- Ocular HI,
- Endocrine HI,
- Hematological HI,
- Immunological HI,
- Skeletal HI,
- Spleen HI,
- Thyroid HI, and
- Whole Body HI.

The reference concentrations for acute health effects include both "no effects" reference levels for the general public such as the California Reference Exposure Levels (RELs), and emergency response levels, such as Acute Exposure Guideline Levels (AEGs) and Emergency Response Planning Guidelines (ERPGs). A more in-depth discussion of the development and

use of these health reference values may be found in the EPA's [Air Toxics Risk Assessment Reference Library](#) (USEPA, 2024h).

**You can add pollutants and associated health effect values, as needed, to the two Excel™ spreadsheets comprising HEM's Toxicity Values Files: the Dose Response Library file and the Target Organ Endpoints file.** These files are located in HEM's *resources* folder:

- HEM\resources\Dose\_Response\_Library.xlsx; and
- HEM\resources\Target\_Organ\_Endpoints.xlsx.

The Dose Response Library file includes a listing of HAP and the URE values, RfC values, and acute benchmark values associated with these pollutants. The Target Organ Endpoints file includes a listing of HAP and the organ(s) or organ system(s) that may be impacted with chronic noncancer health effects by exposure to these pollutants above the RfC level.

**Each pollutant you list in your facility-specific input files (discussed in Section 3) needs to be included and match exactly (the spelling of) a pollutant name in HEM's Dose Response Library file.** The Target Organ Endpoints file need not contain every pollutant listed in your inputs. You should ensure, however, that every pollutant in your input files that has chronic noncancer health effects associated with it – and that you wish to model as such – has an RfC value in the Dose Response Library file and is also listed in the Target Organ Endpoints file, with the impacted organs and organ systems checked. Note: **Only pollutants with RfC values need to be listed in the Target Organ Endpoints file.**

## 2.3. Census Files Library

You will need to obtain nationwide census file from the 2020 Census on the [HEM Download page](#) of EPA's FERA website. This single CSV file is for the entire nation (unlike previous versions of HEM, which used separate state files). Download, unzip and copy the nationwide census file into the *census* folder under the main HEM folder you selected during installation. The census folder is "HEM\census".

### 2.3.1. Description of Census Files

The HEM Census Files include census block identification codes, locations, populations, elevations, and controlling hill heights for the over 5.8 million populated census blocks identified in the 2020 Census. The location coordinates reflect an internal point selected by the Census Bureau to be roughly in the center of the block. For complex shapes, the internal point may not be in the geographic center of the block, but they are still referred to as "centroids". Locations and population data for census blocks in the 50 states, Puerto Rico, and the Virgin Islands are extracted from the U.S. Census Bureau website for Census 2020 (US Census Bureau, 2022b, 2023a).

HEM's Census Files include elevation and controlling hill height data, in addition to the population and location data supplied by the Census Bureau. The AERMOD terrain preprocessor program, AERMAP (USEPA, 2018c), was used to estimate the elevation and hill height of each populated census block in the U.S., including Alaska, Hawaii, Puerto Rico, and the Virgin Islands. The controlling hill height values are used for flow calculations within AERMOD. The elevation data contained within the 2020 Census files were derived from the

United States Geological Survey National Elevation Dataset (NED) at a resolution of 1 arc second, or about 30 meters (USGS, 2024). These block elevations are used if you choose to model with elevated terrain. In addition, if you choose the “offline” option, as discussed later in this guide, HEM uses these block elevations to estimate other elevations used in the modeling.

The HEM Census Files also include the locations for over 120,000 schools and 700 monitors. School location data are for schools spanning pre-kindergarten through high school and are available for both public and private schools (NCES, 2025a, 2025b). You can obtain monitoring locations from the Ambient Monitoring Technology Information Center’s (AMTIC’s) Ambient Monitoring Archive for HAPs, which in 2025 (the date of this User’s Guide) housed records from over 6,000 monitoring sites from 1990 through 2022 (USEPA, 2022). Note: The precision of the latitude/longitude location of these monitors varies and, in some cases, is precise to only two decimal places (roughly  $\pm 600$  meters), making comparison with HEM modeling results inexact.

In addition to the above Decennial Census data (US Census Bureau, 2022b, 2023a), demographic data from the U.S. Census’ American Community Survey (US Census Bureau, 2023b, 2024a, 2024b) is also required by HEM for the Demographic Assessment module. You do not need to separately download the ACS data, as it is already included in HEM’s *resources* folder within the HEM executable in two large files named “acs.csv” and “acs-defaults.csv”. The demographic data used by the Demographic Assessment module is discussed in Section 8 and in Appendix B.

## 2.4. Meteorological Files Library

HEM requires meteorological information for AERMOD’s dispersion modeling, and you can download nationwide meteorological data files from the [HEM Download page](#). Each set of meteorological files contains surface data and upper air data, as required by AERMOD, and is named beginning with the abbreviation for the state in which the station is located. Place the nationwide meteorological files from the HEM Download Page in the *MetData* subfolder of HEM’s *aermod* folder and unzip the met files. After unzipping, verify all the met files are in this folder (“HEM\AERMOD\MetData”). Each met station should have two files: one with an SFC (surface data) extension and one with a PFL (profile data) extension.

When you download the HEM model (as described in Section 2.1), the installation package will place an Excel™ spreadsheet named *metlib\_aermod.xlsx* in your “HEM\resources” folder. This spreadsheet lists all the SFC and PFL met stations that are provided in the nationwide meteorological data files (those available on the HEM Download Page on the date you download the model). You may edit this spreadsheet to include additional met station files, but you must provide the new met station data as both SFC and PFL files in your “HEM\AERMOD\MetData” folder. Be careful that the SFC and PFL file names match the new rows you have added to the *metlib\_aermod.xlsx* spreadsheet in your *resources* folder. You may also edit rows in this spreadsheet or delete met station entries entirely. (A Python error message will be displayed when you initiate a model run, if HEM cannot locate the *metlib\_aermod.xlsx* spreadsheet in your *resources* folder.)

### 2.4.1. Description of Meteorological Files

AERMOD requires surface and upper air meteorological data that meet specific format requirements. HEM includes a library of meteorological data from National Weather Service

(NWS) observation stations. The current HEM AERMOD Meteorological Files library includes over 800 nationwide locations, depicted in **Figure 1**.

EPA meteorologists obtained calendar year 2019 Integrated Surface Hourly Data (ISHD) for approximately 800 [Automated Surface/Weather Observing Systems \(ASOS/AWOS\)](#) spanning the entire US, as well as Puerto Rico and the US Virgin Islands, from the National Centers for Environmental Information (NCEI) (formerly, the National Climatic Data Center (NCDC)). A previous version of the AERMOD meteorological processor, AERMET (USEPA, 2024d) and its supporting modeling system (AERSURFACE and AERMINUTE) were used to process the meteorological data.

To estimate the boundary layer parameters required by AERMOD, AERMET requires hourly surface weather observations (which may include hourly values calculated from 1-minute data) and the full twice-daily upper air soundings (i.e., meteorological variables reported at all levels). The surface and upper air stations are paired to produce the required input data for AERMOD. To support AERMET, ASOS 1-minute data for each surface station were obtained from NCEI in a DSI 6405 format. Further, upper air sounding data for the same time period for over 80 observation sites were obtained from the National Oceanic & Atmospheric Administration (NOAA) Earth System Research Laboratory's (ESRL) online Radiosonde Database (now the [Integrated Global Radiosonde Archive](#)). These datasets were produced by ESRL in Forecast Systems Laboratory (FSL) format.

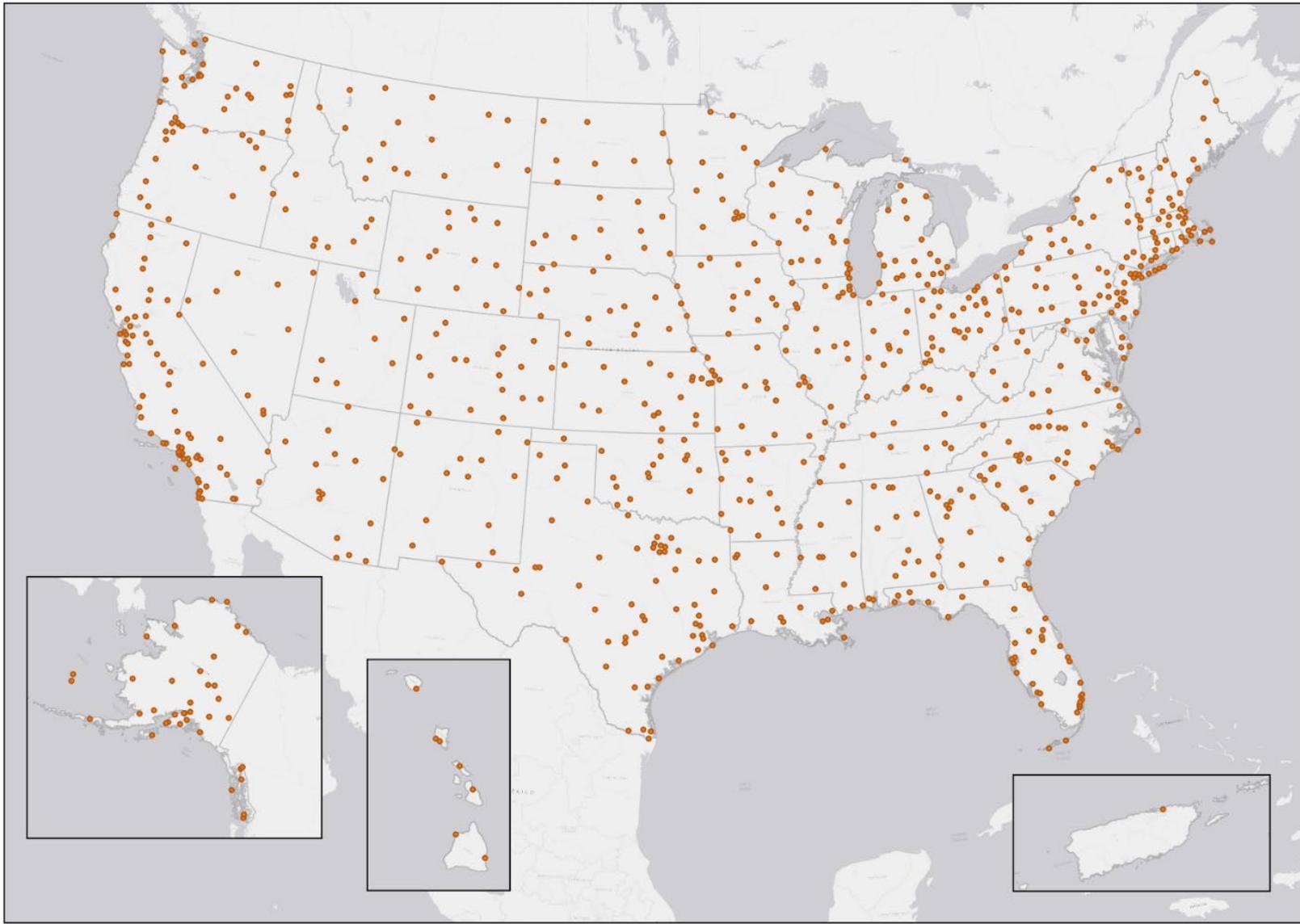
#### **2.4.1.1. AERMET Processing**

Utilizing the AERMET meteorological data pre-processor, and the ASOS surface and FSL upper air stations, surface and profile files for input into AERMOD were generated nationwide. The surface stations were paired with representative upper air stations by using the upper air station closest to each surface station. The AERSURFACE tool was used to estimate the surface characteristics for input into AERMET utilizing land cover data surrounding the surface station. In addition, the AERMINUTE pre-processor was used to process 1-minute ASOS wind data for input into AERMET. The following provide more detail regarding the pre-processors, AERMET and AERMINUTE, used to generate the AERMOD meteorological data:

- **AERMET Options:** Version 19191 used to process ASOS site data; surface data in NCEI TD-3505 (ISHD) format; upper air data in FSL (all levels, tenths m/s) format; used the ADJ\_U\* non-Default BETA option to adjust the friction velocity ( $u^*$  or  $u_{star}$ ) for low wind speed stable conditions.
- **AERMINUTE Options:** Version 15272 used for 1-minute ASOS data in TD-6405 format where available.

The surface files were examined for completeness. If more than 10 percent of the meteorological data were missing within the 2019 calendar year for a station, the next previous calendar year of meteorological data that was considered complete was used for that station in the HEM meteorological database. In all, 838 met station pairs were found suitable and are included in the HEM Meteorological Files library, as depicted in Figure 1. Of these 838 met stations, 791 stations contain 2019 met data, while the rest are 2016 through 2018.

Figure 1. HEM Meteorological Stations



### 3. Preparing HEM Input Files

This section explains how to prepare the required and optional user-supplied input files for HEM. If you will be running AERMOD within your HEM run, in addition to reviewing the instructions provided in Sections 3.1 through 3.5 regarding how to set up your input files, it is important to review the AERMOD documentation for further guidance especially for more advanced modeling options (USEPA, 2024a, 2024b, 2024e). If instead of running AERMOD you are inputting pollutant concentration data for a set of geographic locations, you can ignore the descriptions of the input files associated with an AERMOD run and skip to Section 3.6 that describes the user-supplied concentration input file required for this option.

#### 3.1. Overview of HEM Input Files

HEM (using AERMOD) requires a series of Excel™ spreadsheet files to specify the configuration of the emission sources at the facilities (or facility) you are modeling. HEM accepts all recent Microsoft Excel™ versions using the xlsx spreadsheet format (e.g., Excel 2007/2010 and later). Excel has a 1,048,576-row capacity (and 16,384-column capacity).

To use HEM to calculate ambient pollutant concentrations using AERMOD, you will need the following three files at a minimum: (1) Facility List Options, (2) HAP Emissions, and (3) Emissions Location. **Table 1** describes each of these files. You may also need the additional input files shown in Table 1, depending on the options you choose to use in your modeling run.

**Table 1. Required Input Files and Additional Input Files for HEM-AERMOD run**

Input File	Type	Description
Facility List Options	Required	The primary driver of the model run listing the facilities to be modeled and specifying the model run parameters and options.
HAP Emissions	Required	Provides the names and amounts of the pollutants emitted from each emission source at the modeled facilities.
Emissions Location	Required	Provides emission source locations and configurations for the facilities being modeled.
Polygon Vertex	Additional	Required if one (or more) of your sources is configured as a polygon. It specifies the location of the polygon(s) by providing coordinates of the vertices. Note: This file is not needed for area sources.
Buoyant Line Parameter	Additional	Required if one (or more) of your sources is a buoyant line. It defines the parameters for a group or groups of buoyant line sources (with each group containing one or more buoyant lines) including average parameter values for building length, building height, building width, line source width, building separation (between the individual lines within a group) and buoyancy parameter.

Input File	Type	Description
Building Dimensions	Additional	Required to model building downwash effects. It describes building dimensions or other obstructions near emission sources that would produce wake effects. Note: Your Facility List Options file must indicate the facilities to be modeled with building downwash effects.
Emissions Variation	Additional	Provides emission rate factors for individual sources for one or more of the facilities you specify and is required to model temporally varying emissions (e.g., emissions reflecting diurnal, weekly, monthly, and seasonal variations) or emissions driven by wind speed variations. Note: Your Facility List Options file must indicate the facilities containing the sources to be modeled with emissions variations.
Particle Data	Additional	Required to model particulate deposition. It specifies the particle size distribution for various size ranges.
Gas Parameter	Additional	Included in HEM's <i>resources</i> folder. This file is required to model gaseous deposition. It specifies the parameters needed for modeling dry and/or wet deposition of gaseous (vapor) pollutants including diffusion coefficients, cuticular resistance and Henry's Law coefficients. Note: Defaults are provided by the model automatically, but you should provide pollutant-specific parameters if available by editing the <i>Gas_param.xls/x</i> file as discussed in Section 3.5.4.
Land Use and Month-to-Seasons	Additional	These two files are required to model dry deposition of gaseous pollutants. They describe the land use and vegetative land cover surrounding emission source(s) for facilities listed in the files.
User Receptors	Additional	Specifies the locations of additional discrete receptors and is required if you want HEM to compute pollutant concentrations and risks at locations you specify (e.g., houses, schools, or other sites near a facility) in addition to U.S. census block receptors. Note: Your Facility List Options file must indicate the facilities to be modeled with user receptors.
Alternate Receptors	Additional	Required if you wish to use receptors other than U.S. Census block centroids in your modeling run and instead provide your own list of receptors for modeling within the U.S. or anywhere in the world. Like the U.S. Census file, the alternate receptor file specifies the ID, location, elevation, hill height and population of the receptors to be modeled.

These files are described in more detail in Sections 3.2 through 3.5. In addition to the Table 1 list of input files, you can optionally revise the census database using a Census Update input file (as described below in Section 3.5.9) and revise the Toxicity Value Files – the dose response values and target organ assumptions – used in the model (as described below in Section 3.5.10).

HEM will prompt you to provide the input files required for your model run by opening up *Browse* lines that allow you to identify the name and location on your computer of each required input file. Directly inputting data from spreadsheets avoids having to retype the emission rates and other calculated parameters. However, this method of input has its drawbacks. Notably, HEM will not run successfully unless you have formatted the input files exactly as specified in the format guidelines. This section describes general rules you should follow to avoid common mistakes. To make formatting easier, specific formatting requirements are exemplified in sample input files, which are provided in the default "HEM\Inputs" folder. **Note: If this is your first time running HEM, it is highly recommended that you first run the model with the sample input files provided, as practice, and to confirm that HEM installed properly on your computer.** Most of the sample input files are run-ready, except for certain more advanced emissions variation input files with "template" in their file name (which instead provide instructions for entering your own values before using them in a model run).

### 3.1.1. General Rules for Input Files

- Use a separate Excel™ workbook for each input file. Ensure your Microsoft Office™ Trust Center settings allow your Excel version to be fully opened and operational (i.e., not in protected view only).
- Use only one input file worksheet per workbook.
- Match columns with the format specified for the input file. **You can use the sample input files and substitute actual data for the sample data.** Delete any extra lines of sample data.
- Do not insert columns between data columns. HEM will read these, including any extra hidden columns, as data.
- Use the number of header rows indicated in the sample input files at the top of each spreadsheet file for all required and optional input files.
- Do not include text in numerical data fields (for instance "<0.001"). HEM may read these fields as 0s (zeroes) or may accept only a portion of the number.
- For location coordinates, HEM will accept latitudes and longitudes in decimal degrees as well as Universal Transverse Mercator (UTM) coordinates. **The maximum precision HEM uses for latitude and longitude decimal degrees is 5 places after the decimal.** (HEM will convert latitudes/longitudes to UTM for use in AERMOD.) You must enter coordinates in the World Geodetic System of 1984 (WGS84) format.<sup>1</sup> The 1983 North American Datum (NAD83) and the WGS84 are identical for most applications, so no conversion is needed if using coordinates based on NAD83. However, if coordinates are based on the 1927 North American Datum (NAD27) geographic system format, they would need to be converted to WGS84 before being used in HEM.
- **Match the units used for parameters**, such as emission rates and stack parameters, **with the units given in the file's format guidelines** provided in the following sections (e.g., meters/second, meters, tons/year). The required units are also indicated in parentheses in the header rows of the sample input files which are included HEM's *Inputs* folder.

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<sup>1</sup> WGS84, NAD83 and NAD27 are different world reference frames (a.k.a. geographic systems) that are used as the basis for projected coordinate systems like UTMs. HEM uses WGS84. More information is provided in the following references: (GIS Geography, n.d.), (National Geospatial-Intelligence Agency, n.d.).

- The length indicated in the format guidelines for each field in the various input files is, in most cases, the suggested length based on HEM’s internal rounding conventions. For the Source ID field, however, **AERMOD does not accept Source IDs longer than 8 characters.**

## 3.2. Facility List Options File

The Facility List Options Excel™ file is the primary driver specifying the parameters and options of the modeling run and is required for any HEM run using AERMOD. The file contains one row for every facility that will be run with the various modeling options listed as columns for each facility row. **If you use all default modeling options, the only field requiring input is the Facility ID.** All other fields have defaults which are employed when the field in the Facility List Options file is left blank.

### 3.2.1. Fields in the Facility List Options File

**Table 2** shows the fields included in the Facility List Options file. These fields are columns in the actual *Facility\_List\_Options.xlsx* input file that you must provide to HEM, and each row in the actual file is for a different facility, as identified by the Facility ID. The rows in Table 2 are shown in the same column order required by HEM in the input file. (For a sample template, see *HEM5.0\_Facility\_List\_Options.xlsx* in your HEM *Inputs* folder.) The fields listed in Table 2 are described in more detail following the table.

**Table 2. Fields in the Facility List Options Input File**

Field	Default Setting (if field left blank)	Description of Facility List Options Field
Facility ID (FacilityID)		You must enter an alphanumeric string identifying the facility being modeled. Note: This is the only field in this file that must be filled-in; all other fields have default values when blank.
Met Station (met_station)	Met station selected by model as closest to the facility	The name of the meteorological surface station (e.g., NAME02.SFC) to be used by AERMOD when modeling each facility. The met station closest to the facility is chosen unless you specify a name.
Rural/Urban (rural_urban)	HEM determines when using U.S. Census block receptors or alternate receptors	Used to set the type of dispersion environment for AERMOD. “R” indicates rural land use surrounding the facility; “U” indicates urban land use. If left blank HEM will determine the population density in a circular area centered on the facility center within a radius of 3 km, based on the population of the 2020 Census blocks or the user’s alternate receptors.
Urban Population (urban_pop)	Defaults to 50,000 people if left blank, but only used and needed if “U” specified in Rural/Urban field	If you indicate “U” for urban land use (in Rural/Urban field above), then you should provide the model with the urban population size, otherwise leave blank. Note: If you specify “U” in the Rural/Urban field but provide no urban population value in this field, HEM will use a default urban population of 50,000 people. If you leave the Rural/Urban field blank, then HEM will calculate the urban population as needed.
Max distance (max_dist)	50,000 meters	The outside max radius of the modeling domain in meters (must be $\geq$ the modeling distance and $\leq$ 50,000 meters).

Field	Default Setting (if field left blank)	Description of Facility List Options Field
Modeling distance (model_dist)	3,000 meters	The cutoff distance (in meters) for discrete/explicit modeling of ambient impacts at census blocks or alternate receptors; beyond this distance ambient impacts are interpolated rather than explicitly modeled. Note: For polygon source types, set the modeling distance > the largest distance across the polygon.
Radials (radials)	16	The number of radials in the polar receptor network emanating from the facility center (must be $\geq 4$ ).
Circles (circles)	13	The number of concentric circles in the polar receptor network, centered on the facility center (must be $\geq 3$ ).
Overlap distance (overlap_dist)	30 meters	The distance (in meters) between an emissions source and a census block or alternate receptor within which you do not want the receptor to be considered as a point of maximum exposure/risk, because it might be on facility property. Must be an integer $\geq 1$ meter and $\leq 500$ meters.
First ring distance (ring1)	If left blank, calculated by HEM to be just outside the source locations, but not less than 100 m from facility center	The distance to the first ring (circle) of the polar network as measured from the facility center. You can override the default distance calculated by HEM to fit the size and shape of the facility properties to be modeled.
Facility Center (fac_center)	If left blank, calculated by HEM based on the source locations in the emissions location input file	You can enter the facility center location in this field to override HEM's (default) location. Enter as a comma separated list that should start with either "U" (if using UTM coordinates) or "L" (if using lat/lon coordinates). The list should contain two values if L for latitude followed by longitude (e.g., L, 35.91,-78.89) or three values if U for northing, easting and UTM zone number with hemisphere (e.g., U, 3975044, 690891, 17N). The hemisphere is S or N and defaults to N if omitted.
Ring Distances (ring_dists)	HEM will automatically place 13 polar rings (circles) by default	You can override HEM's placement of polar rings (circles) by specifying a list of distances in this field. Enter a comma separated list that contains at least 3 values representing the distance in meters for each polar ring from the facility center. The distances entered must be > 0 and $\leq 50,000$ meters, and the values must be increasing (e.g., 100,500,1000,5000,10000,50000).
Acute (acute)	N	Entering "Y" directs HEM to calculate short-term (acute) concentrations for that facility. If left blank or "N" is entered, acute impacts are not estimated for the facility.
Hours (hours)	1-hour	If calculating acute concentrations, the short-term (acute) averaging period that AERMOD will use for ambient concentrations, for that facility. The averaging period options are: 1, 2, 3, 4, 6, 8, 12 and 24-hours. The default is 1-hour.
Acute Multiplier (multiplier)	10	If calculating acute concentrations, the acute multiplier applied to the average annual emission rate and used to approximate the short-term emission rate (e.g., 10 times the rate entered in the HAP Emissions file). Note: HEM also assumes that this short-term rate can occur at the same time as the worst-case meteorological conditions. Two-decimal precision is accommodated; minimum value is 1.00

Field	Default Setting (if field left blank)	Description of Facility List Options Field
High Value (high_value)	Maximum acute value is used as the high value when this field is left blank	If calculating acute concentrations, this field indicates which acute concentration to report as the high acute value in the outputs for each facility. If you wish to use a value other than the maximum (e.g., the 98 <sup>th</sup> or 99 <sup>th</sup> percentile), then enter the value in this field. The number you enter must be an integer and is calculated based on the number of hourly values in the modeled run. For example, if you want the 98 <sup>th</sup> percentile acute value used from a data set of 8,760 hourly values (in one year), then enter 175 in this field, which is the truncated product of 0.02 x 8760. Similarly, if you want to use the 99 <sup>th</sup> percentile acute value, then enter 87 in the text box, which is the truncated product of 0.01 x 8760. The default acute high value (if this field is left blank) is the maximum modeled acute concentration.
Deposition (dep)	N	Deposition is not modeled by default; entering "Y" directs the model to calculate deposition in the model run (particle, vapor, or both as designated below) and provide the deposition flux in the output files. However, you can also enter "Y" in this field to produce separate particle and vapor (rather than the standard combined) concentrations in the outputs, even when not calculating deposition; see pdep and vdep fields below. You may model deposition with or without plume depletion. Note: You cannot model deposition/depletion for any facility that contains a buoyant line.
Depletion (depl)	N	Depletion is not modeled by default; entering "Y" directs the model to deplete the plume by the calculated deposition flux. Note: You may enter "Y" here even if you chose "N" for deposition; in that case the model will internally calculate deposition flux to deplete the plume but will not provide the deposition flux values in the output files. (This option saves space if you do not need the deposition flux.) Note: You cannot model deposition/depletion for any facility that contains a buoyant line.
Particle Deposition (pdep)	NO	The value "WD" directs the model to incorporate both wet and dry deposition for particles. Use "WO" for wet only particle deposition; use "DO" for dry only particle deposition; use "NO" (or leave blank) if not modeling deposition of particles and you do not need particle concentrations. Alternatively, enter "CO" for concentration only, if you want particle concentrations provided in the outputs but do not need deposition modeled for particles. If you enter WD, WO or DO in this field for a given facility (or facilities), then HEM will prompt you to provide a particle size input file for that facility (or facilities), if you are using Method 1 for deposition. Note: You cannot model deposition/ depletion for any facility that contains a buoyant line.

Field	Default Setting (if field left blank)	Description of Facility List Options Field
Particle Depletion (pdepl)	NO	The value "WD" directs the model to incorporate both wet and dry depletion of particles from the plume. Use "WO" for wet only particle depletion; use "DO" for dry only particle depletion; use "NO" (or leave blank) if not modeling depletion of particles from the plume. If you enter WD, WO or DO in this field for a given facility (or facilities), then HEM will prompt you to provide a particle size input file for that facility (or facilities), if you are using Method 1 for deposition. Note: You cannot model deposition/depletion for any facility that contains a buoyant line.
Vapor (gaseous) Deposition (vdep)	NO	The value "WD" directs the model to incorporate both wet and dry vapor deposition of pollutants; use "WO" for wet only vapor deposition; use "DO" for dry only vapor deposition; use "NO" (or leave blank) if not modeling deposition of vapor pollutants and you do not need vapor concentrations. Alternatively, enter "CO" for concentration only, if you want vapor concentrations provided in the outputs but do not need deposition modeled for vapor/gases. If you are modeling dry vapor deposition (entered WD or DO here), HEM will prompt you for a land use input file and a month-to-seasons input file, which are needed for dry vapor deposition/ depletion modeling. Note: You cannot model deposition/ depletion for any facility that contains a buoyant line.
Vapor (gaseous) Depletion (vdepl)	NO	The value "WD" directs the model to incorporate both wet and dry depletion of vapor pollutants from the plume. Use "WO" for wet only vapor depletion; use "DO" for dry only vapor depletion; use "NO" (or leave blank) if not considering depletion of vapor pollutants from the plume. If you are modeling dry vapor depletion (entered WD or DO here), HEM will prompt you for a land use input file and a month-to-seasons input file, which are needed for dry vapor deposition/ depletion modeling. Note: You cannot model deposition/ depletion for any facility that contains a buoyant line.
Elevations (elev)	Y	Enter "Y" or leave blank if you want HEM to use elevations provided by USGS web services for source elevations (where not specified by user) and to use elevations/hill heights for polar receptors and user-supplied receptors (where not specified by user). Enter "O" to run using elevations under the "offline" method to interpolate elevations/hill heights from the census blocks or alternate receptors. Enter "N" to run without elevations, as flat terrain.
Flagpole (flagpole)	N	Enter "Y" to use a receptor height above ground level, followed by a comma and the height in meters (e.g., "Y, 5" causes HEM-AERMOD to predict concentrations and impacts at 5 meters above the ground for all census block or alternate receptors). Note: Entering a "Y" only will result in a flagpole height of 0 meters – that is, ground level – for census block or alternate receptors but will enable user receptor flagpole heights. (See user receptor input file for more information.) If left blank or an "N" is entered, by default flagpole heights will not be used at any receptors, and predicted concentrations will be at ground level.

Field	Default Setting (if field left blank)	Description of Facility List Options Field
User receptors (user_rcpt)	N	Enter "Y" to include user receptors in the modeling run for a given facility. User receptors are not included by default. Note: If you are modeling using user receptors, HEM will prompt you for a separate user receptor input file.
Building Downwash (bldg_dw)	N	Enter "Y" in this field for each facility containing point sources for which you wish to model downwash over a nearby building. Building downwash is not included by default. If you are modeling building downwash, HEM will prompt you for a separate input file that must contain building dimension information, for (applicable point sources in) each facility marked with a "Y" in this column. Note: Building downwash may only be modeled with vertical point (P), capped point (C), and horizontal point (H) source types.
FASTALL (fastall)	N	Entering "Y" directs HEM to use AERMOD's control option FASTALL for modeling that facility, which conserves model run time by simplifying AERMOD's dispersion algorithms. FASTALL is not used by default. Note: You cannot use FASTALL for any facility that contains a buoyant line.
Emissions Variation (emiss_var)	N	Entering "Y" indicates that you want to vary the emissions of one or more sources at this facility. This field allows the application of variations to the emission inputs from specific sources by different user-supplied time scales (e.g., by season, month, hour of day, day of week), or by different wind speeds (6 ranges). If you enter a "Y" then HEM will prompt you for a separate emissions variation input file for that facility, and that file must contain variation factors for at least one source.
Annual (annual)	Y	Entering an "N" in the annual field indicates that you want the modeling run to be based on meteorological data from a period other than an annual period. If you enter an "N" then you must enter values in the "period_start" and "period_end" fields (shown next). Leaving this field blank or entering a "Y" will cause HEM-AERMOD to calculate annual concentration averages using the entire met data file, which is the default.
Period Start (period_start)	[Entry required if an "N" is entered in "annual" field above; otherwise leave blank]	The period_start field indicates the start of the meteorological period during which AERMOD will run. You should enter a comma separated list of 3 or optionally 4 values here indicating the year, month, day and (optionally) hour of when the modeling period should begin. For example, if you enter 2016,02,11,12 then the model will use 2016 met data starting on February 11th at the 12th hour (noon) and end on the date and time indicated in the period_end field. If you do not enter an hour here, then the model will use hour 1 as the default.
Period End (period_end)	[Entry required if an "N" is entered in Annual field above; otherwise leave blank]	The period_end field indicates the end of the meteorological period during which AERMOD will run. You should enter a comma separated list of 3 or optionally 4 values here indicating the year, month, day and (optionally) hour of when the modeling period should end. For example, if you enter 2016,06,30,17 then the model will use the met data starting on the date and time indicated in the previous period_start field and ending in 2016 on June 30th at the 17th hour (5 pm). If you do not enter an hour here, then the model will use hour 24 as the default.

**Take care when filling out the Facility List Options File, as this file drives and controls the modeling run. To avoid a model run error, this file must be consistent with your other input files.** For example,

- If you indicate 100% particles in the Percent Particulate column of your HAP Emissions input file (discussed in Section 3.3) and you wish to model deposition and/or depletion, then you cannot choose to model vapor deposition and/or depletion in the Facility List Options file.
- If you indicate options in the Facility List Options file that require additional input files for modeling, you will need to provide these files.
  - For example, if you indicate in the Facility List Options file that you would like building downwash modeled for certain facilities (by entering a “Y” in this field), then one or more point sources at those facilities must be included in the Emissions Location file (discussed in Section 3.4) and in a separate building dimensions input file (discussed in Section 3.5.5) that HEM will prompt you for.
  - Likewise, if you marked a “Y” for any facilities in the user receptor or emissions variations fields, then you will need to provide those separate input files (discussed in Sections 3.5.6 and 3.5.7, respectively).

The various modeling options driven by the Facility List Options file are discussed more in the next sections.

### 3.2.2. Meteorological Station and Period Options

HEM’s library of meteorological (met) station data is described in Section 2.4.1. By default, HEM chooses the met station closest to the facility to be modeled (i.e., if this field is left blank). If you do not want HEM to choose the closest met station’s data to use for your modeling run, enter the name of the met surface station you want AERMOD to use when modeling each facility (e.g., NC13722.SFC) in the meteorological station field (met\_station) column B of the Facility List Options file. Generally, the closest set of stations will be most representative of the meteorology in the modeling domain. However, there are several situations where a different combination of meteorological stations will be more representative. For instance, if the modeling domain is located on the coast, a surface station near the coast may be more representative than an inland station, even if there is a closer inland station.

The names of all stations in the met library can be found in the *metlib\_aermod.xlsx* file in “HEM\resources” folder, and the stations’ met data can be found in the “HEM\AERMOD\MetData” folder. You can also add your own met station to the *metlib\_aermod.xlsx* file in HEM’s *resources* folder and provide the new met station data as both SFC and PFL files in your “HEM\AERMOD\MetData” folder, as explained in more detail in Section 2.4.

The other fields related to met data are at the end of the Facility List Options file, on the far-right side of the spreadsheet, and include “annual” (in column AC), “period\_start” (in column AD), and “period\_end” (in column AE). As noted in Table 2 in Section 3.2.1, these columns allow you to choose to model with a period other than the default annual period of met data.

The **period start and period end fields** allow you to specify exactly what met period HEM should instruct AERMOD to use for your modeling run, down to the year, month, day and even hour. **The period start and end dates you specify must be included in the meteorological files being used. If the set of meteorological files you specify, or that HEM chooses, does not cover the dates you specify, AERMOD will generate an error and that facility will not**

**be modeled.** These period options are useful if modeling, for example, facilities that come on and offline during different parts of a year. The options may also be helpful in performing analyses to determine what time periods in the year produce the highest local concentrations and impacts. **Note:** The selection of the met station and met period for your modeling run can have a significant effect on the air concentrations and therefore risk and HI estimates that HEM produces.

### 3.2.3. Dispersion Environment Options: Rural or Urban

The Rural or Urban field (`rural_urban`) column C is used by HEM to set the type of dispersion environment to be used by AERMOD for the modeling of each facility. The EPA provides guidance on whether to select urban or rural dispersion in its Guideline on Air Quality Models (Appendix W) (USEPA, 2005). That guidance suggests an urban dispersion environment should be used if (1) the land use is classified as urban for more than 50% of the land within a 3-kilometer radius of the emission source, or (2) the population density within a 3-kilometer radius is greater than 750 people per square kilometer. AERMOD's handling of urban versus rural dispersion algorithms is discussed in Section 3 of the AERMOD User's Guide (USEPA, 2024e), Section 5 of the AERMOD Implementation Guide (USEPA, 2024a), and Section 5.10 of the AERMOD Formulation Document (USEPA, 2024b).

Whether you are using U.S. Census blocks or alternate receptors, by default HEM will use the population density to determine if a facility should be modeled as urban or rural. To do so, HEM uses the population of each receptor within 3 km of the facility center to determine the population density surrounding each facility. If that population density is greater than 750 people per square kilometer, HEM will instruct AERMOD to use an urban dispersion environment; otherwise, rural dispersion will be used by AERMOD. In addition, if using an urban dispersion environment for modeling, AERMOD requires a population input for its urban mode, as discussed in Section 5.10 of the AERMOD Formulation Document (USEPA, 2024b). If you left the rural/urban field blank so that HEM determines which dispersion environment to use by default, then you may also leave the urban population field blank. If HEM determines that urban is the appropriate dispersion to use for your facility, HEM will determine this urban population input by tallying the population out to 20 km in all directions around each facility center, using the receptor populations within that 20 km radius.

If you choose the urban dispersion environment for the model run (rather than leaving this field blank in the Facility List Options file indicating HEM's default approach described above), you should specify the population of the urban area surrounding the facility, if known, by entering it in the urban population field (`urban_pop`) column D of the Facility List Options file. This is true whether you are modeling with U.S. Census block receptors or with alternate receptors. If you choose to model using an urban dispersion environment and do not provide a population, HEM will set your urban population column/field (`urban_pop`) to 50,000 people. As noted above, AERMOD uses this urban population value in its dispersion algorithms for urban areas.

### 3.2.4. Modeling Domain Options

You will provide HEM the parameters that define each facility's modeling domain in columns E through L of the Facility List Options file. The modeling domain is circular and centered on each facility, with a user-specified radius. HEM identifies all the receptor locations in the modeling domain – census blocks for U.S. runs based on the census database, or alternate receptors for non-census modeling runs (inside or outside the U.S.). The model then divides the blocks into two groups – inner and outer receptors – based on their distance from the facility. For the inner

group of receptors (closest to the facility), each census block or alternate receptor location is modeled discretely as a separate receptor in AERMOD.

#### **3.2.4.1. Maximum Distance**

In column E (max\_dist) of the Facility List Options file, enter the maximum radius in meters to be modeled; this is the radius around each facility of the modeling domain. The maximum distance must be greater than or equal to the “modeling distance” (discussed next), but not greater than 50,000 meters because, as a Gaussian dispersion model, AERMOD is not recommended beyond 50 kilometers.

If you leave this field blank, HEM will use a default maximum distance of 50,000 meters. The maximum distance is the radius of the circular study area for which HEM will model ambient impacts (at census block centroid receptors or alternate receptors, polar grid receptors, and user receptors, as explained below in this section).

The center of this modeling domain is by default the geographical center of each facility (based on source locations for each facility) you are modeling, but you can change this center using the “facility center” column K, as discussed in Section 3.2.4.7.

#### **3.2.4.2. Modeling Distance**

In column F of the Facility List Options file (model\_dist), enter the distance in meters within which census blocks will be modeled discretely. This is the “cutoff distance” around each facility for explicitly including census block or alternate receptors in the AERMOD run.

Within this radial distance measured from the facility center, AERMOD will model each census block centroid or alternate receptor explicitly as a receptor. Outside of this radius, AERMOD will not model the census blocks or alternate receptors explicitly; ambient impacts at receptors beyond the modeling distance will be interpolated using dispersion modeling results from the polar receptor network, described in Section 3.2.4.9.

If you leave this field blank, HEM will by default use a modeling distance of 3,000 meters. The Modeling Distance may not be greater than the Maximum Distance (above).

Larger values for this cutoff modeling distance will require more time to model, because the number of receptors requiring explicit AERMOD modeling will be higher. However, you should set this cutoff value at a large enough distance so that the maximum risk receptor (discussed in Section 6.1.1) will be modeled explicitly. This distance will vary depending on the configuration of the sources but is generally between 1,500 and 2,000 meters. A typical modeling cutoff distance for larger facilities is 3,000 meters (or 3 km). When modeling large sources configured as polygons (e.g., U.S. Census tracts), set this modeling cutoff distance to be greater than the largest distance across the polygon, to ensure discrete modeling of all census blocks within the polygon.

#### **3.2.4.3. Radials**

In column G of the Facility List Options file (radials), enter the number of radials in the area to be modeled. The polar grid receptors of the polar network are located at the intersection of a radial and a polar ring (or “circle”, described next). A typical run would include 13 concentric rings and 12 or 16 radial directions. HEM will distribute the radial directions evenly around the

facility. For instance, if you select 16 directions, receptors will be modeled at compass bearings of 0, 22.5, 45, 67.5, 90, 112.5, 135, 157.5, 180, 202.5, 225, 247.5, 270, 292.5, 315, and 337.5 degrees.

If you leave this field blank, by default HEM will use 16 radial directions. If you choose to enter a different number of radials, you must specify at least 4 radials in this field.

#### **3.2.4.4. Circles (Polar Rings)**

In column H of the Facility List Options file (circles), enter the number of concentric circles (rings) in the polar receptor network around each facility, centered on the facility center. You must enter at least 3 rings.

If you leave this field blank, by default HEM will use 13 rings. HEM will place the concentric rings at a logarithmic progression of distances starting at the inner ring distance and ending at the outer radius of the modeling domain. However, you have the option to specify different ring distances (than HEM's calculated distances) in the "ring\_dists" column L, described in Section 3.2.4.8.

Although the polar grid receptors are used primarily for interpolating risks at census blocks outside of the modeling cutoff distance, it is important to include some rings close to the facility.

#### **3.2.4.5. Overlap Distance**

In column I of the Facility List Options file (overlap\_dist), enter the distance in meters where source and receptor are considered to be overlapping. The overlap distance is measured from each source at the facility (e.g., stack, edges of area and volume sources). This distance must be greater than or equal to 1 meter and less than or equal to 500 meters. If you leave this field blank, by default HEM will use an overlap distance of 30 meters, which is approximately equal to the width of a narrow buffer and a roadway.

This feature is provided to address situations, for example, wherein U.S. Census blocks are very close to a facility and have complex shapes. In such cases, the centroid of a census block may be much closer to the facility than the nearest actual dwelling. (In fact, if a census block surrounds a portion of the facility, the centroid of the block may be on facility property.) If a receptor falls within this distance, HEM will not calculate risks based on the location of that receptor but will instead assume that the risks associated with the receptor are the same as the highest predicted value for any receptor that does not overlap facility property (including polar receptors).

An exception to this occurs when modeling polygon sources. Unlike other sources, when modeling polygons, overlapping of source and receptor is permitted. This allows the impacts of a U.S. Census tract modeled as a polygon source (e.g., mobile source emissions modeled uniformly across a census tract) to be calculated within the census tract being modeled.

#### **3.2.4.6. Ring1 or First Ring**

In column J of the Facility List Options file (ring1), enter the distance in meters to the first ring (circle) of the polar network for each facility, as measured from the facility center. If you leave this field blank, by default HEM will calculate the inner radius of the polar network. This model-calculated first ring distance is based on the location of the emission sources and the facility

center. HEM uses a distance that places the first modeling ring just beyond all emission sources, but not less than 100 meters from the facility center.

By specifying a distance to the first ring in this column, you can override the default distance to fit the size and shape of the facility properties to be modeled. For example, you can set the first receptor ring to less than 100 meters (or conversely greater than what HEM calculates), if appropriate to the size and shape of the facility property. Place the nearest polar receptor ring as close as possible to the facility boundary – this inner radius of the polar network should be the minimum distance from the facility center that is generally outside of facility property.

For complex or irregularly shaped facilities, however, you may find it useful to specify an inner ring that encroaches on facility property in some directions. Furthermore, you may want to specify a set of boundary receptors by employing the user receptors file (as described in Sections 3.2.9 and 3.5.6).

**The first ring distance must be less than the modeling cutoff distance** (entered in column F “model\_dist”, for explicit modeling of receptors).

#### **3.2.4.7. Facility Center**

In column K of the Facility List Options file (fac\_center), you may specify the facility center location to override HEM's determination of where the facility center is located.

If you leave this field blank, by default HEM will choose the facility center by determining the geographic center of all emission source locations for that facility in your Emissions Location file (discussed in Section 3.4).

If you wish to specify a different facility center location, then enter its location in this field as a comma separated list that starts with either "U" (if using UTM coordinates) or "L" (if using latitude/longitude coordinates). The list must contain two values if L for latitude followed by longitude (L, 35.91, -78.89) or three values if U for northing, easting and UTM zone number with hemisphere (U, 3975044, 690891, 17N). Hemisphere (S or N) defaults to N if omitted.

#### **3.2.4.8. Ring Distances**

In column L of the Facility List Options file (ring\_dists), you may override HEM's placement of polar rings (circles) by specifying a list of distances in this field. To do so, enter a comma separated list that contains at least 3 values representing the distance in meters for each polar ring from the facility center. The distances entered must be greater than 0 and less than or equal to 50,000 meters, and the values must be increasing (e.g., 100,500,1000,5000,10000, 50000).

If you leave this field blank, by default HEM will place 13 polar rings (circles), as noted in Section 3.2.4.4.

#### **3.2.4.9. A Note About the Polar Network**

Columns G (radials) and H (circles) of the Facility List Options file, and optionally columns J (ring1), K (fac\_center) and L (ring\_dists), define HEM's polar network. In addition to modeling ambient impacts at populated receptors (census block centroids or alternate receptors) within the modeling cutoff distance, HEM also uses AERMOD to model ambient impacts explicitly at

polar grid receptors within the polar network. This polar network extends beyond the modeling cutoff distance to the maximum (outside) radius.

The polar receptor network in HEM serves three functions:

- (1) to estimate default impacts if one or more U.S. Census block receptor or alternate receptor locations are inside the overlap cutoff distance;
- (2) to evaluate potential acute effects that may occur due to short-term exposures in unpopulated locations outside the facility boundary; and
- (3) to interpolate long- and short-term impacts at receptors (U.S. Census block locations or alternate receptors) that are within the modeling domain but outside the cutoff distance for explicit/discrete modeling of individual receptors.

If modeling with terrain effects (discussed in Section 3.2.7), the elevation and hill height of each polar receptor is estimated based on how you chose to model elevations in the Facility List Options file. If you chose “Y” (or left blank), HEM will estimate elevations and hill heights using USGS web services (as described in [Section 3.2.7.1](#)). If you chose “O” (for offline), HEM will interpolate elevations and hill heights from the receptors in the census block or alternate receptor files (as described in [Section 3.2.7.2](#)). Currently, you cannot model with terrain effects under the “Y” (or blank) option outside the US (and territories) because the USGS web service is not available. However, you can use still model with terrain effects using the offline ( “O”) option to estimate elevations and hill heights, or you can model as flat. The importance of the polar network is discussed further in Section 5.

### 3.2.5. Acute Options

As introduced in Section 1.2, you can use HEM to estimate chronic health risks and, optionally, acute (short-term) health risks as well. Chronic health risks are estimated based on long-term average concentrations predicted by AERMOD. The time frame of this average is determined by the number of years covered by the meteorological data file selected for the model run: the default is generally one year when running AERMOD, although periods other than one year can be chosen as discussed in Section 3.2.2 regarding met station and period options. Acute health risks, however, are based on short-term average exposures such as 1, 2, 3, 4, 6, 8, 12 and 24 hours.

You can choose to model acute health risks using columns M (acute), N (hours), O (multiplier) and P (high\_value) of the Facility List Options file. HEM uses what you input in these fields for each facility to direct AERMOD to model acute concentrations, and then HEM uses these acute concentration predictions by AERMOD to estimate acute health risks. Enter a Y (for “yes”) in column M (acute) to indicate you want HEM-AERMOD to model short-term/acute concentrations for that facility. If you leave this field blank then by default HEM will not model acute impacts, regardless of what you put in columns N, O and P.

Next, in column N (hours), enter the short-term/acute averaging period that AERMOD will use for ambient concentrations, for each facility. The averaging period options are: 1, 2, 3, 4, 6, 8, 12 and 24 hours. If you entered Y in column M (acute) and leave column N (hours) blank, then HEM will by default use an averaging period of 1 hour.

In column O (multiplier), enter the acute multiplier for each facility. This multiplier is applied to the average annual emission rate (in tons/year from your HAP Emissions input file, which the model converts to grams/second); and it is used to approximate the short-term emission rate. If

you entered a Y in column M (acute), but leave this field blank, then by default HEM will use a multiplier of 10 for that facility (e.g., 10 times the average annual emission rate entered in the HAP Emissions file might be used to approximate short-term emission spikes). Two-decimal precision is accommodated in the multiplier column O, but the multiplier entered must be greater than or equal to 1.00.

Regarding short-term spikes, it is important to note that AERMOD applies this short-term rate over the course of the entire met period chosen (discussed in Section 3.2.2) and **the peak acute value will occur at the same time as the worst-case meteorological conditions**. Therefore, the acute results produced with an appropriate multiplier can be viewed as conservative estimates.

The highest acute value reported by HEM is also impacted by what you enter in column P (high\_value). This field indicates which acute concentration to report as the high acute value in the outputs for each facility. If you wish to use a value other than the maximum (e.g., the 98<sup>th</sup> or 99<sup>th</sup> percentile), then enter the associated value in this field. The number you enter must be an integer and is dependent on the number of hourly values in the model run. For example, if you want the 98<sup>th</sup> percentile acute value used from a dataset of 8,760 hourly values (in one year), then enter 175 in this text box, which is the truncated product of  $0.02 \times 8,760$ . Similarly, if you want to use the 99<sup>th</sup> percentile acute value, then enter 87 in the text box, which is the truncated product of  $0.01 \times 8,760$ . If instead you leave column P (high\_value) blank, then by default HEM will report the maximum modeled acute concentration as the “high value”.

### 3.2.6. Deposition and Depletion Options

#### 3.2.6.1. *Deposition and Depletion Overview*

Deposition and depletion are not modeled by default by HEM. However, depending on the deposition and depletion options you choose in the Facility List Options file in columns Q through V, HEM can (1) calculate and output a deposition flux and (2) deplete the plume (or not) based on the calculated deposition.

Generally speaking, deposition modeled with plume depletion will reduce the ambient impacts from the emission sources by removing pollutants from the plume. Air concentrations will be depleted as pollutants are deposited to the ground. Alternatively, you may choose to calculate the deposition flux but not deplete the plume (to allow for non-depleted air concentrations that a standard run would produce). Deposition without plume depletion will not affect the air concentrations.

Whether you choose to deplete the plume or not, the modeled deposition flux may be then used as an input to a separate multipathway model such as the Total Risk Integrated Methodology (TRIM) (USEPA, 2024i).

**Table 3** lists the Facility List Options entry combinations you can make (“Y” or “N”/leave blank) in columns Q and R, depending on your overall deposition and depletion modeling goals.

**Table 3: Facility List Options Entries based on Deposition/Depletion Modeling Goals**

Deposition/Depletion Modeling Goal for HEM-AERMOD Run	Column Q and R Entries
Model deposition and output a deposition flux column (in g/m <sup>2</sup> /y) for all polar receptors and for the inner discretely modeled receptors. *	Y (for “yes”) in column Q (dep) of your Facility List Options file
Model depletion (i.e., deplete the plume based on a calculated deposition flux).	Y in column R (depl)
Output a deposition flux column AND deplete the plume.	Y in both columns Q (dep) and R (depl)
Deplete the plume (based on an internally calculated deposition flux) but do not output a deposition flux. (This option saves space, if you do not need the deposition flux output by the model.)	Y in only column R (and leave column Q blank or enter an “N”)
Do not model deposition or depletion	Leave both columns Q and R blank (or enter an “N” in each)

\* If you specify a PERIOD average instead of an ANNUAL average of meteorological data, deposition results will be given in g/m<sup>2</sup> instead of g/m<sup>2</sup>/y.

While columns Q and R dictate to AERMOD whether deposition and depletion will be modeled, columns S, T, U, and V of the Facility List Options File identify the specific types of deposition and depletion modeling AERMOD will use for the particulate and gaseous pollutants, as discussed next.

### **3.2.6.2. Particle and Vapor Deposition and Depletion Types (WD, DO, WO)**

HEM uses AERMOD to calculate deposition and depletion effects for particulate matter, vapor (gaseous) pollutants, or both. The make-up of your emissions – that is, the percentage particulate and gas – is dictated to HEM by your HAP Emissions input file, discussed more in Section 3.3. Specifically, column E (Fraction emitted as particulate matter [%]) in the HAP Emission input file indicates to HEM whether your emissions are 100% particle (if column E is populated with 100 for all pollutants), 100% gas (if column E is left blank or populated with 0 for all pollutants), or a mixture of particles and gas (if column E is > 0 and < 100). However, for each facility, you can choose to model deposition and/or depletion for merely the particulate portion of your emissions (if you have a particulate portion), the vapor portion of your emissions (if you have a gas portion), or both (if you have both particle and gas emissions).

If you entered “Y” in column Q (dep) and/or in column R (depl) regarding modeling deposition and/or depletion, you must also indicate what type of deposition and/or depletion you wish HEM to direct AERMOD to model: wet and dry (**WD**), dry only (**DO**), wet only (**WO**), or none (No or leave blank). Use columns S (pdep), T (pdepl), U (vdep) and V (vdepl) of your Facility List Options file to indicate what kinds of deposition and/or depletion you want modeled for particulates and vapor (gas). In column S (pdep) you should indicate the type of particle deposition you want modeled, if any. In column T (pdepl), you should indicate the type of particle depletion you want modeled, if any. Do likewise in columns U (vdep) and V (vdepl) for the types of vapor deposition and vapor depletion of your pollutants, respectively. See the AERMOD User’s Guide (USEPA, 2024e) and AERMOD Implementation Guide (USEPA, 2024a) for a more detailed discussion of these processes.

You can mix and match the type of deposition and depletion you tell HEM to model. For example, you can direct HEM to model wet and dry (WD) deposition, and then deplete the plume based on those wet and dry (WD) deposition processes. Or you can choose wet and dry deposition (WD), but then only deplete the plume based on the wet deposition process (WO). In addition, the “none” option (No or blank) allows you to model deposition for particles (or vapor) only, while ignoring the vapor (or particle) portion of your emissions, even if your HAP Emissions file shows a mixture of particles and gas. For example, if you wish HEM-AERMOD to ignore the vapor portion of your emissions, you can indicate in column S (pdep) and/or column T (pdepl) what type of deposition and/or depletion (respectively) to model for your particle emissions (WD, WO or DO) and then leave both column U (vdep) and column V (vdepl) blank or enter “No”. Alternatively, you can choose to model deposition/depletion for either particles or vapor, while modeling concentrations only (with no deposition/depletion calculated) for the other portion of your emissions (particle or vapor), as described next.

### **3.2.6.3. Concentration Outputs Broken Out into Particle and Vapor**

Even if you do not wish to model deposition/depletion, you can use the deposition fields in the Facility List Options file to produce separate particle and vapor concentrations in the output files (if you have both particle and gas emissions, as indicated in column E of your HAP Emissions input file). In other words, you can direct HEM-AERMOD merely to produce more detailed concentration outputs, showing the breakdown of particle and vapor concentration at each receptor location, without modeling either deposition or depletion.

For standard runs modeled without deposition/depletion (in which columns Q through V are blank), HEM combines the particles and gases into one combined concentration in the output files at each modeled receptor location.<sup>2</sup>

Alternatively, to obtain separate “P” and “V” air concentrations for particles and gases, you can:

- Enter “Y” in the deposition field (column Q) and “CO” for “concentration only” in the pdep field (column S) to obtain particle “P” concentrations in the outputs, plus “CO” in the vdep field (column U) to obtain vapor/gas “V” concentrations in the outputs.
  - Neither deposition nor depletion will be modeled in this case. However, the outputs will show distinct rows for particles (“P”) and vapor (“V”) at each location, rather than the standard combined (“C”) row.
- To produce concentrations only in this way, you should leave all depletion fields blank (**N or No**) in columns R (depl), T (pdepl) and V (vdepl).
  - Note: Using the CO option, you may also choose to produce particle only concentrations while ignoring the vapor portion of your emissions, or vice versa.

You can also mix and match deposition/depletion options with this concentration only (CO) option. For example, you may choose to model deposition (with or without depletion) for the particle portion of your emissions but choose to model concentrations only (with no deposition/depletion processes modeled) for the vapor portion of your emissions. To do this, enter “Y” in column Q (dep) and “CO” in column U (vdep) for your vapor emissions, plus enter

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<sup>2</sup> See for example Table 42 in Section 6.1.10 regarding the All Inner Receptors output file, which explains that a “C” in the field Emission Type means a combined particle/vapor concentration.

whatever deposition/depletion options you wish to model for your particle emissions in columns R (depl), S (pdep), and T (pdepl).

### 3.2.6.4. Sample Deposition and Depletion Modeling Options

As evident from the discussion in this section, there are numerous deposition, depletion, and concentration-only options HEM-AERMOD can model, which are initiated by the many combinations you can enter in the deposition and depletion columns of your Facility List Options file:

- Q (dep),
- R (depl),
- S (pdep),
- T (pdepl),
- U (vdep), and
- and V (vdepl).

To illustrate a few of these options, **Table 4** provides a partial list of some deposition/depletion combinations with their model results. The table indicates the entries you would make in Columns Q - V of the Facility List Options file to achieve each modeling result.

**Table 4. Sample Deposition and Depletion Options and Model Results**

HEM-AERMOD Results *	Entry in Column Q (dep)	Entry in Column R (depl)	Entry in Column S (pdep)	Entry in Column T (pdepl)	Entry in Column U (vdep)	Entry in Column V (vdepl)
Deposition flux will be provided, and the plume will be depleted, using wet and dry processes for both particles and gases, for both deposition and depletion.	Y	Y	WD	WD	WD	WD
Deposition flux will be provided, and the plume will be depleted, using wet and dry processes for particle and gas deposition, but wet-only processes for particle depletion and dry-only processes for gas depletion.	Y	Y	WD	WO	WD	DO
Deposition flux will be provided with no plume depletion, using wet-only processes for particles and dry-only processes for gases.	Y		WO		DO	
No deposition flux will be provided but the plume will be depleted using both wet and dry processes for particles and gases.		Y		WD		WD
Deposition flux will be provided with no plume depletion, using wet and dry processes for particle deposition. (No gas dep/depl modeled)	Y		WD			

<b>HEM-AERMOD Results *</b>	<b>Entry in Column Q (dep)</b>	<b>Entry in Column R (depl)</b>	<b>Entry in Column S (pdep)</b>	<b>Entry in Column T (pdepl)</b>	<b>Entry in Column U (vdep)</b>	<b>Entry in Column V (vdepl)</b>
Deposition flux will be provided, and the plume will be depleted, using dry-only processes for particle deposition and wet-only processes for particle depletion. Vapor/gas concentrations will be provided, but neither deposition nor depletion will be modeled for vapor/gases.	Y	Y	DO	WO	CO	
No deposition flux will be provided but the plume will be depleted using wet-only processes for gases. (No particle dep/depl modeled)		Y				WO
Deposition flux will be provided based on wet and dry processes for particles, with no depletion of the plume. In addition, vapor/gas concentrations will be provided, but neither deposition nor depletion will be modeled for vapor/gases.	Y		WD		CO	
Deposition flux will be provided based on wet and dry processes for gases, and the plume will be depleted based on wet only processes for gases. Particle concentrations will be provided, but neither deposition nor depletion will be modeled for particles.	Y	Y	CO		WD	WO
Separate particle and gas concentrations will be provided in the outputs, but no deposition or depletion will be modeled.	Y		CO		CO	
Particle concentrations will be provided in the outputs, but no deposition or depletion will be modeled. (No gas concentrations provided)	Y		CO			
Vapor concentrations will be provided in the outputs, but no deposition or depletion will be modeled. (No particle concentrations provided)	Y				CO	

Table 4 Note: The above is merely a partial list of some of the possible deposition/depletion combinations (entered in columns Q - V of the Facility List Options file), for illustration purposes. More variations may be chosen that are not illustrated here.

\* These various HEM-AERMOD modeling results listed will be provided if your column entries are consistent with your emissions (e.g., you cannot model deposition and/or depletion of particles if your facility's emissions are 0% particulate in column E of your HAP Emissions file, discussed in Section 3.3.).

### 3.2.6.5. Additional Deposition/Depletion Input Files Required

Depending on the type of deposition and/or depletion you indicate in columns Q through V for each facility, and depending also on the method of particle deposition you indicate for each source at these facilities in your Emissions Location file (discussed in Section 3.4.2), HEM will prompt you to provide additional files. These files are introduced below in **Table 5** and described in more detail in Sections 3.5.3 and 3.5.4.

**Table 5: Additional Input Files Required for Particle and Vapor Deposition/Depletion**

Deposition/Depletion Option	Additional HEM Input File(s) Required
Model deposition and/or depletion of particles in your emissions using Method 1 (described in Section 3.4.2)	Requires a <b>particle data file</b> . This additional input file will need to contain particle size (diameter) information, mass fraction percentages for each size, and particle density for each size, for emissions from each source (for which you wish to model particle deposition and/or depletion using Method 1). The particle data file is described further in Section 3.5.3.
Model dry deposition and/or depletion of gaseous/vapor pollutants	Requires a <b>land use file</b> and a <b>month-to-seasons file</b> . These additional input files are needed to describe the land use and vegetation surrounding each facility at which you wish to model dry only (DO) or wet and dry (WD) deposition and/or depletion of gaseous pollutants, as discussed in Section 3.5.4.
Model deposition and/or depletion of gaseous/vapor pollutants (whether dry or wet)	Requires a <b>Gas Parameter file</b> , described further in Section 3.5.4. This file is included in the HEM <i>resources</i> folder with generic gas parameter values for certain pollutants, but you should review the provided file ( <i>Gas_Param.xlsx</i> ) to ensure that the gaseous pollutants in your HAP Emissions file are included in it. If these pollutants are not included – or if you wish to include updated parameter values – you should edit the Gas Parameter file, as discussed in Section 3.5.4.1. (Per Section 3.5.4.1, default gas parameter values are used for pollutants not included in the <i>Gas_Param.xlsx</i> file.)

In addition to requiring special input files, deposition/depletion runs also require more computing time and resources, as discussed next.

### 3.2.6.6. Deposition/Depletion Run Times, Effects, and Limitations

To model deposition/depletion, HEM requires additional modeling time compared to a standard run (with no deposition and/or depletion modeling). Furthermore, HEM requires significantly more time to run if you opt to model deposition and/or depletion and you are also modeling acute impacts. The exact run time will depend on your source configuration and modeling domain, but the combination of acute calculations and deposition/depletion will generally increase run times from a few minutes to over an hour, or more, per facility.

Deposition and plume depletion have more of an effect on ambient concentrations farther from the facility than these processes do closer to the facility, where the maximum impact generally occurs. Therefore, if you select the deposition and/or depletion options for a model run, you may save time by performing two separate runs. For example, you can use the first HEM run to

calculate chronic effects and include deposition and plume depletion. You can then use the second run to calculate acute effects without deposition and depletion.

It should be noted that HEM does not model deposition and/or depletion at census block and alternate receptors beyond the modeling distance, except at the polar receptors. This means that deposition and/or depletion is modeled at only the “inner receptors” (discussed in Section 6.1.10) and the polar receptors. If you need deposition and/or depletion modeled for the entire modeling domain at all census block or alternate receptors, you should set the modeling distance equal to the maximum distance. HEM will require additional modeling time and computing resources in this scenario, compared to using a smaller modeling distance. As suggested above, you may save modeling time by performing two separate runs, especially if you are also modeling acute impacts.

Finally, it should also be noted that if a facility listed in your Facility List Options file includes a buoyant line source in your accompanying Emissions Location file, you cannot model deposition or depletion for that facility (because deposition/depletion has not been implemented yet in AERMOD for buoyant line source types, as of the date of this User’s Guide). You may, however, model such a facility as two facilities, one with the buoyant line source[s] modeled without deposition/depletion and the other containing the other source types modeled with deposition/depletion.

### 3.2.7. Elevations: Online and Offline Options

By default, HEM includes terrain elevations in your modeling run if you leave column W (elev) blank or enter a “Y” in this field, which directs HEM to use an online method to obtain elevations. Alternatively, if you enter an “O” (for “offline”) in column W, HEM will include terrain elevations but use an offline method. To exclude terrain elevations in your modeling run (i.e., to model as flat terrain), enter an “N” in this field.

Elevated terrain around the facility can cause local impacts to increase, though impacts will differ for each set of sources and elevations. It is especially important to include terrain elevations if the height of receptors around the facility may exceed the height of any stacks at the facility. Consult the EPA's Guideline on Air Quality Models (also published as Appendix W of 40 CFR Part 51) (USEPA, 2005) for more explicit directions on when the use of terrain elevations is recommended. In addition to elevations, AERMOD uses controlling hill heights for flow calculations. Controlling hill height is defined as the highest elevation that is above a 10% grade from the receptor (USEPA, 2018c). HEM will calculate hill heights based on whether you choose the online or offline elevation option.

Whether using the online or offline elevation option, the elevations and hill heights of the census blocks or alternate receptors are used in the AERMOD run. If the user provides all elevations for sources and all elevations and hill heights for the optional user receptors (discussed in Section 3.5.6), then the only difference between the online and offline options is how the elevations and hill heights for polar grid receptors are estimated. The online and offline elevation methods in HEM are described in Sections 3.2.7.1 and 3.2.7.2, respectively.

**Note:** If you are running with elevated terrain and your Census Library contains records with missing elevations or hill heights, HEM will stop the run and give a message in the log indicating that you need to edit the Census Library (via the Census Update file described in Section 3.5.9 under the Revise Census Data HEM option discussed in Section 4.8). If you are using the Census Library from the EPA’s website there should be no receptors without elevations or hill

heights. However, if you have modified the Census Library by adding your own receptors, then it's possible some missing data has been introduced. If you are using alternate receptors, you cannot edit those with the Census Update file and should ensure all alternate receptors have elevations and hill heights if you want to run HEM with elevated terrain.

### **3.2.7.1. Default Online Method for Elevations/Hill Heights**

If the elevation column W is blank or contains a "Y", HEM will attempt to access the internet to obtain elevation data from the USGS website using the [py3DEP](#) Python library. This service provides (10-meter resolution) elevation data for user-provided latitude/longitudes and is available in the US only (including territories). If there is no internet connection available and/or the USGS server is down/not reachable, HEM will stop the run and provide a pop-up message indicating that your computer was unable to obtain elevation data for this model run. In this situation, you may attempt the run using the alternative offline elevation method (described in Section 3.2.7.2) or model the run group with no elevations as flat terrain.

For this online method, HEM will also calculate hill heights using elevation data from the USGS. To calculate hill heights, HEM uses two methods to obtain 30-meter resolution USGS gridded elevation data. With the first method, HEM obtains the necessary number of 1-degree Tagged Image File Format (TIFF) files from the USGS, then calculates the hill height for each receptor by finding the highest elevation that is above a 10% grade from the data in any of the files. The second method calculates hill height in the same way, but obtains the elevation data using the "get\_dem" method of the py3DEP Python library, which requests data from the USGS [3D Elevation Program](#). The get\_dem method (as used in HEM) requests data for a bounding box that includes all receptors plus a buffer of 62 kilometers (ten times the height of the highest peak in the US) to ensure a potential hill height is not missed.

The first method of calculating hill height is typically faster and is attempted first. If that method fails for any reason (e.g., because of a server issue) then the second method is attempted. If the second method fails, then a pop-up message will appear indicating HEM could not obtain elevation data and that HEM stopped the run.

### **3.2.7.2. Alternative Offline Method for Elevations/Hill Heights**

If the elevation column W contains an "O" for the offline option, HEM will estimate missing elevations by interpolating from the census blocks (or alternate) receptors in the modeling domain of each facility. This interpolation method is used for all receptors that fall inside the "envelope" (convex hull) of the input data, and is the same method used for creating contours in HEM (discussed in Section 4.7): the [SciPy griddata](#) method, which uses Delaunay triangulation with linear interpolation. Elevations for (the small number of) receptors that fall outside the convex hull of the input data are assigned the value of the nearest receptor of the input data.

HEM will interpolate hill heights the same way it interpolates elevations described above.

## **3.2.8. Flagpole Option**

Unless otherwise specified, AERMOD predicts concentrations at ground level and all previous HEM versions (including HEM-3 and HEM4) used ground level AERMOD-predicted concentrations. However, AERMOD has the capability of measuring concentrations above ground level by using its flagpole receptor height modeling option (discussed in Section 3.2.11 of the November 2024 [AERMOD User's Guide](#)), and HEM5 includes this AERMOD modeling

capability. It should be noted that flagpole height is unrelated to elevation and the flagpole option can be used with or without using elevated terrain in the modeling run.

Entering "Y" in the "flagpole" field, column X, directs HEM-AERMOD to use receptor heights above ground level. Enter an optional flagpole height by placing a comma after the "Y" and the height in meters. (Note: This height should be an integer. Decimal numbers will be rounded by HEM to the closest integer, and HEM's Python program rounds 0.5 to 0.) For example, "Y, 5" indicates that HEM-AERMOD will predict concentrations and impacts (risk) at 5 meters above the ground for all census block or alternate receptors. If left blank or an "N" is entered in the Flagpole field, by default HEM-AERMOD will not include flagpole heights at any receptors and will predict concentrations at ground level (at elevation above sea level, or not, depending on what you entered in the preceding field for the Elevation option, in column W).

If you enter a "Y" only in the flagpole field (with no number following) HEM will use a flagpole height of 0 meters – that is, ground level – for census block or alternate receptors. However, the "Y" entered in the Flagpole field will enable flagpole heights to be used at user receptor locations you enter in the user receptors input file, discussed in Section 3.5.6.

### 3.2.9. User Receptors Option

If you would like to include additional "user receptors" in your model run for one or more facilities – in addition to the census block or alternate receptors, enter a "Y" in column Y (user\_rcpt) of your Facility List Options file. HEM does not include user receptors by default, so if this column is blank then user receptors will not be included for that facility. If you are modeling impacts at user receptor locations, HEM will prompt you for a separate input file containing the user receptor information, for each facility marked with a "Y". The user receptor input file is described in Section 3.5.6.

### 3.2.10. Building Downwash Option

If you would like to model downwash over a building, which is under or near a point source, then enter "Y" in column Z (bldg\_dw) of your Facility List Options file. HEM does not model building downwash by default, and you should simply leave this field blank if you do not wish to model it as part of the plume dispersion. If you are modeling building downwash, HEM will prompt you for a separate input file that must contain building dimension information, for applicable point sources in each facility marked with a "Y" in this column. **Note:** Building downwash may only be modeled with vertical point (P), capped point (C), and horizontal point (H) source types. These source types are described in Section 3.4.1 regarding the Emissions Location file.

Under AERMOD's regulatory option, the effects of building downwash should be taken into account when a building is close enough to impact dispersion from an emission source. Building downwash will affect dispersion predictions when:

- the stack height is less than either 2.5 times the building height or the sum of the building height and 1.5 times the building width; and
- the distance between the stack and the nearest part of the building is less than or equal to five times the lesser of the height or the projected width of the building (USEPA, 1995, pp. 1–22 & 1–23).

AERMOD incorporates the Plume Rise Model Enhancements (PRIME) algorithms (Schulman et al., 2000) for estimating enhanced plume growth and restricted plume rise for plumes affected

by building wakes (USEPA, 2024b). A building may impact emissions from multiple sources. To model the impact of building downwash, HEM requires information on the configuration of the building when viewed from different wind directions, and this information is contained in the building dimensions input file, described further in Section 3.5.5.

### 3.2.11. FASTALL Option

To conserve model run time by simplifying the dispersion algorithms used to model a given facility's emissions, enter a "Y" in column AA (fastall) of your Facility List Options file. HEM does not employ FASTALL by default, so if you leave this field blank AERMOD will use the more rigorous (non-simplified) dispersion algorithms.

The FASTALL option simplifies the AERMOD algorithms used to represent meander of the pollutant plume. This simplification is achieved by eliminating the upwind component of dispersion for point and volume sources, and by reducing the requirement for uniformity of emissions over the extent of area sources (USEPA, 2024e). For faster runs, you may want to select the FASTALL option which includes these plume and source simplifications.

**Note:** If a facility listed in your Facility List Options file includes a buoyant line source in your accompanying Emissions Location file, you cannot use the FASTALL option for that facility. You may, however, model such a facility as two facilities, one with the buoyant line source[s] and the other with the other source types. You may also use FASTALL for the other facilities in your Facility List Options file.

### 3.2.12. Emissions Variation Option

Enter a "Y" in column AB "emiss\_var" of your Facility List Options to apply variations to the emissions from one or more sources at a given facility. You may vary emissions by different user-supplied time scales (e.g., by season, month, day of week, hour of day), or by different wind speeds (6 ranges). HEM will prompt you for an emissions variation file if you entered "Y" for one or more facilities, and that file must contain variation factors or scalars for at least one source at each facility marked with a "Y". The optional Emission Variation input files are discussed in more detail in Section 3.5.7.

**Note:** These emission variation factors/scalars will compound the effects of the acute multiplier (specified in column O "multiplier") on the short-term/acute emission rates used by AERMOD. For example, whatever numerical factors you supply in an Emission Variations input file will be multiplied by an acute multiplier of 10 (if the default multiplier is used) to derive the short-term emission rate. Therefore, if applying hour-of-day emission variation factors, you may want to set the acute multiplier to 1, unless it is reasonable to assume that the short-term rate may still exceed the hour-of-day factors by an additional multiple.

## 3.3. HAP Emissions File

The HAP Emissions Excel™ file, like the Facility List Options file, is required for any HEM modeling run using AERMOD. This file includes emissions in tons per year (tpy) for each HAP emitted from modeled sources, for all facilities listed in the Facility List Options file. **Table 6 and Table 7** give the format guidelines for the HAP Emissions file and a sample HAP emissions input file, respectively.

**Table 6. Format Guidelines for the HAP Emissions Input File**

Field	Type	Description
Facility ID	Character	An alphanumeric string identifying the facility being modeled
Source ID	Character	An alphanumeric character string up to 8 characters long. It must contain at least one alphabetic character, and all Source IDs must match a Source ID used in the Emissions Location file. Note: AERMOD allows a <b>maximum of 8 characters</b> for the Source ID; and all Source IDs will be converted to uppercase by AERMOD.
Pollutant	Character	The pollutant name must correspond to one of the chemical names listed in the dose response library. (This file, <i>Dose_Response_Library.xlsx</i> , is in the resources folder.)
Emission Amount	Numeric	The emitted amount of the pollutant in tons per year (tpy).
Percent Particulate	Numeric	The percentage of pollutant emitted as particulate. Required if deposition and/or depletion will be modeled, or if a breakdown by particulate and vapor is desired in the concentration outputs. If left blank, defaults to 0% particulate when deposition is modeled. If deposition is not modeled, this field is ignored by HEM.

A sample template is provided in the HEM *Inputs* folder named *HEM5.0\_HAP\_Emiss.xlsx*. The pollutants emitted per source at each facility are required in the HAP Emissions file and are discussed in Section 3.3.1. The percentage particulate emitted from each source is generally only required if you are modeling deposition or depletion (see Section 3.2.6) and is discussed in Section 3.3.2.

**Table 7. Sample HAP Emissions Input File**

Facility ID	Source ID	Pollutant	Emissions (tons/year)	Fraction Emitted as Particulate Matter (%)
Fac2-IL	CT0001	Antimony compounds	1.2E-01	100.0
Fac2-IL	CT0001	Chromium (VI) compounds	3.2E-04	100.0
Fac2-IL	CT0001	Mercury (elemental)	4.2E-02	50.0
Fac2-IL	CV0001	Dibenzofuran	1.1E-01	90.0
Fac2-IL	CV0001	Xylenes (mixed)	1.3E+00	0.0
Fac1-NC	SR0001	Benz(a)anthracene	7.3E-06	11.9
Fac1-NC	SR0001	Benzo(a)pyrene	2.5E-08	23.9
Fac1-NC	SR0001	Benzo(b)fluoranthene	2.8E-06	17.8
Fac1-NC	MS0001	Chrysene	3.2E-05	52.3
Fac1-NC	MS0001	Dibenz(a,h)anthracene	3.6E-08	99.3
Fac1-NC	MS0001	Indeno(1,2,3-cd)pyrene	1.1E-07	98.9
Fac1-NC	RW0001	Chromium (VI) compounds	3.8E-05	100.0
Fac1-NC	RW0001	Mercury (elemental)	3.6E-04	50.0
Fac1-NC	RV0001	Nickel compounds	4.8E-03	100.0

### 3.3.1. Pollutant Emissions per Source at Each Facility

You should include one record (row) for each combination of facility (Facility ID), emission source (Source ID) and chemical (Pollutant) in your HAP Emissions file.

### 3.3.1.1. Source ID

The Source ID is a key parameter in the HAP Emissions file, because HEM uses the Source ID to link the emitted HAP at that source to other input files, such as the Emissions Location input file (discussed in Section 3.4) and other optional input files (discussed in Section 3.5). Source IDs should meet the following conditions:

- The Source ID should provide each source a distinct name.
- Different sources should have unique Source IDs even if they will be modeled at the same location.
- **AERMOD requires that the Source ID be restricted to eight (8) characters (or fewer)** and it must consist of all alphanumeric characters.
- Do not use spaces at the beginning or in the middle of the Source ID.
- AERMOD converts all letters in the Source ID string to uppercase. Therefore, **uppercase and lowercase characters are indistinguishable to AERMOD**; so "ABC" and "abc" would be treated as the same Source ID.
- While each source should have a unique Source ID, it is advantageous to group certain types of sources within part of the Source ID. For example, "ST" could be used in the Source ID to indicate a storage tank, and each distinct storage tank could be given a number (e.g., ST01, ST02). Such grouping is important for certain summary programs, as discussed in Section 4.5.

### 3.3.1.2. Pollutant Names and Emissions in tons/year

Each chemical you name in the HAP Emissions file (under "Pollutant" in the sample shown in Table 7) must match one of the chemical names listed in the dose response table located in the HEM *resources* folder. The dose response values are part of HEM's Toxicity Value Files Library, described in Section 2.2.

If necessary, you can add pollutants to the two Excel™ spreadsheets comprising HEM's Toxicity Value Files Library: the dose response table and the target organ endpoints table. Section 3.5.10 explains how to make changes to the Toxicity Value Files Library.

Finally, **amounts for each HAP emitted from each Source ID must be expressed in tons/year (tpy)**. Be sure your input files use the correct units.

### 3.3.2. Percent Particulate for Deposition and Depletion

If you are modeling deposition or depletion, or if you want separate records for particle phase and vapor phase at each receptor location in the concentration outputs, then you must provide HEM with the breakdown between vapor and particulate matter in the emission inputs.

Provide this breakdown in column E of the HAP Emissions file, expressed as the percentage emitted as particulate for each emission record (each combination of source and pollutant). For a given facility, if you are not modeling deposition or depletion (and do not request a breakdown of particle and vapor in your outputs), then HEM will ignore the field. If you are modeling deposition or depletion (or have requested a particle/vapor breakdown) and have left this field blank, then HEM assigns the blank a default value of 0% particulate.

**Note:** If you are modeling deposition or depletion, you will need additional input files depending on the type of deposition to be modeled, as described in Section 3.2.6 and Sections 3.5.3 and 3.5.4. (You do not need any additional input files if you merely want a breakdown of particle and vapor in your outputs.)

### 3.4. Emissions Location File

The Emissions Location Excel™ file, like the HAP Emissions file and the Facility List Options file, is required for any HEM run using AERMOD. The file includes emission source locations and types (e.g., the latitude and longitude of a stack) for all Source IDs listed in the HAP Emissions file, for all facilities listed in the Facility List Options file. **Table 8** displays the format guidelines for the fields in the Emissions Location file. **Tables 9 and 10** provide a sample file. A sample template is also provided in the HEM *Inputs* folder named *HEM5.0\_Emiss\_Loc.xlsx*.

For each Source ID at every facility, the Emissions Location file includes:

- the location, source type and required parameters, as discussed in Section 3.4.1; and
- the particle deposition method you will identify, for any sources for which you wish to model particle deposition or depletion, as discussed in Section 3.4.2.

**Table 8. Fields in the Emissions Location Input File**

Field	Type	Source type(s) *	Description
Facility ID	Character	All	An alphanumeric string identifying the facility being modeled
Source ID **	Character	All	Source ID is a unique alphanumeric character string <b>up to 8 characters long</b> , with no spaces. It must match exactly the Source ID in other input files (e.g., the HAP Emissions file). Note: AERMOD allows a maximum of 8 characters for the Source ID; and all Source IDs will be converted to uppercase by AERMOD.
Coordinate system	Character	All	Type of coordinates: L = latitude, longitude; U = UTM. Base all coordinates on the WGS84 geographic system. Note: NAD83 and WGS84 are identical for most applications, but coordinates based on NAD27 need to be converted to WGS84 before being used in HEM.
X-coordinate	Numeric	All	UTM east coordinate in meters (if coordinate system = U) or decimal longitude (if system = L) of the center of point or volume sources, the southwest corner of area sources, the first vertex of polygon sources, or the starting point of line and buoyant line sources.*** For longitudes, 5 decimal places are recommended, corresponding to 1-meter precision.
Y-coordinate	Numeric	All	UTM north coordinate in meters (if coordinate system = U) or decimal latitude (if system = L) of the center of point or volume sources, the southwest corner of area sources, the first vertex of polygon sources, or the starting point of line and buoyant line sources.*** For latitudes, 5 decimal places are recommended, corresponding to 1-meter precision.

Field	Type	Source type(s) *	Description
UTM zone with hemisphere	Character	All	UTM zone where the source is located if the coordinate system = U; leave this field blank if the coordinate system = L. If using the UTM coordinate system, enter the UTM Zone from 1 to 60 followed by the hemisphere (S or N). For example, 17N. If you do not include a hemisphere, HEM will default to N.
Source type	Character	All	Type of source *: P = vertical point, C = capped point, H = horizontal point, A = area, V = volume, I (capital "i") = polygon, N = line, B = buoyant line
Length in x direction	Numeric	A, N	Length in meters in x direction for area and line sources. For area source types, the x direction refers to the direction before the source is rotated (if it is rotated). For line source types, enter the width (m), which must be >= 1 meter.
Length in y direction	Numeric	A	Length in meters in y direction for area sources, before the source is rotated (if it is rotated).
Angle	Numeric	A	Angle of rotation: blank except for area sources. For area source types, enter the angle of rotation (from North) between 0 and 90 degrees. (Defaults to 0 if left blank).
Lateral dimension	Numeric	V	Initial lateral/horizontal dimension (in meters) for volume sources.
Vertical dimension	Numeric	V, A, I, N	Initial vertical dimension (in meters) for volume sources. Optional for area, polygon & line sources.
Release height	Numeric	V, A, I, N, B	Emission release height above ground (in meters) for area, volume, polygon, line, and buoyant line sources. Use the height (top) of the source for area and polygon sources and the vertical center for volume sources. Note: that for buoyant line sources, AERMOD requires a minimum release height of 2 meters.
Stack height	Numeric	P, C, H	Emission release height above ground (in meters) for all point source types.
Stack diameter	Numeric	P, C, H	Diameter of stack (in meters) for all point source types.
Exit velocity	Numeric	P, C, H	Velocity at which emissions are released from the stack (in meters/second) for all point source types.
Exit temperature	Numeric	P, C, H	Temperature (in Kelvin) at which emissions exit the stack for all point source types.
Elevation	Numeric	All	Elevation above sea level in meters at the source location. Use when modeling terrain effects and user-specified elevations are desired. This field is optional. If left blank, by default HEM will estimate the source's elevation if you have chosen to model terrain effects (elevations) in the Facility List Options file.
X-coordinate2	Numeric	N, B	Second X (end) coordinate for line and buoyant line source types. UTM east coordinate, in meters (if coordinate system = U) or decimal longitude (if system = L) of the ending point of line and buoyant line sources.*** For longitudes, 5 decimal places are recommended, corresponding to 1- meter precision.
Y-coordinate2	Numeric	N, B	Second Y (end) coordinate for line and buoyant line source types. UTM north coordinate, in meters (if coordinate system = U) or decimal latitude (if system = L) of the ending point of line and buoyant line sources.*** For latitudes, 5 decimal places are recommended, corresponding to 1-meter precision.

Field	Type	Source type(s) *	Description
Method	Numeric	All, except B	The Method field indicates the type of particle deposition AERMOD should use. Enter 1 or leave blank for Method 1 (which is the default); enter 2 for Method 2. Use Method 1 when greater than 10 percent of the total particulate mass has a diameter of 10 µm or larger, or when the particle size distribution is known. For Method 1, the source-specific particle size distributions must be provided in a separate particle data file (described in Section 3.5.3). Method 2 may be used when the particle size distribution is not well-known and when a small fraction (less than 10 percent of the mass) is in particles with a diameter of 10 µm or larger. The particle data required for Method 2 is less specific than Method 1 but requires that you enter the mass fraction of fine particles and the mass-mean particle diameter for the given source in the next two fields.
Mass Fraction	Numeric	All, except B	The Mass Fraction field refers to the fraction of the particle mass emitted from this source as fine particles (less than 2.5 microns). Leave this field blank if you are using Method 1. For Method 2, enter a number between 0 and 1 that is the fraction of particles emitted in the fine category (a blank will be interpreted as a 1, the default, meaning that all are emitted as fine particles). For example, if one-half of the emissions from this source are fine particles (< 2.5 microns), enter a mass fraction in this field of 0.50.
Particle Diameter	Numeric	All, except B	The Particle Diameter field is the representative mass-mean aerodynamic particle diameter in microns emitted from this source when using Method 2 for particle deposition (a blank is interpreted as 1 micron, the default). Leave this field blank for Method 1. For Method 2, enter the mass-mean particle diameter in microns.

\* Source types for which the parameter is used: All = needed for every source type, **A = area**, **P = vertical point**, **C = capped point**, **H = horizontal point**, **V = volume**, **I (capital "i") = polygon**, **N = line**, **B = buoyant line**. Note: Currently AERMOD cannot model deposition/depletion for buoyant lines (B), nor can the FASTALL option be used with buoyant lines. For additional information, see the AERMOD User's Guide.

\*\* If you are modeling deposition or depletion and pollutant properties are known to vary, use a separate record for each pollutant and source. Therefore, for vapor deposition/depletion modeling, use a unique Source ID for each pollutant emitted from a given source (e.g., SAMPLE3A for benzene, SAMPLE3B for 1,3-butadiene). Likewise, use a unique Source ID when modeling particulate deposition or depletion if the particulate properties (size and density distributions) are known and vary by pollutant, not just source. If you are not modeling vapor deposition/depletion and the same properties are assumed for all particulates emitted from a source, one Source ID per emission source is sufficient (e.g., SAMPLE3 for all modeled pollutants from the same source).

\*\*\* Start/end coordinates for buoyant line sources generally should be entered in order from West to East, and from South to North. However, in the case where the buoyant lines are parallel to the Y axis, the order that the lines should be entered is dependent on which endpoint is entered first, the southern or northern endpoint of the lines. If the southern endpoint is entered first, the lines should be entered in the order of the eastern most line to the western most line. If the northern endpoint is entered first, lines should be ordered west to east. Incorrect ordering of these parameters will result in an AERMOD error stating "Input buoyant line sources not in correct order". See page 3-61 of the AERMOD User's Guide for more detail (USEPA, 2024e).

**Table 9. Sample Emissions Location Input File, Excel columns A–M**

Facility ID	Source ID	Coordinate system (U = UTM, L= latitude/longitude (All source types))	X-coordinate Longitude (decimal) or UTM East (m) (All source types)	Y-coordinate Latitude (decimal) or UTM North (m) (All source types)	UTM zone	Source type (P, C, H = point, A = area V= volume I = polygon N = line B = buoyant line)	Length in x-direction (m) A & N sources (width for N sources)	Length in y-direction (m) A sources	Angle (degrees) A sources	Lateral Dim. (m) V sources	Vertical Dim.(m) V sources or optionally A, I and N sources	Release height (m) B sources or optionally A, V, I, and N sources
Fac2-IL	CT0001	L	-88.257293	41.480164		P [or C or H]						
Fac2-IL	CV0001	L	-88.256715	41.481944		A	130	120	45			2
Fac1-NC	SR0001	L	-78.883686	35.900628		V				20	3	10
Fac1-NC	MS0001	L	-78.888792	35.905920		I						5
Fac1-NC	RW0001	L	-78.888430	35.901810		N	20					50
Fac1-NC	RV0001	U	690891	3975044	17	B						40

**Table 10. Sample Emissions Location Input File, Excel columns N–W**

[Source type from column G in Table 9, provided for reference]	Stack height (m) P, C, or H sources	Stack Diameter (m) P, C, or H sources	Exit Velocity (m/s) P, C, or H sources	Exit Temperature (K) P, C, or H sources	Elevation (m) HEM will estimate if blank (if modeling elevations)	X-coord.2 Longitude (decimal) or UTM East (m) B & N sources	Y-coord.2 Latitude (decimal) or UTM North (m) B & N sources	Particle Deposition Method: Method (1 or 2; defaults to 1) All sources, except B	Particle Deposition Method: Mass Fraction (decimal > 0 and < 1 for Method 2 only) All sources, except B	Particle Deposition Method: Particle Diameter (microns, for Method 2 only) All sources, except B
...(P, C or H)	50	2.8	21.83	322				2	0.04	0.0006
...(A)										
...(V)										
...(I)										
...(N)						-78.886303	35.902183			
...(B)						691291	3975044			

### 3.4.1. Source Types and Parameter Requirements

The Emissions Location file must include at least one record for each individual source (e.g., stack/point source, area source, line source, buoyant line source) to be modeled at a facility. For certain modeling situations, more than one record per source is recommended.<sup>3</sup> A record provides information on the location, size, height, and configuration for each source. You must enter every Facility ID to be modeled in column A of the Emissions Location file. Enter each Source ID in column B, taking care to match each named Source ID with a corresponding Source ID in the HAP Emissions file, described in Section 3.3.

#### 3.4.1.1. Source Locations

In column C “Coordinate system”, you can enter source locations as UTM coordinates, or as latitude and longitude (which HEM will convert to UTM coordinates for use in AERMOD). Complete the coordinate system field for each source record and specify which coordinates you are entering. Enter “U” for UTM or “L” for latitude and longitude.

- If using UTM coordinates, specify the UTM zone in each emission source record. Enter the location coordinates for each source in column D “X coordinate, Longitude (decimal) or UTM East (m)” and in column E “Y coordinate, Latitude (decimal) or UTM North (m)”. (The endpoints for line and buoyant line source types, discussed further below, will be entered in columns S and T.).
- If you are using longitudes and latitudes, five decimal places are recommended, which corresponds to a precision of roughly 1 meter. Refer to Table 8 for further specifications for these fields. You must base all coordinates on the WGS84 geographic system. As noted in Section 3.1, NAD83 and WGS84 are identical for most applications, so no conversion is needed if using coordinates based on NAD83. But if coordinates are based on NAD27, they need to be converted to WGS84 before being used in HEM. There are various commercial computer programs available that can perform this conversion.

#### 3.4.1.2. Source Types

Use the source type field in column G to indicate whether the emission source is a vertical non-capped point source (P), a capped point source (C), a horizontal point source (H), an area source (A), a volume source (V), a polygon source (I, for uppercase “i”), a line source (N), or a buoyant line source (B).<sup>4</sup> Each of these source types is discussed more in the following sections, but consult the [AERMOD User's Guide](#) for additional information, including

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<sup>3</sup> If modeling deposition or depletion at a facility (as described in Section 3.2.6), and pollutant properties are known to vary, we recommend you include a separate Source ID record for each pollutant and source—that is, a unique Source ID—for each pollutant being emitted from the same source. This is generally recommended for modeling of vapor deposition/depletion and for modeling of particulate deposition/ depletion if the size or density distributions are known for each pollutant (HAP) and vary for each pollutant. If you are not modeling deposition/depletion of vapor phase pollutants, and the same particulate properties are assumed for all pollutants being emitted from a given source, one record per source in the Emissions Location input file is sufficient.

<sup>4</sup> The AERMOD version 24142 in HEM5.0 cannot model deposition or depletion for buoyant lines (B), nor can AERMOD 24142 use the FASTALL option (in the Facility List Options file) with buoyant lines.

assumptions used by AERMOD to model the emissions from each source type, as well as the additional parameters needed for each.

#### **3.4.1.3. Point Sources – Vertical, Horizontal, and Capped Stacks**

Point source types include vertical stacks (P), horizontal stacks (H) and capped stacks (C) source types. These point sources require you to specify the stack height (in meters in column N), the stack diameter (in meters in column O), the exit velocity (in meters/second in column P), and the exit/release temperature (in Kelvin in column Q) for the pollutant plume. Although capped (C) and horizontal (H) stacks require the same user-specified parameters as vertical stacks (P), AERMOD models these point sources differently than vertical stacks (USEPA, 2024a, 2024e).

#### **3.4.1.4. Non-Point Source Types**

Columns H through M in the Emissions Location file pertain to area (A) sources, volume (V) sources, polygon (I for capital “i”) sources, line (N) sources, and buoyant line (B) sources. Table 8 provides guidance on what you should provide in each of these fields.

- Unlike point source types (P, C, or H), area (A), volume (V), polygon (I) and line (N) source types in AERMOD are modeled using ambient pollutant release temperatures and zero or negligible pollutant release/exit velocities.
- Fugitive emissions are often modeled as rectangular **area** (A) sources.
- A conveyor belt, in which release temperature is assumed to be ambient and release velocity zero or negligible, may be simulated as **volume** (V) sources.
- A **polygon** (I) can be used to represent a complex (non-rectangular) area source with many vertices. A polygon (I) may also be used to represent an entire U.S. Census tract from which a source is modeled as a uniform emission (e.g., for mobile sources). Polygon source types require a Polygon Vertex file as an additional input, as discussed in Section 3.5.1.
- **Line source** (N) types can be used to represent roadways and airport runways and may be used instead of similarly shaped area sources.
- **Buoyant line sources** (B) are useful in simulating continuous vents along a roofline where the emissions, like point sources (P, C or H), are released at an elevated non-ambient temperature and with a non-zero release velocity (unlike the other non-point source types). However, unlike tall stack sources where the plume can move in all directions without impediment, buoyant line source types simulate pollutants emitted close to a building’s roof where vertical wind shear and building downwash effects become important. Buoyant line (B) source types require a Buoyant Line Parameters file as an additional input, as discussed in Section 3.5.2.

These non-point source types are discussed in more detail below.

#### **3.4.1.5. Area Sources**

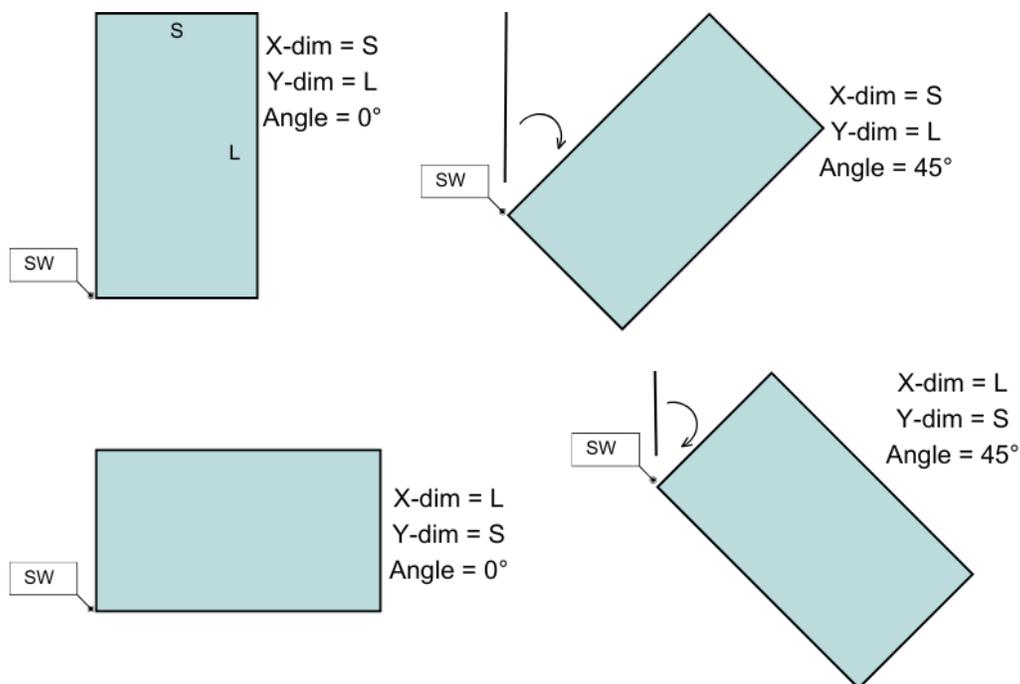
An area source (A) type represents a rectangular area from which emissions are released at ambient temperature and with zero or negligible velocity (e.g., fugitive emissions from a building or tank farm).

In AERMOD, area sources can be at ground level, or at a height above ground level. Specifying a release height (in column M) is optional and defaults to 0.

The default orientation for area sources is with one axis in the north-south direction, but you can rotate these sources using the “angle” parameter (in column J), which specifies the rotation of the source from north (in the clockwise direction), to better fit the orientation of the source you are modeling. The X and Y coordinates you choose (in columns D and E) should reflect the southwest corner of the area source. The length in the X direction you enter (in column H) should reflect the length of the area source in the easterly direction, or in the southeasterly direction if the source is rotated. The length in the Y direction you enter (in column I) should reflect the length of the area source in the northerly direction, or the northeasterly direction if the source is rotated.

Unlike AERMOD, where 360-degree rotation is allowed, the angle parameter for HEM area sources must be between 0 and 90 degrees. You can use this angle to represent any possible orientation by switching the X and Y lengths (shown in **Figure 2**). You can also optionally enter an initial vertical dimension of the area source (in column L).

**Figure 2. Example Orientations of Area Emission Sources for the HEM Model**



#### **3.4.1.6. Volume Sources**

Volume source (V) types – such as multiple vents and conveyor belts – are specified by a lateral/horizontal dimension (you enter in column K), a vertical dimension (you enter in column L), and a release height (you enter in column M).

Emissions from a volume source are assumed to be released at ambient temperature and with zero or negligible velocity.

Both the release height (in column M) and the source location coordinates (in columns D and E) should reflect the center of the source.

#### **3.4.1.7. Polygon Sources**

You can create a polygon source (I, for capital “i”) type to represent a polygon with 3 sides or many more (up to 20 sides). This source type provides considerable flexibility in specifying the shape of an area source. You can use a polygon source type to reflect U.S. Census tract boundaries, for example, when modeling mobile source emissions provided at the tract level.

An associated polygon vertex input file is required when modeling polygon source types. Section 3.5.1 discusses this in more detail. The shape of the polygon source, as defined in the Polygon Vertex Input file, is determined by a list of X and Y coordinates representing the vertices of the polygon. You can order these X and Y coordinates in either a clockwise or counterclockwise direction. However, the first coordinates entered in the Polygon Vertex Input file must match the coordinates entered in the emissions location file (in columns D and E) as the location of the first vertex of the polygon. You can also optionally enter an initial vertical dimension of the polygon (in column L). Emissions from polygon source types are assumed to be released at ambient temperature and zero or negligible velocity.

#### **3.4.1.8. Line Sources**

The line source (N) type allows you to specify long, narrow sources, such as roadways or airport runways. You must enter a start point (in columns D and E) and endpoint of the line (in columns S and T), as well as the width of the line (a value in meters greater than or equal to 1 meter that you enter in column H, Length in x direction.).

Optionally, you can also specify an initial vertical dimension (in column L). In this way, the line source can be used as an alternative to a rectangular area source (A). Like area, volume and polygon source types, emissions from line source types are assumed to be released at ambient temperature and zero or negligible velocity.

Note: According to the AERMOD User’s Guide (USEPA, 2024e) the line source type utilizes the same routines as the area source type and will give identical results, given the same inputs.

#### **3.4.1.9. Buoyant Line Sources**

Like the line source, for the buoyant line source (B), you must enter the starting coordinates (in columns D and E) and the end coordinates (in columns S and T).<sup>5</sup> **Note: AERMOD enforces a minimum release height of 2 meters for buoyant line sources** in your Emissions Location file. (If you enter a release height less than 2 meters, AERMOD will change it to 2 meters.)

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<sup>5</sup> You may wish to use a series of buoyant lines to represent multiple roof vent lines. AERMOD requires a strict ordering of these lines to run properly. The start/end coordinates for buoyant line sources generally should be entered in order from West to East, and from South to North. However, in the case where the buoyant lines are parallel to the Y axis, the order that the lines should be entered is dependent on which endpoint is entered first, the southern or northern endpoint of the lines. If the southern endpoint is entered first, the lines should be entered in the order of the eastern most line to the western most line. If the northern endpoint is entered first, lines should be ordered west to east. See pages 3-57 to 3-58 of the AERMOD User’s Guide for more detail (USEPA, 2024e).

The buoyant line source (B) type was first developed to simulate the transport and diffusion of emissions from aluminum reduction plants in which some emissions from the reduction process escape through continuous (rooftop) ridge ventilators (Schulman & Scire, 1980). In general, the buoyant line source can be used to characterize emissions from a continuous roof vent that spans a portion or the entire building. Emissions from such buoyant line sources result in enhanced plume rise (especially from multiple rows of closely spaced emission lines) and the plume is subject to vertical wind shear and building downwash effects.

This source type incorporates an average buoyancy parameter (in meters<sup>4</sup>/seconds<sup>3</sup>) as well as the average building dimensions (in meters) of the building(s) on which the buoyant line source is located. You must provide HEM with these inputs for your buoyant line source type in a Buoyant Line Parameters Input file, as discussed in Section 3.5.2.

As noted previously, the current version of AERMOD cannot model deposition or depletion for buoyant lines, nor can the FASTALL option in the Facility List Options file be used with buoyant lines. For more detailed information regarding the necessary inputs for the buoyant line source type, see the AERMOD User's Guide (USEPA, 2024e), as well as documentation for the buoyant line and point source (BLP) dispersion model (Schulman & Scire, 1980).

#### **3.4.1.10. Elevation**

If you wish to consider terrain impacts in your modeling, you can specify the elevation above sea level in meters for each emission source in column R. If you leave the elevation field blank for any sources, and you chose to model elevations in the Facility List Options file, then HEM will estimate the missing elevation(s) for the emission source(s) as described in Section 3.2.7.

**Note:** If you chose not to model elevations in your Facility List Options file (by entering an "N" in that file's elevation field/column), then no elevations will be considered in the model run including for sources in the Emissions Location file.

HEM will model area, volume, polygon, line, and buoyant line sources as flat surfaces, which can result in strangely located (underground) impacts if the source is located, for example, on a hillside with varying elevations. To avoid this, either opt to model with no elevations in the Facility List Options file or break up the source into smaller pieces with uniform elevations.

It should also be noted that "release height" (in column M) is different than elevation and indicates the height above the ground elevation where emissions are released (in which the ground is set to an elevation above sea level, or not, depending on whether you chose to model elevations in your Facility List Options file). For point sources, fill in the "stack height" field (in column N) to designate the release height (for vertical stack, horizontal stack and capped stack source types). For all other source types (area, volume, polygon, line and buoyant line), you should fill in the "release height" (in column M) with the source's height above the ground (in meters). If you leave this field blank, HEM will assume the release height is zero (0), meaning at ground level.

#### **3.4.2. Particle Deposition Method**

Columns U (Method), V (Massfrac), and W (Partdiam) of the Emissions Location file should only be filled in if you wish to model particle deposition or depletion using Method 2. If you do not wish to model particle deposition/depletion or if you wish to use AERMOD's Method 1 to model particle deposition/depletion, then leave these fields blank for those sources.

### **3.4.2.1. Particle Deposition/Depletion Method 1**

The Method field (in column U) indicates to HEM the type of particle deposition AERMOD should use for a given source. As noted in Table 8, you should enter 1 or leave this field blank for Method 1 (which is the default). Method 1 should be used when a significant fraction (greater than about 10 percent) of the total particulate mass has a diameter of 10  $\mu\text{m}$  or larger, or when the particle size distribution is known. The particle size distribution must be known reasonably well to use Method 1 and these source-specific particle size distributions must be provided in a separate Particle Data file, as discussed in Section 3.5.3. You should also leave this field (column U) blank if you are not modeling particle deposition/depletion.

### **3.4.2.2. Particle Deposition/Depletion Method 2**

Enter 2 in the Method field (column U) if you wish to model particle deposition or depletion for the given source using AERMOD's Method 2. Method 2 may be used when the particle size distribution is not well known and when a small fraction (less than 10 percent of the mass) is in particles with a diameter of 10  $\mu\text{m}$  or larger. The particle data required for Method 2 is less detailed than Method 1 but does require that you enter the mass fraction of fine particles and the mass-mean particle diameter for the given source in the next two fields.

**Mass Fraction for Method 2:** The Mass Fraction field (in column V) refers to the fraction of the particle mass emitted from this source in the fine particle category (less than 2.5 microns). Leave this field blank if you are using Method 1, or if you are not modeling particle deposition/depletion at all. For Method 2, you should enter a number between 0 and 1 that is the fraction of particles emitted in the fine category (a blank will be interpreted by the model as a 1, the default, meaning that all are emitted as fine particles). For example, if one-half of the emissions from this source are fine particles (< 2.5 microns), enter a mass fraction in this field of 0.50.

**Particle Diameter for Method 2:** The Particle Diameter field (in column W) is the representative mass-mean aerodynamic particle diameter in microns emitted from this source when using Method 2 for particle deposition (a blank is interpreted by the model as 1 micron, the default). Leave this field blank for Method 1, or if you are not modeling particle deposition/depletion at all. For Method 2, enter the mass-mean particle diameter in microns.

## **3.5. Additional Modeling Input Files**

In addition to the three required input files (Facility List Options, HAP Emissions, and Emissions Location) discussed in Sections 3.2, 3.3 and 3.4, other files may be required for your modeling run depending on (a) what modeling options you chose in the Facility List Options file, (b) what source types you are modeling in your Emissions Location file, (c) what kinds of receptors you are modeling with, and/or (d) what changes you may wish to make to HEM's underlying databases and resource files. These additional input files are discussed in the next sections.

### **3.5.1. Polygon Vertex Input File for Modeling Polygon Emission Sources**

If your Emissions Location input file contains one or more polygons (source type "I", for capital "I"), then HEM will prompt you for a Polygon Vertex file. This file provides HEM with the locations of the polygon vertices. Polygons are useful for complex source configurations at a facility, and for modeling U.S. Census boundaries such as blocks and tracts as sources (e.g., for mobile source emissions modeled uniformly across a tract).

Include a separate record (row) for each vertex of the polygon in the Polygon Vertex file. A polygon may have as few as 3 vertices and as many as 20 vertices. Each record must include information for one vertex of the polygon. As noted in Section 3.4.1.7, you can order the X and Y vertex coordinates in either a clockwise or counterclockwise direction. The first and last vertex must have identical coordinates, and these coordinates must match the coordinates listed as the location of the first vertex of the polygon source in your Emissions Location file. The first record must also include the number of vertices for the polygon and the total area of the polygon, in meters squared. You can enter coordinates as UTM coordinates, or as longitudes and latitudes. If using UTM coordinates, you must specify the UTM zone. Base all coordinates on the WGS84 reference system.

Optionally, you can assign an ID (name) to the polygon. This may be useful, for example, if you are using the polygon to model a U.S. Census tract. In this case, you may wish to use the U.S. Census tract ID as the polygon ID and enter it in the last column of the Polygon Vertex file.

**Table 11** and **Table 12** give the format guidelines for the Polygon Vertex file, and a sample Polygon Vertex file, respectively. A sample template is provided in the HEM *Inputs* folder named *HEM5.0\_polygon\_vertex.xlsx*.

**Table 11. Format Guidelines for the Polygon Vertex File**

Field	Type	Description
Facility ID	Character	An alphanumeric character identifying the facility being modeled containing the polygon source(s)
Source ID	Character	An alphanumeric character string up to 8 characters long, with no spaces. The Source IDs must be listed as polygon (Type = I, for capital "i") source types in the Emissions Location file. Note: AERMOD allows a maximum of 8 characters for the Source ID; and all Source IDs will be converted to uppercase by AERMOD.
Coordinate system	Character	Type coordinates: L = longitude, latitude; U = UTM [WGS84].
X-coordinate	Numeric	UTM east coordinate in meters (if Coordinate System = U) or decimal longitude (if System = L). For longitudes, 5 decimal places are recommended, corresponding to 1-meter precision.
Y-coordinate	Numeric	UTM north coordinate in meters (if Coordinate System = U) or decimal latitude (if System = L). For latitudes, 5 decimal places are recommended, corresponding to 1-meter precision.
UTM zone	Numeric	If using the UTM coordinate system (U), enter the UTM Zone from 1 to 60 followed by the hemisphere (S or N). For example, 17N (default hemisphere is N if not specified). If using longitudes/latitudes, leave this cell blank.
Num of Vertices	Numeric	Number of vertices in the polygon. This number must be 3 or greater. The upper limit is 20.
Area	Numeric	Size of area within polygon, in meters squared.
Polygon ID	Character	Optional ID to indicate the name of the polygon (e.g., a U.S. Census tract is sometimes modeled as a polygon and the U.S. Census tract ID may be used as the Polygon ID).

**Table 12. Sample Polygon Vertex File**

Facility ID	Source ID	Coordinate system (U = UTM, L = latitude/longitude)	Longitude (decimal) or UTM East (m)	Latitude (decimal) or UTM North (m)	UTM zone	Num of Vertices ( $\geq 3$ and $\leq 20$ )	Area (m <sup>2</sup> )	Polygon ID (optional)
Fac1-TX	SAMPLE4	L	-95.3586	29.7674		9	402939.4	
Fac1-TX	SAMPLE4	L	-95.3524	29.7685			0	
Fac1-TX	SAMPLE4	L	-95.3515	29.7663			0	
Fac1-TX	SAMPLE4	L	-95.3533	29.7654			0	
Fac1-TX	SAMPLE4	L	-95.3533	29.7622			0	
Fac1-TX	SAMPLE4	L	-95.3574	29.7634			0	
Fac1-TX	SAMPLE4	L	-95.3582	29.7651			0	
Fac1-TX	SAMPLE4	L	-95.3575	29.7661			0	
Fac1-TX	SAMPLE4	L	-95.3586	29.7674			0	
Fac1-TX	SAMPLE5	L	-95.3512	29.7688		11	710176.8	
Fac1-TX	SAMPLE5	L	-95.3524	29.7685			0	
Fac1-TX	SAMPLE5	L	-95.3515	29.7663			0	
Fac1-TX	SAMPLE5	L	-95.3509	29.7653			0	
Fac1-TX	SAMPLE5	L	-95.3533	29.7654			0	
Fac1-TX	SAMPLE5	L	-95.3533	29.7622			0	
Fac1-TX	SAMPLE5	L	-95.3574	29.7634			0	
Fac1-TX	SAMPLE5	L	-95.3582	29.7651			0	
Fac1-TX	SAMPLE5	L	-95.3575	29.7661			0	
Fac1-TX	SAMPLE5	L	-95.3586	29.7674			0	
Fac1-TX	SAMPLE5	L	-95.3512	29.7688			0	

### 3.5.2. Buoyant Line Parameter Input File for Modeling Buoyant Line Sources

If your Emissions Location input file contains one or more buoyant line sources (source type “B”), then HEM will prompt you for a Buoyant Line Parameter file. Buoyant line source types are useful in simulating continuous rooftop vents in which emissions are released at non-ambient (elevated) temperature and non-negligible velocity, as discussed in Section 3.4.1.9. Because building downwash effects are especially important with buoyant line source types, the Buoyant Line Parameter file must provide HEM with the length, width, and height of the building(s) on which the buoyant line source type (e.g., rooftop vent) sits. In addition, the file must contain the width of the buoyant line source(s), the distance between the buildings (zero for a solitary buoyant line), and the buoyancy parameter for the buoyant line source(s).

In a previous version of AERMOD, multiple buoyant lines could be modeled but only one set of “average” parameters for all buoyant lines could be used. The current version of AERMOD allows you to input multiple buoyant line source groups, with individual parameters for each group (containing average building dimensions, average line source width and separation, and average buoyancy parameter). Consequently, HEM now allows multiple buoyant line source groups per facility, with each group containing one or multiple lines. **Note:** The number of individual lines associated with a buoyant line source group is not limited, but each individual buoyant line may belong to one and only one buoyant line group. (Refer to the AERMOD User’s Guide for further information (USEPA, 2024e)).

The buoyancy parameter of a line source is calculated from an equation based on the line source length (m) and width (m), the exit/release velocity (m/s), the exit/release temperature (K), the ambient temperature (K) and the acceleration due to gravity (9.81 m/s<sup>2</sup>), as presented in Equation 2-47 on page 2-37 of the Buoyant Line and Point Source Dispersion Model User’s

Guide (Schulman & Scire, 1980). **These parameters should be average values for the array of buoyant line sources in each group, if more than one parallel buoyant lines are modeled within the group** (USEPA, 2024e). Provide the following parameters in the Buoyant Line Parameter File:

- Facility ID;
- Buoyant Line Group ID associated with facility;
- Source ID(s) included in buoyant line group (one or more);
- Average Building Length (in meters);
- Average Building Height (in meters);
- Average Building Width (in meters);
- Average Line Source Width, of the individual lines (in meters);
- Average Building Separation, between the individual lines (in meters); and
- Average Buoyancy Parameter (in meters<sup>4</sup>/seconds<sup>3</sup>).

**Table 13** and **Table 14** provide the format guidelines for the Buoyant Line Parameter input file and a sample input file, respectively. A sample template is provided in the HEM *Inputs* folder named *HEM5.0\_buoyant\_line\_parameter.xlsx*.

**Table 13. Format Guidelines for the Buoyant Line Parameter Input File**

Field	Type	Description
Facility ID	Character	An alphanumeric character string identifying the facility being modeled containing the buoyant line(s)
Buoyant Line Group ID	Character	An alphanumeric character string identifying a buoyant line group. One or more individual lines may be associated with each buoyant line group. A facility may have more than one buoyant line group, although each must have a unique ID. Different facilities may use the same buoyant line group ID.
Source ID	Character	An alphanumeric character string up to 8 characters long, with no spaces. The Source ID must be listed as a buoyant line (Type = B) source type in the Emissions Location file. Note: AERMOD allows a maximum of 8 characters for the Source ID; and all Source IDs will be converted to uppercase by AERMOD.
Average Building Length	Numeric	The average length of the building or buildings on which the parallel buoyant line source types in the group are located (in meters)
Average Building Height	Numeric	The average height of the building or buildings on which the parallel buoyant line source types in the group are located (in meters)
Average Building Width	Numeric	The average width of the building or buildings on which the parallel buoyant line source types in the group are located (in meters)
Average Line Source Width	Numeric	The average width of the individual buoyant line source types in the group (in meters)
Average Building Separation Distance	Numeric	The average building separation distance between the (parallel) individual buoyant lines in the group (in meters)
Average Buoyancy Parameter	Numeric	The average buoyancy parameter for the buoyant line emission plumes (in meters <sup>4</sup> /seconds <sup>3</sup> ) in the group; See BLP Dispersion Model documentation (Schulman & Scire, 1980).

**Table 14. Sample Buoyant Line Parameter Input File**

Facility ID	Buoyant Line Group ID	Source ID	Avg Building Length (m)	Avg Building Height (m)	Avg Building Width (m)	Avg Line Source Width (m)	Avg Building Separation (m)	Avg Buoyancy (m <sup>4</sup> /s <sup>3</sup> )
Fac1-NC	BLG1A	RV01	454.3	16.76	40	5.73	40.95	3335.49
Fac1-NC	BLG1A	RV02	454.3	16.76	40	5.73	40.95	3335.49
Fac1-NC	BLG2A	RV03	220.5	10.50	20	3.25	35.25	3010.25
Fac1-NC	BLG2A	RV04	220.5	10.50	20	3.25	35.25	3010.25
Fac2-IL	BLG1A	RV01	212	25	35	4.50	25	2750.5

### 3.5.3. Particle Data Input File for Modeling Particulate Deposition and Depletion

As described in Section 3.2.6, AERMOD can implement dry and wet deposition and plume depletion of both particulate and vapor emissions (USEPA, 2024e). This section describes the input file needed for modeling **particulate** deposition and/or particulate depletion.

If you indicated in your Facility List Options file that your run will model deposition or depletion of particulate emissions AND you chose (in your Emissions Location file) to use Method 1 for particle deposition for one or more sources, then you must provide HEM with a separate Particle Data input file describing the particle size distribution. In this file, include a separate record for each particle size range emitted by each emission source, for which HEM-AERMOD will model particle deposition/depletion using Method 1. Each record must include an average particle diameter for the size range, the percentage that the size range represents in terms of the total mass of particulate matter from the given emission source, and the average density of particles in the size range. The mass percentages must sum to 100% for each emission source. **Table 15** and **Table 16** provide format guidelines for the Particle Data input file and a sample input file, respectively. A sample template is provided in the HEM *Inputs* folder named *HEM5.0\_particle\_data.xlsx*.

**Note:** The Particle Date Input File is needed only when modeling deposition/depletion of particulate pollutants. It is not required to model deposition/depletion of vapor/gaseous emissions.

**Table 15. Format Guidelines for the Particle Data Input File**

Field	Type	Description
Facility ID	Character	An alphanumeric character string identifying the facility being modeled
Source ID	Character	The Source ID is a unique alphanumeric character string up to 8 characters long with no spaces. It must match a Source ID in the HAP Emissions and Emissions Location file. Note: AERMOD allows a maximum of 8 characters for the Source ID; and all Source IDs will be converted to uppercase by AERMOD.
Particle diameter	Numeric	The average diameter (in µm) for the particle size range covered by this record.
Mass fraction	Numeric	The percentage (by mass) of particulate matter in this size range. Must add up to 100% for each Source ID.
Particle density	Numeric	The average density of the particles in this size range (in g/cm <sup>3</sup> ).

**Table 16. Sample Particle Data Input File**

Facility ID	Source ID	Particle diameter ( $\mu\text{m}$ )	Mass fraction (%)	Particle density ( $\text{g}/\text{cm}^3$ )
Fac1-TX	SAMPLE1	0.50	72.0	1.00
Fac1-TX	SAMPLE1	1.50	8.0	0.75
Fac1-TX	SAMPLE1	2.50	4.0	0.50
Fac1-TX	SAMPLE1	4.00	4.0	1.00
Fac1-TX	SAMPLE1	10.00	12.0	0.35
Fac1-TX	SAMPLE2	0.50	60.0	1.00
Fac1-TX	SAMPLE2	1.50	8.0	0.80
Fac1-TX	SAMPLE2	2.50	4.0	0.15
Fac1-TX	SAMPLE2	4.00	4.0	0.90
Fac1-TX	SAMPLE2	10.00	24.0	1.00

### 3.5.4. Input Files Required for Modeling Vapor Deposition and Depletion

As described in Section 3.2.6, AERMOD can model dry and wet deposition of both particulate and vapor (gaseous) emissions and the resulting plume depletion (USEPA, 2024e). This section describes the input files required for modeling **vapor** deposition and vapor depletion.

#### 3.5.4.1. Gas Parameter File for Modeling Deposition/Depletion of Vapor Pollutants

To model deposition or depletion of vapor pollutants, wet and/or dry, you must provide HEM with the necessary information to evaluate the scavenging of these pollutants in precipitation and deposition on vegetation and other surfaces. When modeling any type of vapor deposition or depletion (wet, dry, or both wet and dry), HEM accesses a gas parameter file containing pollutant properties related to gaseous deposition. **Note:** The Gas Parameter file is included in HEM's *resources* folder, which is included in the model's installation files; therefore, HEM will NOT prompt you for this file. (The default file pathway is "HEM\resources\Gas\_Param.xlsx".) This file includes the following four parameters for each pollutant:

1. diffusivity in air ( $D_a$ , in  $\text{cm}^2/\text{sec}$ );
2. diffusivity in water ( $D_w$ , in  $\text{cm}^2/\text{sec}$ );
3. cuticular resistance to uptake by lipids for individual leaves ( $r_{cl}$ , in  $\text{sec}/\text{cm}$ ); and
4. Henry's Law coefficient ( $H$ , in  $\text{Pascal}\cdot\text{m}^3/\text{mol}$ ).

Values for these parameters are provided in the Gas Parameter file for 129 pollutants, based on a study by Argonne National Laboratories (Wesely et al., 2002) and a more recent paper which compiles Henry's Law coefficients from numerous other sources (Sander, 2015). When modeling a vapor/gaseous pollutant that is not listed in the Gas\_Param file, HEM uses the following default parameters:

- $D_a$ :  $0.07 \text{ cm}^2/\text{sec}$ ;
- $D_w$ :  $0.7 \text{ cm}^2/\text{sec}$ ;
- $r_{cl}$ :  $2,000 \text{ sec}/\text{cm}$ ; and
- $H$ :  $5.0 \text{ Pascal}\cdot\text{m}^3/\text{mol}$ .

These defaults are based on the logarithmic average of parameters for the 129 pollutant species currently contained in the Gas Parameter file, using one significant figure precision. It should be emphasized that these defaults are averages taken over ranges sometimes in excess of ten orders of magnitude and may not be appropriate for the pollutants of interest to you.

You can calculate parameters for additional pollutants and add these to the *Gas\_Param.xlsx* file or revise the values in this file, as appropriate. For example, you may wish to estimate parameters for pollutants of interest to you by calculating averages based on the values in the Gas Parameter file for smaller groups of pollutants in the same chemical family and of similar molecular weight to your pollutant of interest (e.g., polycyclic aromatic hydrocarbons, PAHs).

Parameter values for additional pollutant species are available in the literature cited here (Wesely et al., 2002; Sander, 2015), as well as in EPA's [Human Health Risk Assessment Protocol for Hazardous Waste Combustion Facilities Final Report](#) (dated September 2005). Wesely et al. also describes a methodology for estimating cuticular resistance, which is less commonly cited in the literature (2002).

**Note:** The Gas Parameter Input File is needed only when modeling deposition/depletion of vapor/gaseous pollutants. It is not required to model deposition/depletion of particulate emissions.

#### **3.5.4.2. Land Use and Month-to-Seasons Input Files for Modeling Dry Deposition of Vapor Pollutants**

If you chose to model **dry** (including dry only or wet and dry) **vapor deposition** or **dry** (including dry only or wet and dry) **vapor depletion** in your Facility List Options file, then HEM will prompt you to provide two additional input files described in this section. To quantify dry deposition of vapor (gaseous) pollutants to vegetation, AERMOD requires information on the land use and vegetation surrounding the emission source. You must provide this information in Excel™ spreadsheets called the land use and month-to-seasons input files.

- **Land Use Input File:** In the land use input file, you must enter a code characterizing the average land use for 36 directions from the emission sources (which emit gaseous pollutants at a facility you chose to model dry deposition or dry depletion at), at increments of 10 degrees compass bearing. **Table 17** gives the format guidelines for the land use input file, and **Table 18** shows a sample land use input file. A sample template is provided in the HEM *Inputs* folder named *HEM5.0\_landuse.xlsx*.
- **Month-to-Seasons Input File:** You must also provide HEM the month-to-seasons input file containing further information on the typical stage of vegetation in the modeled region during each month of the year. As the format guidelines in **Table 19** show, this file associates each month with a season code, describing the stage of vegetation ranging from lush midsummer vegetation to winter snow coverage. **Table 20** shows a sample input table for the month-to-seasons input file. A sample template is provided in the HEM *Inputs* folder named *HEM5.0\_month-to-seasons.xlsx*.

**Note:** The Land Use and Month-to-Seasons input files are required only if you choose to model dry (including wet and dry) vapor deposition or dry (including wet and dry) vapor depletion in your Facility List Options file. These files are not required for modeling wet deposition or depletion of vapor emissions, nor are they required for modeling any kind of deposition or depletion of particulate emissions.

**Table 17. Format Guidelines for Land Use Input File**

Field	Type	Description
Facility ID	Character	An alphanumeric character string identifying the facility being modeled
Direction Sector 1	Numeric	Land use code (value = 1 to 9) for the modeling domain at a compass bearing of 10 degrees from the emission release point: 1) Urban land, no vegetation 2) Agricultural land 3) Rangeland 4) Forest 5) Suburban areas, grassy 6) Suburban areas, forested 7) Bodies of water 8) Barren land, mostly desert 9) Non-forested wetlands
Direction Sector n (n = 2 to 35)	Numeric	Land use code at a bearing of n × 10
Direction Sector 36	Numeric	Land use code at a bearing of 360 degrees

**Table 18. Sample Input File for Land Use**

Facility ID	D01 (10°)	D02 (20°)	D03 (30°)	D04 (40°)	D05 (50°)	...	D36 (360°)
Fac1-NC	1	9	5	5	6	...	1

**Table 19. Format Guidelines for Month-to-Seasons Input File**

Field	Type	Description
Facility ID	Character	An alphanumeric character string identifying the facility being modeled
January	Numeric	Seasonal category (value = 1 to 5) for month 1 (January): 1) Midsummer with lush vegetation 2) Autumn with unharvested crop land 3) Late autumn after frost and harvest, or with no snow 4) Winter with snow on ground 5) Transitional spring with partial green coverage or short annuals
November	Numeric	Seasonal category (value = 1 to 5) for month 11
December	Numeric	Seasonal category (value = 1 to 5) for month 12

**Table 20. Sample Month-to-Seasons Input File**

Facility ID	M01	M02	M03	M04	M05	...	M12
Fac1-NC	4	4	5	5	1	...	4

### 3.5.5. Building Dimensions Input File for Modeling Building Downwash

If you chose to model building downwash in your Facilities List Options file for one or more facilities with point source(s), then HEM will prompt you for a Building Dimensions input file, which is required by AERMOD to model building downwash effects. The following parameters are required in the building dimensions input file:

- building height (keyword=BUILDHGT);
- projected building width perpendicular to the direction of flow (keyword=BUILDWID);
- building length in the direction of flow (keyword=BUILDLEN);
- distance from the stack to the center of the upwind face of the building parallel to the direction of flow (keyword=XBADJ); and
- distance from the stack to the center of the upwind face of the building perpendicular to the direction of flow (keyword=YBADJ).

You must provide these parameters for 36 wind directions, at increments of 10 degrees (compass bearing). Calculate these parameters using the EPA's Building Profile Input Program for PRIME (BPIPPRM). You can download the BPIPPRM model code and documentation from the EPA's [Support Center for Regulatory Atmospheric Modeling \(SCRAM\) website](#). **Table 21** gives the format guidelines for the Excel™ Building Dimensions input file, and **Table 22** shows a sample Excel™ Building Dimensions file. A sample template is provided in the HEM *Inputs* folder named *HEM5.0\_bldg\_dimensions.xlsx*.

**Table 21. Format Guidelines for the Building Dimensions File**

Field	(notes)	Type	Description
Facility ID	--	Character	An alphanumeric character string identifying the facility being modeled
Pathway	--	Character	"SO" should always be entered in this field because it represents a source pathway record, which corresponds to the code used in the AERMOD input file.
Keyword	--	Character	Specifies which values are given in this record (row), as follows: <ul style="list-style-type: none"> <li>• BUILDHGT is building height</li> <li>• BUILDWID is projected building width perpendicular to the direction of flow</li> <li>• BUILDLEN is building length in the direction of flow</li> <li>• XBADJ is along-flow distance from the stack to the upwind face of the building</li> <li>• YBADJ is across-flow distance from the stack to the upwind face of the building</li> </ul>
Source ID	--	Character	The Source ID is a unique alphanumeric character string up to 8 characters long with no spaces. It must match a Source ID in the HAP Emissions and Emissions Location file, and building downwash may only be modeled with vertical point (P), capped point (C), and horizontal point (H) source types. Note: AERMOD allows a maximum of 8 characters for the Source ID; and all Source IDs will be converted to uppercase by AERMOD.

Field	(notes)	Type	Description
Value 1	(n = 1)	Numeric	Dimension or distance (depending on the Keyword parameter) viewed from a compass bearing of 10 degrees from north (clockwise direction) of the emission release point.
Value 2	(n = 2)	Numeric	Dimension or distance of the building at a bearing of 20 degrees.
Value n	(n = 3 to 35)	Numeric	Dimension or distance of the building at a bearing of [n × 10] degrees.
Value 36	(n = 36)	Numeric	Dimension or distance of the building at a bearing of 360 degrees.

**Table 22. Sample Building Dimensions Input File**

Facility ID	Pathway	Keyword	Source ID	Value 1 (10°)	Value 2 (20°)	Value 3 (30°)	...	Value 36 (360°)
Fac1-NC	SO	BUILDHGT	SAMPLE1	26.00	26.00	26.00	...	26.00
Fac1-NC	SO	BUILDWID	SAMPLE1	111.07	107.16	100.00	...	111.60
Fac1-NC	SO	BUILDLEN	SAMPLE1	128.17	115.85	100.00	...	136.60
Fac1-NC	SO	XBADJ	SAMPLE1	-93.97	-98.48	-100.00	...	-86.60
Fac1-NC	SO	YBADJ	SAMPLE1	55.54	53.58	50.00	...	55.80

### 3.5.6. User Receptors File

If you opted to include user receptors in your Facility List Options file for one or more facilities, then HEM will prompt you for a User Receptors file. HEM will automatically calculate ambient concentrations and resultant cancer risks and noncancer hazard indices for all U.S. Census blocks or for all alternate receptors within the defined modeling domain. The User Receptors file allows you to specify additional sites for HEM to model, such as schools, ambient monitors, residential areas other than the census block's centroid, or facility boundaries.

1. Indicate the **Facility ID** associated with the user receptor in column A.
2. **Specify the location** of each User Receptor site in columns B through E, using a separate record (row) to indicate the location of each user receptor, even if associated with the same facility. You must enter locations of each user receptor using longitude and latitude, or UTM coordinates. If using UTM coordinates, you must specify the UTM zone. Base all coordinates on the WGS84 reference system.
3. Column F allows you to enter an **elevation** in meters. If you chose in your Facility List Options file to include elevations in your model run, you can enter the elevation above sea level for each user receptor or leave this field blank for HEM to estimate these elevations.
  - a. If you leave this field blank (but did choose to include elevations in your model run in your Facility List Options file), then HEM will estimate elevations based on whether you chose the online option ("Y" or blank) or the offline option ("O") in the elevation column of the Facility List Options file, as noted in Section 3.2.7.
  - b. For the online HEM elevation option, HEM will attempt to access a USGS website using the [py3DEP](#) Python library, which provides (10m resolution) elevation data for user-provided lat/lons and is available in the US only (including territories). HEM will use this service to obtain elevations for all receptors that are

missing elevations in the User Receptors input file. **Note:** If there is no internet connection available and/or the USGS server is down/not reachable, HEM will stop the run and provide a pop-up message indicating that your computer was unable to obtain elevation data for this model run. In this situation, you may attempt the run using the alternative offline elevation method (described in Section 3.2.7.2) or model the run group with no elevations as flat terrain.

- c. For the offline HEM elevation option, HEM will estimate missing elevations by interpolating from the census blocks (or alternate) receptors in the modeling domain of each facility. This interpolation method is used for all receptors that fall inside the “envelope” (convex hull) of the input data, based on the [SciPy griddata](#) method, which uses Delaunay triangulation with linear interpolation. Elevations for receptors that fall outside the convex hull of the input data are assigned the value of the nearest receptor of the input data.
4. Likewise, if you chose in your Facility List Options file to include elevations in your model run, you may provide a **hill height** in the User Receptor file in column I, or you may leave the hill height field blank for HEM to calculate these values. AERMOD uses the controlling hill height for flow calculations, as discussed in Sections 2.3.1 and 3.2.7. (USEPA, 2018)
    - a. If you leave the hill height field blank in the User Receptors file (but did choose to include elevations in your model run in your Facility List Options file), then HEM will calculate hill heights based on whether you chose the online option (“Y” or blank) or the offline option (“O”) in the elevation field (column) of the Facility List Options file, as described in Section 3.2.7.
    - b. For the online HEM elevation option, HEM will calculate hill heights using elevation data from the USGS using one of two methods to obtain 30-meter resolution USGS gridded elevation data. Under the first method, HEM obtains the necessary number of 1-degree Tagged Image File Format (TIFF) files from the USGS, then calculates the hill height for each receptor by finding the highest elevation that is above a 10% grade from the data in any of the files. Under the second method, HEM calculates hill height in the same way but obtains the elevation data using the “get\_dem” method of the py3dep Python library, which requests data from the USGS [3D Elevation Program](#). The get\_dem method (as used in HEM) requests data for a bounding box that includes all receptors plus a buffer of 62 kilometers (ten times the height of the highest peak in the US) to ensure a potential hill height is not missed. The first method of calculating hill height is typically faster and is attempted first. If that method fails for any reason (e.g., because of a server issue) then the second method is attempted. If the second method fails, then a pop-up message will appear indicating HEM could not obtain elevation data and that HEM stopped the run.
    - c. For the offline HEM elevation option, HEM will interpolate hill heights the same way it interpolates elevations described above in this section (under 3.c.).
  5. In column G, you must specify a **receptor type** indicating the type of receptor. Do not leave this field blank.
    - a. Receptor type codes of P, M, S, or B may be entered:
      - “P” represents populated-type sites like houses and other residences,
      - “M” represents ambient monitors,
      - “S” represents schools, and
      - “B” represents facility boundary sites.

- b. **Only populated type “P” user receptors are considered for sites of maximum risk or maximum TOSHI.** Type M, S, and B receptors are considered unpopulated and therefore HEM will not use M, S, or B receptors as the location of maximum risk or maximum TOSHI because these maxima are defined as populated (although the modeled concentrations for all user receptors will be provided in the concentration outputs, as described in Section 6.1).
6. In column H, you must specify the **Receptor ID** by naming your user receptors using up to 10 characters. HEM will display these names in the output files for ease of reference. Each user receptor name must be unique.
  7. In column J, you may optionally enter a **flagpole height** in meters for your user receptor, if you entered a Y in the flagpole field of the Facility List Options file. Enter the flagpole receptor height if you want HEM-AERMOD to calculate concentrations and risk at a height above ground level for the user receptor.

**Table 23** and **Table 24** give format guidelines for the User Receptors file and a sample input file, respectively. In addition, a sample template is provided in the HEM *Inputs* folder named *HEM5.0\_user\_receptors.xlsx*.

**Table 23. Format Guidelines for the User Receptors File**

Field	Type	Description
Facility ID	Character	An alphanumeric character string identifying the facility being modeled
Coordinate system	Character	Type of coordinates: L = longitude, latitude; U = UTM [WGS84]
X-coordinate	Numeric	UTM east coordinate in meters (if Coordinate System = U) or decimal longitude (if System = L). For longitudes, 5 decimal places are recommended, corresponding to 1-meter precision.
Y-coordinate	Numeric	UTM north coordinate in meters (if Coordinate System = U) or decimal latitude (if System = L). For latitudes, 5 decimal places are recommended, corresponding to 1-meter precision.
UTM zone	Numeric	If using the UTM coordinate system (U), enter the UTM Zone from 1 to 60 followed by the hemisphere (S or N). For example, 17N (default hemisphere is N if not specified). If using longitudes/latitudes, leave this cell blank.
Elevation	Numeric	Elevation of the receptor above sea level, in meters. Optional: HEM will estimate if left blank and you opted to model terrain effects (via the elevations field in the Facility List Options file).
Receptor type	Character	Type of receptor: P = populated site (e.g., house); B = facility boundary; M = monitor, S = school. This field must be filled in.
Receptor ID	Alpha-numeric	Name of receptor provided by user, containing letters and numbers, no symbols or spaces. <b>The name you provide must be 10 characters or less.</b> This name will be displayed in the outputs. This field must be filled in.
Hill Height	Numeric	Hill height scale, in meters. Optional: HEM will estimate if left blank and you are modeling terrain effects/elevations. (You may leave hill heights blank, even if you enter elevations for your user receptors in the elevation field.)
Flagpole Height	Numeric	Optional “flagpole” receptor height (m) if you want concentrations and risk at this height above ground level for the user receptor. Note: HEM will only use this field if you entered a Y in the flagpole field of the Facility List Options file. Defaults to 0 (ground level) if left blank. This field can be used with or without elevations/hill heights included in the model run.

**Table 24. Sample Input File for User Receptors**

Facility ID	Coordinate System (U=UTM, L = latitude/longitude)	X-coord. (decimal) or UTM East (m)	Y-coord. (decimal) or UTM North (m)	UTM zone	Elevation (m)	Receptor type (P, B, M, S)	Receptor ID	Hill Height (m)	Flag-pole height (m)
Fac1	L	-78.88875	35.90016		100	P	Recept1		5
Fac2	U	560005	441000	16N	244	M	Monitor1		

### 3.5.7. Emissions Variation Input Files

If you chose to model emissions variations for one or more facilities in your Facility List Options file, then HEM will prompt you for a separate Emissions Variation input file. AERMOD computes hourly concentration data based on user-supplied emission inputs. AERMOD also gives you the option of specifying variable emission rate factors or scalars for individual sources. You can base these source-specific factors on different temporal scales such as season, month, day of the week, and hour of day, or on wind speed.

For HEM to calculate temporal or wind speed emissions variations, AERMOD requires information on the type of variation and the numerical factors to use for each variation. These variation types and factors/scalars will be applied to one or more sources at each of the facilities you indicated in your Facility List Options file. You must supply this information in an Emissions Variation input file in the form of an Excel™ spreadsheet. **Note: To preserve the total tons per year (TPY) of emissions you entered for each source-HAP combination in the HAP Emissions file, the numerical factors/scalars for each source should average to one** (weighted or unweighted average, depending on the variation type). The types of variations AERMOD can apply include the following (with the HEM sample or template input file provided in parentheses, as well as the “n” number of factors):

- **SEASON** (*HEM5.0\_emisvar\_season.xlsx*): emission rates vary seasonally (n=4);
- **MONTH** (*HEM5.0\_emisvar\_month.xlsx*): emission rates vary monthly (n=12);
- **HROFDY** (*HEM5.0\_emisvar\_hrofdy\_template.xlsx*): emission rates vary by hour-of-day (n=24);
- **HRDOW** (*HEM5.0\_emisvar\_hrdow\_template.xlsx*): emission rates vary by hour-of-day, and day-of-week [M-F, Sat, Sun] (n=72);
- **SEASHR** (*HEM5.0\_emisvar\_seashr\_template.xlsx*): emission rates vary by season and hour-of-day (n=96);
- **HRDOW7** (*HEM5.0\_emisvar\_hrdow7\_template.xlsx*): emission rates vary by hour-of-day, and the seven days of the week [M, Tu, W, Th, F, Sat, Sun] (n=168);
- **SHRDOW** (*HEM5.0\_emisvar\_shrdow\_template.xlsx*): emission rates vary by season, hour-of-day, and day-of-week [M-F, Sat, Sun] (n=288);
- **SHRDOW7** (*HEM5.0\_emisvar\_shrdow7\_template.xlsx*): emission rates vary by season, hour-of-day, and the seven days of the week [M, Tu, W, Th, F, Sat, Sun] (n=672);
- **MHRDOW** (*HEM5.0\_emisvar\_mhrdow\_template.xlsx*): emission rates vary by month, hour-of-day, and day-of-week [M-F, Sat, Sun] (n=864);

- **MHRDOW7** (*HEM5.0\_emisvar\_mhrdow7\_template.xlsx*): - emission rates vary by month, hour-of-day, and the seven days of the week [M, Tu, W, Th, F, Sat, Sun] (n=2,016); and
- **WSPEED** (*HEM5.0\_emisvar\_wspeerd.xlsx*): emission rates vary by wind speed (n=6).
  - The 6 factors are applied to the wind speed categories used by AERMOD that have the following default upper bound speeds in m/s of 1.54, 3.09, 5.14, 8.23, 10.8 and no upper bound.
  - WSPEED is designed to be used for sources where the emission rate depends on wind speed, such as dust emissions from tilled fields or storage piles. **Note:** You will not know the annual emission rate for these sources in advance without analyzing the distribution of hourly wind speeds in the meteorological file. But WSPEED can nonetheless be used without analyzing the meteorological data in advance by calculating the average emissions using just one of the wind speed categories. These average emissions will then represent a baseline that can be used in the HAP Emissions input file (as a stand-in for the annual emission rate). Use a factor of 1.0 for this category in the WSPEED input file and then calculate the factor/scalars for the other wind speed categories in relation to this baseline category.

**Note:** The emissions variation input files that have 24 or more factors, listed above with “template” in their file name, provide instructions for entering your own values before using them in a model run; they are not run-ready as-is. Variation types based on the type of the day-of-the-week (weekday or weekend) – including HRDOW, SHRDOW, and MHRDOW – lend themselves to the use of weighted averages when constructing factors, based on five weekdays and two weekend days. Again, to use the temporal emission variations listed above and not alter your total TPY (entered for each source-HAP combination in the HAP Emissions file), check to ensure the numerical factors you assign for each source in the Emissions Variation input file – whether weighted or unweighted – average to one before initiating your HEM run.

HEM expects a maximum of 12 factor columns across these Emissions Variation input spreadsheets (for a total of 15 columns, including the Facility ID, Source ID and Variation keyword). It should also be noted that although the types of emission variations described above and the samples provided below are for a single type of emissions variation, you can also choose to use different variation types for different sources and/or facilities, within the same input file. The only limitation is that **each source can have only a single type of variation applied in a model run**. A template containing multiple emissions variations in one file is also provided in the HEM *Inputs* folder (*HEM\_emisvar\_multiple\_variations\_template.xlsx*). Refer to the AERMOD User’s Guide (USEPA, 2024e) for more detailed information regarding the temporal and wind speed factors available for varying source-specific emissions.

**Table 25** provides the format guidelines for the Emissions Variation input files. **Table 26**, **Table 27**, and **Table 28** provide sample Emissions Variation input files for a sample of the variations AERMOD can accommodate including: hour of day emission variations (24 factors), monthly emission variations (12 factors), and both season and hour of day emission variations (96 factors), respectively. **Table 29** provides a sample input file for varying source-specific emissions by wind speed.

**Table 25. Format Guidelines for the Emissions Variation Input Files**

Field	Type	Description
Facility ID	Character	An alphanumeric character string identifying the facility being modeled
Source ID	Character	The Source ID is a unique alphanumeric character string up to 8 characters long with no spaces. It must match a Source ID in the HAP Emissions and Emissions Location file. Note: AERMOD allows a maximum of 8 characters for the Source ID; and all Source IDs will be converted to uppercase by AERMOD.
Variation *	Character	Type of variable emission rates being used (SEASON, MONTH, HROFDY, HRDOW, SEASHR, HRDOW7, SHRDOW, SHRDOW7, MHRDOW, MHRDOW7 or WSPEED).*
Factor 1	Character	First factor (scalar) to be applied to emission rate.
Factor 2	Character	Second factor (scalar) to be applied to emission rate.
Factor 3	Character	Third factor (scalar) to be applied to emission rate.
...	...	...
Factor n	Character	nth factor (scalar) to be applied to emission rate.

\* Each emission variation type has a set number of “n” factors (or scalars). The number of factors is as follows: SEASON=4, MONTH=12, HROFDY=24, HRDOW=72, SEASHR=96, HRDOW7=168, SHRDOW=288, SHRDOW7=672, MHRDOW=864, MHRDOW7=2,016, WSPEED=6. Refer to HEM’s template input files for examples and the AERMOD User’s Guide for additional information. **Note:** Running AERMOD does not require the emissions variation factors for a given source to average to one. But **when modeling with HEM-AERMOD, to maintain the total user-provided tons per year of emissions indicated in the HAP Emissions input file, the numerical factors for the temporally based variations must average to one (weighted or unweighted, depending on the variation). Otherwise, these numerical factors would change the total emissions modeled, and not merely distribute that total temporally.** (Refer also to WSPEED variation discussion.)

**Table 26. Sample Emissions Variation File based on Hour of Day (24 factors)**

Facility ID	Source ID	Variation	Hour factor 1,13	Hour factor 2,14	Hour factor 3,15	Hour factor 4,16	Hour factor 5,17	Hour factor 6,18	...	Hour factor 12,24
Fac1	SAMPLE1	HROFDY	(1): 0.2138	(2): 0.1433	(3): 1.2928	(4): 0.098	(5): 0.1342	(6): 0.3301	...	(12): 1.4356
Fac1	SAMPLE1	HROFDY	(13): 1.3959	(14): 1.2728	(15): 0.1079	(16): 1.5255	(17): 1.5255	(18): 1.5519	...	(24): 1.799

**Table 27. Sample Emissions Variation File based on Month (12 factors)**

Facility ID	Source ID	Variation	JAN	FEB	MAR	APR	MAY	JUN	...	DEC
Fac1	SAMPLE 1	MONTH	0.2138	0.1433	1.2928	0.098	0.1342	0.3301	...	1.4356

**Table 28. Sample Emissions Variation File based on Season and Hour of Day (96 factors)**

Facility ID	Source ID	Variation	Season-hour Factor 1,13	Season-hour Factor 2,14	Season-hour Factor 3,15	Season-hour Factor 4,16	Season-hour Factor 5,17	Season-hour Factor 6,18	...	Season-hour Factor 12,24
Fac1	SAMPLE 1	SEASHR	Winter 1: 0.2138	Winter 2: 0.1433	Winter 3: 1.2928	Winter 4: 0.098	Winter 5: 0.1342	Winter 6: 0.3301	...	Winter 12: 1.4356
Fac1	SAMPLE 1	SEASHR	Winter 13: 1.3959	Winter 14: 1.2728	Winter 15: 0.1079	Winter 16: 1.5255	Winter 17: 1.5255	Winter 18: 1.5519	...	Winter 24: 1.799
Fac1	SAMPLE 1	SEASHR	Spring 1: 1.9045	Spring 2: 1.9475	Spring 3: 1.4684	Spring 4: 1.0435	Spring 5: 0.8305	Spring 6: 0.6952	...	Spring 12: 0.3979
Fac1	SAMPLE 1	SEASHR	Spring 13: 0.2138	Spring 14: 0.1433	Spring 15: 1.2928	Spring 16: 0.098	Spring 17: 0.1342	Spring 18: 0.3301	...	Spring 24: 1.4356

Facility ID	Source ID	Variation	Season-hour Factor 1,13	Season-hour Factor 2,14	Season-hour Factor 3,15	Season-hour Factor 4,16	Season-hour Factor 5,17	Season-hour Factor 6,18	...	Season-hour Factor 12,24
Fac1	SAMPLE 1	SEASHR	Summer 1: 1.3959	Summer 2: 1.2728	Summer 3: 0.1079	Summer 4: 1.5255	Summer 5: 1.5255	Summer 6: 1.5519	...	Summer 12: 1.799
Fac1	SAMPLE 1	SEASHR	Summer 13: 1.9045	Summer 14: 1.9475	Summer 15: 1.4684	Summer 16: 1.0435	Summer 17: 0.8305	Summer 18: 0.6952	...	Summer 24: 0.3979
Fac1	SAMPLE 1	SEASHR	Fall 1: 0.2138	Fall 2: 0.1433	Fall 3: 1.2928	Fall 4: 0.098	Fall 5: 0.1342	Fall 6: 0.3301	...	Fall 12: 1.4356
Fac1	SAMPLE 1	SEASHR	Fall 13: 0.2138	Fall 14: 0.1433	Fall 15: 1.2928	Fall 16: 0.098	Fall 17: 0.1342	Fall 18: 0.3301	...	Fall 24: 1.4356

**Table 29. Sample Emissions Variation File based on Wind Speed (6 factors)**

Facility ID	Source ID	Variation*	Cat. 1	Cat. 2	Cat. 3	Cat. 4	Cat. 5	Cat. 6
Fac1	SAMPLE1	WSPEED	0.50	1.25	1.50	1.25	0.75	0.75

Table 29 Note: See discussion above regarding the WSPEED variation. If you know and are using the actual annual emission rate for this source (e.g., storage piles), then these six factors should average to 1.0 for HEM runs. Alternatively, when the annual emission rate is not known, use the method described above that employs factors relative to a baseline.

### 3.5.8. Alternate Receptors File

As noted previously, HEM can model based on U.S. Census blocks or based on alternate receptors you provide. If you check “Use alternate receptors” on the first user interface requiring inputs (discussed below in Section 4.1), then HEM will prompt you for an Alternate Receptor file, in lieu of using U.S. Census blocks for the model run. This allows you to model with HEM anywhere in the world, both within the U.S and outside the U.S.

The Alternate Receptor file must be a CSV file and provide HEM with a list of receptor locations, the type of each receptor (populated “P” or various types of unpopulated receptors, such as boundary “B” and monitor “M” receptors), and the populations represented by each receptor. It is important to note that only populated “P” receptors are chosen by HEM to be the sites of maximum risk or hazard index; and only “P” receptors are used by HEM in cancer incidence calculations. This is discussed further below in Sections 5 and 6. **Note: For HEM to run using alternate receptors, you must provide population values for every Alternate Receptor of type “P”. The population you provide may be any integer value, 0 or greater.** Even if only one populated Alternate Receptor is missing a value in its population field, HEM will not commence the modeling run.

In addition, if you chose in your Facility List Options file to include elevations in your model run, then you must also provide HEM the elevation above sea level for each alternate receptor, as well as the hill height of each receptor. To model terrain effects, the alternate receptor file must be filled-in completely for every elevation and hill height. **Any blanks in the elevation fields or hill height fields of the Alternate Receptors file will cause AERMOD to be run in the FLAT mode with no terrain effects.**

AERMOD uses the controlling hill height for flow calculations. Controlling hill height is defined as the highest elevation that is above a 10% grade from the receptor. For more information on the use and suggested calculation of controlling hill heights using an algorithm in AERMAP, the AERMOD terrain processor (USEPA, 2018), refer to Sections 2.3.1 and 3.2.7. It is important to again note that if you leave any hill height field blank in the Alternate Receptors file, then AERMOD will be run in the FLAT mode with no terrain effects (even if you opt to include

elevations in your model run in your Facility List Options file and also provide elevations for your alternate receptors). You can also opt to model with the elevation option turned off in your Facility List Options file. In such a modeling run, you do not need to provide any elevations or hill heights in the Alternate Receptor file, as HEM will model everything on a flat plane.

**Table 30** and **Table 31** give format guidelines for the Alternate Receptors file and a sample input file, respectively. In addition, a sample template is provided in the HEM *Inputs* folder named *HEM5.0\_alternate\_receptors.csv*.

**Table 30. Format Guidelines for Alternate Receptors File (CSV)**

Field	Type	Sample Value	Description
Receptor ID	Alpha-numeric	1	A unique number identifying the Receptor. The prefix "ALT" will be added to your receptor ID to help identify these receptors in the output files.
Type of receptor	Character	P	Type of receptor: P = populated (e.g., house), B = boundary, M = monitor
Coordinate system	Character	L	Type of coordinates: L = longitude, latitude; U = UTM [WGS84]
X-coordinate	Numeric	-52.74629	UTM east coordinate in meters (if Coordinate System = U) or decimal longitude (if System = L). 5 decimal places are recommended for longitude, corresponding to 1 meter
Y-coordinate	Numeric	47.53796	UTM north coordinate in meters (if Coordinate System = U) or decimal latitude (if System = L). 5 decimal places are recommended for latitude, corresponding to 1 meter
UTM zone with hemisphere	Character	17N	UTM zone where the receptor is located if Coordinate System = U
Elevation	Numeric	219.7	Elevation of the receptor above sea level in meters. Required if you are modeling terrain effects (i.e., choose to model elevations in the Facility List Options file)
Hill Height	Numeric	219.7	Hill height scale in meters. Required if you are modeling terrain effects (i.e., choose to model elevations in the Facility List Options file)
Population	Numeric	45	Population represented by the alternate receptor; required by HEM for every "P" type alternate receptor for incidence calculations.

**Table 31. Sample Input File for Alternate Receptor Input File**

Receptor ID	Type of Receptor (P, B, M)	Coordinate System (U = UTM L = latitude, longitude)	X-coordinate: Longitude (decimal) or UTM East (m)	Y-coordinate: Latitude (decimal) or UTM North (m)	UTM zone with hemisphere	Elevation (m)	Hill Height (m)	Population
1	B	L	-52.74629	47.53880		219.7	219.7	0
2	P	L	-52.74685	47.54225		219.3	219.3	5
3	P	L	-52.74817	47.53796		220.6	220.6	25
4	P	L	-52.74760	47.53683		262.7	262.7	7
5	M	L	-52.75023	47.53795		263.4	263.4	0
6	P	L	-52.74708	47.53599		292.1	292.1	45
n	...	...	...	...	...	...	...	...

### 3.5.9. Census Update File

HEM provides you the option to change the U.S. Census file used for your modeling runs, as described in Section 4.8. Changes are not applied directly to the Census file located in your HEM Census directory. Instead, all changes are reflected in a new file named *census2020-updated.csv* that is located in your HEM Census directory. **To use this changed Census file in HEM, rename or delete the original census2020.csv file and change the name of census2020-updated.csv to census2020.csv.** Note: The official U.S. Census database is available on EPA's [HEM webpage](#), if you need to download another copy of it.

With the Census Update file, you can:

- 1) Zero-out the population of a specific U.S. Census block,
- 2) Move a block to a new latitude and longitude location,
- 3) Delete a U.S. Census block, and
- 4) Add a unique receptor to the Census.

You may wish to **Zero**-out the population of the block if it is clear no residences are present in the block. This change will keep the block in the dataset, so concentrations and risks are modeled, but this receptor will not impact incidence.

You may wish to **Move** a block to different coordinates that better represent the population.

You may wish to **Delete** or remove a block from the dataset; for example, because there are no people living in the block and you do not need concentrations and risks modeled at this location.

You may wish to **Add** a unique receptor to the Census to obtain concentration and risk at this location (e.g., at a facility fence line) or to represent populations not well represented by the current U.S. Census block centroids. You can include a population for your added receptor, as well as specify the elevation and hill height. **Note:** The population, elevation, and hill height fields are for Added blocks only. Although these fields are “optional” and leaving them blank will not cause an error in HEM, if you leave these fields blank, HEM will assign a population of 0, an elevation of 0 meters, and a hill height of 0 meters for your added block. Therefore, if you are running HEM with elevations (either online or offline, as described in Section 3.2.7.), you should enter an elevation and hill height to avoid erroneous modeling results based on a 0 elevation and hill height.

**Table 32** and **Table 33** give format guidelines for the Census Update file and a sample update file, respectively. In addition, a sample template is provided in the HEM *Inputs* folder named *HEM5.0\_Census\_block\_update\_template.xlsx*.

**Table 32. Format Guidelines for the Census Update File**

Field	Type	Sample Value	Description
Change	Character	Move	The potential changes include: Zero, Move, Delete, and Add
Facility ID	Character	Fac2	Optional, can be left blank. You may wish to use it outside of HEM to track the source of changes.
Run Group	Character	Landfills	Optional, can be left blank. You may wish to use it outside of HEM to track the source of changes.

Field	Type	Sample Value	Description
Block ID	Character	170010001001003	Enter the 15-digit U.S. Census block ID as text characters rather than numerals, because some block IDs have leading zeroes.
Latitude	Numeric	39.96789	If the Change is a "Move" or "Add", enter the Latitude (decimal) of where the block should be moved or added. 5 decimal places are recommended, corresponding to 1-meter precision. You can leave this field blank for "Zero" and "Delete" changes.
Longitude	Numeric	-91.37989	If the Change is a "Move" or "Add", enter the Longitude (decimal) of where the block should be moved or added. 5 decimal places are recommended, corresponding to 1-meter precision. You can leave this field blank for "Zero" and "Delete" changes.
Population	Numeric	325	Optional for an "Add" change. Enter the population for added block receptor. A blank is interpreted as 0.
Elevation	Numeric	94	Optional for an "Add" change. Enter the elevation (in meters) above sea level for added block receptor. A blank is interpreted as an elevation of 0 meters.
Hill Height	Numeric	94	Optional for an "Add" change. Enter the hill height scale ( $\geq$ elevation, in meters) for added block receptor. A blank is interpreted as a hill height of 0 meters.

Table 32 Note: This input file will be used to permanently change your copy of the U.S. Census file used by HEM.

**Table 33. Sample Census Update File**

Change	Fac ID	Run Group	Block ID	Latitude	Longitude	Pop.	Elevation	Hill Height
Zero	Fac1	SWL	170318185003007					
Move	Fac1	SWL	170317404003007	41.69741	-87.72994			
Delete	Fac1	SWL	170318185001033					
Zero	Fac2	SWL	370010203022009					
Move	Fac2	SWL	370010203021013	36.34567	-79.45678			
Delete	Fac2	SWL	370010203021016					
Add	Fac2	SWL	RCPT1	35.90016	-78.88875	325	94	94

### 3.5.10. Updating the Toxicity Value Files

As discussed in Section 2.2.1, the Toxicity Value Files Library contains chemical health effects data, including dose response toxicity values. You can make changes to the Toxicity Value Files Library by editing the Excel™ files that comprise the library: the *Dose\_Response\_Library.xlsx* and *Target\_Organ\_Endpoints.xlsx* spreadsheets. These files are located in HEM's *resources* folder. You can add new pollutants to these files or edit the values for the chemicals already in the files.

Follow these guidelines when adding new pollutants to these files:

- **When adding new chemical names to the Dose Response Library file, use the same spelling as used in your HAP emissions input file.**
- The Chemical Abstracts Service (CAS) number field in the Dose Response Library is optional.
- If you do not specify a cancer URE for a new pollutant, then the URE will be assumed to be 0 (zero) and cancer risks will not be evaluated for that pollutant. Similarly, if you do not specify a noncancer chronic RfC or acute benchmark for a new pollutant, HEM will not calculate adverse noncancer chronic or acute health effects, respectively.
- **If you do indicate a noncancer chronic RfC in the Dose Response Library file for a pollutant you add, to assess noncancer health hazards you must also enter the pollutant in the Target Organ Endpoints file and indicate what organs or organ systems may be impacted.**

Before initiating a HEM run, to ensure you have the most recent file versions, you should again check EPA's [HEM Download webpage](#) for the date listed next to the "Toxicity Value Files" link. EPA regularly updates these files. If EPA's update is more recent than the dates shown for the files in HEM's *resources* folder, then you may want to download the newer files and replace your outdated Dose Response Library and/or Target Organ Endpoints files (unless you are purposefully modeling with older dose response values and endpoints). You may also manually modify the files in your HEM's *resources* folder based on updated values (e.g., for the URE, RfC or acute benchmark(s)). For additional information visit EPA's [Dose-Response Assessment for Assessing Health Risks Associated With Exposure to Hazardous Air Pollutants](#) webpage (USEPA, 2024f).

### 3.6. User-Supplied Concentration File

HEM lets you bypass the running of AERMOD and instead provide a file of pollutant concentrations for a gridded or random set of geographic locations. HEM will interpolate from those locations to the census block centroids or to alternate receptors, depending on which set of receptors you direct HEM to use (via the HEM user interface discussed in Section 4.1). HEM will process the interpolated air concentrations in the same way as concentrations generated by AERMOD to estimate cancer risks and noncancer health hazard indices due to inhalation exposure.

To perform the interpolation, HEM uses the [griddata](#) (linear) method of the [SciPy](#) Python library. This method creates Delaunay triangles with the user's set of geographic locations as vertices and linearly interpolates using the values at the triangle vertices to estimate values for any census blocks (or alternate receptors) inside each triangle. All census blocks (or alternate receptors) that are within the convex hull of the user's set of geographic locations will be included in the interpolation.

**Table 34** and **Table 35** provide format guidelines for the User-Supplied Concentrations file and a sample file, respectively. In addition, two sample templates are provided in the HEM *Inputs* folder named *HEM5.0\_User\_Conc\_template\_no\_acute.csv* and *HEM5.0\_User\_Conc\_template\_w\_acute.csv*. **Note:** The User-Supplied Concentrations input file must include an Acute column, although you may leave the values in this column blank (or enter 0's), if you do not have acute concentrations to provide.

**Table 34. Format Guidelines for the User-Supplied Concentrations File**

Field	Type	Description
Receptor ID	Alpha-numeric	Name of receptor provided by user containing letters and numbers, no symbols or spaces. This name will be displayed in the outputs with the prefix "UCONC". This field is required.
Longitude (decimal)	Numeric	Decimal longitude. Five decimal places are recommended, corresponding to 1-meter precision.
Latitude (decimal)	Numeric	Decimal latitude. Five decimal places are recommended, corresponding to 1-meter precision.
Pollutant	Character	The pollutant name must correspond exactly to one of the chemical names listed in the dose response library. (see <i>Dose_Response_Library.xlsx</i> in the <i>resources</i> folder)
Conc (µg/m <sup>3</sup> )	Numeric	Chronic air concentration in µg/m <sup>3</sup>
Acute Conc (µg/m <sup>3</sup> )	Numeric	Acute (short-term) air concentration in µg/m <sup>3</sup>

**Table 35. Sample User-Supplied Concentrations File**

Receptor ID	Longitude	Latitude	Pollutant	Conc (ug/m <sup>3</sup> )	Acute Conc (ug/m <sup>3</sup> )
sect1ring1	-78.8844	35.90762	1,3-butadiene	0.011654	0.116537
sect1ring1	-78.8844	35.90762	2,3,4,6,7,8-hexachlorodibenzofuran	3.00E-10	3E-09
sect1ring1	-78.8844	35.90762	2,3,4,7,8-pentachlorodibenzofuran	8.00E-10	8E-09
sect1ring1	-78.8844	35.90762	2,3,7,8-tetrachlorodibenzofuran	2.40E-09	2.4E-08
sect1ring1	-78.8844	35.90762	2,3,7,8-tetrachlorodibenzo-p-dioxin	1.00E-10	1E-09
sect1ring1	-78.8844	35.90762	acetaldehyde	0.005543	0.055427
sect1ring1	-78.8844	35.90762	acrolein	0.038799	0.387986
sect1ring1	-78.8844	35.90762	arsenic compounds	0.077653	0.776531
sect1ring1	-78.8844	35.90762	benz[a]anthracene	6.35E-07	6.35E-06
sect1ring1	-78.8844	35.90762	benzene	0.005438	0.054384
sect2ring1	...	...	...	...	...
...	...	...	...	...	...

## 4. Step-by-Step Instructions for Running HEM

- 1) **Prepare input files.** Before you initiate a HEM modeling run<sup>6</sup>, you should ensure you have the necessary user-provided input files prepared for your specific modeling needs.
  - a. Section 3 provides detailed descriptions of all HEM input files, and sample templates for each are provided in the HEM *Inputs* folder. **Table 36** lists these template files and when (i.e., for what kind of HEM run) each file is needed.

**Table 36. Summary of User-Provided HEM Input Files**

Sample Input File Name	Description	When Needed
HEM5.0_Fac_List_Options.xlsx	Facility List Options: Provides modeling options for each facility	Every run using AERMOD
HEM5.0_HAP_Emiss.xlsx	HAP Emissions: Provides emission rates for each HAP	Every run using AERMOD
HEM5.0_Emiss_Loc.xlsx	Emissions Location: Provides source types and locations	Every run using AERMOD
HEM5.0_alternate_receptors.csv	Alternate Receptors file	Required if modeling with alternate receptors (whether outside or inside the U.S.) instead of census block receptors
HEM5.0_user_receptors.xlsx	User Receptor file	Required if the user receptor column in the FacList file has a "Y" for any facility
HEM5.0_buoyant_line_parameter.xlsx	Buoyant Line Source Parameter file	Required if a source in the EmissLoc file is a buoyant line
HEM5.0_polygon_vertex.xlsx	Polygon Vertex file	Required if a source in the EmissLoc file is a polygon
HEM5.0_bldg_dimensions.xlsx	Building Dimensions file	Required if the building downwash column in the FacList has a "Y" for any facility
HEM5.0_particle_data.xlsx	Particle Data file containing particle size distribution of emissions per source	Required if the deposition OR depletion column has a "Y" AND Pdep OR Pdepl column in FacList indicates type, AND if Method 1 (the default) is indicated in the EmissLoc file. (HAP_Emiss file must also contain particulates)
HEM5.0_landuse.xlsx	Land use file describing land surrounding emissions source	Required if the deposition OR depletion column has a "Y" AND Vdep OR Vdepl column in FacList indicates DO or WD. (HAP_Emiss file must also contain gases/vapor)
HEM5.0_month-to-seasons.xlsx	Month-to-Season file describing monthly stage of vegetation surrounding emissions source	Required if the deposition OR depletion column has a "Y" AND Vdep OR Vdepl column in FacList indicates DO or WD. (HAP_Emiss file must also contain gases/vapor)
HEM5.0_emisvar_season.xlsx	Emissions Variation file	Required if the Emissions Variation column in FacList has a "Y" and seasonal variations are desired (4 factors)
HEM5.0_emisvar_month.xlsx	Emissions Variation file	Required if the Emissions Variation column in FacList has a "Y" and monthly variations are desired (12 factors)

<sup>6</sup> Note: **It is advisable to close and re-start HEM between modeling runs**, which clears memory for each new run and avoids potential issues by ensuring a full reset.

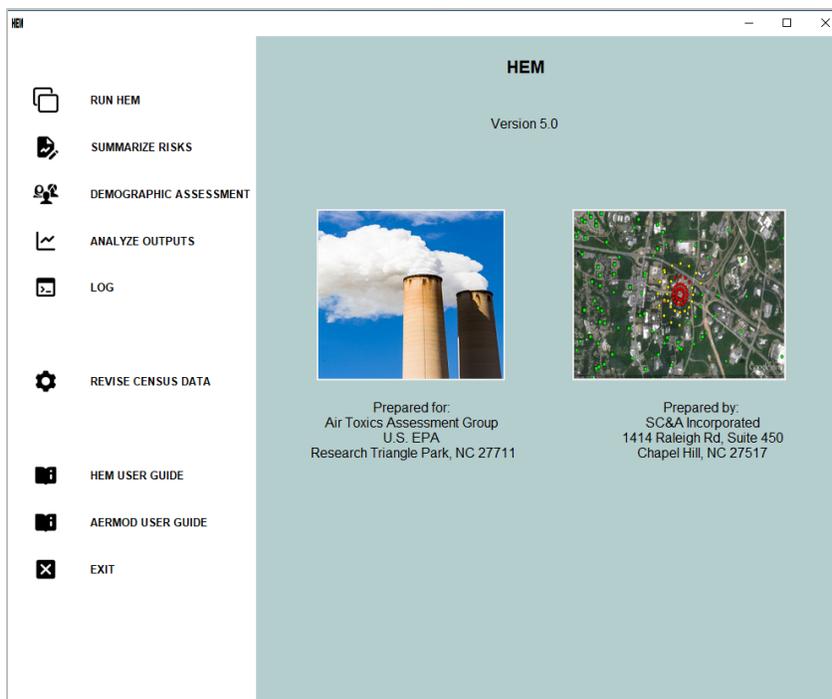
Sample Input File Name	Description	When Needed
HEM5.0_emisvar_hrofdy_template.xlsx	Emissions Variation file	Required if the Emissions Variation column in FacList has a "Y" and hour-of-day variations are desired (24 factors)
HEM5.0_emisvar_hrdow_template.xlsx	Emissions Variation file	Required if the Emissions Variation column in FacList has a "Y" and hour-of-day + type-of-day (M-F, Sat, Sun) variations are desired (72 factors)
HEM5.0_emisvar_seashr_template.xlsx	Emissions Variation file	Required if the Emissions Variation column in FacList has a "Y" and season + hour-of-day variations are desired (96 factors)
HEM5.0_emisvar_hrdow7_template.xlsx	Emissions Variation file	Required if the Emissions Variation column in FacList has a "Y" and hour-of-day + day-of-week (7) variations are desired (168 factors)
HEM5.0_emisvar_shrdow_template.xlsx	Emissions Variation file	Required if the Emissions Variation column in FacList has a "Y" and season + hour of day + type-of-day (weekday, Sat, Sun) variations are desired (288 factors)
HEM5.0_emisvar_shrdow7_template.xlsx	Emissions Variation file	Required if the Emissions Variation column in FacList has a "Y" and season + hour-of-day + day-of-week (7) variations are desired (672 factors)
HEM5.0_emisvar_mhrdow_template.xlsx	Emissions Variation file	Required if the Emissions Variation column in FacList has a "Y" and month + hour-of-day + type-of-day (weekday, Sat, Sun) variations are desired (864 factors)
HEM5.0_emisvar_mhrdow7_template.xlsx	Emissions Variation file	Required if the Emissions Variation column in FacList has a "Y" and month + hour-of-day + day-of-week (7) variations are desired (2,016 factors)
HEM5.0_emisvar_wspped.xlsx	Emissions Variation file	Required if the Emissions Variation column in FacList has a "Y" and wind speed (m/s) variations are desired (6 factors)
HEM5.0_emisvar_multiple_variations_template.xlsx	Emissions Variation file	Required if the Emissions Variation column in FacList has a "Y" and different variations are desired for different sources
HEM5.0_Census_block_update_template.xlsx	Census Update file	Required only if you want to change your Census file prior to the HEM run
HEM5.0_User_Conc_template_no_acute and HEM5.0_User_Conc_template_w_acute	User-Supplied Concentration files	Required if modeling risk based on user-supplied pollutant concentrations. <b>Note:</b> AERMOD will not be run.

- 2) **Ensure your HEM5 model and HEM-provided databases are up to date.** In addition to the files that you must provide, a HEM run also requires its internal databases, including the U.S. Census files (if not using alternate receptors), meteorological files, and the files located in HEM's *resources* folder. These resource files include:
- the *Dose\_Response\_Library.xlsx* file,
  - the *Target\_Organ\_Endpoints.xlsx* file,
  - the *metlib\_aermod.xlsx* (part of HEM's meteorological database),
  - the *Gas\_Param.xlsx* file (for vapor deposition/depletion),
  - the *Pollutant\_CrossWalk.xlsx* file (for multipathway summaries),
  - the *acs.csv* and *acs\_defaults.csv* files (for demographic analyses), and
  - various *png* file types (for graphing applications).

To ensure you have the most recent HEM5 model, U.S. Census files, meteorological files, and toxicity value files, you should check EPA's [HEM Download webpage](#) for updates. EPA updates these files periodically, including to fix bugs in HEM.

- If EPA's HEM5 date is more recent than the HEM5 timestamp on your computer, then download the newer model from EPA's HEM Download webpage.
  - If the toxicity value (chemical health effect) files on the HEM Download webpage are more recent than the ones currently in your HEM's *resources* folder (i.e., Dose Response Library file and Target Organ Endpoints file), then consider replacing the files in your subfolder with the ones you download.
  - Likewise, check the timestamp and consider updating your U.S. Census files (in HEM's "census" subfolder) and the meteorological file (in HEM's "aermod" subfolder), if the dates of these files on the HEM Download webpage are more recent.
- 3) **Start HEM** by using Windows File Explorer™ to navigate to the folder where HEM was unzipped and double click on the HEM executable file (HEM5.0.exe). The HEM title screen will be displayed, as shown in **Figure 3**.
- a. The **HEM USER GUIDE** and the **AERMOD USER GUIDE** buttons on the (left) sidebar menu bar will take you to a HEM webpage linking to this [HEM user guide](#) and directly to the [AERMOD's user guide](#), respectively. Access them whenever you need further instruction and explanation regarding the inputs or outputs of HEM, or when troubleshooting a modeling run issue.

**Figure 3. HEM Title Screen**

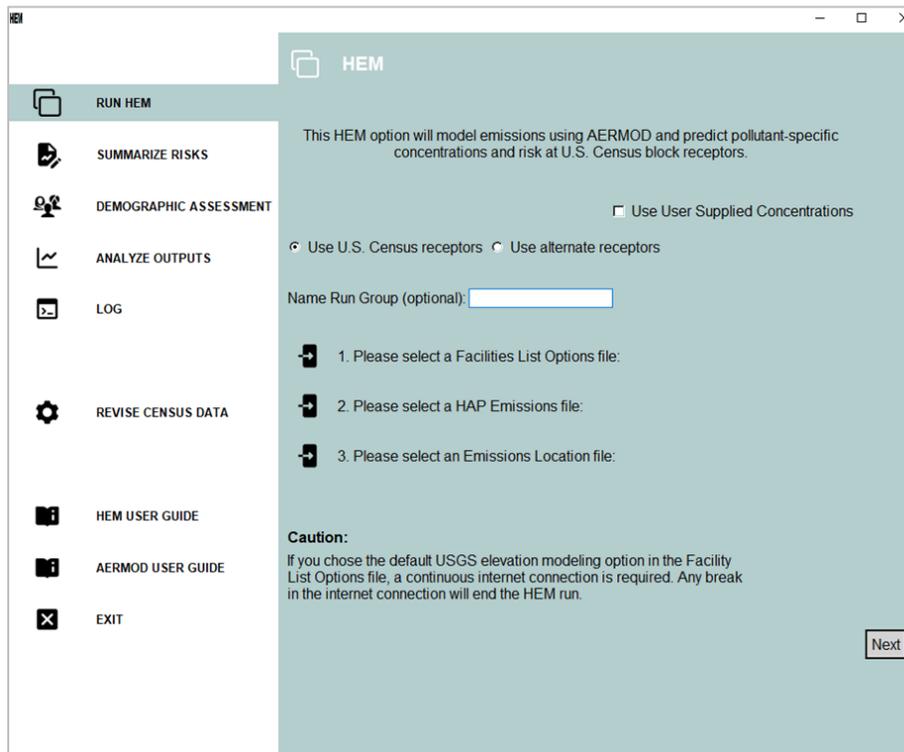


- 4) **Click the *RUN HEM*** button, located on the (left) sidebar menu, to proceed to the next screen, from which you can initiate a model run.
- a. To stop the HEM application on any screen, click the **EXIT** button and close the black DOS window (which may remain open after exiting, on some computers).

## 4.1. Indicate Run Type and Receptors and Provide Input Files

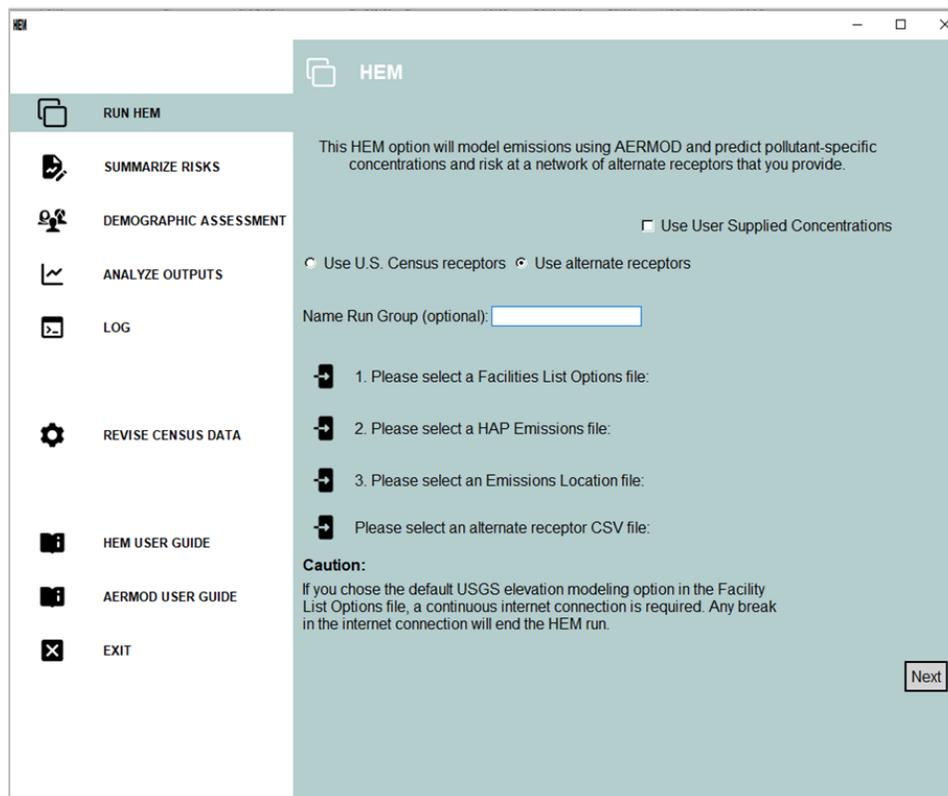
- 1) On the initial input screen (***RUN HEM***) shown below in **Figure 4**, you should first **indicate whether you will using your own file of user-supplied concentrations (and skipping the AERMOD run) or running AERMOD**, which is the default. If using your own file of user-supplied concentrations, check the box to change from the default.
  - a. Whether you are running AERMOD or skipping AERMOD and using your own user-supplied concentrations, you must choose to use either U.S. Census receptors or alternate receptors for your HEM run.
  - b. HEM-AERMOD runs within the U.S. can use U.S. Census or alternate receptors.
  - c. HEM-AERMOD runs outside the U.S. must use alternate receptors.
  - d. User-supplied concentration (non-AERMOD) HEM runs require you to provide [user-supplied concentrations](#) in a CSV file. If you choose to use alternate receptors, you must also provide an alternate receptor CSV file via this first screen. No further inputs are required for this option. You can skip to [Section 6.3](#) regarding the HEM risk results produced using user-supplied concentrations.
- 2) **Click on each input selection button** to browse your computer for the required file. Every HEM-AERMOD run requires the three input files described in Sections 3.2, 3.3 and 3.4: the [Facility List Options](#), [HAP Emissions](#), and [Emissions Location](#) files.
  - a. Depending on the size of your input files, it may take HEM several minutes to load them. Wait until the interface indicates each file has loaded before attempting to load the next input file.
  - b. **Note:** If you chose the default USGS elevation modeling option in your Facility List Options file (described in [Section 3.2.7.1](#)) a continuous internet connection is required. Any break in the internet connection will end the HEM run.

**Figure 4. Run HEM with U.S. Census Receptors**



- 3) If you choose to use alternate receptors in your HEM run, then an additional input selection button will appear that requires you to browse for and select an alternate receptor CSV file.
  - a. Note: It may take several minutes for your Alternate Receptor file to upload for modeling. Do not click the Next button until it has uploaded.
  - b. The [Alternate Receptors file](#) is described in Section 3.5.8.
  - c. For a HEM-AERMOD run using alternate receptors, you must also browse for and select the Facility List Options, HAP Emissions, and Emissions Location input files, as shown in **Figure 5**.

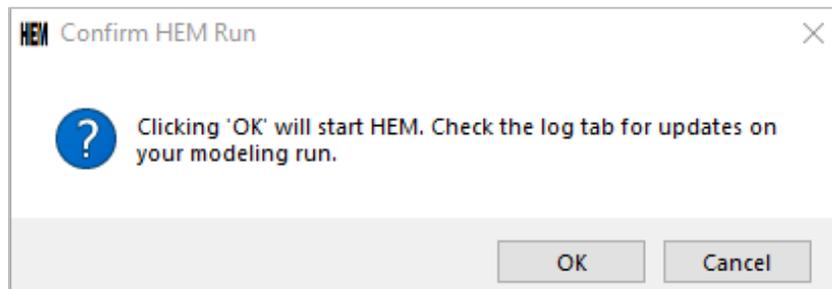
**Figure 5. Run HEM with Alternate Receptors**



- 4) For either type of run, you can (optionally) enter a run group name in the **Name Run Group** box provided.
  - a. This is recommended because the name will be used to identify the subfolder containing the results of your run, located within HEM’s main *output* folder, and will be helpful in identifying which outputs HEM’s post-modeling tools should summarize, demographically assess, and/or view graphically and analyze (discussed in Sections 4.5, 4.6, and 4.7, respectively).
  - b. The name you enter in the “Name Run Group” box will also be prepended to the output files containing the results for the run as a whole.
  - c. Do not enter a name of a subfolder that already exists in the output folder from a previous run. Output files that share identical files names will be replaced by the most current model run.

- d. Do not press the Enter button on your keyboard as part of the run group name, because that will cause a Windows® error.
  - e. If you do not enter a run group name, the model will autogenerate a name for the run group output folder that includes a date and timestamp (e.g., `rungroup_2025_02_21_10_45_01`).
- 5) **Click *Next*** on the screen to continue, after you have indicated what type of receptors should be used for the modeling run and entered the required input files on the initial screen.
- a. If additional input files are required, one or two additional screens will appear after you click the Next button. These additional input files and screens are discussed in more detail in Sections 4.2 and 4.3 below.
  - b. If no additional input files are needed, then a pop-up box will appear asking you to confirm the start of the HEM run, as shown below in **Figure 6**.

**Figure 6. Confirm HEM Run Pop-Up Start Box**



- 6) **Click 'OK' in this box to initiate the HEM run**, and a log of the modeling progress will appear as shown and described in Section 4.4. Click *Cancel* if you need to cancel the model run and/or change any input files already entered.

## 4.2. Provide Additional Input Files

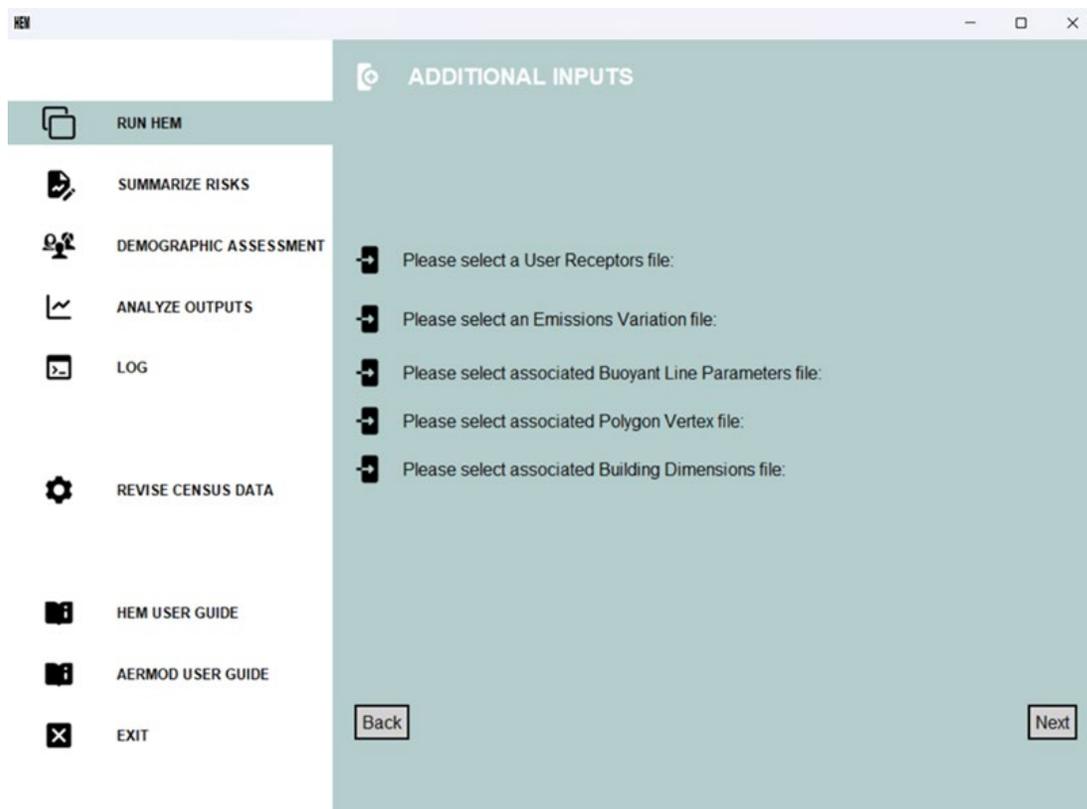
If additional input files are required, one of two supplementary screens will appear next. Depending on the requirements of your HEM-AERMOD run, an example of one of the screens that may appear is shown in **Figure 7**. The other input screen that may appear is shown and discussed in Section 4.3.

- 1) **Click on each input selection button** to browse your computer for the required file. The Additional Inputs screen will prompt you for one or more of the following input files (depending on the modeling options you indicated in your Facility List Options file and the nature of your sources in your Emissions Location file):
  - User Receptors file;
  - Emissions Variation file;
  - Buoyant Line Parameters file;
  - Polygon Vertex file; and/or
  - Building Dimensions file.

When you hover your mouse over each of these input file buttons, instructions will be displayed on the top of the screen describing each file type. For example:

- a. If you indicated in your Facility List Options file that you'd like to include user receptors or emissions variations for one or more facilities to be modeled, then the associated button(s) will appear on this screen asking you to select a [User Receptors](#) file (described in Section 3.5.6) and/or [Emissions Variation](#) file (described in Section 3.5.7).
- b. If one of the sources in your Emissions Location file is a buoyant line source or polygon source, then the button(s) will appear prompting you to browse your computer and select a [Buoyant Line Parameters](#) file (described in Section 3.5.2) and/or [Polygon Vertex](#) file (described in Section 3.5.1).
- c. If you chose to model building downwash in your Facility List Options file, then a button will appear prompting you to provide a [Building Dimensions](#) file (described in Section 3.5.5).

**Figure 7. Provide Additional Input Files**



- 2) **Click the *Next* button** on the screen to continue after you have entered the requested input files. If additional inputs are needed for deposition and depletion modeling, another input screen will open next, as shown and discussed in Section 4.3.
- 3) If no other inputs are needed, HEM will display the pop-up box, shown in Figure 6, which states “*Clicking ‘OK’ will start HEM. Check the log tab for updates on your modeling run.*” Click *Cancel* if you need to change any input files and the ***Back*** button to change any input files on the previous screen. **If you are ready for HEM to start your modeling run, click *OK***, and a log of the modeling progress will appear as shown and described in Section 4.4.

### 4.3. Provide Deposition and Depletion Input Files

When modeling deposition/depletion, HEM can direct AERMOD to (1) calculate a deposition flux and (2) deplete the plume based on the calculated deposition. You can direct HEM to provide the deposition flux in the outputs, or not (to save space). Generally, deposition modeled with plume depletion will reduce the ambient impacts from the emission source by removing pollutants from the plume. Air concentrations will be depleted as pollutants are deposited to the ground. Deposition and plume depletion have more of an effect on ambient concentrations farther from the facility than they do closer to the facility where the maximum impact generally occurs.

Alternatively, you may choose to calculate the deposition flux but not deplete the plume (to allow for higher, more conservative air concentrations). Either way, the modeled deposition flux may be used as an input to a separate multipathway model such as the Total Risk Integrated Methodology (TRIM) (USEPA, 2024i). **Note:** HEM requires significantly more time to run if you opt to model deposition and/or depletion. The exact run-time will depend on your particular source configuration and modeling domain but can be over an hour or more per facility. You can utilize the FASTALL option in the Facility List Options file to expedite the run. As noted in [Section 3.2.11](#), FASTALL conserves model runtime by simplifying the AERMOD algorithms used to represent the meander of the pollutant plume (USEPA, 2024e).

In most cases, if you indicated that you would like to model deposition and/or depletion in the Facility List Options file, HEM will require additional input files.<sup>7</sup> HEM uses AERMOD to calculate deposition and depletion effects for particulate matter, vapor (gaseous) pollutants, or both. The make-up of your emissions – that is, the percentage particulate and gas – is dictated to HEM by your [HAP Emissions](#) input file. Specifically, the column in the HAP Emission input file titled “Fraction emitted as particulate matter” indicates to HEM whether your emissions are:

- 100% particle (if this column is populated with 100 for all pollutants),
- 100% vapor (if this column is left blank or populated with 0 for all pollutants), or
- a mixture of particles and gas.

You will need to browse your computer and select the additional files needed for modeling of deposition and/or depletion, as depicted in **Figure 8**. You will be prompted to provide between one and three deposition/depletion related input files, depending on your modeling options and the nature of the emissions to-be-modeled.

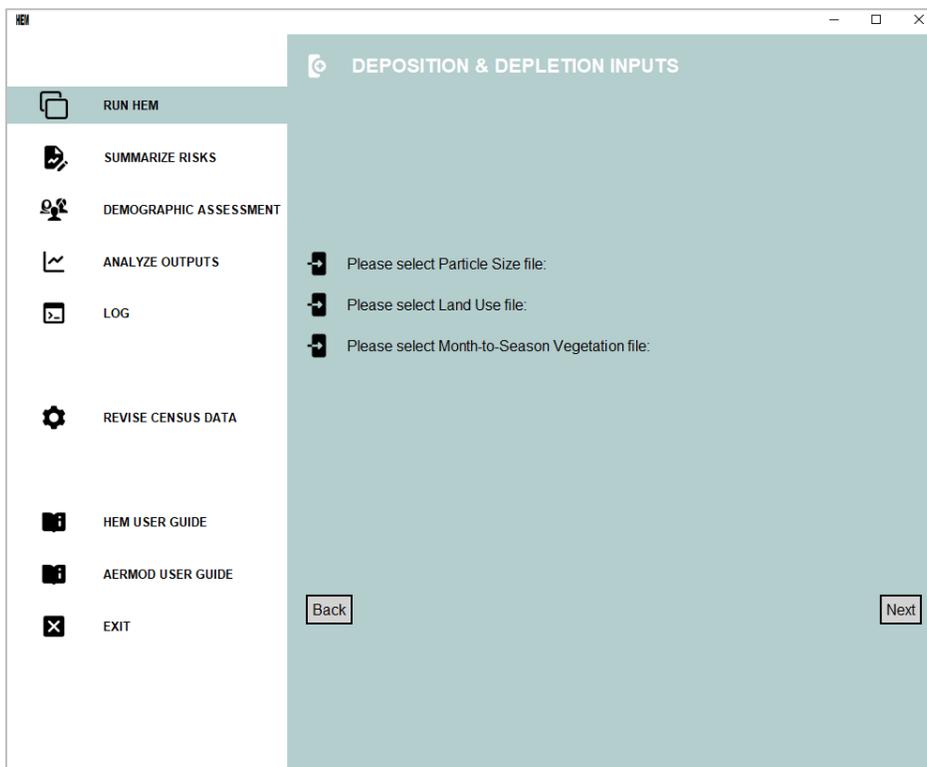
- 1) If your Facility List Options file indicates that you chose to model particle deposition and/or particle depletion using AERMOD’s Method 1 (as discussed in [Section 3.4.2.1](#)) AND your HAP Emissions file indicates that some of the emissions are in particle form, then a particle data file is required by HEM-AERMOD. **Click on the Particle Size file input button** (as shown in Figure 8 below) to browse for the [Particle Data](#) file, which

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<sup>7</sup> Note: The one deposition and/or depletion modeling case, which requires no additional inputs and therefore no deposition/depletion input screen, is if you are modeling only particle deposition and/or depletion AND chose in your Emissions Location input file to use Method 2 for the Deposition Method. It should also be noted that AERMOD does not model deposition or depletion of emissions from buoyant line sources. Therefore, if you indicate in your Facility List Options file that deposition or depletion should be modeled for a facility with buoyant line sources in your Emissions Location file, AERMOD will not run successfully. In this case, remove the buoyant line source IDs from your input files and model that source separately, without deposition or depletion.

provides the particle size information, mass fraction and particle size density for each pollutant (HAP), as described in Section 3.5.3.

**Figure 8. Provide Deposition and Depletion Input Files**



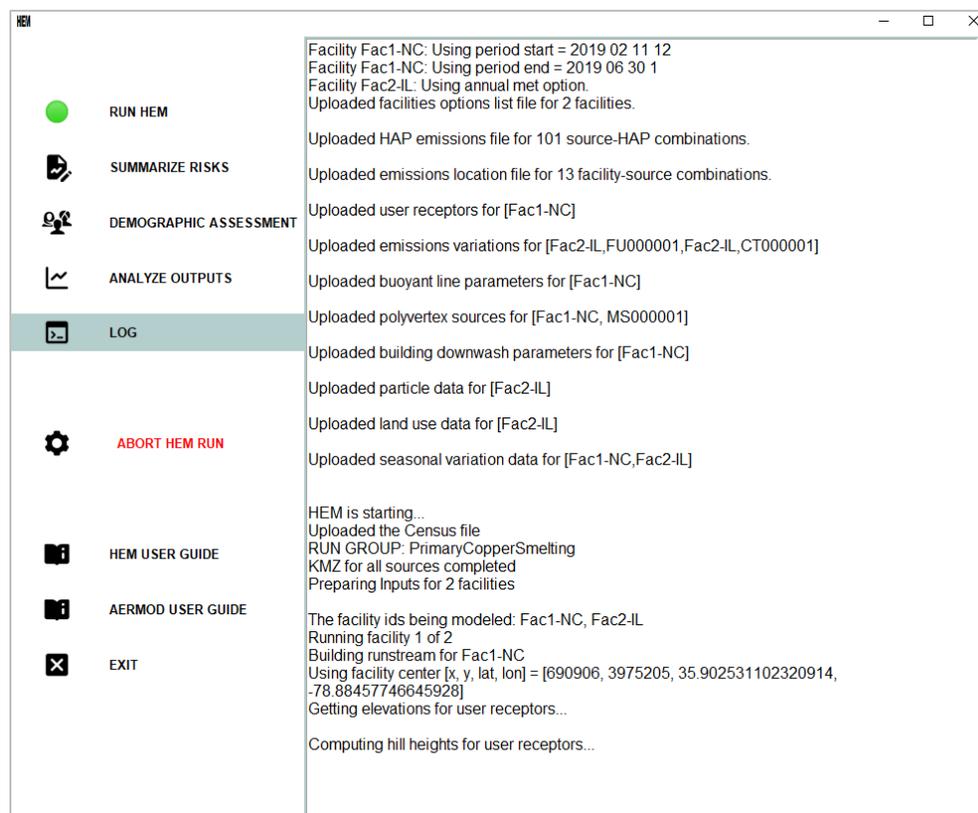
- 2) If your Facility List Options file indicates that you chose to model vapor (gaseous) deposition and/or vapor depletion AND your HAP Emissions file indicates that some of the emissions are in vapor form, then HEM will instruct AERMOD to model vapor deposition and/or depletion. Depending on the type of vapor deposition/depletion you indicated in your Facilities List Option file, two additional inputs may be required by HEM-AERMOD: a [Land Use input file](#) and a [Month-to-Seasons input file](#). **Click on the Land Use file input button** followed by the **Month-to-Season Vegetation file input button** (as shown in Figure 8 above) to provide these files.
  - a. These additional input files are needed only to quantify dry (or “wet and dry”) deposition and/or depletion of vapor emissions, as discussed in Section 3.5.4.
  - b. If you wish to model “wet only” deposition and/or depletion of gaseous pollutants, these additional input files are not needed by HEM. (These files are also not needed to model particle-only deposition and/or depletion.)
- 3) **Check** to ensure that the vapor (gaseous) pollutants in your HAP Emissions file are included in the [Gas Parameter](#) reference file.
  - a. If these pollutants are not included – or if you wish to include different parameter values than the Gas Parameter file currently lists – you should edit the Gas Parameter file located in HEM's *resources* folder (*HEM/resources\Gas\_Param.xlsx*), as discussed in Section 3.5.4. Otherwise, generic default gas parameter values will be used.

- 4) **Click the *Next* button** after you enter the required files on the deposition/depletion input screen. HEM will display the pop-up box (shown in Figure 6) stating “*Clicking ‘OK’ will start HEM. Check the log tab for updates on your modeling run.*” Click “*Cancel*” if you need to change any file locations on this screen, and the **Back** button to change any input files on the previous screen.
- 5) **If you are ready for HEM to start your modeling run, click “OK”** and a log of the modeling progress will appear (as shown and described in Section 4.4).

## 4.4. HEM Log, Aborting a HEM Run, and Run Completion Screens

After HEM starts modeling your facilities (or facility), the **LOG** screen will appear to show you HEM’s progress in real-time including errors in processing, if there are any. A snapshot of the Log screen (during a model run) is shown in **Figure 9**.

**Figure 9. Log Screen**



The log screen will provide you with the following modeling run information:

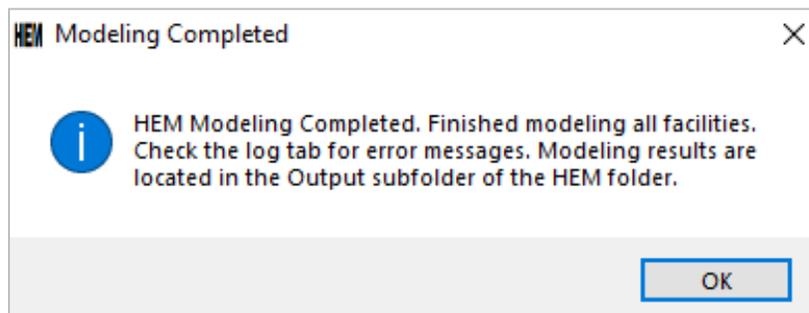
- the meteorological period used, whether annual (the default) or a different period you selected,
- the full list of input files uploaded,
- the method used for obtaining elevations and hill heights, if modeling elevations (e.g., “Using USGS method...”),
- any mismatch between input files prior to you correcting the mismatched files (e.g., mismatched Source IDs between the HAP Emissions and Emissions Location files),

- the default values used for any parameters with out-of-range (unacceptable) values specified in your input files,
- the run group name,
- the Facility IDs modeled and the location of each facility's center,
- the date of each model run (year-month-day),
- the start and end time for the AERMOD portion of the modeling run,
- the full list of outputs produced, and
- the time (number of minutes) required by HEM to model each facility and produce the facility-specific outputs.

No actions are required by you during the HEM-AERMOD run.

- 1) You may abort the HEM run if needed. The log screen shown in Figure 9 also shows an **ABORT HEM RUN** button on the (left) sidebar menu panel next to the log screen. Click on this button to stop your HEM run. Once selected, a pop-up window will appear requesting confirmation that you would like to stop the HEM run. Click the "Ok" button on the pop-up window to confirm or "Cancel" to quit the request.
- 2) After the modeling is complete, a pop-up message box will appear (shown in **Figure 10**) indicating that HEM has finished modeling all facilities and the log tab should be checked for error messages. (Section 6 discusses the outputs produced by the modeling run.)

**Figure 10. Modeling Completed Pop-Up**



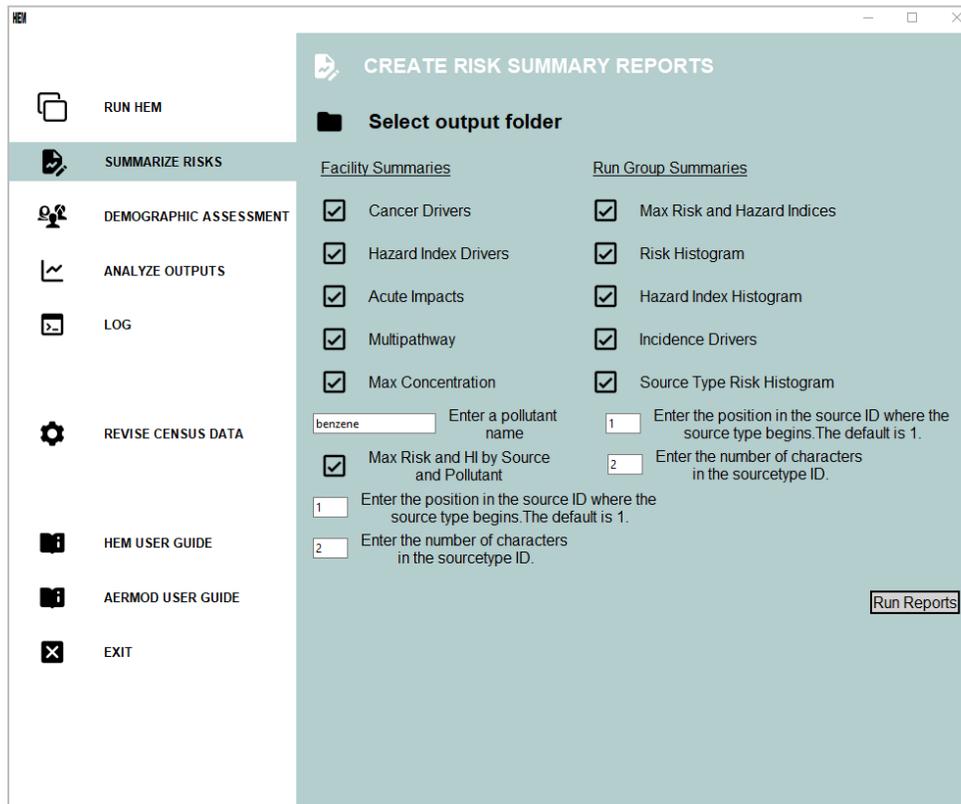
- 3) Once the modeling run is complete, HEM produces a log text file (named *hem.log*) located in the run group output folder as a permanent record of the modeling. The *hem.log* text file will contain information about the facilities modeled in your run. The log file will also indicate what default values HEM used for the required input files (if any), in lieu of erroneous out-of-range values you may have included in your input files.

Failed runs and other modeling errors are discussed further in Section 4.9. **Appendix A** includes a sample *hem.log* file produced for a two-facility modeling run. Section 4.5 next discusses how to run HEM's risk summary programs.

## 4.5. Summarize Risks

The **SUMMARIZE RISKS** button on the (left) sidebar menu allows you to summarize HEM results to produce cancer risk summaries, noncancer HI summaries, and concentration summaries based on the facilities modeled within your run group. This screen is shown in **Figure 11**.

Figure 11. Create Risk Summary Reports



Six of the summaries produce results specific to each facility (i.e., individual facility IDs are connected to the results, which account for impacts from each facility’s emissions in isolation). The other five summaries combine results across the run group (i.e., individual facility IDs are not present in these summaries, which account for multiple impacts on receptors from neighboring facilities). **Note:** Before you choose to summarize your risk results via these reports, you may wish to perform certain quality assurance (QA) checks on the modeled results, as described in **Section 10**.

The “Facility Summaries” available on this screen are:

- Cancer Drivers,
- Hazard Index Drivers,
- Acute Impacts,
- Multipathway,
- Max Concentration, and
- Max Risk and HI by Source and Pollutant.

The “Run Group Summaries” available on this screen are:

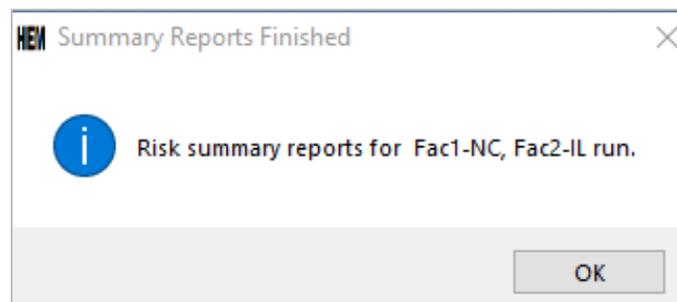
- Max Risk and Hazard Indices,
- Risk Histogram,
- Hazard Index Histogram,
- Incidence Drivers, and

- Source Type Risk Histogram.

Follow these instructions for running the summary reports available on Figure 11's interface:

- 1) First, **click the *Select output folder*** button to browse the output folder for the run group folder where the HEM outputs you want summarized are located.
- 2) Next, **check the box before each summary** you would like to run. There are three summary programs on this screen that will require additional information when you check the box.
  - a. The Max Concentration summary requires you to **enter a pollutant name**. The pollutant name you enter must be a name of a pollutant in your HAP Emissions input file, spelled exactly as it appears in this file. Note: If you would like the maximum concentration for more than one pollutant, you may come back to this screen and enter another pollutant name after you have run and completed the report for the first pollutant entered.
  - b. The Max Risk and HI by Source and Pollutant summary (part of the "Facilities Summaries") and the Source Type Risk Histogram summary (part of the "Run Group Summaries") require you to **indicate where in your Source IDs the source type begins and ends**. As noted in Section 3.3.1, it is helpful to create your Source IDs so that the type of source is always identified in the same location in the Source ID string. For example, if you are modeling a series of storage tanks and wastewater vessels, you could identify them with IDs such as ST01, ST02, ST03, WW01, WW02, and so on. In this example, the source type starts in location 1 of the Source ID string and is 2 characters long (i.e., ST and WW). Therefore, in this case, you would enter a 1 next to "*Enter the position in the source ID where the source type begins...*" You would then enter a 2 next to "*Enter the number of characters in the sourcetype ID.*"
- 3) Then **click the "Run Reports" button to initiate the selected summaries**.
- 4) After you have initiated the summaries you want to run, **check the Log screen for progress**. The *hem.log* text file will also report any errors.
- 5) When the Risk Summary Reports have finished, a pop-up message will appear (shown in **Figure 12**) noting the facilities for which the risk summaries reports were run.

**Figure 12. HEM Summary Reports Finished Pop-Up**



- 6) The Risk Summary Reports you choose to run will be placed in the same output folder where you indicated the HEM results are located, which were summarized using this interface (Figure 11). The outputs produced are risk summary reports for all facilities modeled in your run group and are described in Section 7.

## 4.6. Assess Demographics of Modeled Population

If you used U.S. Census receptors for HEM-AERMOD modeling, the **DEMOGRAPHIC ASSESSMENT** button on the (left) sidebar menu allows you to assess the demographics of the communities surrounding your modeled facility (or facilities). HEM links each U.S. census block receptor around modeled facilities with census-based demographics including racial, ethnic, age, economic, educational, and limited English-speaking population categories. (Alternate receptors do not have demographic data associated with their populations and therefore cannot be used with the Demographic Assessment module. In addition, HEM version 5.0 does not support demographic assessments when using user-supplied concentrations, even with U.S. census blocks.) The Demographic Assessment screen is shown below in **Figure 13**.

**Figure 13. Create Demographic Assessment Reports**

The screenshot shows the HEM software interface. On the left is a sidebar menu with the following options: RUN HEM, SUMMARIZE RISKS, DEMOGRAPHIC ASSESSMENT (highlighted), ANALYZE OUTPUTS, LOG, REVISE CENSUS DATA, HEM USER GUIDE, AERMOD USER GUIDE, and EXIT. The main window is titled 'CREATE DEMOGRAPHIC ASSESSMENT REPORTS'. It contains a note: 'Note: The Demographic Assessment module may be used with HEM runs based on U.S. Census Block receptors only. Demographic results are available out to the smallest radius modeled for any facility in the run group.' Below the note are three numbered steps: 1. Select folder containing modeled risk results; 2. Enter a run group name and prefix to be used for the demographic results. This step includes input fields for 'Name' (with example 'Primary Copper Manufacturing') and 'Prefix' (with example 'PCM'); 3. Choose type of impact (cancer or noncancer) for basis of demographics analysis, the radius around each facility to include, and the impact level at which population percentages will be calculated. Note: proximity statistics will be included at your specified radius. This step includes a table for combinations:

Combination:	Radius (km)	Impact Level
<input checked="" type="radio"/> Cancer Risk Level (in a million)	50	>= 1
<input type="radio"/> Noncancer Hazard Index Level		> (1-10)

Below the table is an 'Add combination' button. At the bottom right of the main window is a 'Run Reports' button.

**Note:** You must have an output folder with modeled results to run the Demographic Assessment module. Do not add or remove files to that output folder, or change the filenames of any output files, as the module's code requires certain files to be present in the output folder (e.g., the Facility Max Risk and HI file) and to contain the same prefix as the output folder that HEM placed them in. After you have run HEM and have modeled results, follow these steps on the Demographic Assessment screen:

- 1) Click the **Select folder containing modeled risk results** button to browse your computer and select the specific HEM output folder containing the modeling results of the group of facilities for which you wish to assess the surrounding demographics.

- 2) Use the “Name” text box to **enter the name you wish to appear within the outputs** produced by the Demographic Assessment. The name you enter will be used in the titles of the demographic tables produced by this module. Use the “Prefix” text box to **enter a prefix that will be used at the beginning of the filenames for the demographic outputs**. The demographic outputs are discussed in Sections 8.2 and 8.3.
  - a. The name and prefix you enter here need not be the same name/prefix used in the HEM output folder you pointed to in step #1.
  - b. Note: Keep the prefix brief; if the path length plus file name length is > 260 characters, Windows® may not write the file.
- 3) Next, **choose the “combination” of three parameters defining your demographic assessment** including whether you wish to assess cancer risk level or noncancer HI level, the radius (in km) within which you wish to assess the community demographics surrounding the facility (or facilities) in your run group, and the impact level – cancer risk level or noncancer HI level – at which population percentages that meet or exceed this level will be provided.
  - a. You may enter a radius up to the smallest radial distance modeled for any facility in your run group, as indicated in the [Max. Distance](#) column of your Facility List Options file. Entering a radius greater than the smallest radial distance modeled for any facility will cause an error message to pop-up.
  - b. You may enter cancer risk levels of 1, 5, 10, 20, 30, 40, 50, 100, 200 or 300-in-1 million, and the module will output population percentages with cancer risk greater than or equal to the level you choose.
  - c. You may enter noncancer HI levels of 1, 2, 3, 4, 5, 6, 7, 8, 9 or 10, and the module will output population percentages with noncancer HI greater than the level you choose.
  - d. The **Add combination** button allows you to choose up to four cancer and non-cancer combinations for a single Demographic Assessment, all of which will be based on the HEM outputs you selected in step #1. Proximity statistics, which are the total demographic populations and percentages around your modeled facility (or facilities) irrespective of risk or HI levels, will also be provided at the radius you specify ( $\leq$  the smallest radial distance modeled for any modeled facility).
  - e. The **Remove** button allows you to delete a combination.
- 4) After you have specified between one and four combinations, click **Run Reports** to initiate the Demographic Assessment.

**Figure 14** provides an example of a Demographic Assessment in which four combinations are chosen for a run group that will be named “Primary Copper Smelting” in the demographic output tables produced. In this example, all outputs will have filenames beginning with the prefix “PrimCop” and the following outputs will be provided, based on the four combinations chosen:

- Demographic-specific population percentages for people with a cancer risk greater than or equal to 1 in a million at a radius of 50 km,
- Demographic-specific population percentages for people with a cancer risk greater than or equal to 10 in a million at a radius of 5 km,
- Demographic-specific population percentages for people with a noncancer HI level greater than 1 at a radius of 50 km, and
- Demographic-specific population percentages for people with a noncancer HI level greater than 2 at a radius of 5 km.

Figure 14. Sample Demographic Assessment Run Combinations

**CREATE DEMOGRAPHIC ASSESSMENT REPORTS**

Note: The Demographic Assessment module may be used with HEM runs based on U.S. Census Block receptors only. Demographic results are available out to the smallest radius modeled for any facility in the run group.

- Select folder containing modeled risk results
- Enter a run group name and prefix to be used for the demographic results.  
Name: Primary Copper Smelting  
Prefix: PrimCop
- Choose type of impact (cancer or noncancer) for basis of demographics analysis, the radius around each facility to include, and the impact level at which population percentages will be calculated. Note: proximity statistics will be included at your specified radius.

Combination:	Radius (km)	Impact Level	Action
<input checked="" type="radio"/> Cancer Risk Level (in a million) >= 1	50	>= 1	
<input type="radio"/> Noncancer Hazard Index Level > (1-10)		> (1-10)	
<input checked="" type="radio"/> Cancer Risk Level (in a million) >= 10	5	>= 10	Remove
<input type="radio"/> Noncancer Hazard Index Level > (1-10)		> (1-10)	
<input type="radio"/> Cancer Risk Level (in a million) >= (1-300)	50	>= (1-300)	Remove
<input checked="" type="radio"/> Noncancer Hazard Index Level > 1		> 1	
<input type="radio"/> Cancer Risk Level (in a million) >= (1-300)	5	>= (1-300)	Remove
<input checked="" type="radio"/> Noncancer Hazard Index Level > 2		> 2	

Run Reports

If you require more than four combinations for your Demographic Assessment, you may come back to this screen after running the first four reports, to run more combinations. Based on the radii indicated in the above combinations shown in Figure 14, proximity demographics at 5 km and 50 km will be provided (irrespective of cancer or HI level). Binned cancer risk and noncancer HI levels for the full array of HEM results at each of these radii will also be provided, as discussed further in Sections 8.2 and 8.3.

It should also be noted that, if the noncancer radio button is selected, noncancer HI results will be provided for whatever TOSHI is the maximum plus any other TOSHIs that are greater than 1. (As discussed in Section 2.2.1, there are a total of 14 TOSHIs modeled by HEM.)

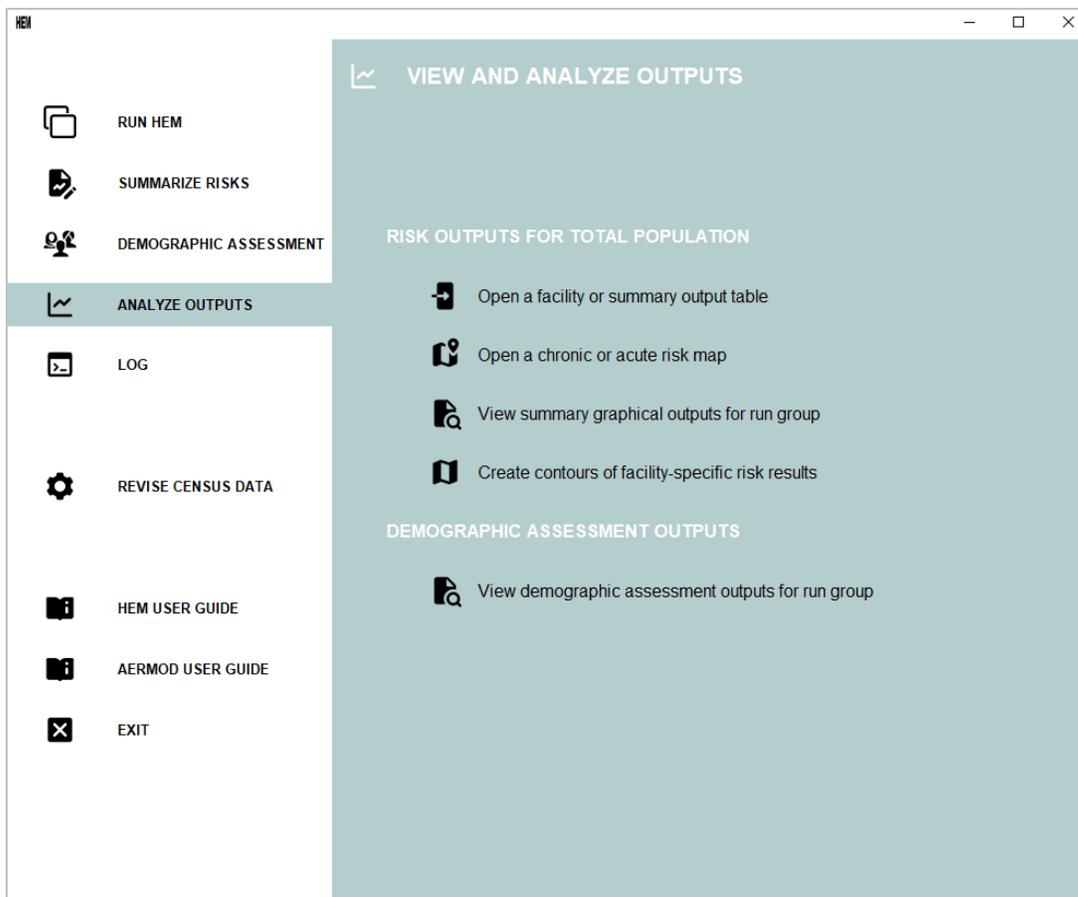
**Upon commencement of the Demographic Assessment, HEM will create a new subfolder named “pop” in your run group output folder (short for “population”), and the demographic results will be placed in this subfolder, each with a date (month-day-year) and time stamp. The Demographic Assessment methodology and results are discussed in more detail in Section 8.**

## 4.7. Analyze Outputs

The **ANALYZE OUTPUTS** button on the (left) sidebar menu allows you to view and analyze HEM’s (1) Risk Outputs for the Total Population, including facility-specific modeling results as

well as the run group-wide Risk Summary outputs, and (2) the Demographic Assessment Outputs, which break down the total population into specific demographics, as discussed in Section 4.6. The Analyze Outputs interface is shown below in **Figure 15**.

**Figure 15. View and Analyze Outputs**



#### 4.7.1. Risk Outputs for Total Population

The top portion of the “Analyze Outputs” interface consists of four buttons that allow you to:

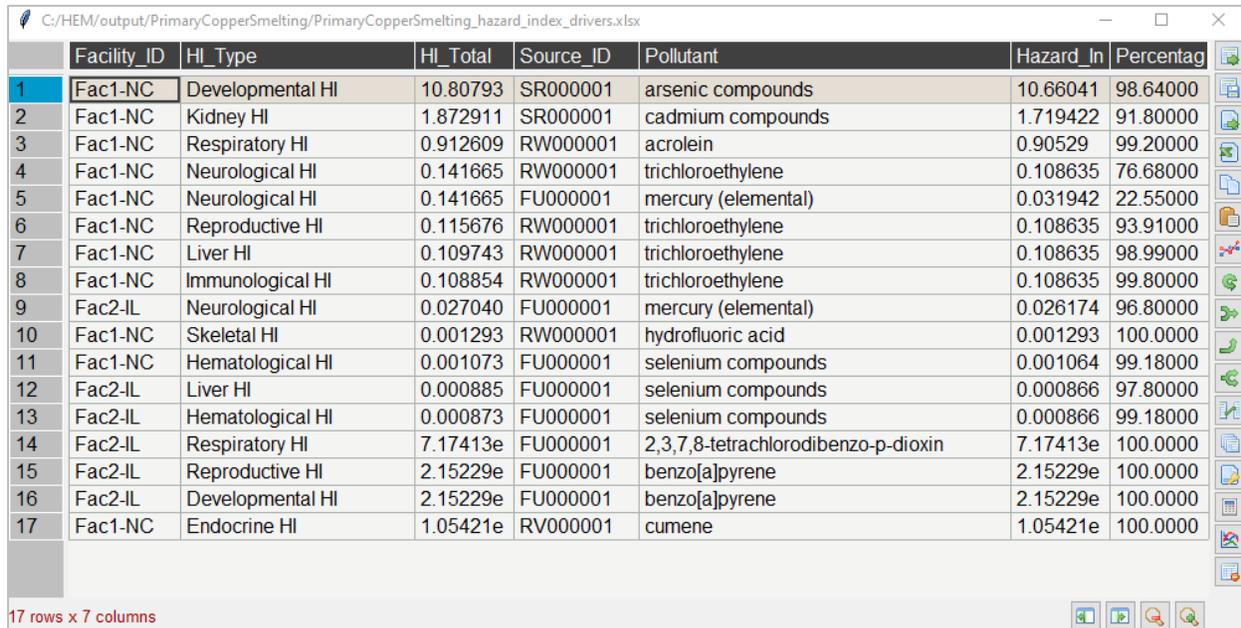
1. Open a facility or summary output table,
2. Open a chronic or acute risk map,
3. View summary graphical outputs for your run group, and
4. Create contours of facility-specific risk results.

After you click on each of these buttons, HEM will prompt you to identify the location of the output files you wish to view and analyze further. The types of output files that can be viewed and analyzed with each of these four buttons are discussed below.

#### 4.7.1.1. Open a facility or summary output table

If you choose to **Open a facility or summary output table** (Excel or CSV) using the button (shown in Figure 15), HEM will open the file within a spreadsheet app with numerous widgets<sup>8</sup> available for further analysis and graphing. This collection of widgets is provided by a [pandastable](#) library for the purpose of offering users an interactive way to review and analyze HEM's tabular output data. An example of a Hazard Index Drivers output (spreadsheet) with widgets is shown in **Figure 16**.

**Figure 16. Hazard Index Drivers File Opened via Spreadsheet App**



	Facility_ID	HI_Type	HI_Total	Source_ID	Pollutant	Hazard_In	Percentag
1	Fac1-NC	Developmental HI	10.80793	SR000001	arsenic compounds	10.66041	98.64000
2	Fac1-NC	Kidney HI	1.872911	SR000001	cadmium compounds	1.719422	91.80000
3	Fac1-NC	Respiratory HI	0.912609	RW000001	acrolein	0.90529	99.20000
4	Fac1-NC	Neurological HI	0.141665	RW000001	trichloroethylene	0.108635	76.68000
5	Fac1-NC	Neurological HI	0.141665	FU000001	mercury (elemental)	0.031942	22.55000
6	Fac1-NC	Reproductive HI	0.115676	RW000001	trichloroethylene	0.108635	93.91000
7	Fac1-NC	Liver HI	0.109743	RW000001	trichloroethylene	0.108635	98.99000
8	Fac1-NC	Immunological HI	0.108854	RW000001	trichloroethylene	0.108635	99.80000
9	Fac2-IL	Neurological HI	0.027040	FU000001	mercury (elemental)	0.026174	96.80000
10	Fac1-NC	Skeletal HI	0.001293	RW000001	hydrofluoric acid	0.001293	100.0000
11	Fac1-NC	Hematological HI	0.001073	FU000001	selenium compounds	0.001064	99.18000
12	Fac2-IL	Liver HI	0.000885	FU000001	selenium compounds	0.000866	97.80000
13	Fac2-IL	Hematological HI	0.000873	FU000001	selenium compounds	0.000866	99.18000
14	Fac2-IL	Respiratory HI	7.17413e	FU000001	2,3,7,8-tetrachlorodibenzo-p-dioxin	7.17413e	100.0000
15	Fac2-IL	Reproductive HI	2.15229e	FU000001	benzo[a]pyrene	2.15229e	100.0000
16	Fac2-IL	Developmental HI	2.15229e	FU000001	benzo[a]pyrene	2.15229e	100.0000
17	Fac1-NC	Endocrine HI	1.05421e	RV000001	cumene	1.05421e	100.0000

- The spreadsheet and graphing widgets positioned along the right-hand side of the spreadsheet app screen include Load table, Save, Import CSV, Load Excel file, Copy table to clipboard, Paste table, Select data to plot, Transpose, Aggregate, Pivot, Melt, Merge/concatenate/join, Prepare a sub-table, Filter table, Calculate, Model fitting, and Clear table.
- The spreadsheet and graphing widgets positioned along the bottom, right-hand side of the spreadsheet app screen include Contract columns, Expand columns, Zoom out, and Zoom in.

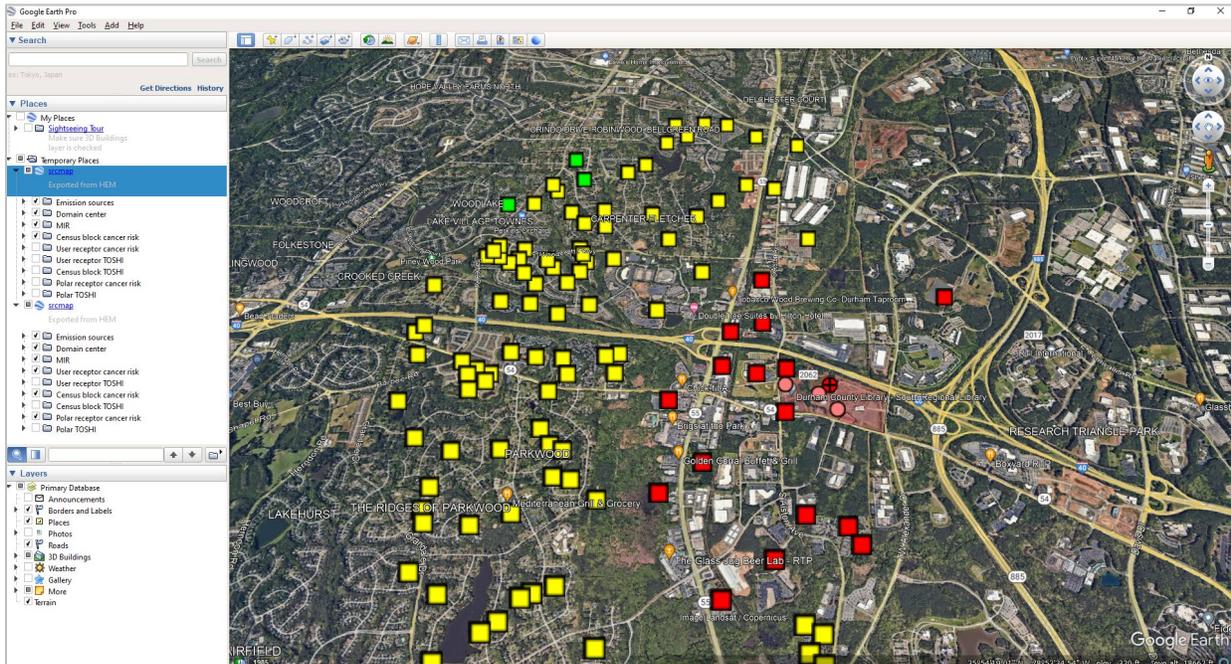
#### 4.7.1.2. Open a chronic or acute risk map

If you choose to **Open a chronic or acute risk map** via the Analyze Outputs user interface (shown in Figure 15), you can select a chronic kmz file from your modeled outputs, which HEM will launch in Google Earth™. Or you can select an acute map html file to view on a satellite street map.

<sup>8</sup> A widget is an element of a graphical user interface (GUI), like a Save File icon, that displays information or provides a specific way for a user to interact.

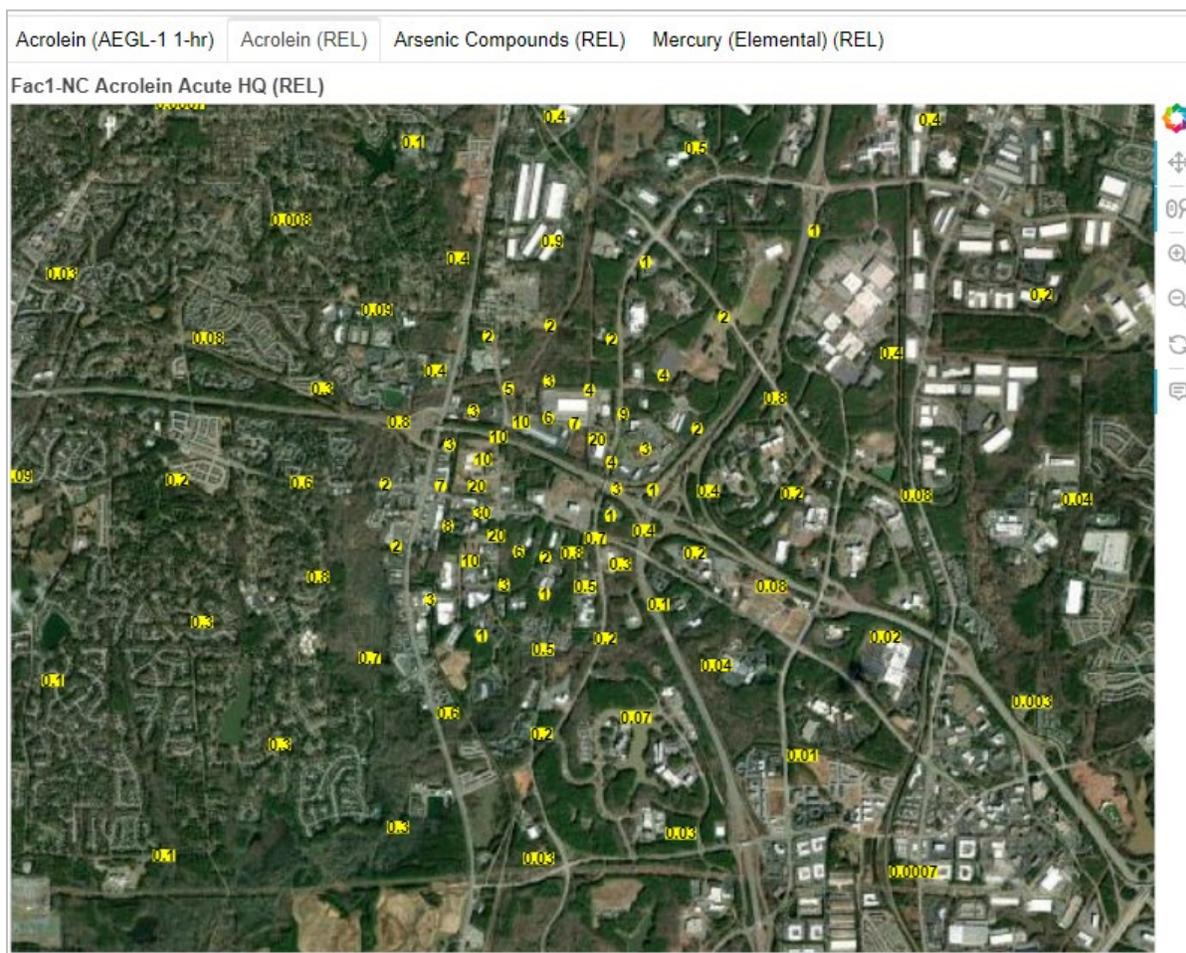
- 1) An example of a chronic kmz file is shown in **Figure 17** displayed via Google Earth™, with the cancer and noncancer chronic results overlaid on the map. These results are discussed further in Section 6. Note: The first time you run HEM, your computer may take several minutes to open Google Earth™, but the application will open more quickly after subsequent runs.

**Figure 17. Chronic Risk Map shown in Google Earth™**



- 2) To open an acute map, you must first run the **Acute Impacts summary** from the Summarize Risks (“Create Risk Summary Reports”) screen, shown in Figure 11. After you run the Acute Impacts summary program, *if there is an acute HQ greater than or equal to 1.5 based on any benchmark*, then HEM will produce an output subfolder called “Acute Maps”. This subfolder will be in the same location on your computer as the other facility-specific and summary outputs from your run. Note: No Acute Maps folder is produced if all acute HQ are less than 1.5.
  - After clicking on the “Open a chronic or acute map” button under “Risk Outputs for Total Population” on the “Analyze Outputs” interface (shown in Figure 15). HEM will ask you to select the html file you wish to view. Choose an html file from the “Acute Maps” subfolder and HEM will display the map in your default browser window. An example of a html acute map is shown below in **Figure 18**, for one of the acute benchmarks (REL) noted in Section 2.2.1. The acute output files underlying these mapped results are explained in Sections 6 and 7.

**Figure 18. Acute Map View of HTML File**



#### **4.7.1.3. View summary graphical outputs for run group**

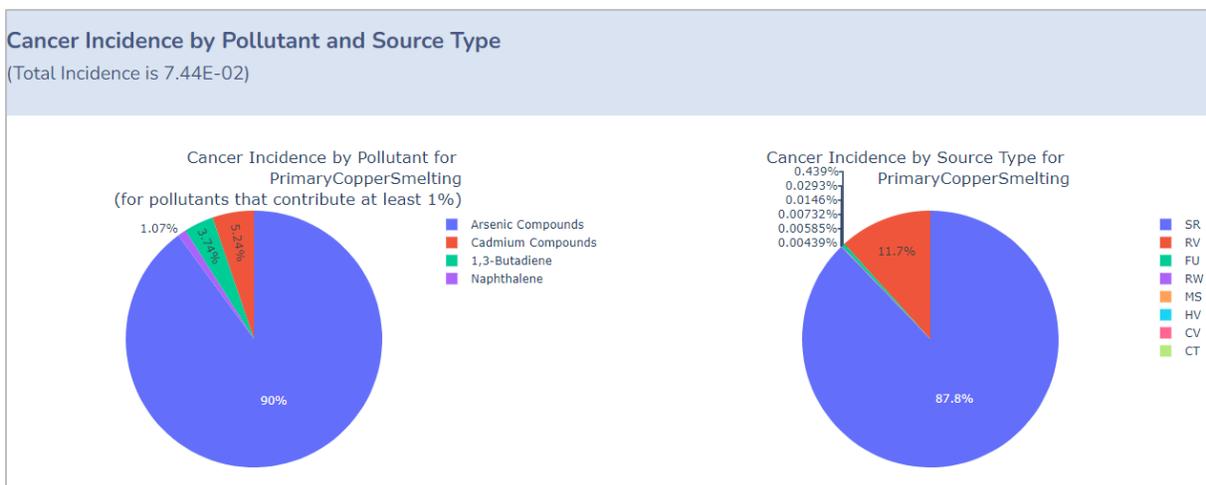
You can also choose to **View summary graphical outputs for run group** in your default web browser by clicking on this button under "Risk Outputs for Total Population" (shown in Figure 15).

- 1) To use these statistical and graphical visualization tools, you must choose a folder containing Risk Summary reports run from the Summarize Risk screen (shown in Figure 11). **Note:** All risk summary reports must be present in your selected folder to use these statistical and graphing tools, except the Max Risk report, Multipathway report and Acute Impact report. These three reports may be present in your selected folder but are not required.
- 2) After you select your desired output folder, the graphical visualizations of your results that appear in your default web browser are constructed via the Dash app, which is a Python framework for building interactive web applications. The graphical displays of your results offered by this application include:
  - a map of your modeled facility or facilities,
  - pie charts based on the cancer incidence percentages by pollutant and source type,

- bar charts showing the number of people at increasing levels of cancer risk (e.g., less than 1-in-1 million risk, greater than or equal to 1-in-1 million risk, greater than or equal to 10-in-1 million risk, greater than or equal to 100-in-1 million risk),
- bar charts showing the number of people at increasing noncancer hazard index levels for each of the 14 modeled target organ specific hazard indices (e.g., less than or equal to 1, greater than 1, greater than 10),
- bar charts showing the source and pollutant risk drivers of your modeling run for both cancer and noncancer,
- bar charts showing the acute screening hazard quotients by benchmark and pollutant for each facility with modeled acute impacts, and
- an interactive and exportable spreadsheet displaying the maximum cancer risk and noncancer hazard index values for each modeled facility.

An example of one of the several graphical visualizations offered by this application is shown in **Figure 19**. This figure displays pie charts based on the cancer incidence percentages by pollutant and source type, for a modeling run based on 4 different pollutants and 8 different source types. It is worth noting that the Cancer Incidence summary results present information that differs slightly from incidence drivers and source type histogram summary results because pollutants less than 1% are excluded from the summary. In addition, you may choose to exclude or “gray out” a pollutant(s) by clicking on the pollutant(s) name. When one or more pollutants are selected, the Dash app’s pie chart summary will automatically recalculate cancer incidences percentage amounts based on these selections.

**Figure 19. Example Graphical Visualization of Incidence by Pollutant and Source Type**



#### 4.7.1.4. Create contour maps of facility-specific risk results

Finally, you can choose to **create contour maps of facility-specific risk results** by clicking on this button under “Risk Outputs for Total Population” (shown in Figure 15). After choosing to create risk contours, HEM will open your default web browser and redirect you to the “HEM Risk Contour Maps” site, shown in **Figure 20**. From this site you will be able to select from your computer the facility-specific output files (ring summary and/or block summary files) upon which the risk contours will be based. **Note:** This application produces risk contours around one facility at a time.

**Figure 20. HEM Risk Contour Maps Web App**

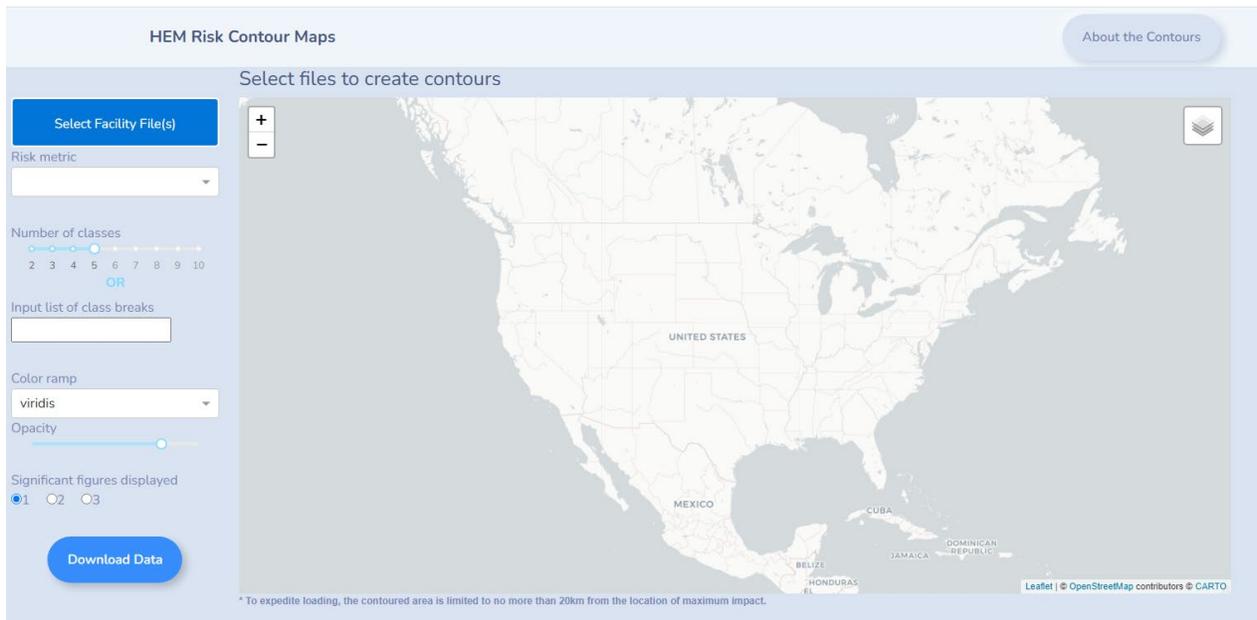
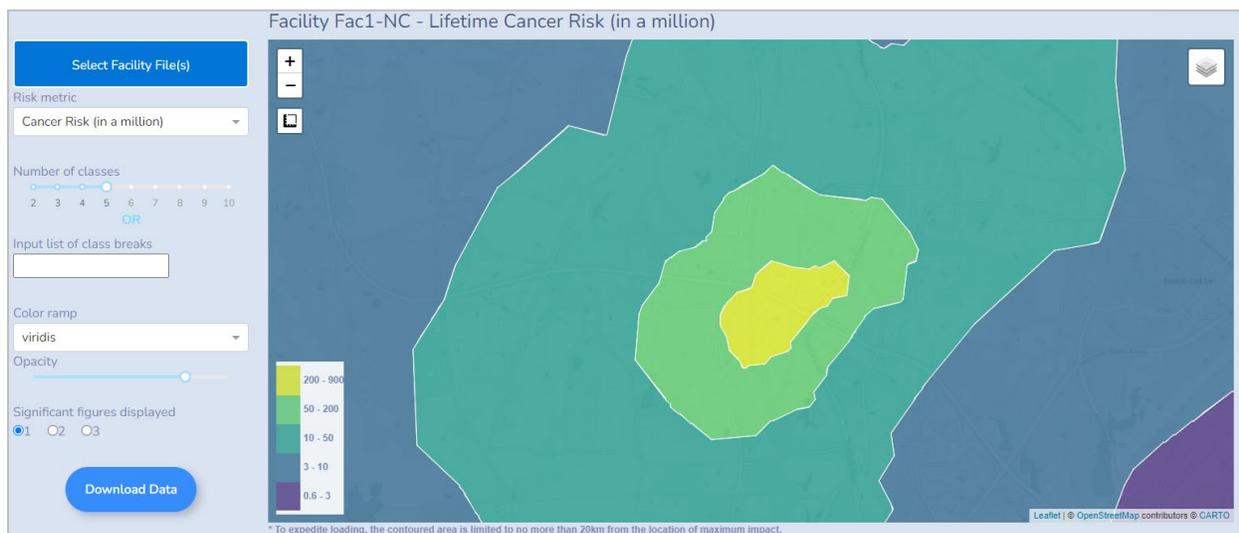


Figure 20, depicting the web app that will open in your default browser, displays an empty map and several buttons, dropdowns, and numerical inputs which allow you to create a contour map. The following provides detailed instructions for using these risk contour applications.

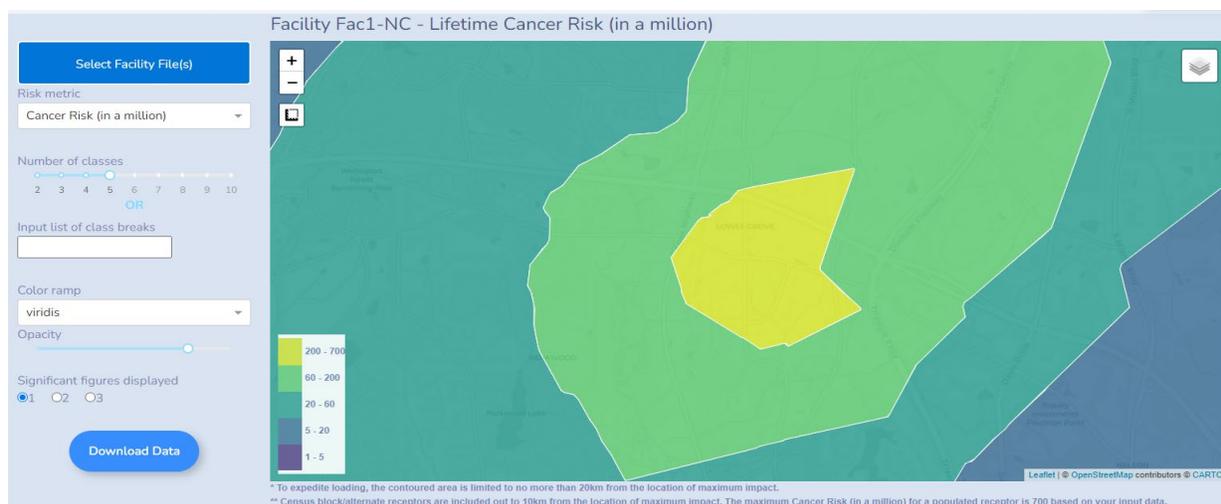
1. Click the **Select Facility File(s) Button** to indicate the data files you want to use to create the contours around a facility. You may use the Ring Summary Chronic file, the Block Summary Chronic file, or both.
  - Attempting to use files other than these, or more than two files, or files for different facilities will fail to create contours, and a popup message will indicate why the attempt failed.
  - In cases where AERMOD is not run, but instead you have provided [user-supplied concentrations](#) for some geographic locations, there won't be a Ring Summary Chronic file, and the Block Summary Chronic file will contain risk estimates for both the user's provided locations and the interpolated block or alternate receptors. However, HEM will use only the risk estimates at user's geographic locations to create contours because the block or alternate receptor risks are interpolated and don't add any new information.
  - For the typical HEM run, both the Ring Summary Chronic file and the Block Summary Chronic file are generated for each facility modeled. While both files can be used to create contours, the Ring Summary Chronic file will likely be the most important for creating contours because the default set of polar receptors spans the entire modeling domain and provides good coverage for most areas. Also, the user can control how the polar receptors cover the modeling domain by using the Facility List Options file to specify the desired number of radials and the ring distances. The contour interpolation is more accurate when more input data are used, so it is recommended that your polar receptor network have at least the default number of rings (13) and radials (16). **Figure 21** shows an example of contours around a facility where on the Ring Summary Chronic file is used.

**Figure 21. Risk Contour Based on Ring Summary Chronic File**



- The Block Summary Chronic file can be used to add some finer resolution near the facility where people may live. However, by default HEM interpolates census or alternate receptors beyond 3 kilometers from the facility, so receptors beyond that distance are not useful for creating contours. Also, when using the Block Summary Chronic file, be aware that if the density of the receptors is high, the resulting contours may have sharp edges or islands. **Figure 22** shows an example of contours around a facility where both the Ring Summary Chronic and Block Summary Chronic files are used. Experiment using ring summary with and without block summary data, to balance contour smoothness with resolution around the modeled facility.

**Figure 22. Risk Contour Based on Ring Summary Chronic and Block Summary Chronic Files**



2. **Select a risk metric** to contour from the dropdown list. The list potentially includes cancer risk (in a million) and all of the TOSHIs, but the only metrics that appear in the dropdown list are those with at least one nonzero value in the data.

3. **Specify the number of data classes to be displayed using the slider**, which allows a minimum of 2 and a maximum of 10 classes, and defaults to 5 classes. HEM uses a logarithmic scale and will automatically set the upper limit of the highest class at the maximum value of the selected risk metric; and HEM will automatically set the lower limit of the lowest class at the minimum value of the selected risk metric. **Note:** When a Block Summary Chronic file is used, the maximum value used will be a populated-type census block or alternate receptor (i.e., not a school, monitor, or boundary receptor).
4. **Instead of using the slider to set the number of classes, you can input a comma-separated list of class breaks to specify the number of classes** and the class break levels.
  - To activate the input box, after entering a list of values, either press enter, or click anywhere outside of the input box.
  - HEM does not enforce any limit on the number of classes when using this option, but you should exercise caution such that the map doesn't become too cluttered or contain class breaks that may not be meaningful.
  - If you input a list where the highest value is less than the lowest value in the data for the risk metric chosen, or the lowest list value is greater than the highest value in the data for the risk metric, HEM will ignore the list and revert to the slider (described above) to set the number of classes.
  - As long as there is a valid list of values, HEM will use the list instead of the slider value, but if you activate the slider by changing the number of classes, HEM will use that instead.
5. **Select the color ramp** for the contours from a dropdown list, which includes 28 color ramps from the [matplotlib color ramp gallery](#). The list includes common color ramps like Viridis (purple to yellow) and Blues (a sequence of blue colors). Fourteen of the 28 color ramps listed also include their reversed color ramps, indicated with an “\_r” suffix. Viridis is the default color ramp.
6. **Adjust the opacity of the contours** (in 10 percent increments) with the opacity slider. The default is 80 percent.
7. **Specify the number of significant figures** that will be shown in the map legend, footnotes, and popups with this radio button. The default is 1 significant figure. For data values greater than 1, HEM uses an integer data type for purposes of contour display, so the values displayed may not have the full number of significant figures you specify. For example, if you specify 3 significant figures, a value of 1.23 would be displayed as 1, a value of 12.3 would be displayed as 12, and a value of 123 would be displayed as 123.
8. Download the spatial data for the contours using the **Download Data Button**. Clicking this button opens a sidebar with another button for downloading the contour spatial data in GeoJSON format. Clicking this button will save (to your computer's downloads folder) a GeoJSON file containing the spatial data for the contours as they appear in the app, with the same color ramp and classes. The GeoJSON file can be viewed and used in another web map or in GIS software. After importing the saved GeoJSON file into some GIS applications like ArcGIS Pro, the symbology may need to be adjusted by the user to exactly replicate the contours as they appear in HEM.
9. Once a contour map is created, you can control which basemap is displayed and which additional layers are displayed using the **layer list widget** that appears in the upper right corner of the map. The basemap choices are satellite, dark, light, and OpenStreetMap. The additional layers that you can check on or off in the layer list include:

- US Roads – contains primary roads, secondary roads, local roads, and railroads within the US.
- Places/Roads – contains cities/towns, places, and road names for the entire world.  
**Note:** The road names in this layer may overlap those in the US Roads layer.
- Block/User Receptors – If a Block Summary Chronic file was used to create contours, this layer can be checked and will display (as points) these receptors.  
**Note:** This layer is limited to receptors that are within a 20-kilometer square centered on the maximum metric value location. Hovering your mouse over a receptor will display that receptor’s ID and risk metric value.
- Polar Receptors – If a Ring Summary Chronic file was used to create contours, this layer can be checked and will display (as points) these receptors. All polar receptors are displayed and, like the block/user receptors, hovering your mouse over them will display receptor information and risk metric value.
- Contours – The contours may be checked on or off.

The output files underlying these results (the Ring Summary Chronic and the Block Summary Chronic files) are explained in Section 6. In addition, **it is helpful to review and understand the following methodology and tips when generating risk contour maps:**

- The raw data used to create contours are the Ring Summary Chronic file and/or the Block Summary Chronic file. HEM uses these data and the [griddata](#) (linear) interpolation method of the [SciPy](#) Python library to interpolate from the raw data points to a regular grid (10m resolution). This is the same basic method (described in Sections 3.2.7.2 and 3.6) used to interpolate concentration values to census blocks (or alternate receptors), but in this application HEM interpolates risk estimates to a regular grid of locations. HEM uses the regular grid of interpolated risk values in the matplotlib filled contour ([contourf](#)) method to create the contours. There is inherent uncertainty involved in any interpolation.
- Depending on the size of the modeling domain, HEM may limit the geographic extents of the contoured area. To expedite loading, the contoured area is limited to no more than 20km from the location of maximum impact, where the risks are the highest. Because the time it takes to process data and render contours depends on the amount of input data and the resolution of the generated regular data point grid used in the contour method, HEM limits the extents to a square with 40 kilometer sides when a Ring Summary Chronic file is used, and to a square with 20 kilometer sides when only a Block Summary Chronic file is used. HEM centers the contours on the receptor with the highest risk value for the metric being contoured.
- The boundary of the contoured area could be square, circular, or irregular depending on the size of the modeling domain and whether the inputs are block or polar receptor data.
  - If your modeling domain spans more than 40 kilometers and the Ring Summary Chronic file is used (with or without the Block Summary Chronic file) then the boundary of the contoured area will be square.
  - If the span is less than 40 kilometers, the boundary will be nearly circular (and will be determined by the convex hull of the polar receptors).
  - If only a Block Summary Chronic file is used, then the shape of the boundary is determined by the convex hull of the census block or alternate receptors.

- If you specify your own class breaks, then the contours will be limited to values above the lowest class break and the boundary may take the shape of the contour line representing that value.
- If your contours are based on both unpopulated receptors (e.g., polar rings from the Ring Summary Chronic file) and populated receptors (e.g., census blocks from the Block Summary Chronic file), and you are using the automatically generated class breaks, unpopulated areas of higher impact (than predicted for populated receptors) may appear close to the facility as areas outside the color-coded contours. **Note:** To include unpopulated areas of higher impact in the maximum contour, you can use the “Input list of class breaks” option to enter a class break higher than the populated max impact (but  $\leq$  the unpopulated max impact).
- The contours’ functionality is designed to use data from a single facility. If you have used HEM to estimate risks from [user-supplied concentration](#) data, then HEM generates only a Block Summary Chronic file and not a Ring Summary Chronic file. You can still use this file to create contours, but because your provided concentration data could cover a broad area, HEM will only create contours around the area of maximum risk, and it could take a long time to process the data.

#### 4.7.2. Demographic Assessment Outputs

The bottom portion of the “Analyze Outputs” interface (shown in Figure 15) allows you to **View demographic assessment outputs for run group** in your web browser.

- 1) When you click this button, HEM will prompt you to identify the location of the output files you wish to view and analyze further. **To use these statistical and graphical visualization tools, you must choose a folder containing Demographic Assessment reports**, generated from a completed run under the Demographic Assessment screen (shown in Figure 13).
  - a. You will receive an error message if the directory (folder) selected does not contain one or more of the required files needed to run.
- 2) After you select an output folder, the graphical visualizations of that run’s demographic results will appear in your default web browser and are constructed via the Dash app, which, as previously mentioned, is a Python framework for building interactive web applications.

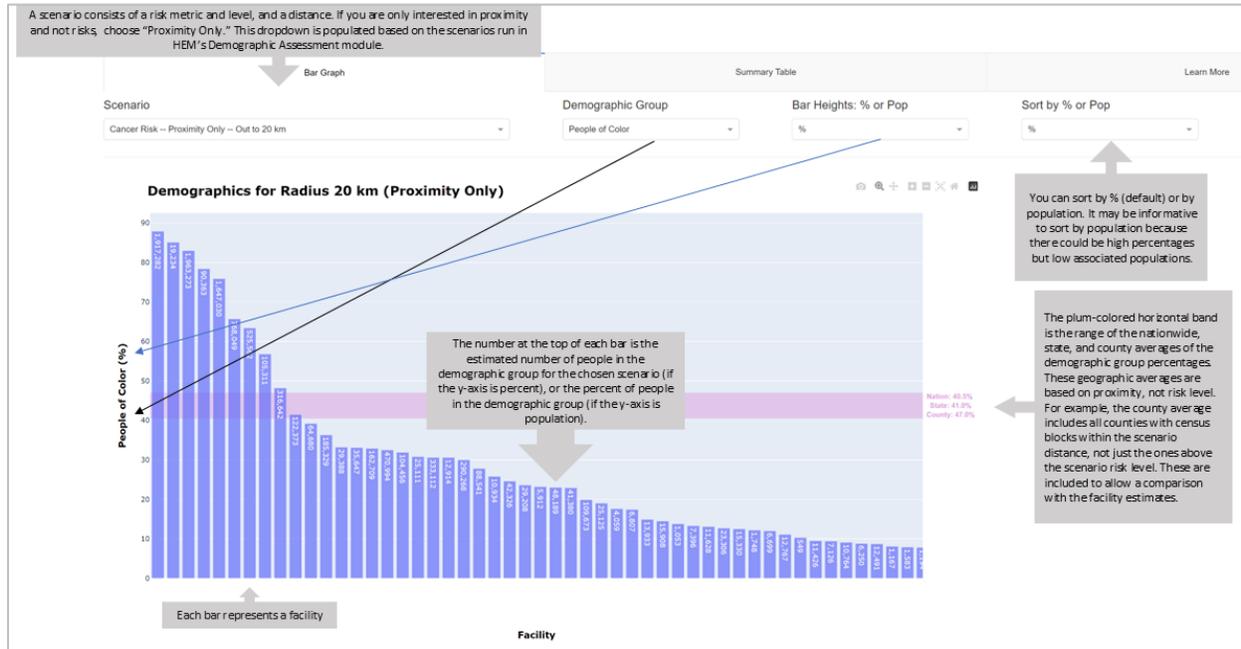
The graphical displays of your demographic results offered by this app’s dashboard include:

- a **Bar Graph** tab displaying the risk at each facility according to parameters determined by selections on four dropdown menus:
  - **Scenario**, which includes (1) risk metric (cancer or noncancer HI), (2) risk/HI level or proximity only, and (3) radial distance (in km) based on what you requested via the Demographic Assessment interface (Figure 13);
  - **Demographic Group** (14 groups provided, which are listed later in this section);
  - **Bar Heights** preference (by percentage or population); and
  - **Sort** preference (by percentage or population).
- a **Summary Table** tab, which is an interactive and exportable spreadsheet displaying the number or percentage of facilities exceeding the nationwide, state, and county geographic average for varying metrics, distances, and risk levels by a selected percentage amount; and

- a **Learn More** tab that provides more information about both the Bar Graph tab and the Summary Table tab.

**Figure 23** shows a sample Bar Graph with annotation from the “Learn More” tab and provides helpful information about the contents of the bar graph. The Bar Graph and Summary Table tabs that will appear in your web browser are also described more below.

**Figure 23. The Demographic Assessment Bar Graph under “Analyze Outputs”**



The Bar Graph tab displays the results of HEM's Demographic Assessment module, which as discussed in Section 4.6, provides demographic estimates for scenarios that are based on distance and risk level. The 14 demographic groups included are:

- People of Color (which is the Total population minus the White population),
- Black,
- American Indian and Alaskan Native,
- Asian,
- Other races and multiracial,
- Hispanic or Latino,
- Children 17 years of age and under,
- Adults 18 to 64 years of age,
- Adults 65 years of age and over,
- Adults without a high school diploma,
- People living below the poverty level,
- People living below twice the poverty level,
- Limited English speaking households (previously called Linguistic Isolation), and
- People living with one or more disabilities.

As discussed more in Section 8, statistics on total population, race, ethnicity, age, high school education level, household income relative to the poverty level, and limited English speaking households are obtained from the Census' American Community Survey (ACS) five-year averages for 2018-2022 (US Census Bureau, 2023b, 2024a, 2024b).

The Bar Graph tab is interactive, allowing you to change several properties. If you hover your mouse over the graph, a widget bar appears in the (upper righthand) corner of the graph. There are several widgets, including zoom and pan, and a widget that allows you to download the graph as an image file.

The Summary Table tab provides the number (or percent) of facilities that exceed the nationwide, state, and county geographic averages for each of the 14 demographic groups listed above. Similar to the bar graph, the table is interactive with changeable properties. There is a radio button below the table that allows you to show either the number of facilities (default) or the percent of facilities that exceed the geographic averages. Because you may be interested in how many facilities exceed the geographic averages by a certain amount, there is a slider widget below the table that allows you to select any percentage above the geographic averages, from 0 to 100%, in increments of 5%. For example, if you wanted to know how many facilities were twice each of the geographic averages, you would select 100% from the slider. There is also a button at the top of the table that allows you to export the table to a spreadsheet.

It should be noted that the nationwide, state, and county geographic averages provided in both the Bar Graph tab and Summary Table tab are population statistics not based on cancer or noncancer risk levels. For example, the county and state averages include all counties and states, respectively, with census block centroids within the scenario distance, not just the ones above the scenario risk level. These are included to allow a comparison with the facility estimates. The output files underlying these results are explained in Section 8.

## 4.8. Revise Census Data Option

The **REVISE CENSUS DATA** button, located on HEM's (left) sidebar menu allows you to change your U.S. Census file using the [Census Block Update](#) input file described in Section 3.5.9. Under the "Update Census" screen, as shown in **Figure 24**, click on the "Please select a census update file" button to select an update file from your computer. Once your census update file is selected, click on the "Update" button on this screen, which will apply the changes to a new version of the census file.

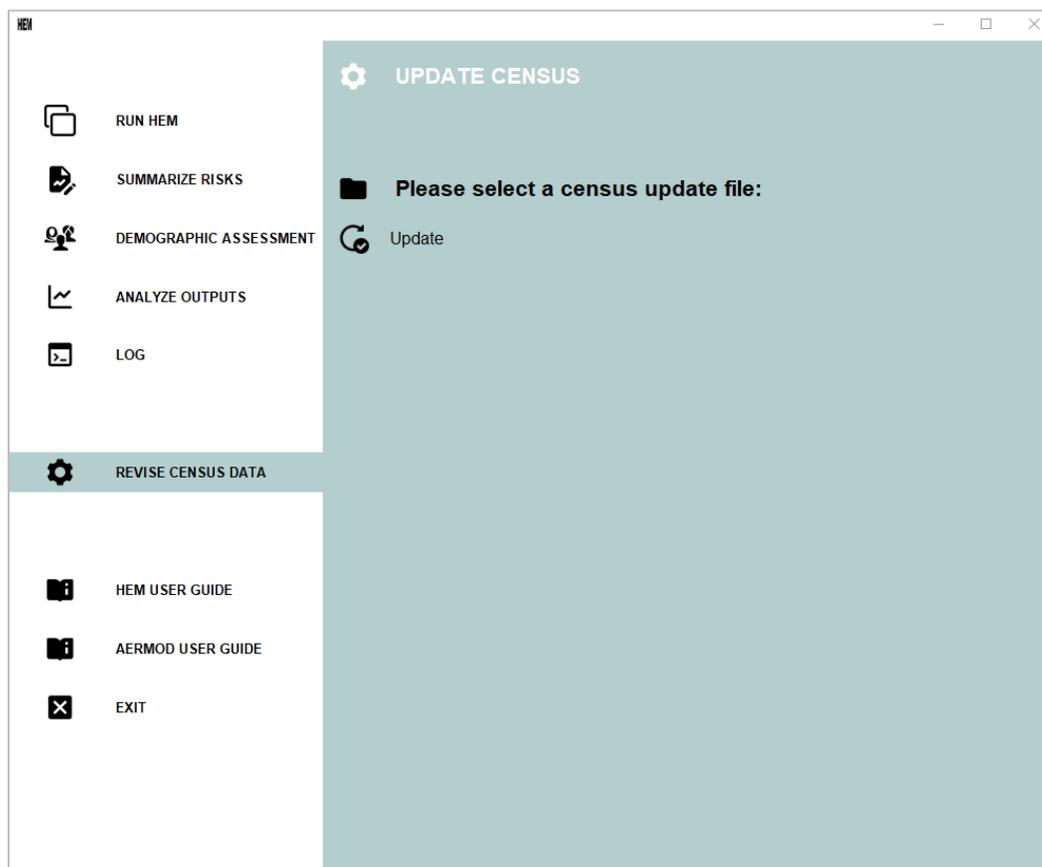
- **Note:** Changes are not applied directly to the Census file located in your HEM Census directory. Instead, all changes are reflected in a new file named census2020-updated.csv that is located in your HEM Census directory. **To use this changed Census file in HEM, rename or delete the original census2020.csv file and change the name of census2020-updated.csv to census2020.csv.**

You can use the census update file via this HEM interface to:

- Zero-out the population of a specific U.S. Census block,
- Move a block to a new latitude and longitude location,
- Delete/remove a census block, and
- Add a block receptor.

The reasons for making such revisions to your census dataset are discussed in Section 3.5.9.

**Figure 24. Revise Census Data Screen**



## 4.9. Error Messages and Failed Runs

When initiating a model run, HEM will perform a series of checks on your inputs to identify obvious errors that would cause the model (including AERMOD) to fail. Identifying these input errors prior to HEM attempting to model the erroneous values avoids most unsuccessful model runs and provides you with instructions to rectify the problem. Reviewing the AERMOD documentation (USEPA, 2024a, 2024e, 2025) is also important and helpful if you receive an error from HEM or from AERMOD (via the aermod.out file, described in Section 6.1.13) and the resolution of the error is not clear.

- For example, on the user interfaces that instruct you to select input files (discussed above in Sections 4.1 through 4.3), if you attempt to upload an input file with the wrong number of columns (fields), then an error message will pop-up indicating that the file you uploaded had “x” columns but should have “y” columns.
- HEM will also compare the Source IDs in your input files to ensure they match. If the Source IDs in your Emissions Location file do not match the Source IDs in your HAP Emissions file, then an error message will pop-up indicating that “Your Emissions Location and HAP Emissions files have mismatched Source IDs. Please correct one or both files with matching sources and upload again.”

- Additionally, if you entered a value for an input parameter that is out-of-range of the acceptable values for that parameter, then HEM will replace your problematic value with the default value, and indicate the replacement in the log file, noted above in Section 4.4. The values HEM defaults to are listed for applicable parameters within each standard input file starting in Section 3.2.

A sample of the kinds of pop-up and log error messages and their meanings are listed in **Table 37**. Note: The error messages listed in Table 37 are not exhaustive with respect to the out-of-range messages HEM provides.

**Table 37. Sample List of Error Messages and Causes in HEM**

Pop-Up and/or Log Error Message	Meaning / Cause
"One or more facility IDs are missing in the <file> List."	The uploaded file contains records without a valid Facility ID.
"One or more records are duplicated in the <file> List (key=fac_id)"	The uploaded Facility List Options file contains duplicate facility ID's.
"One or more met stations referenced in the Facility List are invalid."	The uploaded Facility List Options file contains facilities with met station references that are not present in the master list of met stations.
"rural_urban value invalid. Will be defaulted based on census data."	The rural_urban field in the Facility List Options file is not "R", "U" or blank. The field will be set to blank and HEM will determine rural/urban status based on population density.
"Invalid value (urban_pop): Defaulting to 50,000."	Rural_urban field in the Facility List Options file is set to "U" but an invalid urban population value (< 0) is present. The urban population will be set to 50,000.
"model distance value out of range. Defaulting to 3000."	The uploaded Facility List Options file contains a modeling distance that is out of range (< 0 or > 50,000m). The modeling distance will be set to 3,000m.
"max distance value out of range. Defaulting to 50000."	The uploaded Facility List Options file contains a maximum distance that is out of range (<= 0 or > 50,000m). The maximum distance will be set to 50,000m.
"model distance value is larger than maximum distance. Defaulting max_dist to 50000."	The uploaded Facility List Options file contains a modeling distance that is larger than the maximum distance. The maximum distance will be set to 50,000m.
"One or more source IDs are missing in the <file> List."	The uploaded file contains records without a valid Source ID.
"One or more pollutants are missing in the <file> List."	The uploaded file contains records without a valid pollutant (HAP).
"One or more locations are missing a coordinate system in the <file> List."	The uploaded file contains records without valid coordinate system values.
"There is at least one elevation value in the Alternate Receptor file that is less than -415m or greater than 8850m. Please correct and retry."	The uploaded Alternate Receptor file contains at least one elevation that is out of range (< -415m or > 8,850m). The file must be corrected.
"Some receptors have negative population values in the Alternate Receptor file. Please correct and retry."	The uploaded Alternate Receptor file contains at least one receptor with a negative population value. The file must be corrected.
"Some 'P' receptors are missing population values in the Alternate Receptor file. Please correct and retry."	The uploaded Alternate Receptor file contains at least one receptor of "P" type that has no population value. The file must be corrected.

Pop-Up and/or Log Error Message	Meaning / Cause
"One or more receptors have an invalid Location Type in the Alternate Receptors file. Valid types are L or U. Please correct and retry."	The uploaded Alternate Receptor file contains at least one receptor whose Location Type is not L or U. The file must be corrected.
"There are longitudes in the Alternate Receptors file that are < -180 or > 180. Please correct these values."	The uploaded Alternate Receptor file contains at least one receptor with an out-of-range longitude. The file must be corrected.
"There are latitudes in the Alternate Receptors file that are < -80 or > 85. Please correct these values."	The uploaded Alternate Receptor file contains at least one receptor with an out-of-range latitude. The file must be corrected.
"There are UTM Easting coordinates in the Alternate Receptors file that are < 160000 or > 850000. Please correct these values."	The uploaded Alternate Receptor file contains at least one receptor with an out-of-range UTM Easting. The file must be corrected.
"There are UTM Northing coordinates in the Alternate Receptors file that are < 0 or > 1000000. Please correct these values."	The uploaded Alternate Receptor file contains at least one receptor with an out-of-range UTM Northing. The file must be corrected.
"Alternate Receptors file contains malformed UTM zone."	The uploaded Alternate Receptor file contains at least one receptor with a UTM zone that is not correctly formatted. The UTM zone must contain the zone number plus hemisphere string ("S" or "N"). The file must be corrected.
"Alternate Receptors file contains at least one invalid UTM zone that is < 1 or > 60. "	The uploaded Alternate Receptor file contains at least one receptor with a UTM zone that is out-of-range (<1 or >60). The file must be corrected.
"Alternate Receptors file contains receptor types that are not P, B, or M."	The uploaded Alternate Receptor file contains at least one receptor with a receptor type that is not "P", "B", or "M". The file must be corrected.
"One or more source types are missing a valid value in the Emissions Locations List."	The uploaded Emissions Location file contains records without a valid source type value for one or more fields.
"The following pollutants were not found in HEM's Dose Response Library: [list of HAP names not found]. Would you like to amend your HAP Emissions file? (They will be removed otherwise.)"	One or more HAP listed in the HAP Emissions file is not included in the Dose Response Library. Note: If you do not revise your HAP Emissions file to include only HAP listed in your Dose Response library, then HEM will drop those HAP for the current run. Alternatively, you may exit the run and amend the Dose Response Library before starting a new run.
"Facility <fac>: [lat/lon] value out of range in the Emissions Locations List."	The uploaded Emissions Location file contains an out-of-range latitude or longitude value for one or more sources.
"Facility <fac>: UTM zone value malformed or invalid in the Emissions Locations List."	The uploaded Emissions Location file contains an invalid UTM zone value.
"Error: Some non-numeric values were found in numeric columns in this data set."	The uploaded file contains non-numeric values in a field that should have only numbers.
"Length Mismatch: Input file has x columns but should have y columns."	The uploaded file contains the wrong number of columns.
"<file> parameters are specified in the Facilities List Options file. Please upload a <file> File."	The Facility List Options file specifies modeling options requiring additional input files that have not been uploaded.

Pop-Up and/or Log Error Message	Meaning / Cause
<p>"AERMOD models building downwash from point sources only (i.e., vertical P, horizontal H, or capped C point sources). Your building dimensions file includes non-point sources. Please edit your building dimensions file to remove all non-point sources."</p>	<p>AERMOD models building downwash of emissions from vertical point (P), capped point (C), and horizontal point (H) source types only. The uploaded Facility List Options file indicates building downwash for one or more facilities and the Source IDs for those facilities in the uploaded building dimensions input file include sources other than P, C, or H types.</p>
<p>"AERMOD cannot currently model deposition or depletion of emissions from buoyant line sources, and the Emissions Location file includes a buoyant line source for one or more facilities. Please disable deposition and depletion for each of these facilities or remove the buoyant line source(s)."</p>	<p>The current AERMOD version can model deposition and/or depletion from all source types except buoyant lines. The uploaded Facility List Options file indicates deposition and/or depletion for one or more facilities and one or more Source IDs for those facilities in the uploaded Emissions Location file are buoyant lines.</p>
<p>"AERMOD's FASTALL option cannot be used with buoyant line sources, and the Emission Location file includes a buoyant line source for one or more facilities. Please disable FASTALL for each of these facilities or remove the buoyant line source(s)."</p>	<p>The current AERMOD version does not allow the FASTALL option with buoyant line sources. The uploaded Facility List Options file indicates FASTALL for one or more facilities and one or more Source IDs for those facilities in the uploaded Emissions Location file are buoyant lines.</p>
<p>"AERMOD ran unsuccessfully. Please check the error Section of the aermod.out file in the &lt;fac&gt; output folder."</p>	<p>AERMOD didn't run successfully, for a reason specified in the aermod.out file.</p>
<p>"At least one buoyant line group ID in the Buoyant Line Parameter file is longer than 8 characters."</p>	<p>The Buoyant Line Parameter input file contains at least one buoyant line group ID that is longer than 8 characters, which is the maximum length.</p>
<p>"There is at least one buoyant line group in the Buoyant Line Parameter file with source IDs that do not have the same parameters."</p>	<p>All Source IDs within one buoyant line group must use the same parameters. The Buoyant Line Parameter input file contains at least one buoyant line group where this is not the case.</p>
<p>"The Buoyant Line Parameter file contains one or more facilities with non-unique source IDs."</p>	<p>The Source IDs of each buoyant line group must be unique. This Buoyant Line Parameter input file contains at least one facility with non-unique Source IDs.</p>
<p>"For at least one facility, there are mismatched buoyant line Source IDs in the Emission Location file and the Buoyant Line Parameter file."</p>	<p>All Source IDs identified as buoyant line sources in the Emission Location file and part of a buoyant line group must also appear in the Buoyant Line Parameter file. Either a Source ID is in the Buoyant Line Parameter file and is not identified as a buoyant line source in the Emissions Location file, or the Source ID is identified as a buoyant line source in the Emissions Location file but is missing in the Buoyant Line Parameter file.</p>
<p>"Buoyant line parameters for &lt;facility list&gt; have not been assigned. Please edit the 'source type' column in the Emissions Location file."</p>	<p>The Buoyant Line Parameter input file contains at least one facility that does not have any Source IDs identified as buoyant line sources in the Emissions Location input file. The Emissions Location file should be edited to correct this.</p>
<p>"_ At least one buoyant line group ID in the Buoyant Line Parameter file is blank. Please add an ID._"</p>	<p>The Buoyant Line Parameter file cannot contain a blank Group ID. At least one Group ID is blank in this file.</p>
<p>"Cannot generate summaries because there is no Facility_Max_Risk_and_HI Excel file in the folder you selected."</p>	<p>The Risk Summary reports could not be run because the Facility_Max_Risk_and_HI output file is needed, but is missing.</p>

Pop-Up and/or Log Error Message	Meaning / Cause
"You must have at least one configuration."	At least one combination (configuration), including radius and risk/HI level, must be entered on the Demographic Assessment interface to initiate a run.
"Please ensure all run combinations contain a value for radius and the selected risk threshold."	For one or more combinations requested, the needed parameters (radius and/or risk/HI level) were not entered on the Demographic Assessment interface.
"Please ensure all radius values are numbers."	One or more radius values were input with non-numeric characters on the Demographic Assessment interface.
"Please ensure all radius values satisfy 1 <= radius <= 50."	A radius value less than 1 km or greater than 50 km was entered on the Demographic Assessment interface, which are outside the allowable range of radius values.
"The selected HEM output folder included a facility run at max dist = [X] km. Please ensure all radii are <= this value."	A radius requested on the Demographic Assessment interface was larger than that used for the modeling domain of at least one facility (i.e., the max distance in the Facility List Options file).
"Please ensure all cancer risk values are one of the following: [1, 5, 10, 20, 30, 40, 50, 100, 200, 300]"	For the current HEM version, the value entered for the risk level on the Demographic Assessment interface must be one of the values shown.
"Please ensure all HI values are one of the following: [1, 2, 3, 4, 5, 6, 7, 8, 9, 10]"	For the current HEM version, the value entered for the HI level on the Demographic Assessment interface must be one of the values shown.
"The folder selected for a Demographic Assessment contains HEM outputs that use Alternate Receptors. These cannot be used with the Demographic Assessment Tool."	HEM's Demographic Assessment module can only run a demographic analysis on outputs of a modeling run that used U.S. Census receptors.
"The folder selected for a Demographic Assessment is deeply nested or contains long names. Consider using a different path to avoid unexpected behavior that arises from exceeding the Windows path length limit of 260 characters."	HEM's Demographic Assessment output file names tend to be long to cover the run parameters (especially the facility-specific output file names). If the path length plus file name length is longer than 260 characters, the file may not be written.
"Unable to find required ACS data. Please check your HEM resources folder and try again."	HEM could not find required American Community Survey data necessary for a Demographic Assessment run.
"Please check the output folder for a properly named Facility Max Risk and HI file."	HEM could not find a facility max risk and HI file with the expected name. For a Demographic Assessment run, the prefix used for this file must be the same as the run group folder name: '[rungroup] facility_max_risk_and_hi.xlsx'.
"The directory chosen does not contain a pop sub-directory. Please ensure that the Demographic Assessment tool has been run on this directory."	The directory chosen for the "View Demographic Assessment outputs in web browser" selection on the Analyze Outputs interface does not contain a sub-directory named "pop". This viewing tool can only be run on a directory where a Demographic Assessment has been performed [and has produced a pop folder].
"There are no discrete receptors within the max distance of this facility. Aborting processing of this facility."	No Census blocks or Alternate Receptors could be found within the maximum modeling distance of the facility. The facility will not be processed.

Pop-Up and/or Log Error Message	Meaning / Cause
"The following user receptors have coordinates that are already in the Alternate Receptor data. They will be removed from the user receptor list."	User receptors cannot have IDs that already exist within the Alternate Receptor data. Such user receptors will not be used in the modeling of this facility.
"The following user receptors have IDs that are already in the Census data: They will be removed from the user receptor list."	User receptors cannot have IDs that already exist within the Census data. Such user receptors will not be used in the modeling of this facility.
"Error! Modeling distance is less than first ring."	The modeling distance must be larger than the radius of the first polar ring. If not, this facility will be skipped.
"Some polar elevations are higher than the hill height. Aborting processing for this facility."	The elevation of a polar receptor cannot be higher than the hill height of that receptor. If the elevation is higher than the hill height, then the facility is skipped.
"Your computer was unable to obtain elevation data for this model run. This HEM run will stop. This problem may be due to your Internet connection or the elevation data not being available from the USGS. Your options are to run this Run Group with no elevation or to use the off-line elevation method. More detail about this error is available in the log."	You chose (via your Facility List Options file) to use elevated terrain with the online method for this facility but there is no Internet connection available and/or the USGS server is down/not reachable. HEM will abort this run, indicate in the log that elevation data was not able to be obtained, and provide the associated python error message.

If HEM is unable to model a facility or facilities due to errors in the inputs, HEM will not only note the errors in the log file but will also produce an Excel file entitled "Skipped Facilities" in the run group's output subfolder (as noted in Section 6.2.4). You can use the list of skipped facilities in column A of this output file to create a new Facility List Options file, after you fix the errors, to model these facilities. This is discussed further in Section 10.

Finally, **in the event of a failed modeling run, you should close down HEM and then re-start before your next modeling run.** A full shutdown and re-start of HEM ensures the memory has been cleared, which will reset values in the underlying model code and avoid a variety of potential issues in the next run.

## 5. HEM Modeling Calculations for Each Facility

Section 3 of this User's Guide describes the HEM input files, and Section 4 describes the step-by-step instructions for initiating a HEM run. This section describes the internal modeling algorithms and simplifying assumptions employed by HEM during the modeling run.

We list the AERMOD options used to model emission dispersion from each facility and describe the methodology HEM implements to transform AERMOD's single pollutant concentration modeling into multiple pollutant concentration estimations. This section also discusses HEM's post-dispersion computation of health impacts at modeled receptors, including cancer risk and noncancer health hazards, as well as HEM's calculations to estimate the contributions of individual pollutants and emission sources to the estimated concentrations and health impacts at the modeled receptors.

### 5.1. Dispersion Modeling

As previously noted, HEM carries out dispersion modeling by running EPA's preferred and recommended steady-state Gaussian plume air dispersion model, AERMOD. AERMOD version 24142 is used in HEM5.0. Section 3 describes a number of input options you can specify for running AERMOD—for example, incorporating building downwash, deposition and depletion, and emissions variations. This section discusses the AERMOD options that HEM implements by default. In addition, this section describes the dilution factor methodology used in HEM for modeling multiple pollutants based on AERMOD's unit-emission rate modeling.

#### 5.1.1. Regulatory Default, ALPHA and BETA Options

HEM uses primarily the regulatory default options when running AERMOD. These options include the following:

- Uses the elevated terrain algorithms requiring input of terrain height data,
- Uses stack-tip downwash (except for building downwash cases),
- Uses the calms processing routines, and
- Uses missing data processing routines.

However, it should also be noted that AERMOD includes model option keywords ALPHA and BETA for certain modeling options. The ALPHA keyword indicates one or more options are being used that are scientific/formulation updates considered to be in the research phase and have not been fully evaluated and peer reviewed by the scientific community; and/or non-scientific model options in development that still need rigorous testing and for which EPA is seeking feedback from the user community. The BETA keyword indicates one or more options are being used that have been fully vetted through the scientific community with appropriate evaluation and peer review. BETA options are planned for future promulgation as regulatory options in AERMOD. See the AERMOD Model Formulation document for more information (Appendix B of USEPA, 2024b).

For the current version of HEM-AERMOD, the only ALPHA options available are Method 2 particle deposition and gaseous (vapor) deposition. There are no BETA options in AERMOD version 24142. To keep HEM general, the ALPHA and BETA keywords will always be included in

the AERMOD runstream file prepared by HEM, even when no ALPHA or BETA options are being used.

### 5.1.2. Dilution Factors

HEM uses AERMOD to compute a series of dilution factors, in units of  $\mu\text{g}/\text{m}^3$  per g/sec, specific to each emission source and receptor. This approach more quickly analyzes the impacts of multiple pollutants than if separately modeling each pollutant. The dilution factor for a particular emission source and receptor is defined as the predicted ambient impact from the given source and at the given receptor, divided by the emission rate from the given source.

If you choose not to analyze deposition or depletion, then the dilution factor does not vary from pollutant to pollutant. If you do select deposition or depletion, HEM will compute separate dilution factors for gaseous and particulate pollutants. In addition, you can specify different particle sizes and densities for each particulate matter emission source. To use pollutant-specific parameters for particulates and/or gases requires a separate Source ID for each pollutant at a given source. As noted in Section 3.4 (Table 8), you can create multiple Source IDs using the same locations and source parameters to accommodate different pollutants when modeling deposition or depletion.

## 5.2. Estimating Risks and Hazard Indices

HEM estimates the total cancer risk, noncancer hazard indices (HIs) and optionally acute hazard quotients (HQs) for all U.S. Census block locations or alternate receptor locations in the modeling domain, all user receptors, and all receptors in the polar network. Receptors in the HEM domain fall into two categories: those with impacts explicitly modeled by HEM-AERMOD, and those with impacts estimated via interpolation rather than explicit modeling. Section 5.2.1 describes methods used to calculate cancer risks and noncancer health hazards for receptors that HEM-AERMOD explicitly models. Section 5.2.2 describes the interpolation approach used to estimate cancer risks and noncancer health hazards at receptors not explicitly modeled.

Based on the results for U.S. Census blocks or alternate receptors, and other receptors, HEM estimates the maximum individual risk (MIR), maximum target organ specific HI (TOSHI), and optionally high acute value for populated receptors (Section 5.2.3); as well as the maximum impacts for all offsite receptors, including unpopulated locations (Section 5.2.4). For these locations, the model calculates the contributions of individual pollutants and emission sources to cancer risks, chronic HI, and optionally acute HQ (Section 5.2.5).

### 5.2.1. Explicit Modeling of Inner Receptors, User Receptors and Polar Receptors

HEM calculates cancer risks, TOSHIs, and optionally acute HQs for three types of discrete receptors that are explicitly modeled by AERMOD:

1. U.S. Census blocks or alternate receptors within the user-defined modeling [“cutoff” distance](#) for explicit modeling of individual receptors,
2. all [user receptors](#), and
3. the user-defined [polar receptor network](#).

As noted above in Section 5.1.2 regarding Dilution Factors, HEM combines pollutants into two categories — particulates and gases (vapor) — for the purposes of dispersion modeling. The

model retains these categories to calculate cancer risks, noncancer HI and optionally acute HQ. HEM uses Equations 1, 2, 3, and 4:

For cancer risk:

$$CR_T = \sum_{i,j} CR_{i,j} \quad (1)$$

$$CR_{i,j} = DF_{i,j} \times CF \times \sum_k [E_{i,k} \times URE_k] \quad (2)$$

For noncancer hazard indices:

$$HI_T = \sum_{i,j} HQ_{i,j} \quad (3)$$

$$HQ_{i,j} = DF_{i,j} \times CF \times \sum_k \left[ \frac{E_{i,k}}{RfC_k \times 1000 \frac{\mu g}{mg}} \right] \quad (4)$$

where:

- CR<sub>T</sub> = total cancer risk at a given receptor (probability for one person)
- Σ<sub>i,j</sub> = the sum over all sources i and pollutant types j (particulate or gas)
- CR<sub>i,j</sub> = cancer risk at the given receptor for source i and pollutant type j
- DF<sub>i,j</sub> = dilution factor [(μg/m<sup>3</sup>) / (1000 g/sec)] at the given receptor for source i and pollutant type j
- CF = conversion factor, 0.02877 [(g/sec) / (tons/year)]
- Σ<sub>k</sub> = sum over all pollutants k within pollutant group j (particulate or gas)
- E<sub>i,k</sub> = emissions (tons/year) of pollutant k from source i
- URE<sub>k</sub> = cancer unit risk estimate [1/(μg/m<sup>3</sup>)] for pollutant k (cancer risk for an individual exposed to 1 μg/m<sup>3</sup> over a lifetime)
- HI<sub>T</sub> = TOSHI at a given receptor and for a given organ
- HQ<sub>i,j</sub> = organ-specific hazard quotient at the given receptor for source i and pollutant type j
- RfC<sub>k</sub> = noncancer health effect reference concentration (mg/m<sup>3</sup>) for pollutant k (concentration at and below which no adverse health effect is expected)

The above equations are equivalent to the following simpler Equations 5 and 6:

$$CR_T = \sum_{i,k} AC_{i,k} \times URE_k \quad (5)$$

$$HI_T = \sum_{i,k} AC_{i,k} / \left( RfC_k \times \frac{1000 \mu g}{mg} \right) \quad (6)$$

where:

- AC<sub>i,k</sub> = ambient concentration (μg/m<sup>3</sup>) for pollutant k at the given receptor. This is the same as [E<sub>i,k</sub> × DF<sub>i,j</sub> × CF]

However, the use of these simpler equations would require modeling all pollutants individually in AERMOD and performing separate risk calculations for each pollutant.

If the cancer unit risk estimate (URE) is not available for a given pollutant, then that pollutant is not included in the calculation of cancer risk. Likewise, if the noncancer reference concentration (RfC) is not available for a given pollutant, that pollutant is not included in the calculation of HI.

**Note:** Separate reference concentrations are used for acute HQ and chronic HQ. As discussed in Section 2.2.1, for acute impacts, instead of the chronic RfC, the short-term concentration is compared with various threshold or benchmark levels for acute health effects (e.g., the California EPA reference exposure level [REL] for no adverse effects).

## 5.2.2. Interpolated Modeling of Outer Receptors using the Polar Receptor Network

At U.S. Census blocks and alternate receptors outside of the user-defined modeling [“cutoff” distance](#) for individual block modeling, HEM estimates cancer risks, noncancer HI and optionally acute HQ by interpolation from the [polar receptor network](#). HEM estimates impacts at the polar grid receptors using AERMOD modeling results and the algorithms described in Section 5.2.1.

If you choose to model terrain effects with the elevation option in your Facility List Options file, then HEM estimates an elevation and hill height for each polar receptor as described in Section 3.2.7, depending on whether your run uses the [default online method](#) for determining elevations and hill heights, or the [alternative offline method](#).

HEM interpolates the impacts at each outer U.S. Census block receptor or alternate receptor (outside the modeling cutoff distance) from the four nearest polar grid receptors. The interpolation is linear in the angular direction, and logarithmic in the radial direction, as summarized in Equations 7, 8, and 9:

$$I_{a,r} = I_{A1,r} + (I_{A2,r} - I_{A1,r}) \times \frac{a-A1}{A2-A1} \quad (7)$$

$$I_{A1,r} = \exp\{\ln(I_{A1,R1}) + [\ln(I_{A1,R2}) - \ln(I_{A1,R1})] \times [(\ln r) - \ln(R1)] / [\ln(R2) - \ln(R1)]\} \quad (8)$$

$$I_{A2,r} = \exp\{\ln(I_{A2,R1}) + [\ln(I_{A2,R2}) - \ln(I_{A2,R1})] \times [(\ln r) - \ln(R1)] / [\ln(R2) - \ln(R1)]\} \quad (9)$$

where:

- $I_{a,r}$  = the impact (cancer risk, chronic HI or acute HQ) at an angle,  $a$ , from north, and radius,  $r$ , from the center of the modeling domain
- $a$  = the angle of the target receptor, from north
- $r$  = the radius of the target receptor, from the center of the modeling domain
- $A1$  = the angle of the polar network receptors immediately counterclockwise from the target receptor
- $A2$  = the angle of the polar network receptors immediately clockwise from the target receptor
- $R1$  = the radius of the polar network receptors immediately inside the target receptor
- $R2$  = the radius of the polar network receptors immediately outside the target receptor

### 5.2.3. Maximum Individual Risks, Hazard Indices, and Hazard Quotients

HEM evaluates the predicted chronic impacts for all populated receptors to identify the locations of the MIR and the highest HI for various target organs (maximum TOSHIs). For these calculations, populated receptors include all U.S. Census block locations or alternate receptors and any user receptors you included in the run designated as type P (for populated). In general, type P receptors should include houses near the facility, as well as other residences not represented well by the location of the U.S. Census block centroids or alternate receptors.

The maximum cancer risk may occur at a location other than the maximum HI for a given organ, or TOSHI. Likewise, TOSHI locations may differ: the location of the maximum HI for one organ will not necessarily be the same as the location for a different organ. HEM performs a separate evaluation of the maximum impact location for each health impact.

The model also tests for instances where U.S. Census block centroids, alternate receptors or type P user receptors may be located on facility property. To do so, HEM calculates the distance between each receptor and each emission source. These distances are compared with the [overlap distance](#) that you specified in the Facility List Options file. If a populated-type receptor is located within the overlap distance, then HEM does not use these calculated results for this receptor to estimate the maximum individual cancer risk or maximum HI for populated areas, because the MIR and max TOSHI locations are defined as being off facility property. Instead, the model assumes the impacts at the overlapping receptor to be equal to the maximum impacts for any receptors that do not overlap facility property. This could include both populated receptors and unpopulated polar receptors, as long as they do not overlap facility property.

If you chose to model [acute \(short-term\) impacts](#) in the Facility List Options file, HEM will also evaluate predicted acute impacts for all receptors to identify the locations of the highest acute HQs. For the acute calculations, all receptors are evaluated – both populated and unpopulated receptors – including U.S. Census blocks or alternate receptors, all user receptors you may have specified and all polar receptors. As described in the preceding paragraph, HEM also checks to ensure that the maximum populated acute receptor is not overlapped. In the case of an overlapped populated receptor, then the next highest non-overlapped populated receptor is chosen.

### 5.2.4. Maximum Offsite Impacts

In addition to evaluating the maximum cancer risks, chronic HI, and acute HQ (if modeled) for populated receptors (including census blocks, alternate receptors, and P type user receptors), HEM evaluates maximum offsite impacts for all receptors, including unpopulated receptors. All U.S. Census blocks or alternate receptors, all user receptors (populated and unpopulated types), and all points (unpopulated receptors) on the polar receptor network are included in the evaluation of maximum offsite impacts. Only receptors that are found to be overlapping emission sources are excluded in the evaluation.

### 5.2.5. Contributions of Different Pollutants and Emission Sources

HEM calculates the contributions of different pollutants and emission sources to cancer risks, chronic HI, and acute HQ (if modeled) at the receptors where impacts are highest, both for populated receptors and for all offsite receptors. As noted in Section 5.2.1, HEM groups pollutants together when calculating total risks, HI, and acute HQ (if modeled) for the large number of receptors that are typically included in an overall modeling domain. Thus, the model

does not compute the contributions of individual pollutants and emission sources for all receptors.

However, HEM retains the information needed to determine the contributions of individual pollutants and emission sources at the receptors where impacts are highest. HEM calculates these contributions using Equations 10, 11, and 12:

$$AC_{i,k,m} = E_{i,k} \times DF_{i,j,m} \times CF \quad (10)$$

$$CR_{i,k,m} = AC_{i,k,m} \times URE_k \quad (11)$$

$$HQ_{i,k,m} = \frac{AC_{i,k,m}}{RfC_k \times \frac{1000 \mu g}{mg}} \quad (12)$$

where:

- $AC_{i,k,m}$  = the predicted ambient concentration ( $\mu\text{g}/\text{m}^3$ ) for pollutant k, from source i, at receptor m (as shown in **sample calculation below**<sup>9</sup>)
- $E_{i,k}$  = emissions (tons/year) of pollutant k from source i
- $DF_{i,j,m}$  = the dilution factor [ $(\mu\text{g}/\text{m}^3) / (1000 \text{ g/sec})$ ] for source i, receptor m, and pollutant group j, which includes pollutant k
- CF = conversion factor,  $0.02877 [(g/sec) / (ton/year)]$
- $CR_{i,k,m}$  = the estimated cancer risk from source i, and pollutant k, at receptor m
- $URE_k$  = cancer unit risk estimate [ $1/(\mu\text{g}/\text{m}^3)$ ] for pollutant k (cancer risk for an individual exposed to  $1 \mu\text{g}/\text{m}^3$  over a lifetime)
- $HQ_{i,k,m}$  = the organ-specific hazard quotient as a result of emissions of pollutant k, from source i, at receptor m
- $RfC_k$  = noncancer health effect reference concentration ( $\text{mg}/\text{m}^3$ ) for pollutant k concentration at and below which no adverse health effect is expected)

**Note:** The methodology outlined above for cancer and chronic noncancer impacts is similar for acute impacts, although acute emissions are used (including any [acute factor/multiplier](#) you may have indicated in your Facility List Options files) and acute benchmarks are used (discussed in Section 2.2.1).

### 5.3. Population Exposures and Incidence

Using the predicted impacts for U.S. Census blocks or alternate receptors, HEM estimates the populations exposed to various cancer risk levels and noncancer HI levels. To do so, the model adds up the populations for receptors that have predicted cancer risks or noncancer HI above a

<sup>9</sup> **Sample calculation:** If at a particular receptor location, AERMOD (in the AERMOD outputs discussed in Section 6.1.13) calculates a unit concentration of  $3,853.5 \mu\text{g}/\text{m}^3$  caused by a specific source, to derive the concentration of a specific pollutant (e.g., arsenic) at that receptor location caused by that source, HEM uses the tons per year (tpy) emission rate of arsenic from that source in your HAP Emissions input file (e.g., 0.01164 tpy) as follows:

$$0.01164 \text{ tpy arsenic} * (3,853.48 \mu\text{g}/\text{m}^3) / (1,000 \text{ g/sec}) * 0.02877 \text{ (g/sec)/tpy} = 0.00129 \mu\text{g}/\text{m}^3 \text{ arsenic at that location caused by that source}$$

given threshold. For cancer risk, around each facility HEM predicts the number of people exposed to a risk greater than or equal to the following thresholds:

- 1 in 1,000 (or 1,000-in-1 million) risk,
- 1 in 10,000 (or 100-in-1 million) risk,
- 1 in 20,000 risk,
- 1 in 100,000 (or 10-in-1 million) risk,
- 1 in 1,000,000 (or 1-in-1 million) risk, and
- 1 in 10,000,000 (or 0.1-in-1 million) risk.

For noncancer HI, around each facility HEM predicts the number of people exposed to each of the [14 TOSHIs](#) above the following thresholds:

- Greater than 100,
- Greater than 50,
- Greater than 10,
- Greater than 1.0,
- Greater than 0.5, and
- Greater than 0.2.

If you opt to model acute impacts, HEM will provide the acute concentration for every pollutant at every receptor, including every populated receptor, and will also include the population of those receptors (whether U.S. Census blocks or alternate receptors). Because of the transitory nature of acute exposures, acute health impacts are modeled not only where people reside but at all receptors in the modeling domain. Therefore, the highest acute health impacts often occur at unpopulated polar receptor locations close to the modeled facility. **Note:** The maximum acute impacts will occur at different times for different spatial locations (receptors) and are therefore not additive. For this reason, population exposures are not tallied by HEM for acute health impacts, as they are for cancer and chronic noncancer TOSHI.

HEM also estimates the contributions of different pollutants and emission sources to total annual cancer incidence for the overall modeling domain using Equations 13, 14, and 15:

$$CI_{i,k,m} = CR_{i,k,m} \times P_m / LT \quad (13)$$

$$CI_m = \sum_{i,k} [CI_{i,k,m}] \quad (14)$$

$$TCI = \sum_m [CI_m] \quad (15)$$

where:

- $CI_{i,k,m}$  = the estimated annual cancer incidence (excess cancer cases/year) for populated receptor m due to emissions from pollutant k and emission source i
- $CR_{i,k,m}$  = the estimated cancer risk from source i, and pollutant k, at populated receptor m
- $P_m$  = the population of populated receptor m
- $LT$  = the average lifetime used to develop the cancer unit risk estimate, 70 years
- $\sum_{i,k}$  = the sum over all modeled pollutants k and emission sources i

- $CI_m$  = the estimated total cancer incidence for populated receptor  $m$  due to emissions from all modeled pollutants and emission sources
- $\Sigma_m$  = the sum over all populated receptors  $m$  in the modeling domain
- TCI = the estimated total annual cancer incidence (excess cancer cases/year) for the population living within the modeling domain from all modeled pollutants and emission sources

Note the above incidence calculations are made for the pollutant group/types “ $j$ ” being modeled (whether particulate, gas, or combined) to which each pollutant “ $k$ ” belongs. For each facility, HEM provides the estimated total annual cancer incidence (excess cancer cases/year) predicted to be caused by all modeled pollutants emitted from all modeled sources. Increasing in specificity, HEM also provides the annual cancer incidence predicted to be caused by each emission source at a facility for all pollutants emitted from that source, as well as by each pollutant from all sources emitting that pollutant at a facility. At the greatest level of specificity, HEM provides the estimated cancer incidence broken down by both pollutant and emission source – that is, for every pollutant individually from each source separately.

## 5.4. Summarizing Human Health Impacts

Section 5.1 discusses how HEM uses AERMOD for dispersion modeling of your inputs to produce multi-pollutant concentration predictions at the receptors in your modeling domain, around a given facility. Sections 5.2 and 5.3 discuss the methodology and algorithms used by HEM to transform predicted concentrations into human health impacts around each modeled facility. The following sections describe the outputs produced by HEM for each facility and for your run group as a whole, which allow you to summarize the risk and health impacts per facility and across all facilities you choose to group together in a modeling run.

## 6. HEM Output Files

After running the AERMOD dispersion model to determine receptor-specific concentrations, HEM completes the post-AERMOD risk and exposure calculations (explained in Section 5). HEM then produces a variety of facility-specific, source-specific, and pollutant-specific files containing concentration, cancer risk and incidence, noncancer hazard quotients (HQ) and hazard indices (HI), and population exposure output results. These outputs are discussed in Section 6.1. HEM also produces three summary output files, based on the results for the entire run group (e.g., source category/sector) of modeled facilities. These multi-facility outputs are updated after the output files for the individual facilities have been created and essentially concatenate the individual facility results into group-wide summary files. These run group summary files are discussed in Section 6.2.

If AERMOD was not run and instead you provided a user-supplied concentration file, then the output files created by HEM are similar to the facility-specific files created in a typical HEM run when AERMOD is used (discussed in Section 6.1) but are fewer because some files are not relevant. The files created under the user-supplied concentrations option are discussed in Section 6.3.

### 6.1. Facility-Specific Outputs

A standard HEM-AERMOD run produces the following facility-specific output files:

- 6 risk and HI files (maximum individual risk [MIR], maximum offsite impacts, risk breakdown, block summary chronic, ring summary chronic, and source risk KMZ);
- 3 incidence and population exposure files (incidence, cancer risk exposure, noncancer risk exposure);
- 3 concentration files (all inner receptors, all outer receptors, all polar receptors);
- dispersion model output file(s) from AERMOD (the number depends on the type run); and
- 1 file cataloging modeling options used (input selection options).

In addition, depending on the modeling options chosen, a HEM run may produce 3 other non-standard/optional files, including the following 3 acute files:

- acute breakdown;
- acute chem populated; and
- acute chem max.

These facility-specific standard and optional files are described below in this section. Note: In addition to the HEM output files described in this section, several additional files are available via HEM's Analyze Outputs screen described in Section 4.7 (e.g., you can download data after generating risk contours, as noted in Section 4.7.1.4).

#### 6.1.1. Maximum Individual Risk

The Maximum Individual Risk output file provides the MIR value for cancer and the max TOSHI value for noncancer chronic health effects predicted for any populated receptor that does not

overlap facility property, such as census blocks, alternate receptors, and user receptors that are designated as “populated”.

- Note: User “P” receptors are considered populated receptors because of how HEM treats them (e.g., they can be the MIR location), even though they are assigned a population of zero.

This file also indicates the population and location of the receptors where these maxima occur.

**Note:** The MIR and max TOSHIs may or may not occur at the same receptors/locations, depending on what pollutants are being emitted from one source versus another source (indicated in the HAP Emissions input file) and the locations and parameters of the sources (indicated in the Emissions Location input file). **Table 38** describes the fields of information provided in the Maximum Individual Risk file. A sample Maximum Individual Risk output file is provided in Appendix A.

**Table 38. Fields Included in the Maximum Individual Risk & Maximum Offsite Impacts Files**

Field	Description
Parameter	Maximum individual cancer risk (MIR) or maximum TOSHI including maximum respiratory HI, maximum liver HI, maximum neurological HI, etc. for 14 TOSHIs
Value of MIR or TOSHI	MIR value or maximum TOSHI value, including a rounded value and a value in scientific notation
Population	Population at the location of the MIR or maximum HI, if it is a census block or alternate receptor
Distance	Distance from the center of the modeling domain, in meters
Angle	Angle from north
Elevation	Elevation in meters above sea level
Hill Height	Controlling hill height of receptor, in meters above sea level, as described in Section 2.3.1.
FIPS code	Five-digit Federal Information Processing Standard (FIPS) code which uniquely identifies the county of the receptor, if the receptor is a census block. (Note: For alternate receptor run, there is a field called “Receptor ID”)
Block ID	10-digit census block ID for linking to census demographic data, if the receptor is a census block. (Note: For alternate receptor run, there is a field called “Receptor ID”)
UTM east coordinate	In meters
UTM north coordinate	In meters
Latitude	Decimal
Longitude	Decimal
Receptor type	Census block receptors, P-type populated user receptors, and alternate receptors can be sites of MIR and max TOSHI in the Maximum Individual Risk file. The Maximum Offsite Impacts file includes this list of populated receptors plus unpopulated receptors including polar grid receptors, B-type boundary user receptors, monitors (M), and schools (S).
Notes	This field indicates whether the receptor was modeled discretely or interpolated and also indicates if the original maximum receptor was overlapped (and therefore not used). In the case of interpolation or an overlap, you may wish to re-model the facility.

For the Maximum Individual Risk file, if any populated receptor is located within the minimum [overlap distance](#), then it is assumed that either the source location or the receptor location is

inappropriate. (A block centroid may be inappropriate as a receptor location if the block partially encompasses an emission source, such as at a corner of the facility.) When an overlap condition occurs, this is indicated in the Notes field/column and the calculated results for the overlapping receptor are not used. Instead, the maximum cancer risk and TOSHI are assumed equal to the maximum (next highest) impacts for any receptor that does not overlap facility property. This could include both populated (census, alternate, and populated user) receptors and unpopulated (polar and user boundary) receptors, as long as they do not overlap facility property. In this situation, check the source coordinates in the [emissions location](#) input file, and define a set of facility boundary receptors in the [user receptors](#) file.

### 6.1.2. Maximum Offsite Impacts

The Maximum Offsite Impacts output file provides similar information to the Maximum Individual Risk output file, but the receptors of maximum impact in this file include any receptors, not only populated receptors. This file lists the highest cancer risks and TOSHI predicted at any receptor that does not overlap with the emission sources, whether the receptor is populated or unpopulated. The receptors in this file include all discretely modeled census blocks (a.k.a. “inner receptors”), all user receptors (including populated-type P receptors, boundary receptors, monitors, and schools), and all points in the polar receptor network, except for those receptors overlapping emission sources. **Table 38** (above) describes the fields of information provided in the Maximum Offsite Impacts file. A sample Maximum Offsite Impacts output file is provided in Appendix A.

### 6.1.3. Risk Breakdown

The Risk Breakdown output file provides the breakdown of risk and TOSHI by pollutant and source, including a listing of pollutant concentrations and unit risk estimates (URE) and reference concentration (RfC) values. This file includes information about the MIR and HI (for populated census block receptors, P type user receptors, and alternate receptors), as well as the maximum offsite impacts (for any receptor, including unpopulated receptors such as polar grid receptors, boundary receptors, monitors, and schools), as discussed in Section 5.2.

This file also shows the contributions of gaseous and particulate emissions for any pollutants that are emitted in both forms, if you opted to model deposition/depletion or if you merely elected to show the particulate/gaseous breakdown, as explained in Section 3.2.6.

**Table 39** describes the fields of information provided in the Risk Breakdown file. A sample Risk Breakdown output file is provided in Appendix A.

As previously noted, HEM computes cancer risks using the EPA’s recommended UREs for HAP and other toxic air pollutants. The resulting estimates reflect the risk of developing cancer for an individual breathing the ambient air at a given receptor site over a 70-year lifetime. Noncancer health effects are quantified using HQ and HI for various target organs. The HQ for a given pollutant and receptor site is the ratio of the ambient concentration of the pollutant to the RfC level at which no adverse effects are expected. The HI for a given organ is the sum of HQs for substances that affect that organ.

**Table 39. Fields Included in the Risk Breakdown File**

Field	Description
Site type	MIR (for max populated receptor) or maximum offsite impact (for max of any receptor, populated or not)
Parameter	Cancer risk, all 14 TOSHIs (e.g., respiratory HI, liver HI, neurological HI)
Source ID	Individual source identification code, "Total by pollutant all sources", or "Total" for all pollutants and all sources combined
Pollutant	Pollutant name, "all modeled pollutants" for all pollutants combined for each source, or "all pollutants all sources" for all pollutants and all sources combined
Emission (Pollutant) type	P = particulate, V = vapor (gas), C = combined, NA = not applicable (e.g., NA is used for rows for "all modeled pollutants")
Value	Cancer risk or noncancer HQ
Value_rnd	Cancer risk or noncancer HQ rounded to one significant figure
Conc_ugm <sup>3</sup>	Pollutant concentration ( $\mu\text{g}/\text{m}^3$ )
Conc_rnd	Pollutant concentration ( $\mu\text{g}/\text{m}^3$ ) rounded to two significant figures
Emissions_tpy	Modeled tons per year (tpy) emitted of pollutant
URE	Unit risk estimate used to compute cancer risks for the pollutant [ $1 / (\mu\text{g}/\text{m}^3)$ ]
RfC	Reference concentration used to compute HQs for the pollutant ( $\text{mg}/\text{m}^3$ ); <b>Note:</b> HEM converts this to $\mu\text{g}/\text{m}^3$ to compute TOSHIs

#### 6.1.4. Block Summary Chronic

The Block Summary Chronic file provides the total cancer risk and all 14 TOSHIs for every populated census block receptor, populated alternate receptor, and all user receptors (including types P, B, M, and S receptors), and also indicates whether the receptor is an overlap location. As noted above, if any populated receptor is located within the minimum [overlap distance](#), then it is assumed that either the source location or the receptor location is inappropriate. (For example, a block centroid may be inappropriate as a receptor location if the block partially encompasses an emission source, such as at a corner of the facility.) When an overlap condition occurs, the calculated results for the overlapping receptor are not used. Instead, the maximum cancer risk and HI are assumed equal to the maximum impacts for any receptor that does not overlap facility property. This could include both populated (census block, populated user, or alternate) receptors and unpopulated (polar and boundary) receptors, as long as they do not overlap facility property. In the case of an overlap, you may wish to check the coordinates in your Emissions Location input file, and define a set of facility boundary receptors in the [user receptors](#) file.

To facilitate detailed geographic information system (GIS) analyses of HEM results, the file gives the latitude and longitude, and the UTM coordinates of each receptor, in addition to cancer risk estimates and HI. This output file also gives the county FIPS code and block identification number for U.S. Census-based runs or alternate Receptor ID for non-census runs, as well as the population of each receptor. This information is intended to facilitate studies linking HEM results with census information, such as demographic or economic data. **Table 40** below describes the fields of information provided in the Block Summary Chronic file. A sample Block Summary Chronic output file is provided in Appendix A.

#### 6.1.5. Ring Summary Chronic

The Ring Summary Chronic file provides the same information provided by the Block Summary Chronic File, but for points in the polar receptor network. However, because these are polar

receptors, the FIPS, Block, and population fields are not included in the Ring Summary Chronic File, while three additional fields are provided: distance from center of polar network, angle from north, and sector number. **Table 40** describes the fields of information in the Ring Summary Chronic file, and a sample file is provided in Appendix A.

**Note:** For both the Block Summary Chronic and Ring Summary Chronic files, in the case of an overlapped receptor, the risk and TOSHI values for that receptor displayed in these files will not be the originally modeled values. Instead, the maximum cancer risk and TOSHIs are assumed equal to the maximum (next highest) impacts for any receptor that does not overlap facility property. This could include both populated (census, alternate, populated P-type user) receptors and unpopulated (polar and boundary) receptors, as long as they do not overlap facility property. The originally modeled values that occurred in the location of the overlap are available in the All Inner Receptor, All Outer Receptor, and/or All Polar Receptor files described in Sections 6.1.10, 6.1.11, and 6.1.12, respectively.

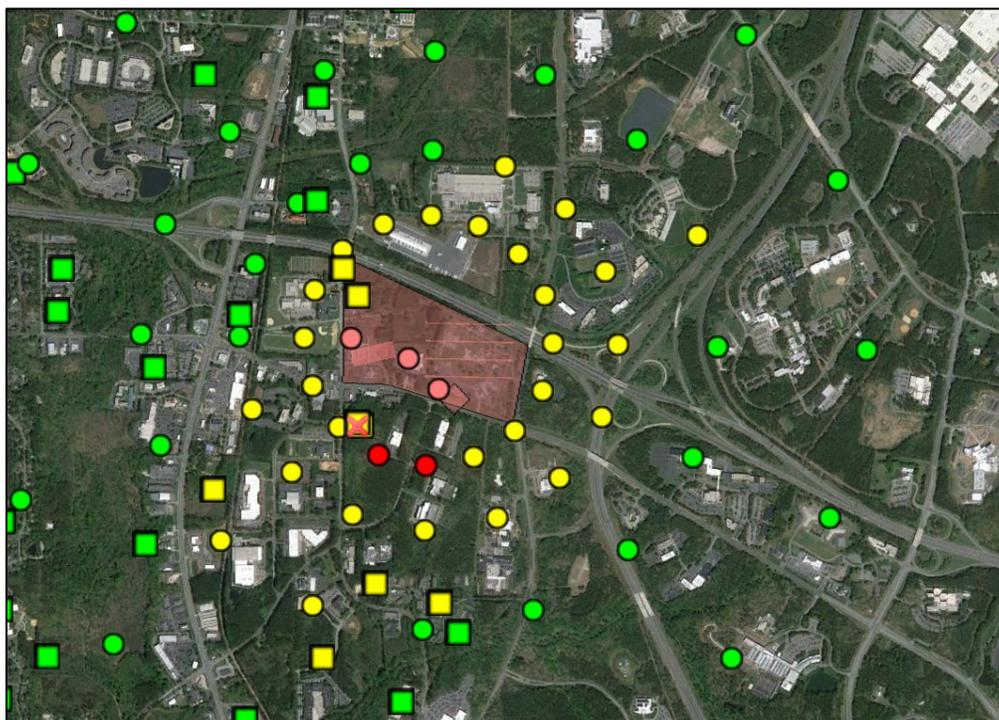
**Table 40. Fields Included in the Block Summary and Ring Summary Chronic Files**

Field	Description
Latitude	Decimal
Longitude	Decimal
Overlap	N for No, Y for Yes. If Yes, the values shown for the receptor in that row are the next highest receptor (whether populated or unpopulated), not overlapped. See also the Overlapping Source Receptors file.
Elevation	Elevation in meters above sea level
FIPS code	Five-digit Federal Information Processing Standard (FIPS) code which uniquely identifies the county of the receptor, if the receptor is a census block. (Not part of Ring Summary Chronic File) Note: For alternate receptor run, there is a field called "Receptor ID".
Block ID	10-digit census block ID for linking to census demographic data, if the receptor is a census block. (Not part of Ring Summary Chronic File) Note: For an alternate receptor run, there is a field called "Receptor ID".
X	UTM Easting Coordinate
Y	UTM Northing Coordinate
Hill Height	Controlling hill height of receptor, in meters above sea level, as described in Section 3.2.7
Population	Population at the location of the MIR or maximum HI, if it is a census block, or has user-provided population in the case of an alternate receptor. (Not part of Ring Summary Chronic File)
Parameter	Cancer risk, all 14 TOSHIs (e.g., respiratory HI, liver HI, neurological HI)
Discrete/ Interpolated	D for Discretely modeled receptor (within the modeling distance, aka "inner receptors"), I for Interpolated receptor (outside the modeling distance, aka "outer receptors") (Not part of Ring Summary Chronic File)
Receptor Type	C for census block; P for populated user or alternate receptor; B for boundary user receptor; M for monitor; S for school. (Not part of Ring Summary Chronic File)
Distance	Distance in meters from the center of the polar network of the polar receptor's location on polar ring (Not part of Block Summary Chronic File)
Angle (from north)	Angle from north of the polar radial on which the polar receptor is located (0 to 360 degrees) (Not part of Block Summary Chronic File)
Sector	Sector number within the polar network (the number depends on number of radials indicated in your Facility List Options file; default is 1-16) (Not part of Block Summary Chronic File)

### 6.1.6. Source Risk KMZ Image

The Source Risk KMZ file is a Google Earth™ map centered on the facility, as shown in **Figure 25**. The map displays the emission sources in the center as circles for point/stack sources, rectangles for area sources, polygons for polygon-shaped sources, and lines for line and buoyant line sources. All these source types are shown in red. The map also displays all receptors within the modeled area including populated census block centroid receptors or alternate receptors (displayed as squares), polar grid receptors (displayed as circles), unpopulated monitors and schools (displayed as squares with a “U”), and all user receptors (also displayed as squares with a “U”). The MIR receptor is marked with a red “X”.

**Figure 25. Sample Google Earth™ Map of Results**



You can click on the square census block receptors to see the total cancer risk and maximum TOSHI for that receptor, the FIPS and block ID of the receptor (for census blocks) or receptor ID (for alternate and user receptors), as well as a listing of the top pollutants contributing to that receptor's total cancer risk and maximum TOSHI.

You can click on the circular polar receptors to view similar information for each polar receptor. The cancer and noncancer risk at the census block and polar receptors are color coded on the Google Earth™ map. For cancer risk, red indicates a receptor with a modeled total cancer risk greater than 100 in a million. Yellow indicates a risk level between 20 and 100 in a million. Green indicates a risk less than 20 in 1 million.

Figure 25 shows an example in which only two unpopulated polar grid receptors have a cancer risk greater than 100 in a million (shown as dark red circles). All populated census block receptors have modeled risks between 20 and 100 in a million (shown as yellow squares) or

less than 20 in a million (shown as green squares). No unpopulated census block or user receptors are shown in this example.

### 6.1.7. Incidence

The facility-specific Incidence file provides the overall total incidence for all modeled pollutants from all sources in the given facility, the pollutant-specific total incidence for all sources combined, and the individual incidence per source for each pollutant. As explained in Section 5.3, the incidence is calculated as the cancer risk of each populated receptor (e.g., census block or alternate receptor) times the receptor population, divided by a 70-year average lifespan. This individual populated receptor incidence is then summed over all populated receptors in the modeling domain of the facility. **Table 41** describes the fields of information provided in the facility-specific Incidence file. A sample Incidence output file is provided in Appendix A.

**Table 41. Fields Included in the Incidence File**

Field	Description
Source ID	Individual source identification code, or "Total" for all sources combined
Pollutant	Pollutant name, or "All modeled pollutants" for all pollutants combined for each source and for the Total
Emission (Pollutant) type	P = particulate, V = vapor (gas), C = combined
Incidence	Incidence calculated as (cancer risk) X (population) / 70-year lifespan, summed over all populated receptors
Incidence, rounded	Incidence, rounded

### 6.1.8. Cancer Risk Exposure

The Cancer Risk Exposure file is a simple two column (two field) file that provides the population numbers exposed to various cancer risk levels in the modeling domain surrounding the facility. Population numbers are provided for the following cancer risk levels:

- Greater than or equal to 1 in 1,000 ( $\geq 1,000$ -in-a-million risk),
- Greater than or equal to 1 in 10,000 ( $\geq 100$ -in-a-million risk),
- Greater than or equal to 1 in 20,000 ( $\geq 50$ -in-a-million risk),
- Greater than or equal to 1 in 100,000 ( $\geq 10$ -in-a-million risk),
- Greater than or equal to 1 in 1,000,000 ( $\geq 1$ -in-a-million risk), and
- Greater than or equal to 1 in 10,000,000 ( $\geq 0.1$ -in-a-million risk).

A sample Cancer Risk Exposure output file is provided in Appendix A.

### 6.1.9. Noncancer Risk Exposure

The Noncancer Risk Exposure file, like the Cancer Risk Exposure file described above, is a simple file that provides the population numbers exposed to various HI levels for all 14 TOSHIs, in the modeling domain surrounding the facility. Population numbers are provided for the following noncancer HI levels:

- Greater than 100,
- Greater than 50,

- Greater than 10,
- Greater than 1.0,
- Greater than 0.5, and
- Greater than 0.2.

Population numbers at each of the above noncancer HI levels are provided for the following TOSHIs:

- Respiratory HI,
- Liver HI,
- Neurological HI,
- Developmental HI,
- Reproductive HI,
- Kidney HI,
- Ocular HI,
- Endocrine HI,
- Hematological HI,
- Immunological HI,
- Skeletal HI,
- Spleen HI,
- Thyroid HI, and
- Whole Body HI.

A sample Noncancer Risk Exposure output file is provided in Appendix A.

#### **6.1.10. All Inner Receptors**

The All Inner Receptors file provides the chronic concentration (in  $\mu\text{g}/\text{m}^3$ ) and (if optionally modeled) the acute concentration of every populated (census block or alternate) receptor inside the modeling distance, as well as every user receptor, both populated and unpopulated.

**Note:** All concentrations in this file are discretely (explicitly) modeled, not interpolated. If you opted to calculate deposition with or without depletion, this file will also contain the deposition flux (in  $\text{g}/\text{m}^2/\text{y}$  if modeled using annual averages, or in  $\text{g}/\text{m}^2$  if modeled using period averages). Columns for both dry and wet deposition flux results are provided and will be populated with non-zero results depending on the type of deposition modeling (wet, dry or both) you selected in the Facility List Option fields.

**Table 42** describes the fields of information provided in the All Inner Receptors file. A sample All Inner Receptors file output file is provided in Appendix A.

#### **6.1.11. All Outer Receptors**

The All Outer Receptors file includes nearly the same information provided in the All Inner Receptor file (described above) for every receptor located between the modeling distance (often specified as 3 km) and the outer edge of the modeling domain (the “maximum distance” often

specified as 50 km). The dry and wet deposition fluxes provided in the All Inner Receptors file, however, are not provided in this file, for the outer receptors.

**Note:** All concentrations in this file are interpolated using the polar grid receptors, not discretely (explicitly) modeled.

**Table 42** describes the fields of information provided in the All Outer Receptors file. A sample All Outer Receptors file output file is provided in Appendix A.

**Table 42. Fields Included in the All Inner and All Outer Receptor Files**

Field	Description
FIPS code	Five-digit Federal Information Processing Standard (FIPS) code which uniquely identifies the county of the receptor if the receptor is a census block. (Note: For alternate receptor run, there is a field called "Receptor ID")
Block ID	10-digit census block ID for linking to census demographic data, if the receptor is a census block. (Note: For alternate receptor run, there is a field called "Receptor ID")
Latitude	Decimal
Longitude	Decimal
Source ID	Individual source identification code affiliated with given concentrations
Emission (Pollutant) type	P = particulate, V = vapor (gas), C = combined
Pollutant	Pollutant name affiliated with given concentrations
Conc	Chronic air concentration in $\mu\text{g}/\text{m}^3$
Acute Conc	Acute (short-term) air concentration in $\mu\text{g}/\text{m}^3$ , if modeled
Elevation	Elevation in meters above sea level
Dry deposition	Dry deposition flux in $\text{g}/\text{m}^2/\text{year}$ if modeled using annual averages, or in $\text{g}/\text{m}^2$ if using period option (not included in All Outer Receptor file)
Wet deposition	Wet deposition flux in $\text{g}/\text{m}^2/\text{year}$ if modeled using annual averages, or in $\text{g}/\text{m}^2$ if using period option (not included in All Outer Receptor file)
Population	Population of receptor
Overlap	N for No, Y for Yes. Note: The value shown is the originally modeled value, even if overlapped (and therefore not used in other files such as the Maximum Individual Risk, Risk Breakdown, and Block Summary Chronic files)
Receptor Type	C for census block; P for populated user receptor or alternate receptor; B for boundary receptor; M for monitor; S for school

### 6.1.12. All Polar Receptors

The All Polar Receptors file provides similar information to the All Inner Receptors and All Outer Receptors for the nodes of the polar receptor grid, including the chronic concentration (in  $\mu\text{g}/\text{m}^3$ ) and (if optionally modeled) the acute concentration of every polar receptor.

**Note:** Like the All Inner Receptors file, all concentrations in the All Polar Receptors file are discretely (explicitly) modeled, not interpolated. If you opted to calculate deposition with or without depletion, this file will also contain the deposition flux (in  $\text{g}/\text{m}^2/\text{y}$  if modeled using annual averages, or in  $\text{g}/\text{m}^2$  if modeled using period averages). Columns for both dry and wet deposition flux results are provided and will be populated with non-zero results depending on the type of deposition modeling (wet, dry or both) you selected in the Facility List Option fields. In addition, this file will contain the distance from the center of the polar network, the angle, sector, and ring number that describes the location of each polar receptor.

**Table 43** describes the fields of information provided in the All Polar Receptors file. A sample All Polar Receptors file output file is provided in Appendix A.

**Table 43. Fields included in the All Polar Receptors File**

Field	Description
Source ID	Individual source identification code
Emission (Pollutant) type	P = particulate, V = vapor (gas), C = combined
Pollutant	Pollutant name affiliated with given concentrations
Conc	Chronic air concentration in $\mu\text{g}/\text{m}^3$
Acute Conc	Acute air concentration in $\mu\text{g}/\text{m}^3$
Distance	Distance in meters from the center of the polar network of the polar receptor's location on polar ring
Angle (from north)	Angle from north of the polar radial on which the polar receptor is located (0 to 360 degrees)
Sector	Sector number within the polar network (the number depends on number of radials indicated in your Facility List Options file; default is 1-16)
Ring number	The number of the ring ("circle") in the polar network on which the receptor is located, beginning with number 1 closest to facility center
Elevation	Elevation in meters above sea level
Latitude	Decimal
Longitude	Decimal
Overlap	N for No, Y for Yes. Note: the value shown is the originally modeled value, even if overlapped (and therefore not used in other files such as the Maximum Individual Risk, Risk Breakdown, and Ring Summary Chronic files).
Wet deposition	Wet deposition flux in $\text{g}/\text{m}^2/\text{year}$ if modeled using annual averages, or in $\text{g}/\text{m}^2$ if using period option
Dry deposition	Dry deposition flux in $\text{g}/\text{m}^2/\text{year}$ if modeled using annual averages, or in $\text{g}/\text{m}^2$ if using period option

### 6.1.13. AERMOD Outputs

With each run, HEM automatically provides a set of AERMOD text files that track the inputs and keywords (modeling commands) passed to AERMOD, including the receptor network and meteorological files, as well as the AERMOD outputs. The outputs produced by AERMOD are then passed back to HEM and used to produce the other outputs described in this guide. You should review these AERMOD text files (especially the `aermod.out` file described below) to confirm that AERMOD completed its modeling without error. These text files include:

- aermod.inp** – a text file for combined particle and vapor phase emissions listing the inputs passed to AERMOD for modeling, including modeling control options (explained in the [AERMOD User's Guide](#)), rural or urban dispersion environment, averaging time, specific input parameters (including from the Facility List Options and Emissions Location files), the network of discrete receptor coordinates (census block or alternate receptors in UTM), elevations and hill heights, meteorological data, and designated text formatted output files. Note: If particle and vapor phase emissions are modeled separately, then the above information will be provided for particle phase emissions in an **aermod\_P.inp** file and for vapor phase emissions in an **aermod\_V.inp** file.
- aermod.out** – a text file for combined particle and vapor phase emissions listing the inputs received by AERMOD in the `aermod.inp` file (noted above), any fatal error messages, warning messages, informational messages, indication of successful

AERMOD set-up or not, AERMOD version number used for modeling, type of deposition and depletion modeled if any, modeling options employed, whether short-term (acute) concentrations were modeled along with their period, number and type of sources, number of receptors, vintage of meteorological data used, emission rates modeled for each source (in grams per second), elevations and hill heights of every discrete (census block or alternate) receptor and every polar grid receptor, UTM coordinates and unit HAP chronic concentration at every receptor for each source, UTM coordinates and unit HAP short-term/acute concentration (if modeled) based on the acute high value selected, the number of hours processed, the number of calm (very low wind) hours identified, the number of missing hours in the meteorological data used for modeling, and an indication whether AERMOD finished the modeling run successfully or not. Note: If particle and vapor phase emissions are modeled separately, then the above information will be provided based on particle phase emissions in an **aermod\_P.out** file and for vapor phase emissions in an **aermod\_V.out** file. Deposition fluxes (wet/dry) will be provided with depletion applied to concentrations, if modeled.

- **plotfile.plt** – a text file for combined particle and vapor phase emissions listing the average modeled chronic concentration at every UTM receptor location and each modeled source. Note: If particle and vapor phase emissions are modeled separately, then these concentrations will be provided based on particle phase emissions in a **plotfile\_p.plt** file and in a **plotfile\_v.plt** file for vapor phase emissions. Deposition fluxes (wet/dry) will be provided with depletion applied to concentrations, if modeled.
- **maxhour.plt** – a text file for combined particle and vapor phase emissions listing the modeled short-term/acute concentration (based on the acute high value indicated in your Facility List Options file) at every UTM receptor location and each modeled source. Note: If particle and vapor phase emissions are modeled separately, then these acute concentrations will be provided based on particle phase emissions in a **maxhour\_p.plt** file and for vapor phase emissions in a **maxhour\_v.plt** file.

**Note:** Concentration results provided by AERMOD in the above files should not be interpreted as predicted concentrations of any pollutant listed in the HEM input files. Rather, **these AERMOD results reflect concentrations attributable to a unit-emission rate (1 kg/s), which HEM converts to specific modeled pollutant emissions, as explained in Section 5.** To fully understand the AERMOD processing and output files, refer to the AERMOD documentation for further guidance (USEPA, 2024a, 2024e, 2025).

#### 6.1.14. Input Selection Options

The Input Selection Options output file is a useful QA file to refer to because it provides a record of the modeling options you chose for the run, as well as the names and location of the input files you indicated. The following information is provided in this file:

- Facility ID,
- AERMOD control options used,
- Phase of emissions,
- Dispersion environment (rural or urban),
- Whether deposition was modeled,
- Whether depletion was modeled,
- Type of deposition modeled for particle and vapor,
- Type of depletion modeled for particle and vapor,

- Whether elevations were modeled (or flat terrain used),
- Acute averaging period (e.g., 1 hour),
- Acute multiplier (factor applied to annual average emissions, if any),
- Whether building downwash was modeled,
- Whether user receptors were modeled,
- Maximum distance used for modeling domain (in meters),
- Modeling distance used for discrete modeling of receptors (in meters),
- Overlap distance used (in meters),
- Number of polar rings used,
- Number of polar radials used,
- Whether acute was modeled,
- Distance to first ring (meter),
- Whether FASTALL was used,
- Run group name,
- Facility List Options file – name/location,
- Emissions Location file – name/location,
- HAP Emissions file – name/location,
- User Receptor file – name/location (if used),
- Particle Size file – name/location (if used),
- Building downwash file – name/location (if used),
- Buoyant line file – name/location (if used),
- Land use file – name/location (if used),
- Month-to-Seasons file – name/location (if used),
- Polygon vertex file – name/location (if used),
- Whether Alternate Receptors were used, and
- Whether any of the Alternate Receptors were missing population values. Note: To compute incidence, population values are needed at every populated alternate receptor. Even if only one Alternate Receptor is missing a value in its population field, incidence is not computed by HEM.

#### **6.1.15. Acute Maximum Concentrations (Optional)**

If you chose to model acute impacts for a given facility, HEM will produce an Acute\_Chem\_Max output file. The Acute Chem Max output provides the maximum acute (short-term) pollutant concentration at any receptor for all sources of that pollutant combined. The “maximum” reported in this file refers to the acute high value you identified (e.g., the absolute maximum, the 99th percentile, the 98th percentile) and is based on the acute multiplier you provided (e.g., 10 times the average annual emission rate), as well as the acute averaging period (e.g., 1-hour) you indicated in the respective acute fields of your Facility List Options file. The maxima provided in the Acute Chem Max output may occur at any receptor—populated or unpopulated—including census blocks, alternate receptors, polar grid receptors, and user receptors.

This file also provides the specific location of the receptor with highest modeled concentration for each pollutant – including UTM and latitude/longitude coordinates, FIPS, Block, distance from facility center, and angle from north – as well as the elevation and hill height of the receptor. **Note:** Each pollutant may cause a different receptor to be the maximum (based on emissions of that specific pollutant).

This output file also lists the acute reference concentrations for five different acute benchmarks above which adverse short-term health impacts can be expected. For example, the file provides:

- the California Acute Reference Exposure Level (**REL**) benchmark,
- the Acute Exposure Guideline Level (**AEGL1**) for transient reversible effects and the **AEGL2** for long-lasting irreversible effects, both based on one hour of exposure, and
- the Emergency Response Planning Guideline (**ERPG-1**) for mild or transient effects and the **ERPG-2** for irreversible or serious effects, both based on one hour of exposure.

The EPA’s [Air Toxics Risk Assessment Library](#) (USEPA, 2024h) provides a more detailed description of these acute benchmarks.

**Table 44** below describes the fields of information provided in the Acute Chem Max file, and a sample file output file is provided in Appendix A. **Note:** the concentrations reported in Table 44 are in  $\mu\text{g}/\text{m}^3$ , while the acute benchmark values (reference concentrations) are in  $\text{mg}/\text{m}^3$  and should therefore be multiplied by 1,000 for comparison to the modeled concentrations.

#### 6.1.16. Acute Populated Concentrations (Optional)

If you chose to model acute impacts for a given facility, HEM will also produce an Acute\_Chem\_Pop output file. The Acute Chem Pop file provides the same information described above in the Acute Chem Max file, but for only populated receptors (census blocks, alternate receptors and user receptors), not unpopulated receptors. Therefore, the concentrations shown in this file may or may not be the acute maxima/high values for all receptors; but they are the acute high values for the populated receptors. Refer also to discussion above in Section 6.1.15.

**Table 44** below describes the fields of information provided in the Acute Chem Pop file, and a sample file output file is provided in Appendix A.

**Table 44. Fields included in the Acute Chem Max and Acute Chem Pop Files**

Field	Description
Pollutant	Pollutant name
Conc	High value Acute Concentration in $\mu\text{g}/\text{m}^3$
Conc sci	High value Acute Concentration, scientific notation, in $\mu\text{g}/\text{m}^3$
AEGL-1, 1-hour	Acute Exposure Guideline Level 1 (AEGL-1) for a 1-hour exposure: the concentration above which it is predicted that the general population, including susceptible individuals, could experience notable discomfort, irritation, or certain asymptomatic, non-sensory effects ( $\text{mg}/\text{m}^3$ )
AEGL-2, 1-hour	Concentration above which it is predicted that the general population, including susceptible individuals, could experience irreversible or other serious, long-lasting adverse health effects or an impaired ability to escape for a 1-hour exposure ( $\text{mg}/\text{m}^3$ )

Field	Description
ERPG-1	Emergency Response Planning Guideline 1 (ERPG-1): concentration below which it is believed nearly all individuals could be exposed for up to 1 hour without experiencing other than mild transient adverse health effects or perceiving a clearly defined objectionable odor (mg/m <sup>3</sup> )
ERPG-2	Concentration below which it is believed nearly all individuals could be exposed for up to 1 hour without experiencing or developing irreversible or other serious health effects or symptoms that could impair an individual's ability to take protective action (mg/m <sup>3</sup> )
Acute REL	Reference Exposure Level: concentration below which no adverse health effects are anticipated, based on the most sensitive adverse health effect reported (mg/m <sup>3</sup> )
Population	If the receptor is a census block or alternate receptor
Distance	From the center of the modeling domain (in meters)
Angle	From north
Elevation	In meters above sea level
Hill	Controlling hill height in meters above sea level, as described in Section 3.2.7
County FIPS	If the receptor is a census block. (Note: For alternate receptor run, there is a field called "Receptor ID")
Census block ID	If the receptor is a census block. Allows linking to demographic data. (Note: For an alternate receptor run, there is a field called "Receptor ID")
UTM east coordinate	In meters
UTM north coordinate	In meters
Latitude	Decimal
Longitude	Decimal
Receptor type	C = census block, P = populated user receptor or alternate receptor, PG = polar grid receptor, B = boundary receptor, M = monitor, S = school
Notes	Indicates whether the receptor was discretely (explicitly) modeled or interpolated

Table 44 Note: The concentrations reported in the acute output tables are in  $\mu\text{g}/\text{m}^3$ , while the acute benchmark values (reference concentrations) are in  $\text{mg}/\text{m}^3$  and must therefore be multiplied by 1,000 for comparison to the modeled concentrations.

### 6.1.17. Acute Breakdown (Optional)

If you chose to model acute impacts for a given facility, HEM also produces a third acute output file entitled Acute\_Bkdn, which provides the contribution ("breakdown") of each emission source to the receptor of maximum acute impact for each pollutant (i.e., the acute concentration of pollutant at the maximum receptor for that pollutant, caused by each source). This information is provided for both the maximum/high value receptor (whether populated or unpopulated) and for the highest populated receptor. **Note:** Concentration values are interpolated outside the modeling distance (e.g., between 3 km and 50 km if defaults are used).

The acute breakdown file includes the following fields, and a sample file output file is provided in Appendix A.:

- Pollutant,
- source ID,
- emission type (P for particle, V for vapor, C for combined),
- the maximum pollutant concentration ( $\mu\text{g}/\text{m}^3$ ) at a populated receptor,

- the maximum pollutant concentration ( $\mu\text{g}/\text{m}^3$ ) at all receptors (both populated and unpopulated), and
- columns indicating whether the pollutant's concentration at each receptor was interpolated or not.

## 6.2. Run Group Outputs

In addition to the facility-specific outputs listed in Section 6.1, a HEM-AERMOD run produces three summary output files, based on the results for the entire run group of modeled facilities. These multi-facility outputs are updated after the output files for the individual facilities have been created and essentially concatenate the individual facility results into group-wide summary files. In each of these three Excel™ (.xlsx) files, HEM writes one row of information for each facility upon completion of that facility's individual modeling run. The three group-wide output files created by HEM are described in the following sections and sample files are provided in Appendix A. Note: These files will be produced even if HEM-AERMOD models only one facility.

### 6.2.1. Facility Max Risk and HI

The Facility Max Risk and HI output file provides the maximum modeled risk and hazard index results for every facility as well as additional facility-specific modeling results, including:

- a listing of all Facility IDs modeled,
- the cancer risk at the receptor that experiences the highest risk in the modeled radius around each facility (i.e., facility-specific MIR),
- whether or not the MIR (max cancer risk) is interpolated from nearby receptors<sup>10</sup>,
- the type of receptor where the MIR (max cancer risk) occurs (e.g., census block, alternate receptor, polar grid, user P-type receptor),
- the latitude and longitude of the MIR (cancer) receptor,
- the census block ID, alternate receptor ID or user receptor ID of the MIR receptor,
- the 14 TOSHIs at the receptors that experience the maximum TOSHI for each facility including: whether or not the TOSHI value is interpolated, the receptor type(s) where the max TOSHIs occur, the latitude and longitude for certain max TOSHI receptors (e.g., respiratory, neurological), and the census block ID, alternate receptor ID or user receptor ID of each max TOSHI receptor,
- the population, if any, excluded from the modeling run because of any census block centroid(s) located within the overlap distance around each emission source (and therefore considered on facility property)<sup>11</sup>,
- the cancer incidence (predicted excess cancers per year due to modeled emissions) at each facility,
- the file name of the meteorological station used in the modeling of each facility,

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<sup>10</sup> An interpolated MIR generally suggests that the modeling distance should be increased, and the facility remodeled as discussed more in Section 10.

<sup>11</sup> A value in the population overlap field generally indicates that the facility should be remodeled (e.g., with a smaller overlap distance specified) to ensure that the population associated with the census block centroid(s) is accounted for.

- the distance (in kilometers) from the facility center to the meteorological station used in the modeling run,
- the latitude and longitude location of the facility center, and
- the dispersion environment used by HEM for modeling each facility – rural or urban.

The TOSHIs modeled by HEM can impact the following organs and organ systems: respiratory, liver, neurological, developmental, reproductive, kidney, ocular, endocrine, hematological, immunological, skeletal, spleen, thyroid, and whole body. In the sample abbreviated Facility Max Risk and HI provided in Appendix A, only respiratory HI is shown, which is commonly the highest TOSHI level based on the dispersion and inhalation modeling performed by AERMOD and HEM.

### 6.2.2. Facility Cancer Risk Exposure

The Facility Cancer Risk Exposure output file lists the facilities by ID, their corresponding latitudes and longitudes (of the calculated facility centers), and the population exposed to different cancer risk levels surrounding each facility, including:

- the number of people from each facility exposed to a cancer risk level greater than or equal to 1 in 1,000 (or 1,000 in a million),
- the number of people from each facility exposed to a cancer risk level greater than or equal to 1 in 10,000 (or 100 in a million),
- the number of people from each facility exposed to a cancer risk level greater than or equal to 1 in 100,000 (or 10 in a million),
- the number of people from each facility exposed to a cancer risk level greater than or equal to 1 in 1,000,000 (or 1 in a million), and
- the number of people from each facility exposed to a cancer risk level greater than or equal to 1 in 10,000,000 (or 0.1 in a million).

**Note:** Each row of this output file is facility-specific and does not reflect the impacts of multiple facilities with overlapping modeling domains (which may impact the same receptor and increase population numbers at various risk levels beyond what each single facility causes). A sample Cancer Risk Exposure file is provided in Appendix A.

### 6.2.3. Facility TOSHI Exposure

The Facility TOSHI Exposure output file lists the facilities by ID and the number of people with a TOSHI greater than 1 for each facility and for each of the 14 TOSHIs currently modeled by HEM. Note: Because the convention of one significant figure is employed, an HI greater than 1 equates mathematically to an HI greater than or equal to 1.5. A Facility TOSHI Exposure file is provided in Appendix A.

### 6.2.4. Additional Run Group Outputs

HEM will also produce several other group output files with each run, including:

- An **Inputs folder** containing every input file used by HEM (that you provided) for your modeling run - a useful QA feature to ensure the inputs you intended to be modeled were indeed the ones modeled,

- A Google Earth™ map showing the source locations at every facility in your modeling run - named **AllFacility\_source\_locations.kmz**,
- A **hem.log** text file, as described in Section 4.4, which provides a permanent record of your model run – includes the files uploaded, the output files produced, whether the run was successful and/or any errors that occurred, and
- If HEM could not model all facilities listed in your inputs, a **Skipped Facilities** file (*Skipped\_Facilities.xlsx*) will be produced which simply lists the IDs of those skipped facilities. You may use this to remodel those facilities, after correcting or amending the issues that caused the facilities to be skipped. This is discussed further in Section 10.

Note: **Do not change the names of the facility-level or HEM output files** discussed in Section 6, as several of these files are referenced by their specific names in the code of the Risk Summary Report programs (that produce the outputs described in Section 7), and in the code of the Demographic Assessment module (that produce the outputs described in Section 8).

### 6.3. User-Supplied Concentration Outputs

As previously noted, if you provided pollutant concentration data for a set of geographic locations, then fewer output files are created (compared to a typical HEM-AERMOD run) because some files are not relevant. For example, since there is no AERMOD run under this option, there are no AERMOD input and output files. Also, there are no polar receptors created, and there is no separation of census blocks (or alternate receptors) into inner and outer data sets. There is only one file created that contains the concentration data for each receptor and pollutant combination. There is also no ring summary file created because there are no polar receptors. Since there are no facility-specific data under this option, there are no run group outputs. Currently, in HEM version 5.0, only risk data are estimated under this option, and no demographic information is associated with any census blocks which have interpolated risk estimates.

Although there are only concentrations specified under this option and not facilities, HEM treats the user's input file like the "all inner receptors" file created for a single facility when AERMOD is run, and HEM processes those data in the same way to create outputs files. These output files are included in a subdirectory generically named "Facility1" within the run group directory, and include:

- Maximum Individual Risk,
- Block Summary Chronic,
- Incidence,
- Cancer Risk Exposure,
- Noncancer Risk Exposure,
- All Inner Receptors, and
- Acute Maximum Concentrations and Acute Populated Concentrations (if you provided acute concentrations in your user-supplied concentration input file).

The Maximum Individual Risk, Cancer Risk Exposure, Noncancer Risk Exposure, and Incidence files provide information based on the risks at interpolated receptors (either census blocks or alternate receptors) and are the same as described in Section 6.1 for these file types.

The Block Summary Chronic file is similar to that described in Section 6.1.4. but includes risk estimates for the locations of your user-supplied concentrations in addition to the census blocks (or alternate receptors). The user's concentration locations can be identified by the "UCONC" assigned to them in the FIPs column (or the Receptor ID having a "UCONC" prefix where alternate receptors are used). **Note:** Some of the fields in this file have no meaning in the context of this option (e.g., overlap), and others simply carry forward information that may be of interest (e.g., elevation, hill height).

The All Inner Receptors file is similar to that described in Section 6.1.10. but includes the locations of your user-supplied concentrations in addition to concentration estimates at the census blocks (or alternate receptors). The user's concentration locations can be identified as described above for the Block Summary Chronic file. The All Inner Receptors file usually contains concentration estimates at each receptor for each source/pollutant combination. But since no source-specific information is included under this option, the source ID field has no meaning, and each row is assigned a generic value of "sourceID". Likewise, the receptor type column uses a "C" for the output rows pertaining to the user-supplied concentration sites (when run with the census or with alternate receptor sites), primarily because these sites are similar to discrete census type receptors. Also in this file the deposition fields are blank because deposition is not interpolated.

The Acute Maximum Concentrations and Acute Populated Concentrations files are similar to those described in Sections 6.1.15 and 6.1.16, respectively. When determining the maximum acute concentrations in the Acute Maximum Concentrations file, the locations of your user-supplied concentrations are considered in addition to the census blocks (or alternate receptors). The user's concentration locations can be identified as described above for the Block Summary Chronic file.

Finally, it should be noted that the output files contain rows for both the interpolated receptors (whether census blocks or alternate receptors) and the sites of user-supplied concentration data, where applicable. However, if there is one or more census blocks or alternate receptors that have the same coordinates as the locations of your user-supplied concentrations, only the census block or alternate receptor data are provided.

The sample outputs provided in Appendix A (for the output files listed in this Section 6.3) also describe the user-supplied concentration outputs except for the minor differences noted above.

## 7. HEM Summary Reports

You may choose to run 11 different Risk Summary Reports, as described in the step-by-step HEM instructions in Section 4.5. These summary reports, similar to the run group outputs described in Section 6.2, are based on risk results from all facilities modeled in your run group. However, certain Risk Summary Reports have the added benefit of taking into account multiple impacts on the same receptor(s) from neighboring facilities. The 11 Risk Summary Reports are described in this section.

### 7.1. Facility-Specific Summaries

As noted in Section 4.5, six of the 11 summaries produce results specific to each facility. These summaries include individual facility IDs connected to the results, for all facilities in your run group, which account for impacts from each facility's emissions in isolation (i.e., not considering impacts from other facilities, including neighboring facilities). The six facility-specific summaries discussed in this section include: cancer drivers, hazard index drivers, acute impacts, multipathway, max concentration, and max risk and HI by source and pollutant.

#### 7.1.1. Cancer Drivers Summary

The Cancer Drivers output (*cancer\_drivers.xlsx*) provides the pollutants and sources that are driving the risk at the receptor with the highest risk (the MIR receptor), for each facility. This file lists the facilities by ID; the MIR modeled at each facility from all pollutants and emission sources acting on the receptor; the predominant pollutant(s) and emission source(s) contributing to at least 90% of that facility's MIR; the cancer risk associated with each of those pollutant-source combinations; and the percentage risk contribution to the MIR for each. **Table 45** shows a sample output.

**Table 45. Sample Cancer Drivers Summary Output**

Facility ID	MIR	Pollutant	Cancer Risk	Risk Contribution	Source ID
270536222111	1.13E-06	Arsenic compounds	8.90885E-07	78.84	CEPM0005
270536222111	1.13E-06	Nickel compounds	2.35101E-07	20.81	CEPM0005
3605517127011	1.02585E-06	Arsenic compounds	9.7294E-07	94.84	CEPM0002
484535678711	3.45674E-07	Arsenic compounds	4.61526E-08	13.35	CEPM0006
484535678711	3.45674E-07	Arsenic compounds	4.25802E-08	12.32	CEPM0026
484535678711	3.45674E-07	Arsenic compounds	3.81743E-08	11.04	CEPM0024
484535678711	3.45674E-07	Arsenic compounds	3.30016E-08	9.55	CEPM0007
484535678711	3.45674E-07	Arsenic compounds	3.27424E-08	9.47	CEPM0001
484535678711	3.45674E-07	Arsenic compounds	3.24023E-08	9.37	CEPM0004
484535678711	3.45674E-07	Arsenic compounds	2.62015E-08	7.58	CEPM0029
484535678711	3.45674E-07	Arsenic compounds	2.52855E-08	7.31	CEPM0005
484535678711	3.45674E-07	Arsenic compounds	2.46037E-08	7.12	CEPM0003
484535678711	3.45674E-07	Arsenic compounds	2.29875E-08	6.65	CEPM0002
...	...	...	...	...	...

Table 45 Note: The Risk Contribution column for each facility will not sum to 100%, because only the pollutant-source combinations that sum to at least 90% are displayed.

#### 7.1.2. Hazard Index Drivers Summary

The Hazard Index Drivers output (*hazard\_index\_drivers.xlsx*) provides the sources and pollutants that are driving the maximum TOSHI at each modeled facility. This file lists the facilities by ID; the "HI type" (respiratory, neurological, liver, etc., for all non-zero TOSHI values);

the maximum TOSHI (“HI Total”) modeled at each facility from all pollutants and emission sources acting on the receptor, the predominant sources and pollutants contributing to at least 90% of each maximum TOSHI; the TOSHI (“Hazard Index”) value associated with each of these source-pollutant combinations; and the percentage each source-pollutant combination contributes to each maximum TOSHI (for all nonzero TOSHIs at each facility). **Table 46** shows a sample output.

**Table 46. Sample Hazard Index Drivers Summary Output**

Facility ID	HI Type	HI Total	Source ID	Pollutant	Hazard Index	Percentage
Fac1-NC	Developmental HI	8.9969812	SR000001	arsenic compounds	8.964020301	99.63
Fac1-NC	Kidney HI	1.4796741	SR000001	cadmium compounds	1.445809726	97.71
Fac1-NC	Respiratory HI	0.6770494	RW000001	acrolein	0.557883699	82.4
Fac1-NC	Respiratory HI	0.6770494	FU000001	bis(2-ethylhexyl)phthalate	0.113999602	16.84
Fac1-NC	Liver HI	0.1816668	FU000001	bis(2-ethylhexyl)phthalate	0.113999602	62.75
Fac1-NC	Liver HI	0.1816668	RW000001	trichloroethylene	0.066946044	36.85
Fac1-NC	Neurological HI	0.0882496	RW000001	trichloroethylene	0.066946044	75.86
Fac1-NC	Neurological HI	0.0882496	FU000001	mercury (elemental)	0.020602338	23.35
Fac1-NC	Reproductive HI	0.0746997	RW000001	trichloroethylene	0.066946044	89.62
Fac1-NC	Reproductive HI	0.0746997	RV000001	1,3-butadiene	0.007751977	10.38
Fac1-NC	Immunological HI	0.0671872	RW000001	trichloroethylene	0.066946044	99.64
Fac2-IL	Liver HI	0.0405107	FU000001	bis(2-ethylhexyl)phthalate	0.037081163	91.53
Fac2-IL	Respiratory HI	0.039644	FU000001	bis(2-ethylhexyl)phthalate	0.037081163	93.54
Fac2-IL	Neurological HI	0.0266972	FU000001	mercury (elemental)	0.023278107	87.19
Fac2-IL	Neurological HI	0.0266972	FU000001	mercury (elemental)	0.00256432	9.61
...	...	...	...	...	...	...

Table 46 Note: The Percentage column for each facility will not sum to 100%, because only the source-pollutant combinations that add to at least 90% are displayed.

### 7.1.3. Acute Impacts Summary

The Acute Impacts output (*acute\_impacts.xlsx*) provides the maximum acute concentration for every modeled pollutant, five acute benchmark values (REL, AEGL-1, AEGL-2, ERPG-1, and ERPG-2, as defined above in Table 44), and the hazard quotient (HQ) based on the ratio of the pollutant’s max acute concentration to those five benchmark values. **Note:** The max acute concentration is based on the [acute high value](#) you chose in your Facility List Options file. The file also provides the receptor ID at which this max acute concentration occurs, including the FIPS and block ID for a census block receptor, the alternate receptor ID, the user receptor ID, or the distance and angle for a polar receptor.

The Acute Impacts Summary is able to be generated only if you entered Y in the [acute column](#) of the Facility List Options input file prior to modeling, for one or more facilities in your run group.

Note: **The pollutant concentration is provided in mg/m<sup>3</sup> in this output** (not µg/m<sup>3</sup> as provided by HEM at receptor locations in other output files) and the benchmark values are also based on mg not µg. **Table 47** below shows an abbreviated sample screenshot of the Acute Impacts Summary file.

### 7.1.4. Multipathway Summary

The Multipathway Summary output (*multi\_pathway.xlsx*) provides arsenic, polycyclic aromatic hydrocarbon (PAH) and dioxin/furan (D/F) concentrations and risk at MIR receptors and within directional octants around each facility, which are useful for a post-HEM multipathway analysis.

This file lists the following information:

- the run group’s name,

- the Facility ID,
- whether the facility was modeled using an urban or rural dispersion environment,
- whether the receptor in a given output row is an MIR or the closest receptor to the facility center in a specific octant direction (E, N, NE, NW, S, SE, SW, W),
- the pollutants the MIR is attributable to (All HAP, As for Arsenic, PAH, or D/F for Dioxins/Furans),
- whether the closest octant receptor is at a census block centroid, alternate receptor, or a discrete user receptor,
- the FIPS plus Block ID of the census receptor, or the ID of alternate and user receptor,
- the latitude and longitude location of the receptor,
- the population of the receptor,
- the total inhalation risk of that receptor (for all HAP),
- the total inhalation risk of that receptor attributable to Arsenic compounds,
- the total inhalation risk of that receptor attributable to PAHs, and
- the total inhalation risk of that receptor attributable to Dioxins/Furans.

**Table 48** shows a screenshot of a sample Multipathway Summary file. **Note:** Blank cells indicate that emissions from this sample facility do not include arsenic, PAH, or D/F.

**Table 47. Sample Acute Impacts Summary Output (abbreviated)**

Facility ID	Pollutant	CONC_MG/M <sup>3</sup>	REL	AEGL_1_1H	[3 other benchmark columns]	HQ REL	HQ AEGL1	[3 other HQ columns based on 3 other benchmarks]	[4 columns indicating Receptor ID or distance and angle for polar receptor]
Fac1-NC	acetaldehyde	0.014339116	0.47	81	...	0.03050876	0.00017703	...	...
Fac1-NC	acrolein	0.100373815	0.0025	0.069	...	40.149526	1.45469297	...	...
Fac1-NC	arsenic compounds	0.069242032	0.0002	0	...	346.210161	0	...	...
Fac1-NC	benz[a]anthracene	1.61754E-06	0	0	...	0	0	...	...
Fac1-NC	benzene	0.029947323	0	170	...	0	0.00017616	...	...

**Table 48. Sample Multipathway Summary Output**

Run Group	Facility ID	Rural/Urban	Octant or MIR	Chem, Centroid, or Discrete	Fips + Block	Lat	Lon	Population	Total Inhalation Cancer Risk	Total Inhalation As Cancer Risk	Total Inhalation PAH Cancer Risk	Total Inhalation D/F Cancer Risk
test 8-8-2020	Fac1-NC	U	MIR	All HAP	370639801001074	35.89908	-78.888	3	0.000610761	0	0	0
test 8-8-2020	Fac1-NC	U	MIR	As					0	0	0	0
test 8-8-2020	Fac1-NC	U	MIR	PAH					0	0	0	0
test 8-8-2020	Fac1-NC	U	MIR	DF					0	0	0	0
test 8-8-2020	Fac1-NC	U	E	Centroid	370630020283011	35.89548	-78.8494	1	1.28285E-05	0	0	0
test 8-8-2020	Fac1-NC	U	N	Centroid	370630020271050	35.91643	-78.8859	55	7.45249E-05	0	0	0
test 8-8-2020	Fac1-NC	U	NE	Centroid	370630020281025	35.92024	-78.8455	3	2.99575E-05	0	0	0
test 8-8-2020	Fac1-NC	U	NW	Centroid	370630020272047	35.90438	-78.8882	7	0.000248176	0	0	0
test 8-8-2020	Fac1-NC	U	S	Centroid	370630020272057	35.89265	-78.8873	219	0.00017255	0	0	0
test 8-8-2020	Fac1-NC	U	SE	Centroid	370630020283042	35.88258	-78.864	41	1.48092E-05	0	0	0
test 8-8-2020	Fac1-NC	U	SW	Discrete	U00000000URCPT1	35.90016	-78.8888	0	0.000518777	0	0	0
test 8-8-2020	Fac1-NC	U	W	Discrete	U00000000URCPT2	35.90434	-78.8909	0	0.00018499	0	0	0

### 7.1.5. Max Concentration Summary

The Max Concentration Summary (*max\_conc\_locations.xlsx*) provides the maximum concentration and the location of that maximum, for each facility, of the pollutant you identify on the *Summarize Risks* interface, as noted in Section 4.5. The summary lists the maximum concentration of this pollutant (in  $\mu\text{g}/\text{m}^3$ ) for every facility that emits that pollutant, the latitude and longitude of the location where this maximum concentration occurs, the receptor type (e.g., polar grid receptor, census block receptor, user receptor), and the FIPS and Block ID for the receptor, if it is a census block.

**Table 49** shows a screenshot of a sample Max Concentration Summary, in which the user entered “arsenic compounds” on the *Summarize Risks* interface, under the Max Concentration check box. The “PG” listed under Receptor Type in this example indicates that the maximum occurs at a polar grid receptor; hence the FIPS and Block ID columns are blank.

**Table 49. Sample Max Concentration Summary**

Facility ID	Pollutant	Max Concentration ( $\mu\text{g}/\text{m}^3$ )	Lat	Lon	FIPS	Block	Receptor Type
Fac1-NC	arsenic compounds	0.004157229	33.01296	-110.784			PG
Fac2-SC	arsenic compounds	0.03816163	33.00462	-110.778			PG
Fac3-IL	arsenic compounds	0.175248289	33.41242	-110.856			PG

Table 49 Note: Only facilities containing the pollutant will appear in this summary; if you ask for the max concentration of a pollutant not contained in certain facilities, those facilities will not appear in this output. Likewise, if you ask for a pollutant not in your HAP Emissions input file at all, no max concentrations will be provided.

### 7.1.6. Max Risk and HI by Source and Pollutant Summary

The Max Risk and HI by Source and Pollutant Summary (*facility\_risk\_hi\_byrchap.xlsx*) provides the maximum risk for each facility, the facility-wide incidence, the maximum noncancer hazard index (HI) for each facility, and the target organ type for that facility-specific maximum HI from the 14 modeled TOSHIs (e.g., respiratory, neurological, developmental). The summary also provides the risk, incidence, and noncancer hazard quotient (HQ) by source type and by pollutant, for each modeled facility.

**Table 50** shows a screenshot of a portion of a sample Max Risk and HI by Source and Pollutant Summary. In this sample, results are shown for one modeled facility and the facility’s ID/name, MIR, incidence, noncancer max TOSHI value, and TOSHI type (for all pollutants and sources combined) are listed in each row of this output in the first five columns. In addition, each row provides a different risk, noncancer HQ, and incidence caused by each modeled source type and pollutant (“HAP”) combination. For example, the risk caused by trichloroethylene from source type “RW” is 6.43E-07 (or 0.6 in a million), as shown in row 2 of Table 50. The noncancer HQ caused by trichloroethylene from source type RW is 0.0669, and the incidence caused by trichloroethylene from source type RW is 4.17E-06.

**Table 50. Sample Max Risk and HI by Source and Pollutant Summary**

Facility	Facility MIR	Facility Incidence	Facility Max HI	Max HI Type	Source Type	Pollutant	Risk by Source and HAP	HQ by Source and HAP	Incidence by Source and HAP
Fac1-NC	0.000611	0.0480683	8.998161	developmental	RV	xylenes (mixed)	0	0.000111	0
Fac1-NC	0.000611	0.0480683	8.998161	developmental	RW	trichloroethylene	6.43E-07	0.066946	4.171E-06
Fac1-NC	0.000611	0.0480683	8.998161	developmental	FU	selenium compounds		0.00091	
Fac1-NC	0.000611	0.0480683	8.998161	developmental	RV	naphthalene	4.49E-07	0.004401	4.268E-05

Facility	Facility MIR	Facility Incidence	Facility Max HI	Max HI Type	Source Type	Pollutant	Risk by Source and HAP	HQ by Source and HAP	Incidence by Source and HAP
Fac1-NC	0.000611	0.0480683	8.998161	developmental	FU	mercury (elemental)	0	0.027301	0
Fac1-NC	0.000611	0.0480683	8.998161	developmental	CT	indeno[1,2,3-c,d]pyrene	3.13E-14	0	3.071E-12
Fac1-NC	0.000611	0.0480683	8.998161	developmental	CV	indeno[1,2,3-c,d]pyrene	1.51E-13	0	1.201E-11
Fac1-NC	0.000611	0.0480683	8.998161	developmental	HV	indeno[1,2,3-c,d]pyrene	1.59E-13	0	1.651E-11
...	...	...	...	...	...	...	...	...	...

As suggested by the above example, this summary output provides a detailed breakdown of cancer risk, noncancer HQ, and incidence for every modeled pollutant and source type.

## 7.2. Run Group Summaries

As noted in Section 4.5, five of the 11 summaries produce results for the entire run group that account for impacts on receptors from multiple, neighboring facilities if their modeling domains intersect. Individual facility IDs are not connected to the results. The five run group-wide summaries discussed in this section include: the max risk and hazard indices summary, the risk histogram summary, the hazard index histogram summary, the incidence drivers summary, and the source type risk histogram summary.

### 7.2.1. Max Risk and Hazard Indices Summary

The Max Risk Summary output (*max\_risk.xlsx*) provides the maximum cancer risk and maximum noncancer risk (HI) for all 14 TOSHI's at any populated receptor in the run group, accounting for multiple impacts on receptors from neighboring facilities. This summary also provides the FIPS and block ID for census blocks, the alternate receptor ID, or the user receptor ID of each of the maxima, as well as the receptor's population.

The Max Risk Summary also lists the Facility ID(s) of the facility or facilities that impact these max receptors (i.e., contribute to the max risk and max TOSHIs at these receptors).

**Note:** The maxima reported in this summary will equal the highest facility-specific risk and HI listed in the Facility Max Risk and HI output (discussed in Section 6.2.1), except when multiple facilities' impacts on the same receptor cause the max risk and HI to be greater than the highest individual facility-specific risk and HI.

A sample Max Risk Summary file is shown split up into **Table 51** and **Table 52**.

**Table 51. Sample Max Risk Summary Output, Rows 1-16**

RISK_TYPE	FIPS	BLOCK	POPULATION	RISK
mir	36045	0613001004	126	4.8218E-07
respiratory	36045	0613001004	126	0.003784775
liver	36045	0613001004	126	0.00010653
neurological	37165	0104001092	16	0.115473556
developmental	36045	0613001004	126	2.37305-05
reproductive			0	0
kidney			0	0
ocular			0	0
endocrine			0	0

RISK_TYPE	FIPS	BLOCK	POPULATION	RISK
hematological			0	0
immunological			0	0
skeletal			0	0
spleen			0	0
thyroid			0	0
whole body			0	0

**Table 52. Sample Max Risk Summary Output, Rows 17-18**

Facilities Impacting mir Block	Facilities Impacting respiratory Block	Facilities Impacting liver Block	Facilities Impacting neurological Block	Facilities Impacting developmental Block
3604511259	3604511259	3604511259	3604511259	3604511259

## 7.2.2. Risk Histogram Summary

The Risk Histogram output (*histogram\_risk.xlsx*) provides the population and facility counts at various risk levels. This file lists the number of people and facilities in the modeled run group in the following risk bins:

- less than 1 in 1 million risk (displayed as “<1e-6”),
- greater than or equal to 1 in 1 million risk (displayed as “>= 1e-6”),
- greater than or equal to 10 in 1 million risk (displayed as “>=1e-5”),
- greater than or equal to 100 in 1 million risk (displayed as “>=1e-4”), and
- greater than or equal to 1,000 in 1 million risk (displayed as “>=1e-3”).

**Note:** This program assigns populations and facilities to cancer risk bins based on their risk level after rounding to one significant figure, per EPA convention. The Risk Histogram Summary takes into account multiple impacts on the same receptor (from facilities located close to one another). This may cause the population numbers from this file to differ slightly from the population numbers provided by the Facility Cancer Risk Exposure file. **Table 53** shows a sample output. Note that the total population modeled in the run group can be determined by summing cells B2 and B3; and the total number of facilities modeled can be determined by summing cells C2 and C3.

**Table 53. Sample Risk Histogram Summary Output**

Risk level	Population	Facility count
<1e-6	3088984	0
>=1e-6	835305	2
>=1e-5	45866	1
>=1e-4	435	1
>=1e-3	0	0

### 7.2.3. Hazard Index Histogram Summary

The Hazard Index Histogram output (*hi\_histogram.xlsx*) provides the population and facility counts at various noncancer HI levels, for all 14 TOSHIs. This file lists the number of people and facilities in the modeled run group in the following noncancer HI bins:

- 1,000,
- 100,
- 10,
- 1, and
- <= 1.

**Note:** This program assigns populations and facilities to noncancer HI bins based on their HI level after rounding to one significant figure, per EPA convention. The Hazard Index Histogram Summary takes into account multiple impacts on the same receptor (from facilities located close to one another). This may cause the population numbers from this file to differ slightly from the population numbers provided by the Facility TOSHI Exposure file. **Table 54** shows an abbreviated sample output for 3 TOSHIs; the actual file shows results for all 14 TOSHIs.

**Table 54. Sample Hazard Index Histogram Summary Output (Partial)**

HI Level	Respiratory Pop	Respiratory Facilities	Liver Pop	Liver Facilities	Neurological Pop	Neurological Facilities
> 1000	0	0	0	0	0	0
> 100	0	0	0	0	0	0
> 10	0	0	0	0	0	0
> 1	167	1	0	0	22	1
<= 1	3924289	1	3924289	2	3924434	1

### 7.2.4. Incidence Drivers Summary

The Incidence Drivers output (*incidence\_drivers.xlsx*) provides the pollutants driving the incidence across the entire run group of modeled facilities. (As noted in previous sections, the incidence is equal to the cancer risk of each block times the population of that block, divided by a 70-year lifetime, and summed over all blocks in the modeling domain.) In this file, the total incidence and individual incidence attributable to each pollutant are provided, as well as the percentage that each pollutant-specific incidence is of total incidence. The pollutants are listed in descending order of contribution to the total incidence. **Table 55** shows a sample output.

**Table 55. Sample Incidence Drivers Summary Output**

Pollutant	Incidence	% of Total Incidence
arsenic compounds	0.039060199	81.83%
1,3-butadiene	0.003666767	7.68%
cadmium compounds	0.003205572	6.72%
naphthalene	0.00105277	2.21%
benzene	0.000444901	0.93%
bis(2-ethylhexyl)phthalate	0.000219206	0.46%
chromium (vi) compounds	5.6644E-05	0.12%
trichloroethylene	1.01883E-05	0.02%
Total incidence	0.04773414	100%

## 7.2.5. Source Type Risk Histogram Summary

The Source Type Risk Histogram Summary (*source\_type\_risk.xlsx*) output provides the maximum cancer risk overall for the run group, as well as individually by emission source type. For the maximum overall risk and for the source type-specific risk, the file also provides the number of people estimated at three risk levels:  $\geq 1$  in 1 million,  $\geq 10$  in 1 million, and  $\geq 100$  in 1 million. The overall incidence and the incidence attributable to each emission source type is also provided.

**Table 56** shows a sample Source Type Risk Histogram Summary file. In this example, the source types included in the input files for the run on which this summary file is based are SR, RV, FU, MS, RW, CV, HV, and CT. As shown in Table 56, the SR source type contributes almost all of the risk to the overall cancer risk.

**Table 56. Sample Sourcetype\_Histogram\_Sorted RTR Summary Output**

	Maximum Overall	SR	RV	FU	MS	RW	CV	HV	CT
<i>Cancer Risk: Maximum (in 1 million)</i>	600	600	5	4	0.5	0.4	0.009	0.007	0.002
<i>Number of people <math>\geq 100</math> in 1 million</i>	435	435	0	0	0	0	0	0	0
<i>Number of people <math>\geq 10</math> in 1 million</i>	48,998	37,478	0	0	0	0	0	0	0
<i>Number of people <math>\geq 1</math> in 1 million</i>	800,229	528,652	214,494	239	0	0	0	0	0
Incidence	0.047	0.035	0.012	0.00022	5.9E-06	0.000011	3.3E-06	3.8E-06	2.1E-06
<b>Run Group MIR (in a million) = 600.0</b>									

Table 56 Note: The Maximum Overall column lists the population at various risk levels attributable to all source types/emission process groups combined, while the other columns list the population at various risk levels attributable to each individual source type in isolation. The sum of the population tallies across the individual source types may not necessarily equal the corresponding value in the maximum overall column, at a given risk level, because: (a) two or more source types' impact in combination may be required to cause a census block population to exceed a given risk level; or conversely (b) an individual source type's impact in isolation may be enough to cause a census block population to exceed a given risk level, while other source types may similarly impact the same census block population and also (in isolation) cause that population to exceed the given risk level.

## 8. Demographic Assessment Methodology & Results

HEM's Demographic Assessment module can be used only when modeling with U.S. Census block receptors because the Census provides demographic estimates for its population counts. This section discusses the data sources and methodology behind HEM's Demographic Assessment results and describes the outputs produced using sample results. **Appendix B** contains a more detailed description of the calculations used within the methodology.

### 8.1. U.S. Census Demographic Data used by HEM

When modeling with U.S. Census receptors, HEM estimates population exposures to air pollution at the census block level, which is the finest level of spatial resolution reported in the U.S. Decennial Census. HEM Version 5.0's Demographic Assessment module links your modeled population (including cancer and noncancer estimates for each census block receptor) to demographic data from the Census' 2018-2022 American Community Survey (ACS) on race and ethnicity, age, poverty status, educational attainment, limited English speaking households, and disabilities. **Note:** The ACS data is included in HEM's *resources* folder when you download the model in the form of two CSV files named *acs.csv* and *acs\_defaults.csv*.

The ACS (US Census Bureau, 2023b, 2024a, 2024b) is a population survey continuously carried out by the Census Bureau, in parallel with the Decennial Census (US Census Bureau, 2022b, 2023a) and independent of the decennial schedule. The ACS dataset is a five-year rolling average updated annually, with a lag time of about two years from the last year of the rolling average. The ACS also produces one year and three-year surveys for states and counties, although HEM's Demographic Assessment module uses the five-year (2018-2022) averages from the ACS for the nationwide, state, county, and modeling domain demographic statistics, for greater spatial resolution. Most demographic data in the five-year ACS are computed at the block group level; but some statistics are only computed at the tract level.

- **Note about the U.S. Census:** Within the Census, census blocks are aggregated into block groups, and block groups are aggregated into tracts. Tracts do not cross county boundaries, so each tract is contained entirely within a county. On average nationwide, there are about 20 tracts in a county. In the 2020 Census, there are approximately 240,000 block groups and 85,000 census tracts in the U.S. and Puerto Rico.<sup>12</sup> A census tract typically contains about three block groups and is designed to average 4,000 people. A census block group contains about 30 populated census blocks on average, with about 1,400 people in the block group. There are approximately 8.2 million census blocks in the 2020 Census and approximately 5.8 million of these are populated, with a block population of 58 people on average for these populated blocks (or 41 people on average for all census blocks including those with zero population). These statistics are merely averages; actual block populations vary widely.

HEM computes demographic statistics within the radius/proximity you chose on the Demographic Assessment interface (described in Section 4.6) for each individual facility's modeling domain and for your run group as a whole, including demographic-specific cancer and

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<sup>12</sup> 2020 Census Tallies are provided by the U.S. Census Bureau at <https://www.census.gov/geographies/reference-files/2020/geo/tallies.html>.

noncancer risk for your modeled population. HEM uses demographic data extracted from the 2018-2022 five-year ACS, which includes data from the 50 States, the District of Columbia, and Puerto Rico, to compute population impacts in the six following demographic categories:

- Race and ethnicity:
  - Percent White (not Hispanic or Latino),
  - Percent People of Color (the Total population minus the White population, including Black, American Indian or Alaska Native, Asian, Other or Multiracial, and Hispanic or Latino ethnicity of any race),
  - Percent Black (not Hispanic or Latino),
  - Percent American Indian or Alaska Native (not Hispanic or Latino),
  - Percent Asian (not Hispanic or Latino),
  - Percent Other races or Multiracial (not Hispanic or Latino),
  - Percent Hispanic or Latino (any race),
- Age:
  - Percent under age 18,
  - Percent aged 18 to under 65,
  - Percent aged 65 and older,
- Poverty status:
  - Percent living in households with total household income below the poverty line,
  - Percent living in households with total household income below twice the poverty line,
- Educational attainment:
  - Percent of people over age 25 without a High School Diploma,
- Limited English speaking households:
  - Percent of households in which no one over age 14 is proficient in English, and
- Disabilities:
  - People living with one or more disabilities.

The above demographic data is available at the census block group level for all demographic categories shown except for disabilities data, which is available at the tract level (US Census Bureau, 2023b, 2024a, 2024b). **Table 57** summarizes the census data used by HEM, showing the source of each dataset and the level of geographic resolution.

As previously noted, HEM's Demographic Assessment module links your modeling results for each census block to the appropriate ACS census block group and (for disabilities) tract demographic statistics. The demographic characteristics of the population potentially impacted by emissions from facilities in your run group are thereby determined by applying the ACS block group and tract characteristics to all modeled census block populations located within that block group or tract. As such, the demographic characteristics of a given block group or tract are presumed to also describe each census block located within that block group or tract.

Appendix B describes the calculation methods used to estimate the total population exposed to different risk levels, as well as the calculation methods used to compute risks for racial, ethnic, age, high school education status, low household income, poverty status, limited English-speaking, and disabilities demographic categories. Appendix B also describes the gap-filling

approach used by HEM when block group statistics are not available for a given block, based on computing default averages for the missing demographic(s) at the tract level or from the nearest block group.

**Table 57. Summary of Census Data used for Demographic Groups**

Type of population category	Source of data	Level of geographic resolution
Total population (sum of block centroid counts)	2020 Census, P.L. 94-171 Tables <sup>(a)</sup>	Census block
Total population (sum of block group counts, used for demographic percentages)	2018-2022 ACS Table B03002 (e1) (US Census Bureau, 2023b, 2024a, 2024b)	Census block group
Race/ethnicity categories (percentages):	ACS Table B03002, Hispanic or Latino Origin by Race (Tiger table X03): <ul style="list-style-type: none"> <li>• <b>White (non-hispanic):</b> e3/e1</li> <li>• <b>People of Color (non-white and hispanic):</b> (e1-e3)/e1</li> <li>• <b>Black (non-hispanic):</b> e4/e1</li> <li>• <b>American Indian and Alaskan Native (non-hispanic):</b> e5/e1</li> <li>• <b>Asian (non-hispanic):</b> e6/e1</li> <li>• <b>Other and Multiracial (non-hispanic):</b> (e6+e7+e8+e9)/e1</li> <li>• <b>Hispanic (all races):</b> e12/e1</li> </ul>	Census block group
Age groups	ACS Table B01001, Sex by Age (Tiger table X01)	Census block group
Individuals living in households earning below the poverty level (percentage of individuals)	ACS Table C17002, Ratio of Income to Poverty Level (Tiger table X17): (e2+e3)/e1	Census block group
Individuals living in households earning below twice the poverty level (percentage of individuals)	ACS Table C17002, Ratio of Income to Poverty Level (Tiger table X17): (e1-e8)/e1	Census block group
Adults 25 years and older without a high school diploma	ACS Table B15002, Sex by Educational Attainment (Tiger table X15)	Census block group
Individuals living in limited English speaking households (percentage of households)	ACS Table C16002, Household Language by Household (Tiger table X16): (e4+e7+e10+e13)/e1	Census block group
Individuals with one or more disabilities	ACS Table B99181, Allocation of Disability Items for the Civilian Noninstitutionalized Population: e2/e1	Census tract

(a) ArcGIS feature layer from Esri containing block level 2020 Decennial Census data as reported by the U.S. Census Bureau with attributes from the 2020 Public Law 94-171 (P.L. 94-171) tables (US Census Bureau, 2022b). Also refer to following reference: (US Census Bureau, 2023a).

## 8.2. Overview of Demographic Results

When you initiate a Demographic Assessment, the module will access the ACS data described above and will also access every facility's Block Summary Chronic output from the run group to create a large file called *MIR\_HI\_allreceptors.csv*. The *MIR\_HI\_allreceptors* file contains the FIPS, Block ID, latitude/longitude, population, MIR, and all 14 TOSHI values for every modeled block in your run group. It also contains the number of facilities that impact each block (to account for multiple impacts from neighboring facilities) and the distance of the block from the

facility center (used to determine if the block is within your specified radius). Depending on the size of your run group, this file may be quite large and will be placed by HEM in the output directory you pointed to on the [Demographic Assessment interface](#) (i.e., the same folder in which the *Facility\_Max\_Risk\_and\_HI.xlsx* file is located). The Demographic Assessment module will select blocks from the *MIR\_HI\_allreceptors* file that fall within the radius you specified on the interface and then determine their demographics from the ACS data.

- **Note about the *MIR\_HI\_allreceptors* file:** The *MIR\_HI\_allreceptors* file will not be overwritten during a subsequent Demographic Assessment run in which you have pointed to the same HEM output folder. This saves time when processing additional Demographic Assessment scenarios (beyond the initial four combinations). However, **you must move or delete an existing *MIR\_HI\_allreceptors* file if you do wish for a new one to be created.** No new *MIR\_HI\_allreceptors* file will be created in an output folder if one already exists.

For each combination of radius and risk/HI level you select on the Demographic Assessment interface (discussed in Section 4.6), **HEM produces four types of output files that are placed in the “pop” (population) subfolder created in your output folder:**

1. Run group wide Excel™ workbooks of binned results covering all risk/HI levels for each demographic category (listed in Table 57), which include:
  - a. the total population in the run group’s modeled domain exceeding your chosen risk/HI level, broken out into demographic percentages (exceeding your chosen risk/HI level),
  - b. the max risk/HI for your entire run group of modeled facilities as a whole,
  - c. run group wide proximity results showing the total population (at your chosen radius) broken out into demographic percentages (irrespective of risk/HI), and
  - d. nationwide, state, and county total populations, broken out into demographic percentages for comparison.
2. Facility-specific Excel™ workbooks of binned results covering all risk/HI levels for each demographic category (listed in Table 57), which include results similar to those listed in #1 except at the facility-level instead of the run group-level:
  - a. the total population in the facility’s modeled domain exceeding your chosen risk/HI level, broken out into demographic percentages (exceeding your chosen risk/HI level),
  - b. the max risk/HI at that facility,
  - c. facility-specific proximity results showing the total population (at your chosen radius) broken out into demographic percentages (irrespective of risk/HI), and
  - d. nationwide, state, and county total populations, broken out into demographic percentages for comparison.
3. Summary Excel™ worksheets that display the results contained in #1 and #2 above in rows collected into one summary table, including:
  - a. run group wide “Proximity” row results showing the total population (at your chosen radius) broken out into demographic percentages (irrespective of risk/HI),
  - b. “At Risk” or “Above HI” population rows for the run group’s modeled domain exceeding your chosen risk/HI level, broken out into demographic percentages (exceeding your chosen risk/HI level),
  - c. facility-specific “Proximity” rows showing the total population surrounding each facility (at your chosen radius) broken out into demographic percentages and irrespective of risk/HI,

- d. “At Risk” or “Above HI” population rows for each modeled facility’s modeled domain exceeding your chosen risk/HI level, broken out into demographic percentages (exceeding your chosen risk/HI level); and
      - e. nationwide, state, and county total populations, broken out into demographic percentages for comparison.
4. Defaulted block groups text files at each radius you selected, at both the facility-specific and run group wide levels, listing the populated (non-zero) Census blocks that could not be matched to block groups.
  - a. These listed blocks required the use of tract or nearest block group defaults to estimate their demographic compositions. (See Appendix B, Section B.7 for a discussion regarding demographic defaulting by HEM’s Demographic Assessment module.)
  - b. These text files do not contain any demographic results but are useful for QA reviews because they indicate the degree to which spatially resolved demographic statistics were available for your demographic assessment.

In addition to the above four file types, the Demographic Assessment module also produces a *hem.log* file that chronicles the Demographic Assessment run. This is similar to the *hem.log* files produced for your modeling run and discussed in Sections 4.4 and 6.2.4, although this *hem.log* tracks the activity performed by the Demographic Assessment module.

Finally, the Demographic Assessment module may also produce another type of QA output named *Skipped demographic facilities.xlsx*. This file is produced if one or more of the facility-specific folders are empty to alert you to the fact that not all facilities are included in the demographic assessment outputs. (Empty facility folders may occur when AERMOD fails to run during HEM modeling due to errors in the input files, as discussed in Section 4.9 and Section 6.2.4.)

- **Note regarding run group-wide versus facility-specific outputs:** Run group wide cumulative risk is accounted for from neighboring facilities with overlapping domains of impact, while at the facility level only risk from that individual facility is accounted for, regardless of how close a neighboring facility may be. This allows for consideration of the demographic impacts from each individual facility in isolation, as well as from the group of facilities modeled as a whole.

### 8.3. Sample Demographic Results

As noted in Section 4.6 and Section 8.2, when you initiate a Demographic Assessment run, **HEM will automatically create a new subfolder named “pop” in your run group output folder, and the results described above will be placed in this subfolder.** The outputs containing the demographic results will contain both the date and time stamp in their file names, indicating when they were produced. Samples of several Demographic Assessment output files are provided in this section, along with a short discussion to explain the demographic data shown.

**Table 58** is a sample of one of the tables provided in the workbook described above in #1 of Section 8.2, based on run-group wide results for cancer at 50 km and demographics by race/ethnicity. A similar table and workbook are produced for each facility (described above in #2 of Section 8.2).

Table 58 shows the number of people in each binned cancer risk level that the Demographic Assessment provides (i.e., 0 to <1-in-1 million risk up to >=300-in-1 million risk), as well as the *Total Number* of people modeled at all risk levels combined. This table also provides the population of each race/ethnicity category for each of the cancer risk bins, as well as the *Total Population* of all races/ethnicities combined within each risk bin.

**Table 58. Sample Demographic Output: Distribution of Cancer Risk for Racial and Ethnic Categories – 50 km Study Area Radius**

Range of Lifetime Individual Cancer Risk from the NC-IL Source Category (Chance in One Million) <sup>a</sup>	Total Population	White	Black	American Indian or Alaska Native	Asian	Other and Multiracial	Hispanic or Latino <sup>c</sup>
0 to < 1	3,325,002	2,075,203	444,229	3,347	178,776	111,572	511,875
1 to < 5	733,391	468,424	103,468	1,225	66,685	31,244	62,345
5 to < 10	173,873	76,566	44,615	416	22,527	7,430	22,319
10 to < 20	44,800	18,916	14,910	86	5,934	1,500	3,454
20 to < 30	26,199	10,666	8,685	102	3,412	961	2,373
30 to < 40	8,058	2,900	3,593	9	418	295	842
40 to < 50	3,379	1,739	1,037	7	144	169	283
50 to < 100	8,048	4,011	2,510	11	585	485	446
100 to < 200	573	154	337	0	8	39	35
200 to < 300	273	66	184	0	3	17	3
>= 300	72	17	50	0	1	4	0
Total Number	4,323,668	2,658,661	623,618	5,203	278,493	153,717	603,976
Average Risk (Chance in One Million) <sup>b</sup>	1	1	2	2	2	1	0.8

Table 58 Note: The demographic populations are based on the 2020 Decennial Census' total block populations that are located within the indicated radius, which are linked to the Census' 2018-2022 American Community Survey five-year demographic averages at the block group level.

- <sup>a</sup> Risks from the modeled emissions are at the census block level, based on the predicted outdoor concentration over a 70-year lifetime, and not adjusted for exposure factors.
- <sup>b</sup> The population-weighted average risk takes into account risk levels at all populated block receptors in the entire modeled domain.
- <sup>c</sup> In order to avoid double counting, the "Hispanic or Latino" category is treated as a distinct demographic category for these analyses. A person is identified as one of six racial/ethnic categories: White, Black, American Indian or Alaska Native, Asian, Other and Multiracial, or Hispanic/Latino.

Based on the sample output shown above in Table 58:

- For this run group, there are a total of 4,323,668 people in the 50 km modeling domain.
- Out of those 4,323,668 people, there are 3,325,002 people at a cancer risk less than 1-in-1 million, 733,391 people at a risk at least 1-in-1 million but less than 5-in-1 million and so on, with 72 people at a risk greater than or equal to 300-in-1 million.
- Of the 3,325,002 people with a modeled risk less than 1-in-1 million, 2,075,203 identify as White, 444,229 identify as Black, 3,347 identify as American Indian or Alaskan Native, 178,776 identify as Asian, 111,572 identify as "Other and Multiracial", and 511,875 identify as Hispanic or Latino.
- Of the 72 people in the highest cancer risk bin (greater than or equal to 300-in-1 million), 17 identify as White, 50 identify as Black, none identify as American Indian or Alaskan

Native, one identifies as Asian, 4 identify as “Other and Multiracial”, and none identify as Hispanic or Latino.

Finally, the bottom row of Table 58 provides the average cancer risk (chance in one million) for the total population and for each racial/ethnic demographic category in the modeled population in this run group as a whole.

- **Note about average risk versus maximum risk:** The average risk is less than the maximum risk (MIR) because the average risk takes into account risk levels at all populated block receptors for the entire modeled domain of the source category (a 50 km radius in this sample run), whereas the maximum risk occurs at an individual populated receptor (that receptor with the highest modeled risk level). The average risk statistic encompasses higher risk levels (generally) closer into facility emissions as well as lower risk locations (generally) farther away in the domain.

Similar tables to the one shown in Table 58 are produced by the Demographic Assessment module for the other demographic categories listed in Table 57 (i.e., by age, education level, poverty status, limited English speaking households, and disabilities), at both the run group level and the individual facility level. These tables are produced for every radius you selected on the Demographic Assessment interface.

**Figure 26** shows another sample table in the workbook described in #1 (of Section 8.2), labeled the “**Proximity & Ave. Risk Summary**” on its worksheet tab. The results depicted in this sample table are based on run-group wide results for cancer risk at 5 km, for all demographic categories provided by the Demographic Assessment module. A similar table is produced for each facility (described in #2 of Section 8.2).

- This table provides proximity statistics at the radius you selected on the Demographic Assessment interface as both number of people and percentage.
- The average risk (in one million) for every demographic category provided by the Demographic Assessment module is also listed.
- In addition, the table shown in Figure 26 provides nationwide, state and county demographic breakdowns.
  - The nationwide population counts and percentages are based on the five-year U.S. national averages provided in the 2018-2020 ACS (US Census Bureau, 2023b, 2024a, 2024b) and include Puerto Rico. Average(s) based on fewer years will differ slightly and will be impacted more by the value in any one year.
  - The state and county demographic breakdowns are tabulated by HEM’s Demographic Assessment module based on the average statistics of every state and county within which any facility’s receptor is located, at the radius you chose for your run group. Even if only one receptor is located in a given state or county, that state or county is included in the demographic breakdowns shown. It should also be noted that the nationwide, state, and county demographic breakdowns are not based on risk or HI levels, but are merely total population counts and percentages, or “proximity statistics”.

Following Figure 26, another sample table output by the Demographic Module is shown in **Table 59**. This table, labeled the “**Pop. at Risk Summary**” on the workbook’s tab, is also provided at the run group level and the individual facility level. In addition to the nationwide, state and county percentages, Table 59 also provides:

- the maximum risk (or HI) for the run group (or for the individual facility for the facility-specific outputs) in table note “i”, and
- the total population above the risk or HI level you selected on the Demographic Assessment interface, with the demographic breakdown of that same population exceeding the risk/HI threshold you selected.

A tab labeled “**Preamble Summary**” (not depicted here) produces similar results as the “Pop. at Risk Summary” but is organized differently and grouped into the following categories: Race and Ethnicity by Percent, Income by Percent, Education by Percent, Disabilities by Percent, and Limited English Speaking Households by Percent.

Finally, following Table 59, the table shown in **Table 60** is a sample of the “**Pop Summary**” output file, noted in #3 above (of Section 8.2). This summary provides the nationwide, state, and county demographic breakdowns as well as the “At Risk” (or “Above HI”) demographic percentages above the risk/HI level and at the radius you selected, for the run group and for each individual facility. The Pop Summary output provides the comprehensive results of your Demographic Assessment in one file and is used by Python’s Dash app to produce the interactive browser-based graphs of the demographic results, described in Section 4.7.2.

The Demographic Assessment module produces a separate Pop Summary output file, for cancer risk and for noncancer HI, at each radius you selected (as explained in Section 4.6). Then, within each radius-specific Pop Summary file, there are separate Excel™ workbook tabs for each risk/HI level you selected on the interface. For example, if you choose to run a Demographic Assessment for cancer risk at 50 km with a risk level greater than or equal to 1-in-1 million, and also at 50 km with a risk level greater than or equal to 10-in-1 million, then one Pop Summary output file will be produced that will contain “50\_km\_Cancer” in the filename (with the date), and within that file will be a two-tabbed workbook. One worksheet tab will be labeled “Risk >= 1-in-1 million” and the other worksheet tab will be labeled “Risk >= 10-in-1 million”. The same is true for different noncancer HI levels you choose at a given radius on the Demographic Assessment interface.

**Figure 26. Sample Demographic Proximity and Average Risk Summary – 5 km Study Area Radius**

	A	B	C	D	E	F	G	H	I	J	K	L	M	N	O	P	Q	R
1	<b>Proximity and Average Risk Results for All Demographic Groups Analyzed - 5 km Study Area Radius *</b>																	
2		Total Population	White	People of Color <sup>b</sup>	Black	American Indian or Alaska Native	Asian	Other and Multiracial	Hispanic or Latino <sup>c</sup>	Age (Years) 0-17	Age (Years) 18-64	Age (Years) >=65	Below the Poverty Level <sup>d</sup>	Below Twice the Poverty Level <sup>d</sup>	Total Number >= 25 Years Old	Over 25 without a High School Diploma <sup>e</sup>	People Living in Limited English Speaking Households <sup>f</sup>	People with One or More Disabilities <sup>g</sup>
3	<b>Nationwide Demographic Breakdown</b>																	
4	Total population <sup>h</sup>	334,369,975	194,913,654	139,456,321	40,150,435	1,826,398	18,875,968	13,616,327	64,987,193	73,779,881	205,129,512	55,460,582	41,977,891	95,614,101	229,010,904	25,093,509	17,072,312	40,368,464
5	Percentage of total		58.3%	41.7%	12.0%	0.5%	5.6%	4.1%	19.4%	22.1%	61.3%	16.6%	12.6%	28.6%	68.5%	11.0%	5.1%	12.1%
6	<b>State Demographic Breakdown</b>																	
7	Total population <sup>h</sup>	23,227,848	14,057,603	9,170,245	3,905,992	101,718	1,054,092	781,731	3,326,712	5,104,365	14,304,651	3,818,832	2,828,766	6,532,929	15,918,598	1,620,894	807,283	2,790,208
8	Percentage of total		60.5%	39.5%	16.8%	0.4%	4.5%	3.4%	14.3%	22.0%	61.6%	16.4%	12.2%	28.1%	68.5%	10.2%	3.5%	12.0%
9	<b>County Demographic Breakdown</b>																	
10	Total population <sup>h</sup>	2,416,151	1,407,971	1,008,180	426,399	3,338	151,937	91,027	335,479	562,302	1,533,782	320,067	192,796	479,457	1,631,342	119,848	68,393	282,733
11	Percentage of total		58.3%	41.7%	17.6%	0.1%	6.3%	3.8%	13.9%	23.3%	63.5%	13.2%	8.0%	19.8%	67.5%	7.3%	2.8%	11.7%
12	<b>Proximity Results plus Average Risk based on test1 modeled emissions</b>																	
13	Total population within 5 km of any facility	58,133	28,533	29,600	16,265	68	5,811	2,297	5,159	11,705	38,486	7,942	3,935	10,736	42,458	1,499	790	6,041
14	Percentage of total		49.1%	50.9%	28.0%	0.1%	10.0%	4.0%	8.9%	20.1%	66.2%	13.7%	6.8%	18.5%	73.0%	3.5%	1.4%	10.4%
15	Average risk (in one million) <sup>i</sup>	20	20	30	30	30	20	30	20	20	20	30	30	30	30	30	20	30
16																		

Figure 26 Notes:

**Note on table title shown in the figure, Proximity and Average Risk Results for all Demographic Groups Analyzed – 5 km Study Area Radius:** The demographic percentages are based on the 2020 Decennial Census' block populations, which are linked to the Census' 2018-2022 American Community Survey (ACS) five-year demographic averages at the block group level. To derive demographic percentages, it is assumed a block's demographics are the same as the block group in which it is contained. Demographics are tallied for all blocks falling within the indicated radius.

**Note on the People of Color column shown in the figure:** A person is identified as one of six racial/ethnic categories: White, Black, American Indian or Alaska Native, Asian, Other and Multiracial, or Hispanic/Latino. The People of Color population is the total population minus the White population.

**Note on the Hispanic or Latino column shown in the figure:** To avoid double counting, the "Hispanic or Latino" category is treated as a distinct demographic category. A person who identifies as Hispanic or Latino is counted only as Hispanic/Latino for this analysis (regardless of other racial identifiers).

**Note on the Below the Poverty Level and Below Twice the Poverty Level columns shown in the figure:** The demographic percentages for people living below the poverty line and below twice the poverty line are based on Census ACS surveys at the block group level that do not include people in group living situations such as dorms, prisons, nursing homes, and military barracks. To derive the nationwide demographic percentages shown, these block group level tallies are summed for all block groups in the nation and then divided by the total U.S. population based on the 2018-2022 ACS. The study area's population counts are based on the methodology noted in footnote 'a' to derive block-level demographic population counts, which are then divided by the respective total block-level population to derive the study area demographic percentages shown.

**Note on the Over 25 without a High School Diploma column shown in the figure:** The demographic percentage for people >= 25 years old without a high school diploma is based on Census ACS data for the total population 25 years old and older at the block group level, which is used as the denominator when calculating this demographic percentage.

**Note on the People Living in Limited English Speaking Households column shown in the figure:** The Limited English speaking population is estimated at the block group level by taking the product of the block group population and the fraction of Limited English speaking households in the block group, assuming that the number of individuals per household is the same for Limited English speaking households as for the general population, and summed over all block groups.

**Note on the *People with One or More Disabilities* column shown in the figure:** The demographic percentages for people with one or more disabilities are based on Census ACS surveys at the tract level of civilian non-institutionalized people (i.e., all U.S. civilians not residing in institutional group quarters facilities such as correctional institutions, juvenile facilities, skilled nursing facilities, and other long-term care living arrangements). To derive the nationwide demographic percentages shown, these tract level tallies are summed for all tracts in the nation and then divided by the total U.S. population based on the 2018-2022 ACS. The study areas' population counts are based on applying the Census tract level percentage of people with one or more disabilities to each block group and block within the respective tract. The methodology noted in footnote "a" is then used to derive block-level demographic population counts, which are then divided by the respective total block-level population to derive the study area demographic percentages shown.

**Note on the *Total Population* rows for the *Nationwide Demographic Breakdown, State Demographic Breakdown, and County Demographic Breakdown* shown in the figure:** The total nationwide population includes all 50 states, the District of Columbia, and Puerto Rico. The state and county populations include any states and counties, respectively, with census block centroids within the radius of the modeled area.

**Note on the *Average risk (in one million)* row shown in the figure:** The population-weighted average risk takes into account risk levels at all populated block receptors in the entire modeled domain. Risks from the modeled emissions are at the census block level, based on the predicted outdoor concentration over a 70-year lifetime, and not adjusted for exposure factors.

**Table 59. Population at Risk Summary: Demographic Assessment of Risk Results Based on NC-IL Emissions - 50 km Study Area Radius**

Population Basis	Total Population	People of Color <sup>a</sup>	Black	American Indian or Alaska Native	Asian	Other and Multiracial	Hispanic or Latino <sup>b</sup>	Age (Years) 0-17	Age (Years) 18-64	Age (Years) >=65	Below the Poverty Level <sup>c</sup>	Below Twice the Poverty Level <sup>c</sup>	Over 25 Without a High School Diploma <sup>d</sup>	People Living in Limited English Speaking Households <sup>e</sup>	People with One or More Disabilities <sup>f</sup>
Nationwide <sup>g</sup>	334,369,975	41.7%	12.0%	0.5%	5.6%	4.1%	19.4%	22.1%	61.3%	16.6%	12.6%	28.6%	11.0%	5.1%	12.1%
State <sup>g</sup>	23,227,848	39.5%	16.8%	0.4%	4.5%	3.4%	14.3%	22.0%	61.6%	16.4%	12.2%	28.1%	10.2%	3.5%	12.0%
County <sup>g</sup>	10,412,933	49.0%	18.2%	0.1%	6.8%	3.2%	20.6%	22.2%	62.8%	14.9%	11.1%	25.3%	10.3%	5.3%	12.5%
Population With Risk Greater Than or Equal to 1 in 1 million <sup>h,i</sup>	998,666	41.6%	18.0%	0.2%	10.0%	4.2%	9.2%	21.1%	64.7%	14.2%	8.7%	19.8%	6.0%	2.8%	10.6%

Table 59 Notes: The demographic percentages are based on the 2020 Decennial Census' block populations, which are linked to the Census' 2018-2022 American Community Survey (ACS) five-year demographic averages at the block group level. To derive demographic percentages, it is assumed a block's demographics are the same as the block group in which it is contained. Demographics are tallied for all blocks falling within the indicated radius.

- <sup>a</sup> A person is identified as one of six racial/ethnic categories: White, Black, American Indian or Alaska Native, Asian, Other and Multiracial, or Hispanic/Latino. The People of Color population is the total population minus the White population.
- <sup>b</sup> To avoid double counting, the "Hispanic or Latino" category is treated as a distinct demographic category. A person who identifies as Hispanic or Latino is counted only as Hispanic/Latino for this analysis (regardless of other racial identifiers).
- <sup>c</sup> The demographic percentages for people living below the poverty line or below twice the poverty line are based on Census ACS surveys at the block group level that do not include people in group living situations such as dorms, prisons, nursing homes, and military barracks. To derive the nationwide demographic percentages shown, these block group level tallies are summed for all block groups in the nation and then divided by the total U.S. population based on the 2018-2022 ACS. The study area's population counts are based on the methodology noted in footnote 'a' to derive block-level demographic population counts, which are then divided by the respective total block-level population to derive the study area demographic percentages shown.
- <sup>d</sup> The demographic percentage for people >= 25 years old without a high school diploma is based on Census ACS data for the total population 25 years old and older at the block group level, which is used as the denominator when calculating this demographic percentage.
- <sup>e</sup> The Limited English Speaking population is estimated at the block group level by taking the product of the block group population and the fraction of Limited English speaking households in the block group, assuming that the number of individuals per household is the same for Limited English speaking households as for the general population, and summed over all block groups.
- <sup>f</sup> The demographic percentages for people with one or more disabilities are based on Census ACS surveys at the tract level of civilian non-institutionalized people (i.e., all U.S. civilians not residing in institutional group quarters facilities such as correctional institutions, juvenile facilities, skilled nursing facilities, and other long-term care living arrangements). To derive the nationwide demographic percentages shown, these tract level tallies are summed for all tracts in the nation and then divided by the total U.S. population based on the 2018-2022 ACS. The study areas' population counts are based on applying the Census tract level percentage of people with one or more disabilities to each block group and block within the respective tract. The methodology noted in footnote "a" is then used to derive block-level demographic population counts, which are then divided by the respective total block-level population to derive the study area demographic percentages shown.
- <sup>g</sup> The total nationwide population includes all 50 states, the District of Columbia, and Puerto Rico. The state and county populations include any states and counties, respectively, with census blocks within the radius of the modeled area.
- <sup>h</sup> The at-risk population and its demographic breakdown are the people residing within the indicated study area radius of each modeled facility with a cancer risk greater than or equal to the indicated level.
- <sup>i</sup> **The maximum modeled risk is 700 in 1 million based on NC-IL emissions.** This maximum occurs at the single populated receptor with the highest modeled risk.

**Table 60. Summary of Demographic Assessment of Risk Results for Facilities in the NC-IL run group - Population with Risk Greater Than or Equal to 1 in 1 million within a 50 km Study Area Radius around each facility**

Population Basis	Analysis Type <sup>b</sup>	Total Population <sup>c</sup>	People of Color <sup>d</sup>	Black	American Indian or Alaska Native	Asian	Other and Multi-racial	Hispanic or Latino <sup>e</sup>	Age (Years) 0-17	Age (Years) 18-64	Age (Years) >=65	Below the Poverty Level <sup>f</sup>	Below Twice the Poverty Level <sup>f</sup>	Over 25 Without a High School Diploma <sup>g</sup>	People Living in Limited English Speaking Households <sup>h</sup>	People with One or More Disabilities <sup>i</sup>
Nationwide (2018-2022 ACS) <sup>j</sup>	N/A	334,369,975	41.7%	12.0%	0.5%	5.6%	4.1%	19.4%	22.1%	61.3%	16.6%	12.6%	28.6%	11.0%	5.1%	12.1%
State <sup>j</sup>	Proximity	23,227,848	39.5%	16.8%	0.4%	4.5%	3.4%	14.3%	22.0%	61.6%	16.4%	12.2%	28.1%	10.2%	3.5%	12.0%
County <sup>j</sup>	Proximity	10,412,933	49.0%	18.2%	0.1%	6.8%	3.2%	20.6%	22.2%	62.8%	14.9%	11.1%	25.3%	10.3%	5.3%	12.5%
NC-IL	Proximity	4,323,668	38.5%	14.4%	0.1%	6.4%	3.6%	14.0%	22.5%	62.3%	15.1%	8.1%	19.8%	7.4%	3.1%	11.9%
NC-IL	At Risk	998,666	41.6%	18.0%	0.2%	10.0%	4.2%	9.2%	21.1%	64.7%	14.2%	8.7%	19.8%	100.0%	2.8%	10.6%
Fac1-NC	Proximity	1,899,432	41.6%	20.1%	0.2%	6.5%	4.1%	10.7%	21.8%	64.4%	13.8%	9.2%	22.3%	7.0%	2.7%	11.0%
Fac1-NC	At Risk	998,666	41.6%	18.0%	0.2%	10.0%	4.2%	9.2%	21.1%	64.7%	14.2%	8.7%	19.8%	100.0%	2.8%	10.6%
Fac2-IL	Proximity	2,424,236	36.1%	9.9%	0.1%	6.4%	3.1%	16.6%	23.2%	60.7%	16.1%	7.3%	17.9%	7.7%	3.5%	12.6%
Fac2-IL	At Risk	0	0.0%	0.0%	0.0%	0.0%	0.0%	0.0%	0.0%	0.0%	0.0%	0.0%	0.0%	0.0%	0.0%	0.0%

Table 60 Notes: The demographic percentages are based on the 2020 Decennial Census' block populations, which are linked to the Census' 2018-2022 American Community Survey (ACS) five-year demographic averages at the block group level. To derive demographic percentages, it is assumed a block's demographics are the same as the block group in which it is contained. Demographics are tallied for all blocks falling within the indicated radius or "proximity" and for blocks within that radius at the indicated risk level. Demographic-specific populations may be determined by multiplying the total population provided in each row by the respective demographic percentages in the same row.

- <sup>b</sup> The "Proximity" analysis is for the entire population irrespective of risk (i.e., for all risk levels combined). The "At Risk" analysis is for only the population within Census blocks having HEM5-modeled risk at and above the risk level indicated in the table title.
- <sup>c</sup> The total population values for the run group and each individual facility are based on block level data from the 2020 Decennial Census, with block populations summed over the area defined by the indicated radius around each facility.
- <sup>d</sup> A person is identified as one of six racial/ethnic categories: White, Black, American Indian or Alaska Native, Asian, Other and Multiracial, or Hispanic/Latino. The People of Color population is the total population minus the White population.
- <sup>e</sup> To avoid double counting, the "Hispanic or Latino" category is treated as a distinct demographic category. A person who identifies as Hispanic or Latino is counted only as Hispanic/Latino for this analysis (regardless of other racial identifiers).
- <sup>f</sup> The demographic percentages for people living below the poverty line or below twice the poverty line are based on Census ACS surveys at the block group level that do not include people in group living situations such as dorms, prisons, nursing homes, and military barracks. To derive the nationwide demographic percentages shown, these block group level tallies are summed for all block groups in the nation and then divided by the total U.S. population based on the 2018-2022 ACS. The study area's facility-specific and run group-wide population counts are based on the methodology noted in footnote 'a' to derive block-level demographic population counts for the study area, which are then divided by the respective total block-level population to derive the study area demographic percentages shown.
- <sup>g</sup> The demographic percentage for people >= 25 years old without a high school diploma is based on Census ACS data for the total population 25 years old and older at the block group level, which is used as the denominator when calculating this demographic percentage.
- <sup>h</sup> The Limited English Speaking population is estimated at the block group level by taking the product of the block group population and the fraction of Limited English speaking households in the block group, assuming that the number of individuals per household is the same for Limited English speaking households as for the general population, and summed over all block groups.
- <sup>i</sup> The demographic percentages for people with one or more disabilities are based on Census ACS surveys at the tract level of civilian non-institutionalized people (i.e., all U.S. civilians not residing in institutional group quarters facilities such as correctional institutions, juvenile facilities, skilled nursing facilities, and other long-term care living arrangements). To derive the nationwide demographic percentages shown, these tract level tallies are summed for all tracts in the

nation and then divided by the total U.S. population based on the 2018-2022 ACS. The study areas' facility-specific and run group-wide population counts are based on applying the Census tract level percentage of people with one or more disabilities to each block group and block within the respective tract. The methodology noted in footnote "a" is then used to derive block-level demographic population counts for the study area, which are divided by the respective total block-level population to derive the study area demographic percentages shown.

j The total nationwide population includes all 50 states, the District of Columbia, and Puerto Rico. The state and county populations include any states and counties, respectively, with census blocks within the radius of the modeled area.

## 9. Understanding the Risk Results

This section contains an overview on using the HEM outputs, Risk Summary Reports, and Demographic Assessment tables to ascertain the cancer risks, noncancer hazards and acute impacts posed by your group of modeled facilities to the population in your modeling domain.

**Note:** The below steps are an example of how you might approach reviewing the output files' risk results; they are not the only way to interact with the results, nor are these steps comprehensive (as not all output files are mentioned below).

1. **Step 1:** Open the *Max\_Risk.xlsx* summary report output to obtain the highest cancer risk and noncancer TOSHI for all the modeled facilities in your run group, as well as the max receptor IDs and population at each max receptor. With this output, you can also view the number of facilities impacting each maximum receptor, if nearby facilities are impacting the same receptor(s).
2. **Step 2:** Open the *Facility\_max\_risk\_and\_HI.xlsx* output to obtain the facility-specific MIR in column B (mx\_can\_rsk), as well as the facility-specific maximum TOSHI values in each of their respective columns. Note: Multi-facility impacts on the same receptor (from facilities located close to one another) are not accounted for in the *Facility\_max\_risk\_and\_HI.xlsx* output file, because each row of this output file is specific to each individual facility. Therefore, the run group maximum reported in the *Max\_Risk.xlsx* summary report (which, as mentioned in Step 1, accounts for multiple impacts on the same receptor from more than one facility) will either be equal to or greater than the highest facility-specific MIR in the *Facility\_max\_risk\_and\_HI.xlsx* output.
3. **Step 3:** Open the *Cancer\_drivers.xlsx* output to obtain the pollutant and emission source type driving the modeled risk. To report the top cancer drivers for a run group, use the Pollutant from column C and the Source ID from column F for all rows associated with the facility showing the highest risk. The MIR value from this highest facility will equal that listed in the *Facility\_max\_risk\_and\_HI.xlsx* file from Step 2. Note: This output does not account for 100% of the modeled risk but rather provides those pollutant-emission source combinations that contribute at least 90% to each facility's MIR (from one or more pollutant-emission source combinations, depending on how many combinations are needed to describe 90% of the modeled risk at each facility).
4. **Step 4:** Open the *Histogram\_risk.xlsx* output to obtain the number of people and facilities at various risk levels. The total population within the modeling domain (by default a 50-kilometer radius around each facility or your user-specified radius) equals the sum of cells B2 + B3. This histogram output counts facilities based on modeled risk at populated census blocks, alternate receptors, and user receptors. Consequently, this file's facility count numbers will be in accord with the manual counting of facilities at each risk level from *the Facility\_max\_risk\_and\_HI.xlsx* file. Note: What risk bin a facility falls into in this output is based on the EPA's one significant figure rounding convention (e.g., 14-in-1 million rounds to 10-in-1 million and 18-in-1 million rounds to 20-in-1 million).
5. **Step 5:** Open the *Hazard\_Index\_Drivers.xlsx* output to obtain the pollutants and emission sources driving all (non-zero) TOSHIs at each modeled facility. To report the top HI drivers for a run group, use the Pollutant from column E and the Source ID from column D for all rows associated with the facility showing the highest total TOSHI in column C ("HI Total"). The TOSHI value from this highest facility should equal the TOSHI value listed in the *Facility\_max\_risk\_and\_HI.xlsx* file from Step 2. Note: This output does not account for 100% of the modeled TOSHI but rather provides those pollutant-emission source combinations that contribute at least 90% to the facility's total TOSHI.

6. **Step 6:** Open the *Hi\_histogram.xlsx* output to obtain the number of people and facilities at various HI levels for each of the 14 TOSHIs. These numbers are based on the one significant figure rounding convention (e.g., an HI of 1.4 rounds to 1 and so is considered  $\leq 1$ , an HI of 1.5 rounds to 2 and so is considered  $>1$ ).
7. **Step 7:** Open the *Incidence\_drivers.xlsx* output to obtain the run group-wide incidence attributable to each pollutant. This file is sorted in descending order of incidence and column C provides the percentage each pollutant drives the total incidence for all of your modeled facilities.
8. **Step 8:** Open the *Source\_type\_risk.xlsx* output to obtain the number of people at various risk levels caused by each emission source type, and the incidence attributable to each source type. This output also shows the run group max risk and the number of people at various risk levels attributable to all source types combined (“Maximum Overall” which accounts for impacts on the same receptor by different source types), as well as the overall incidence.
9. **Step 9:** Open the *Acute\_impacts.xlsx* output, if you modeled acute impacts, to obtain the hazard quotients (HQs) based on various benchmarks for each pollutant of interest, as well as the highest acute concentration for each HAP. You can perform a manual count using this output file to determine the number of facilities with an HQ  $\geq 1.5$  for any benchmark. (Note: An HQ  $\geq 1.5$  is the mathematical definition of “greater than 1” when using EPA’s one significant figure rounding convention.) This output file also provides (in the far-right columns) the receptors experiencing the maximum acute concentration for each pollutant at every modeled facility.
10. **Step 10:** Open the *AllFacility\_source\_locations.kmz* output to see all modeled sources at each facility in your run group on a Google Earth™ map. This map provides a ready view of the distance between your modeled facilities, and it allows you to perform QA to determine whether the modeled locations of your sources are reasonable.

For additional details regarding the modeling results for each of the facilities in the run group, open the individual facility subfolders in the output folder. Section 6 discusses these facility-specific output files. Each facility folder also contains a *source\_risk.kmz* output file which displays the detailed modeled risk results for that facility on a Google Earth™ map.

The tables produced by the Demographic Assessment module (described in Sections 8.2 and 8.3) provide the demographic breakdown of the population in your modeling domain and include risk and HI results consistent with the outputs discussed above, if **at the same radii**. For example, the maximum risk/HI for your run group that is reported in one of the Demographic Assessment tables (shown in footnote “i” of Table 59, “Population at Risk Summary”) is the same maximum risk/HI that is reported by the *Max\_Risk.xlsx* summary noted in Step 1 above. The facility-specific risk/HI maxima provided in similar Demographic Assessment tables at the facility level are the same risk/HI maxima listed for each facility in the *Facilty\_max\_risk\_and\_HI.xlsx* in Step 2 above. The number of people in various risk/HI bins in the run group wide Demographic Assessment table (exemplified in Table 58, “Distribution of Cancer Risk for the Total Population”) is consistent with the number of people listed in the cancer risk histogram (*Histogram\_risk.xlsx*) and HI histogram (*Hi\_histogram.xlsx*) noted in Steps 4 and 6 above, respectively, although grouped into fewer bins than provided by the Demographic Assessment module.

Finally, HEM provides numerous graphical ways to review and analyze the cancer and noncancer risk outputs from your run including bar charts, maps, and risk contours, as discussed in Section 4.7 regarding the *Analyze Outputs* interface of HEM.

## 10. Quality Assurance Remodeling

There are several quality assurance (QA) checks that you should perform after HEM has completed modeling each of your facilities. Ideally, these QA checks should be made before you run the Risk Summary Reports (described in Section 4.5), to determine if any facility inputs need to be revised and the facilities remodeled prior to being summarized with the run group.

### 10.1. Ensure Maxima are Located at Populated Receptors

For cancer risk and chronic noncancer HI, it is generally considered best practice to ensure the maximum for each (i.e., the cancer MIR and noncancer max TOSHI) occur where people reside, at populated receptors.

First, open and review the ***Facility\_max\_risk\_and\_HI.xlsx*** file to ensure that:

- the number of facilities modeled in column A equals the number of facilities in the input files (e.g., ***Facility\_List\_Options.xlsx***),
- the maximum cancer risk values in column B occur at census blocks, alternate receptors, or populated user receptors rather than at unpopulated polar grid (or boundary or monitor) receptors, as noted in column D, and
- the TOSHI values in the various HI columns occur at census blocks, alternate receptors, or populated user receptors rather than at unpopulated polar grid (or boundary or monitor) receptors.

The cancer risk and noncancer TOSHI QA checks described above are especially important for facilities of interest, such as those facilities with relatively high cancer risk or TOSHI values in the modeled set. Remodel those facilities (as described below) that failed one or more of the QA checks before running the Risk Summary Reports. Re-running HEM for such facilities will ensure that all facilities in the run group are modeled and that the modeled maximum risk and TOSHI values occur at populated receptors.

Follow these steps to rerun a facility when the MIR or the maximum TOSHIs occur at an unpopulated receptor (such as a polar grid receptor).<sup>13</sup>

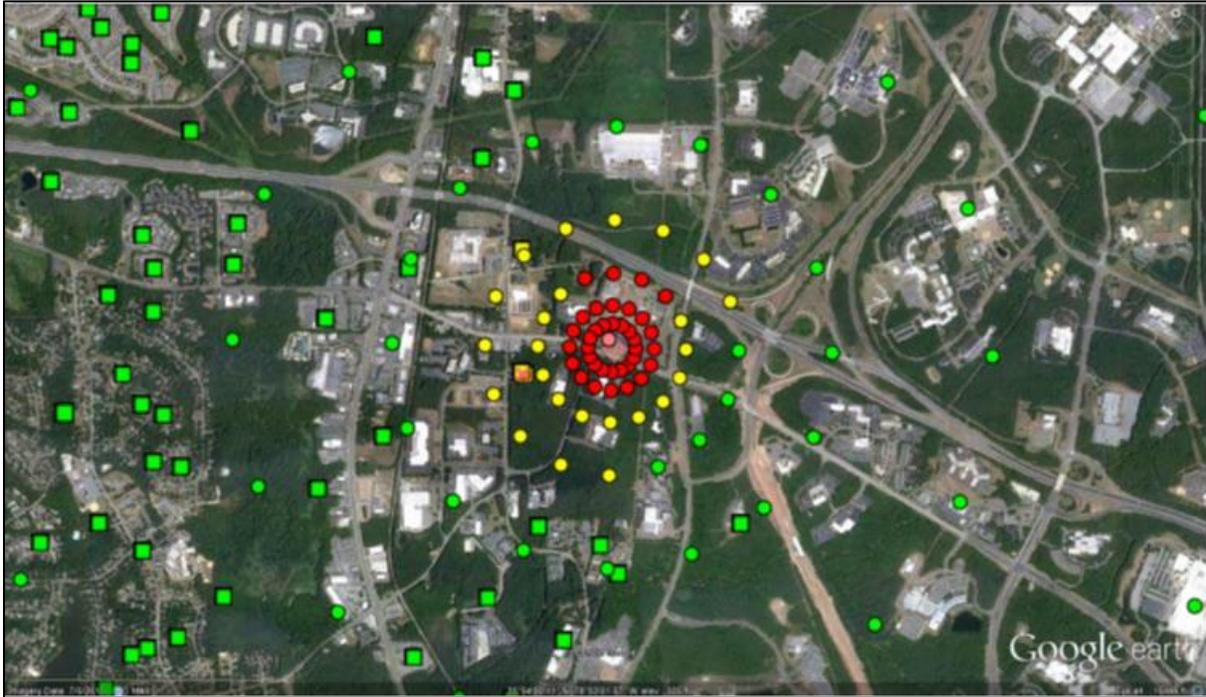
1. Review the ***Source\_risk.kmz*** file located in the individual facility subfolder. Opening this file will start Google Earth™ if it is installed on your computer. **Figure 27** shows a sample Google Earth™ kmz output file.

Zoom in on the facility center and turn on the polar grid (by checking the box next to “Polar receptor cancer risk” in the Places key) to make visible the polar grid receptor at which the MIR or TOSHI value occurs.

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<sup>13</sup> The MIR or maximum TOSHIs can occur at a polar grid receptor if the populated receptor (census block, user receptor or alternate receptor) with highest risk or TOSHI is located within the overlap distance of the facility boundary. In this case, HEM will select the next highest receptor (whether populated or unpopulated) that is not overlapped. If a polar grid receptor is the next highest receptor that is not overlapped, it will be chosen as the MIR or max TOSHI receptor.

Figure 27. Sample Source\_risk.kmz HEM Output



2. Find the census block centroid closest to the MIR polar receptor. Use the 'ruler' tool to measure the distance (in meters) from the census block centroid to the approximate facility center. Increase this distance enough to ensure that a census block centroid near the current polar MIR receptor will be closer to the facility center than this revised first polar ring when the facility is rerun, as explained further below. Follow these steps for all facilities of interest requiring remodeling due to an overlapped populated receptor.
3. To rerun the facility or facilities, create a copy of the input file **Facility\_List\_Options.xlsx**. Be careful to name the new file so that it is obvious it is not the original **Facility\_List\_Options.xlsx** file (e.g., **QA1\_Facility\_list\_options.xlsx** to indicate it is the first QA run). Delete the rows for the facilities that do NOT have to be rerun.
4. Under the column heading 'ring1', enter the value determined from the above instructions (i.e., the distance in meters between the approximate facility center and the census block centroid closest to the MIR polar receptor, rounded up). Save these changes and close the file.
5. Re-start HEM using the new **QA1\_Facility\_list\_options.xlsx** file as an input.
  - Note: There may be extra facilities in the HAP Emissions and Emissions Location files from your original run, because HEM will only use data for the facilities listed in the Facility List Options file you specify for the QA run.
6. HEM will then remodel the facilities with revised first ring distances. This "bumping out" of the first polar ring will allow HEM to choose a populated census block or alternate receptor as the MIR or TOSHI receptor, because the first polar ring of polar receptors will be more distant from the facility center than the closest populated receptor. When re-running HEM, it is advisable to name the output folder using "QA1" in case additional QA runs are necessary.

7. Once you have rerun the facility or facilities, check the outputs to determine if the relevant MIR or TOSHI is now at a populated receptor by opening the **QA1\_Facility\_max\_risk\_and\_HI.xlsx** file. If the MIR or TOSHI is still at a polar grid receptor, repeat the above steps (starting with Step #1, opening the **Source\_risk.kmz** file) using the identifier QA2 for the naming convention. Make the first ring of the polar grid more distant from the facility center than in the first adjustment.
8. After you have successfully adjusted the distance so that the MIR and maximum TOSHIs occur at populated receptors, copy the most recent facility rows from all **QA\_Facility\_max\_risk\_and\_HI.xlsx** files (e.g., QA1, QA2, QA3) into the original **Facility\_max\_risk\_and\_HI.xlsx** file.
9. Perform this row replacement for each remodeled facility, using the most recent QA run applicable to that facility. In addition, replace the original subfolder for each remodeled facility by copying the most recent facility output subfolder (including all its revised contents) from the QA run to the location of the original facility output. Move or delete the original subfolder.

## 10.2. Ensure Maxima are Discretely Modeled, not Interpolated

A facility may require remodeling (using the steps described above) if the MIR and/or max TOSHI values of that facility are interpolated, rather than explicitly modeled. The **Facility\_max\_risk\_and\_HI.xlsx** output indicates interpolated maximum risk values in column C and maximum TOSHI values in the columns to the right of each TOSHI value (e.g., column I for the respiratory HI). If these fields contain an N, then the values are not interpolated. Generally, a value is interpolated if the maximum receptor is located outside the modeling distance within which receptors are explicitly modeled (e.g., at a default value of 3,000 m or 3 km). This can occur if a modeled facility is located in a sparsely populated area, where there are no census block centroids or alternate receptors within the modeling distance (e.g., 3 km) of the facility center. Follow these steps:

1. Open the **Source\_risk.kmz** file located in the individual facility subfolder to determine if a facility with an interpolated MIR and/or TOSHI should be remodeled with an increased modeling distance. This Google Earth™ kmz file will show where the closest populated receptors are located.
2. Increase the modeling distance to include the populated receptor(s).
3. Use Google Earth's™ ruler tool to determine the new modeling distance. Remember to increase this distance slightly before remodeling the facility in a QA run, as discussed above.
  - Note: If the risk and all TOSHIs are considered low—and if the reason for the low values is that the facility is located in a sparsely populated area—you may decide that revising the modeling distance and remodeling is not necessary.
4. Inspect the location of modeled sources by reviewing the facility specific **Source\_risk.kmz** or the run group-wide **AllFacility\_source\_locations.kmz** file. If one or more source is mislocated, perform a QA rerun for that facility using a corrected Emissions Location file (and a corrected polygon vertex file and/or buoyant line parameters file, if the misplaced source is configured as a polygon or buoyant line source).
  - Note: An interpolated MIR or TOSHI value may occur if one or more of the emission sources is mislocated – for example, with an incorrect latitude or longitude that

places a source too far from the actual facility location and other modeled sources. This interpolated situation requires remodeling to correct the location inaccuracy.

5. It is best practice to review each **Source\_risk.kmz** file, even if all MIR and TOSHI values listed in the **Facility\_max\_risk\_and\_HI.xlsx** output occur at populated receptors and no values are interpolated. In general, the image of each facility's emission sources and receptors on a Google Earth™ satellite map (i.e., the **Source\_risk.kmz** file) is a powerful tool for QA checks of the inputs and modeling parameters that HEM uses (see Figure 27 above as an example).
  - Reviewing these map images allows you to determine if sources are mislocated and require remodeling and if the surrounding populations are represented well enough by the populated receptors. If surrounding populations are not represented sufficiently by the receptors, you can remodel with the addition of user receptors placed near residences.
  - Even a QA check of a kmz image that shows nothing amiss may prove useful. For example, if nothing looks incorrect in the **Source\_risk.kmz** image, but the MIR and/or TOSHI values seem too high to be reasonable, this may indicate an error in the emission amounts or pollutant names provided in the HAP Emissions input file.
6. Once you have performed all QA checks and remodeled any facilities, you are ready to run the Risk Summary Reports, as described in Section 4.5. The Risk Summary programs need as inputs the final **Facility\_max\_risk\_and\_HI.xlsx** and several facility-specific outputs (depending on the HEM options you selected and which Risk Summary Reports you run). Therefore, do not rename the HEM output files (e.g., after row replacement).

### 10.3. Model Skipped Facilities

As noted in Sections 4.9 and 6.2.4, if HEM is unable to model a facility or facilities due to errors in the inputs, HEM will produce an Excel file titled "Skipped Facilities" (*Skipped\_facilities.xlsx*) in the run group's output subfolder.

1. After you fix the errors in the inputs, you can use the list of skipped facilities in column A of this output file to create a new Facility List Options file.
2. Use the new Facility List Options file to model the facilities as a group.
3. Copy the resulting skipped facility output folders back into the directory/folder containing the original group's modeled outputs.
4. Append the resulting Facility Mask Risk and HI rows into the original Facility Max Risk and HI file (described in Section 6.2.1).
5. Do the same appending for the Facility Cancer Risk Exposure file (described in Section 6.2.2) and the Facility TOSHI Exposure file (described in Section 6.2.3).
6. Run the Risk Summary Reports on the full set of HEM outputs (as described in Section 4.5 and Section 7).
7. Finally, if you have remodeled any facilities, you should rerun the Demographic Assessment module, discussed in Section 4.6, to ensure the demographic results are based on the remodeled cancer risks, noncancer risks, and proximity statistics of the current domain.

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## 12. Appendix A: Sample HEM Output Files

This appendix contains examples (some abbreviated to fit) of the facility-specific and run group HEM output files discussed in Section 6. Sample risk summary reports are provided in Section 7. Sample results for Demographic Assessments are provided in Section 8.

**Table 61. Sample Maximum Individual Risk HEM Output (facility-specific)**

Parameter	Value	Value rounded	Value scientific notation	Population	Distance (m)	Angle (from north)	Elevation (m)	Hill height (m)	FIPs	Block	UTM easting	UTM northing	Latitude	Longitude	Receptor type	Notes
Cancer risk	0.00061	0.0006	6.1e-04	3	491.8557	217.7	89.7	89.7	37063	9801001074	690605	3974816	35.89908	-78.888	Census block	Discrete
Respiratory HI	0.67705	0.7	6.8e-01	0	459.4366	233.9	90.5	90.5	U0000	0000URCPT1	690535	3974934	35.90016	-78.88875	User receptor	Discrete
Liver HI	0.18167	0.2	1.8e-01	0	459.4366	233.9	90.5	90.5	U0000	0000URCPT1	690535	3974934	35.90016	-78.88875	User receptor	Discrete
Neurological HI	0.08825	0.09	8.8e-02	0	459.4366	233.9	90.5	90.5	U0000	0000URCPT1	690535	3974934	35.90016	-78.88875	User receptor	Discrete
Developmental HI	8.99698	9	9.0e+00	3	491.8557	217.7	89.7	89.7	37063	9801001074	690605	3974816	35.89908	-78.888	Census block	Discrete
Reproductive HI	0.0747	0.07	7.5e-02	0	459.4366	233.9	90.5	90.5	U0000	0000URCPT1	690535	3974934	35.90016	-78.88875	User receptor	Discrete
Kidney HI	1.47967	1	1.5e+00	3	491.8557	217.7	89.7	89.7	37063	9801001074	690605	3974816	35.89908	-78.888	Census block	Discrete
Ocular HI	0	0	0	0	0	0	0	0			0	0	0	0		
Endocrine HI	2.3E-06	2E-06	2.3e-06	219	1124.139	191.4	85.8	85.8	37063	0020272057	690684	3974103	35.89265	-78.8873	Census block	Discrete
Hematological HI	0.00092	0.0009	9.2e-04	3	491.8557	217.7	89.7	89.7	37063	9801001074	690605	3974816	35.89908	-78.888	Census block	Discrete
Immunological HI	0.06719	0.07	6.7e-02	0	459.4366	233.9	90.5	90.5	U0000	0000URCPT1	690535	3974934	35.90016	-78.88875	User receptor	Discrete
Skeletal HI	0.0008	0.0008	8.0e-04	0	459.4366	233.9	90.5	90.5	U0000	0000URCPT1	690535	3974934	35.90016	-78.88875	User receptor	Discrete
Spleen HI	0	0	0	0	0	0	0	0			0	0	0	0		
Thyroid HI	0	0	0	0	0	0	0	0			0	0	0	0		
Whole body HI	0	0	0	0	0	0	0	0			0	0	0	0		

**Table 62. Sample Maximum Offsite Risk HEM Output (facility-specific)**

Parameter	Value	Value_rnd	Value_sci	Population	Distance (in meters)	Angle (from north)	Elevation (in meters)	Hill height (in meters)	Fips	Block	Utm_east	Utm_north	Latitude	Longitude	Rec_type
Cancer risk	0.000783	0.0008	7.8e-04	0	565	67.5	92	92			691428	3975421	35.90438	-78.878745	Polar grid
Respiratory HI	0.677049	0.7	6.8e-01	0	459.43661	233.85	90.5	90.5	U0000	0000URC PT1	690535	3974934	35.90016	-78.88875	User receptor
Liver HI	0.277505	0.3	2.8e-01	0	565	90	92	92			691471	3975205	35.90242	-78.878321	Polar grid
Neurological HI	0.08825	0.09	8.8e-02	0	459.43661	233.85	90.5	90.5	U0000	0000URC PT1	690535	3974934	35.90016	-78.88875	User receptor
Developmental HI	11.47101	10	1.1e+01	0	565	67.5	92	92			691428	3975421	35.90438	-78.878745	Polar grid
Reproductive HI	0.0747	0.07	7.5e-02	0	459.43661	233.85	90.5	90.5	U0000	0000URC PT1	690535	3974934	35.90016	-78.88875	User receptor
Kidney HI	1.974576	2	2.0e+00	0	565	67.5	92	92			691428	3975421	35.90438	-78.878745	Polar grid
Ocular HI	0	0	0	0	0	0	0	0			0	0	0	0	
Endocrine HI	4.2E-06	4E-06	4.2e-06	0	565	90	92	92			691471	3975205	35.90242	-78.878321	Polar grid
Hematological HI	0.001641	0.002	1.6e-03	0	565	90	92	92			691471	3975205	35.90242	-78.878321	Polar grid
Immunological HI	0.067187	0.07	6.7e-02	0	459.43661	233.85	90.5	90.5	U0000	0000URC PT1	690535	3974934	35.90016	-78.88875	User receptor
Skeletal HI	0.000797	0.0008	8.0e-04	0	459.43661	233.85	90.5	90.5	U0000	0000URC PT1	690535	3974934	35.90016	-78.88875	User receptor
Spleen HI	0	0	0	0	0	0	0	0			0	0	0	0	
Thyroid HI	0	0	0	0	0	0	0	0			0	0	0	0	
Whole body HI	0	0	0	0	0	0	0	0			0	0	0	0	

**Table 63. Sample Risk Breakdown HEM Output (facility-specific, abbreviated)**

Site type	Parameter	Source ID	Pollutant	Emission type	Value	Value rounded	Conc (ug/m <sup>3</sup> )	Conc rounded (ug/m <sup>3</sup> )	Emissions (tpy)	URE 1/(ug/m <sup>3</sup> )	RFC (mg/m <sup>3</sup> )
Max indiv risk	Cancer risk	CT000001	All modeled pollutants	NA	1.88E-09	2E-09	6.95E-10	7E-10	2.456E-07	0	0
Max indiv risk	Cancer risk	CT000001	2,3,4,7,8-pentachlorodibenzo-furan	C	1.04E-09	1E-09	1.05E-10	1E-10	3.7E-08	9.9	1.3E-07
Max indiv risk	Cancer risk	CT000001	1,2,3,7,8-pentachlorodibenzo-p-dioxin	C	2.25E-10	2E-10	6.82E-12	7E-12	2.41E-09	33	4E-08
...	...	...	...	...	...	...	...	...	...	...	...
Max indiv risk	Cancer risk	Total	All pollutants all sources	NA	0.000611	0.0006	1.964495	2	39.355593	0	0
Max indiv risk	Cancer risk	Total by pollutant all sources	arsenic compounds	NA	0.000579	0.0006	0.134549	0.1	1.06	0	0
Max indiv risk	Cancer risk	Total by pollutant all sources	cadmium compounds	NA	2.61E-05	0.00003	0.014526	0.01	0.2	0	0
...	...	...	...	...	...	...	...	...	...	...	...
Max offsite impact	Cancer risk	CT000001	All modeled pollutants	NA	6.26E-09	6E-09	2.31E-09	2E-09	2.456E-07	0	0
Max offsite impact	Cancer risk	CT000001	2,3,4,7,8-pentachlorodibenzo-furan	C	3.44E-09	3E-09	3.48E-10	3E-10	3.7E-08	9.9	1.3E-07
...	...	...	...	...	...	...	...	...	...	...	...
Max offsite impact	Cancer risk	Total	All pollutants all sources	NA	0.000783	0.0008	2.157177	2	39.355593	0	0
Max offsite impact	Cancer risk	Total by pollutant all sources	arsenic compounds	NA	0.000739	0.0007	0.171925	0.2	1.06	0	0
Max offsite impact	Cancer risk	Total by pollutant all sources	cadmium compounds	NA	3.54E-05	0.00004	0.019652	0.02	0.2	0	0
...	...	...	...	...	...	...	...	...	...	...	...
Max indiv risk	Developmental HI	CT000001	2,3,4,7,8-pentachlorodibenzo-furan	C	0	0	1.05E-10	1E-10	3.7E-08	9.9	1.3E-07
Max indiv risk	Developmental HI	CT000001	1,2,3,6,7,8-hexachlorodibenzo-p-dioxin	C	0	0	5.15E-12	5E-12	1.82E-09	3.3	4E-07
...	...	...	...	...	...	...	...	...	...	...	...
Max indiv risk	Developmental HI	CT000001	All modeled pollutants	NA	0	0	6.95E-10	7E-10	2.456E-07	0	0
...	...	...	...	...	...	...	...	...	...	...	...
Max indiv risk	Developmental HI	Total	All pollutants all sources	NA	8.996981	9	1.964495	2	39.355593	0	0
Max indiv risk	Developmental HI	Total by pollutant all sources	arsenic compounds	NA	8.969901	9	0.134549	0.1	1.06	0	0
Max indiv risk	Developmental HI	Total by pollutant all sources	trichloroethylene	NA	0.027078	0.03	0.054157	0.05	0.24	0	0
...	...	...	...	...	...	...	...	...	...	...	...
Max offsite impact	Developmental HI	CT000001	2,3,4,7,8-pentachlorodibenzo-furan	C	0	0	3.48E-10	3E-10	3.7E-08	9.9	1.3E-07

Site type	Parameter	Source ID	Pollutant	Emission type	Value	Value rounded	Conc (ug/m <sup>3</sup> )	Conc rounded (ug/m <sup>3</sup> )	Emissions (tpy)	URE 1/(ug/m <sup>3</sup> )	RFC (mg/m <sup>3</sup> )
Max offsite impact	Developmental HI	CT000001	1,2,3,6,7,8-hexachlorodibenzo-p-dioxin	C	0	0	1.71E-11	2E-11	1.82E-09	3.3	4E-07
...	...	...	...	...	...	...	...	...	...	...	...
Max offsite impact	Developmental HI	CT000001	All modeled pollutants	NA	0	0	2.31E-09	2E-09	2.456E-07	0	0
...	...	...	...	...	...	...	...	...	...	...	...
Max offsite impact	Developmental HI	Total	All pollutants all sources	NA	11.47101	10	2.157177	2	39.355593	0	0
Max offsite impact	Developmental HI	Total by pollutant all sources	arsenic compounds	NA	11.46165	10	0.171925	0.2	1.06	0	0
Max offsite impact	Developmental HI	Total by pollutant all sources	trichloroethylene	NA	0.009358	0.009	0.018716	0.02	0.24	0	0
...	...	...	...	...	...	...	...	...	...	...	...

Table 63 Note: To capture the full extent of the kind of information provided in this output, the above sample Risk Breakdown file includes missing rows as indicated by the ellipses (...) for risk by individual source and pollutant, for risk by individual source and all pollutants combined, and for risk by individual pollutant and all sources combined. The above sample file also depicts only one of the 14 TOSHIs (Developmental HI) included in the actual file. The actual file includes the above breakdown for cancer risk and for all 14 (noncancer) TOSHIs, for both populated receptors ("Max indiv risk") and for any receptor whether populated or unpopulated ("Max offsite impact").

**Table 64. Sample Block Summary Chronic HEM Output (facility-specific, abbreviated)**

Latitude	Longitude	Overlap	Elevation	FIPs	Block	X	Y	Hill	Population	MIR	Respiratory HI	Liver HI	Neuro-logical HI	...
36.09438	-79.38606	N	181.3	37001	203004018	645293	3995623	181.3	66	3.86E-07	0.000246666	3.85E-05	1.43E-05	...
36.09624	-79.37883	N	173.5	37001	203005002	645941	3995840	173.5	3	3.89E-07	0.000248244	3.87E-05	1.43E-05	...
36.09475	-79.38259	N	178.3	37001	203005005	645605	3995669	178.3	3	3.88E-07	0.000247772	3.86E-05	1.43E-05	...
36.09726	-79.38345	N	173.7	37001	203005007	645523	3995946	173.7	55	3.85E-07	0.000245794	3.83E-05	1.42E-05	...
36.09843	-79.38333	N	171.2	37001	203005008	645534	3996075	171.2	35	3.84E-07	0.00024509	3.82E-05	1.42E-05	...
36.08863	-79.3819	N	174.5	37001	203005010	645678	3994991	174.5	57	3.94E-07	0.0002521	3.93E-05	1.46E-05	...
36.092	-79.38435	N	185.3	37001	203005011	645452	3995361	185.3	2	3.89E-07	0.000248895	3.88E-05	1.44E-05	...
36.09427	-79.38459	N	179.3	37001	203005012	645426	3995613	179.3	13	3.87E-07	0.000247309	3.86E-05	1.43E-05	...
36.09397	-79.38536	N	183.4	37001	203005013	645357	3995577	183.4	2	3.87E-07	0.000247214	3.86E-05	1.43E-05	...
36.09193	-79.38555	N	185.4	37001	203005014	645343	3995351	185.4	13	3.88E-07	0.000248466	3.88E-05	1.44E-05	...
36.09238	-79.38517	N	184.4	37001	203005015	645377	3995402	184.4	10	3.88E-07	0.000248321	3.87E-05	1.44E-05	...
36.09002	-79.38582	N	181	37001	203005017	645323	3995140	181	14	3.90E-07	0.000249604	3.90E-05	1.44E-05	...
36.08975	-79.38621	N	178	37001	203005018	645288	3995109	178	11	3.90E-07	0.000249626	3.90E-05	1.44E-05	...
36.08996	-79.3878	N	183.5	37001	203005019	645144	3995129	183.5	19	3.89E-07	0.000248859	3.89E-05	1.44E-05	...
36.0873	-79.38689	N	183.1	37001	203005039	645232	3994836	183.1	36	3.91E-07	0.000250958	3.92E-05	1.45E-05	...
36.08769	-79.3852	N	181.4	37001	203005040	645383	3994881	181.4	37	3.92E-07	0.00025139	3.93E-05	1.46E-05	...
36.08671	-79.3833	N	174.7	37001	203005042	645556	3994776	174.7	24	3.94E-05	0.000252807	3.95E-05	1.46E-05	...
36.08729	-79.38956	N	189.6	37001	203005046	644991	3994831	189.6	82	3.90E-05	0.000249883	3.90E-07	1.45E-05	...
36.08615	-79.38586	N	181.1	37001	203005048	645326	3994709	181.1	26	3.93E-07	0.000252133	3.94E-07	1.46E-05	...
36.08476	-79.38295	N	171.2	37001	203005050	645591	3994560	171.2	12	3.96E-07	0.000254249	3.97E-05	1.47E-05	...
36.08756	-79.37782	N	169.4	37001	203005052	646047	3994878	169.4	24	3.97E-07	0.000254489	3.97E-05	1.47E-05	...
36.0909	-79.37605	N	166.8	37001	203005053	646200	3995251	166.8	99	3.95E-07	0.000252943	3.94E-05	1.46E-05	...
36.0907	-79.37304	N	156.3	37001	203005054	646472	3995234	156.3	19	3.98E-07	0.000254301	3.96E-05	1.47E-05	...
36.09164	-79.37145	N	157.3	37001	203005056	646614	3995340	157.3	8	3.98E-07	0.000254305	3.96E-05	1.47E-05	...
36.09327	-79.37612	N	166	37001	203005057	646190	3995514	166	24	3.93E-07	0.000251308	3.92E-05	1.45E-05	...
36.0889	-79.37362	N	154.5	37001	203005061	646424	3995033	154.5	46	3.99E-07	0.00025531	3.98E-05	1.48E-05	...
36.08887	-79.371	N	157	37001	203005062	646659	3995034	157	16	4.01E-07	0.000256407	4.00E-05	1.48E-05	...
36.08803	-79.37061	N	159.1	37001	203005063	646696	3994941	159.1	17	4.02E-07	0.000257159	4.01E-05	1.49E-05	...
...	...	...	...	...	...	...	...	...	...	...	...	...	...	...

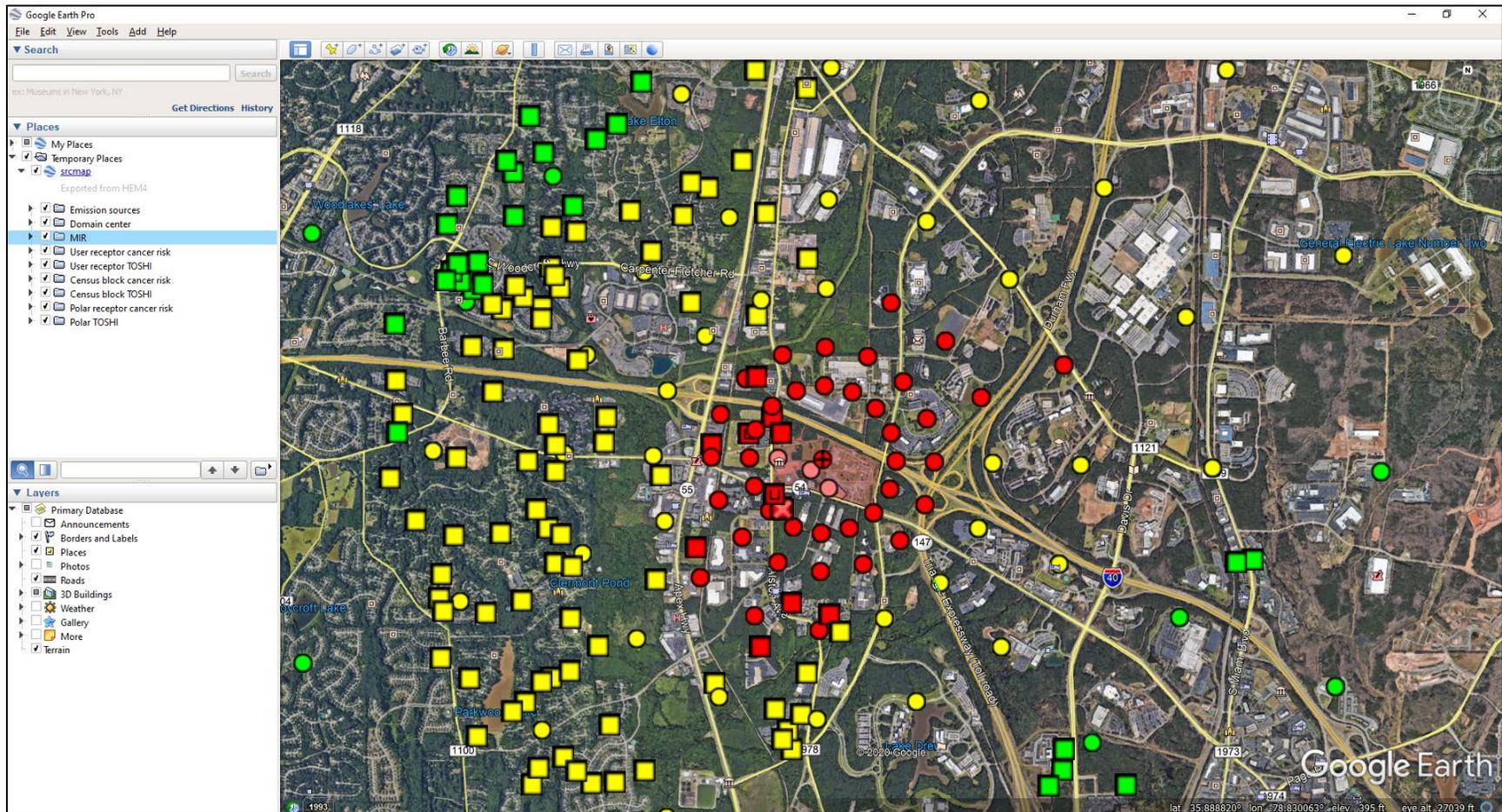
Table 64 Note: The Block Summary Chronic file is large because it includes the cancer risk (“MIR”) and all 14 TOSHIs for every modeled block or alternate receptor. The above sample file includes ellipses (...) as it shows only a partial list of rows and only 3 of the 14 TOSHIs (Respiratory HI, Liver HI and Neurological HI). In addition to providing all the TOSHIs, the actual file includes a column indicating whether the concentration at each receptor was discretely modeled or interpolated, as well as a final Receptor Type column (not shown above), which indicates C for census block, P for populated user or alternate receptor, B for boundary receptor, M for monitor, or S for school.

**Table 65. Sample Ring Summary Chronic HEM Output (facility-specific, abbreviated)**

Latitude	Longitude	Overlap	Elevation (m)	X	Y	Hill	MIR	Respiratory HI	Liver HI	Neuro-logical HI	Developmental HI	...	Distance (m)	Angle (from north)	Sector
35.90762	-78.88444	N	92	690906	3975770	92	0.000276	0.16267133	0.06719334	0.022959781	4.061680358	...	565	0	1
35.91028	-78.88437	N	85	690906	3976065	85	0.000163	0.08834714	0.03991907	0.012732447	2.405209191	...	860	0	1
35.91433	-78.88426	N	86	690906	3976515	86	9.86E-05	0.05006334	0.02351642	0.007284751	1.449323028	...	1310	0	1
35.92046	-78.8841	N	86	690906	3977195	86	5.67E-05	0.02748919	0.01321489	0.004022705	0.830353561	...	1990	0	1
35.92956	-78.88386	N	98	690906	3978205	98	3.29E-05	0.01497071	0.00728229	0.002192643	0.476986257	...	3000	0	1
35.94127	-78.88355	N	108	690906	3979505	108	1.98E-05	0.00851103	0.00414235	0.001235919	0.283698446	...	4300	0	1
35.95749	-78.88311	N	128	690906	3981305	128	1.19E-05	0.00487219	0.00221982	0.000669144	0.164677271	...	6100	0	1
35.98092	-78.88249	N	128	690906	3983905	128	7.18E-06	0.00297086	0.00127924	0.000389865	0.098200187	...	8700	0	1
36.01425	-78.88159	N	126	690906	3987605	126	4.30E-06	0.00182397	0.00072968	0.000225519	0.057813435	...	12400	0	1
36.0611	-78.88034	N	134	690906	3992805	134	2.61E-06	0.0011715	0.00040331	0.000128775	0.03383493	...	17600	0	1
36.12777	-78.87855	N	174	690906	4000205	174	1.60E-06	0.00087183	0.00020231	7.08E-05	0.018804954	...	25000	0	1
36.22237	-78.87599	N	234	690906	4010705	234	9.40E-07	0.00061899	9.59E-05	3.64E-05	0.00985544	...	35500	0	1
36.35301	-78.87245	N	207	690906	4025205	207	6.14E-07	0.00039616	6.43E-05	2.42E-05	0.00651898	...	50000	0	1
35.90719	-78.88206	N	92	691122	3975727	92	0.000317	0.20423035	0.08411586	0.028758088	4.672317905	...	565	22.5	2
35.90963	-78.88074	N	92	691235	3976000	92	0.000192	0.10610333	0.04725769	0.015216162	2.82876806	...	860	22.5	2
35.91334	-78.87874	N	86	691407	3976415	86	0.000106	0.05416447	0.02491204	0.007832226	1.5593033	...	1310	22.5	2
35.91895	-78.8757	N	86	691668	3977044	86	5.91E-05	0.02814812	0.01306979	0.004078483	0.86713832	...	1990	22.5	2
35.92728	-78.8712	N	98	692054	3977977	98	3.20E-05	0.01471825	0.00679289	0.002115014	0.466186678	...	3000	22.5	2
35.938	-78.86539	N	115	692552	3979178	115	1.81E-05	0.00825512	0.00360303	0.001123976	0.256202648	...	4300	22.5	2
35.95285	-78.85736	N	126	693240	3980841	126	1.10E-05	0.00516917	0.00198365	0.000625377	0.149211565	...	6100	22.5	2
35.9743	-78.84575	N	126	694235	3983243	126	6.79E-06	0.00327005	0.00114822	0.000363808	0.089533991	...	8700	22.5	2
36.00481	-78.82921	N	122	695651	3986661	122	4.11E-06	0.00201365	0.00066383	0.000211097	0.053338866	...	12400	22.5	2
36.04769	-78.80594	N	119	697641	3991465	119	2.48E-06	0.00123679	0.00037985	0.000121813	0.031601403	...	17600	22.5	2
36.1087	-78.77279	N	128	700473	3998302	128	1.51E-06	0.00079302	0.00020903	6.91E-05	0.018536631	...	25000	22.5	2
36.19526	-78.72566	N	185	704491	4008003	185	9.14E-07	0.00055697	0.00010008	3.60E-05	0.010134297	...	35500	22.5	2
36.31474	-78.66039	N	161	710040	4021399	161	5.74E-07	0.0003369	6.18E-05	2.22E-05	0.006426578	...	50000	22.5	2
35.90606	-78.88005	N	92	691306	3975605	92	0.000421	0.26615504	0.10388434	0.036941868	6.177728359	...	565	45	3
35.90789	-78.8777	N	92	691514	3975813	92	0.000272	0.16583271	0.06683816	0.023219576	3.998420365	...	860	45	3
...	...	...	...	...	...	...	...	...	...	...	...	...	...	...	...

Table 65 Note: The Ring Summary Chronic file includes the cancer risk (“MIR”) and all 14 TOSHIs for every modeled polar receptor. The above sample file includes ellipses (...) as it shows only a partial list of rows and only 4 of the 14 TOSHI’s (Respiratory HI, Liver HI, Neurological HI, and Developmental HI). The final 3 columns shown (above) cycle through polar receptor ring distances over each angle from north (or sector) for a total of 16 angles/sectors by default, unless you indicate a different number of radials in your Facility List Options file.

Figure 28. Sample Source Risk KMZ Google Earth™ Image (facility-specific)



**Table 66. Sample Incidence HEM Output (facility-specific, abbreviated)**

Source ID	Pollutant	Emission type	Incidence	Incidence rounded
Total	All modeled pollutants	C	0.047682	0.048
CT000001	1,2,3,4,6,7,8-heptachlorodibenzo-p-dioxin	C	1.513E-09	1.5E-09
CT000001	1,2,3,4,6,7,8-heptachlorodibenzofuran	C	6.008E-09	6E-09
CT000001	1,2,3,4,7,8-hexachlorodibenzo-p-dioxin	C	1.238E-08	1.2E-08
CT000001	1,2,3,4,7,8-hexachlorodibenzofuran	C	1.44E-07	1.4E-07
CT000001	1,2,3,6,7,8-hexachlorodibenzo-p-dioxin	C	1.317E-08	1.3E-08
CT000001	1,2,3,6,7,8-hexachlorodibenzofuran	C	1.296E-07	1.3E-07
CT000001	1,2,3,7,8,9-hexachlorodibenzofuran	C	2.316E-08	2.3E-08
CT000001	1,2,3,7,8-pentachlorodibenzo-p-dioxin	C	1.744E-07	1.7E-07
...	...	...	...	...
Total	1,2,3,4,6,7,8,9-octachlorodibenzo-p-dioxin	C	5.041E-10	5E-10
Total	1,2,3,4,6,7,8,9-octachlorodibenzofuran	C	5.209E-11	5.2E-11
Total	1,2,3,4,6,7,8-heptachlorodibenzo-p-dioxin	C	8.953E-09	9E-09
Total	1,2,3,4,6,7,8-heptachlorodibenzofuran	C	3.556E-08	3.6E-08
...	...	...	...	...
CT000001	All modeled pollutants	C	1.462E-06	0.0000015
CV000001	All modeled pollutants	C	3.309E-06	0.0000033
FU000001	All modeled pollutants	C	0.0001703	0.00017
HV000001	All modeled pollutants	C	3.88E-06	0.0000039
MS000001	All modeled pollutants	C	5.983E-06	0.000006
RV000001	All modeled pollutants	C	0.0051644	0.0052
RV000002	All modeled pollutants	C	3.079E-06	0.0000031
RV000003	All modeled pollutants	C	1.772E-06	0.0000018
RV000004	All modeled pollutants	C	0.0069082	0.0069
RW000001	All modeled pollutants	C	1.116E-05	0.000011
SR000001	All modeled pollutants	C	0.0354084	0.035

Table 66 Note: The sample Incidence file above includes ellipses (...) for some rows because the file is too long to depict fully. The above rows indicate the kinds of information provided in this file.

**Table 67. Sample Cancer Risk Exposure HEM Output (facility-specific)**

Level	Population
Greater than or equal to 1 in 1,000	0
Greater than or equal to 1 in 10,000	435
Greater than or equal to 1 in 20,000	2119
Greater than or equal to 1 in 100,000	48998
Greater than or equal to 1 in 1,000,000	800221
Greater than or equal to 1 in 10,000,000	1545731

**Table 68. Sample Noncancer Risk Exposure HEM Output (facility-specific)**

Level	Respira- tory HI	Liver HI	Neuro- logical HI	Develop- mental HI	Repro- ductive HI	Kidney HI	Ocular HI	Endo- crine HI	Hemato- logical HI	Immun- ologi- cal HI	Skeletal HI	Spleen HI	Thyroid HI	Whole body HI
Greater than 100	0	0	0	0	0	0	0	0	0	0	0	0	0	0
Greater than 50	0	0	0	0	0	0	0	0	0	0	0	0	0	0
Greater than 10	0	0	0	0	0	0	0	0	0	0	0	0	0	0
Greater than 1.0	0	0	0	435	0	0	0	0	0	0	0	0	0	0
Greater than 0.5	0	0	0	3065	0	12	0	0	0	0	0	0	0	0
Greater than 0.2	12	0	0	19289	0	432	0	0	0	0	0	0	0	0

**Table 69. Sample All Inner Receptors HEM Output (facility-specific, abbreviated)**

FIPS	Block	Latitude	Longitude	Source ID	Emission type	Pollutant	Conc (ug/m <sup>3</sup> )	Elevation (m)	Dry deposition (g/m <sup>2</sup> /yr)	Wet deposition (g/m <sup>2</sup> /yr)	Population	Overlap
17063	1022007	41.459428	-88.264967	CT000001	P	2,3,4,7,8-pentachlorodibenzofuran	1.00E-11	189.2	2.15E-12	2.46E-12	11	N
17063	1022007	41.459428	-88.264967	CT000001	P	1,2,3,6,7,8-hexachlorodibenzo-p-dioxin	6.50E-13	189.2	1.40E-13	1.60E-13	11	N
17063	1022007	41.459428	-88.264967	CT000001	P	1,2,3,7,8-pentachlorodibenzo-p-dioxin	6.93E-13	189.2	1.49E-13	1.70E-13	11	N
17063	1022007	41.459428	-88.264967	CT000001	P	1,2,3,6,7,8-hexachlorodibenzofuran	6.25E-12	189.2	1.34E-12	1.53E-12	11	N
17063	1022007	41.459428	-88.264967	CT000001	P	1,2,3,4,7,8-hexachlorodibenzofuran	6.97E-12	189.2	1.49E-12	1.71E-12	11	N
17063	1022007	41.459428	-88.264967	CT000001	P	1,2,3,7,8,9-hexachlorodibenzofuran	1.11E-12	189.2	2.38E-13	2.72E-13	11	N
17063	1022007	41.459428	-88.264967	CT000001	P	2,3,4,6,7,8-hexachlorodibenzofuran	4.56E-12	189.2	9.78E-13	1.12E-12	11	N
17063	1022007	41.459428	-88.264967	CT000001	P	1,2,3,4,6,7,8-heptachlorodibenzofuran	2.95E-12	189.2	6.32E-13	7.24E-13	11	N
17063	1022007	41.459428	-88.264967	CT000001	P	1,2,3,4,7,8-hexachlorodibenzo-p-dioxin	5.92E-13	189.2	1.27E-13	1.45E-13	11	N
17063	1022007	41.459428	-88.264967	CT000001	P	1,2,3,7,8-pentachlorodibenzofuran	6.37E-12	189.2	1.37E-12	1.56E-12	11	N
17063	1022007	41.459428	-88.264967	CT000001	P	indeno[1,2,3-c,d]pyrene	4.06E-11	189.2	8.70E-12	9.96E-12	11	N
17063	1022007	41.459428	-88.264967	CT000001	P	1,2,3,4,6,7,8-heptachlorodibenzo-p-dioxin	7.57E-13	189.2	1.62E-13	1.86E-13	11	N
17063	1022008	41.4587614	-88.2642443	CT000001	P	2,3,4,7,8-pentachlorodibenzofuran	9.21E-12	189.1	2.00E-12	2.27E-12	16	N
17063	1022008	41.4587614	-88.2642443	CT000001	P	1,2,3,6,7,8-hexachlorodibenzo-p-dioxin	5.97E-13	189.1	1.29E-13	1.47E-13	16	N
17063	1022008	41.4587614	-88.2642443	CT000001	P	1,2,3,7,8-pentachlorodibenzo-p-dioxin	6.36E-13	189.1	1.38E-13	1.57E-13	16	N
17063	1022008	41.4587614	-88.2642443	CT000001	P	1,2,3,6,7,8-hexachlorodibenzofuran	5.73E-12	189.1	1.24E-12	1.41E-12	16	N
17063	1022008	41.4587614	-88.2642443	CT000001	P	1,2,3,4,7,8-hexachlorodibenzofuran	6.39E-12	189.1	1.39E-12	1.58E-12	16	N
17063	1022008	41.4587614	-88.2642443	CT000001	P	1,2,3,7,8,9-hexachlorodibenzofuran	1.02E-12	189.1	2.21E-13	2.51E-13	16	N
17063	1022008	41.4587614	-88.2642443	CT000001	P	2,3,4,6,7,8-hexachlorodibenzofuran	4.18E-12	189.1	9.07E-13	1.03E-12	16	N
17063	1022008	41.4587614	-88.2642443	CT000001	P	1,2,3,4,6,7,8-heptachlorodibenzofuran	2.71E-12	189.1	5.87E-13	6.68E-13	16	N
17063	1022008	41.4587614	-88.2642443	CT000001	P	1,2,3,4,7,8-hexachlorodibenzo-p-dioxin	5.43E-13	189.1	1.18E-13	1.34E-13	16	N
17063	1022008	41.4587614	-88.2642443	CT000001	P	1,2,3,7,8-pentachlorodibenzofuran	5.84E-12	189.1	1.27E-12	1.44E-12	16	N
17063	1022008	41.4587614	-88.2642443	CT000001	P	indeno[1,2,3-c,d]pyrene	3.72E-11	189.1	8.08E-12	9.19E-12	16	N
...	...	...	...	...	...	...	...	...	...	...	...	...

Table 69 Note: The Dry deposition and Wet deposition flux units will be in g/m<sup>2</sup>/yr if you modeled with annual averages, or in g/m<sup>2</sup> if you modeled with period averages. These columns will be blank if you did not choose to model deposition in your Facility List Options file. Receptor Type (not shown above) is also provided in this output: C for census block, P for populated user or alternate receptor, B for boundary receptor, M for monitor, S for school.

**Table 70. Sample All Outer Receptors HEM Output file (facility-specific, abbreviated)**

FIPS	Block	Latitude	Longitude	Source ID	Emission type	Pollutant	Conc (ug/m <sup>3</sup> )	Elevation (m)	Population	Overlap
17093	8907002213	41.5097585	-88.271948	CT000001	P	2,3,4,7,8-pentachlorodibenzofuran	8.50E-12	177.7	5	N
17093	8907002213	41.5097585	-88.271948	CT000001	P	1,2,3,6,7,8-hexachlorodibenzo-p-dioxin	5.51E-13	177.7	5	N
17093	8907002213	41.5097585	-88.271948	CT000001	P	1,2,3,7,8-pentachlorodibenzo-p-dioxin	5.87E-13	177.7	5	N
17093	8907002213	41.5097585	-88.271948	CT000001	P	1,2,3,6,7,8-hexachlorodibenzofuran	5.29E-12	177.7	5	N
17093	8907002213	41.5097585	-88.271948	CT000001	P	1,2,3,4,7,8-hexachlorodibenzofuran	5.90E-12	177.7	5	N
17093	8907002213	41.5097585	-88.271948	CT000001	P	1,2,3,7,8,9-hexachlorodibenzofuran	9.40E-13	177.7	5	N
17093	8907002213	41.5097585	-88.271948	CT000001	P	2,3,4,6,7,8-hexachlorodibenzofuran	3.86E-12	177.7	5	N
17093	8907002213	41.5097585	-88.271948	CT000001	P	1,2,3,4,6,7,8-heptachlorodibenzofuran	2.50E-12	177.7	5	N
17093	8907002213	41.5097585	-88.271948	CT000001	P	1,2,3,4,7,8-hexachlorodibenzo-p-dioxin	5.01E-13	177.7	5	N
17093	8907002213	41.5097585	-88.271948	CT000001	P	1,2,3,7,8-pentachlorodibenzofuran	5.39E-12	177.7	5	N
17093	8907002213	41.5097585	-88.271948	CT000001	P	indeno[1,2,3-c,d]pyrene	3.44E-11	177.7	5	N
17093	8907002213	41.5097585	-88.271948	CT000001	P	1,2,3,4,6,7,8-heptachlorodibenzo-p-dioxin	6.41E-13	177.7	5	N
17093	8907002186	41.4973643	-88.294909	CT000001	P	2,3,4,7,8-pentachlorodibenzofuran	5.56E-12	173.3	11	N
17093	8907002186	41.4973643	-88.294909	CT000001	P	1,2,3,6,7,8-hexachlorodibenzo-p-dioxin	3.61E-13	173.3	11	N
17093	8907002186	41.4973643	-88.294909	CT000001	P	1,2,3,7,8-pentachlorodibenzo-p-dioxin	3.84E-13	173.3	11	N
17093	8907002186	41.4973643	-88.294909	CT000001	P	1,2,3,6,7,8-hexachlorodibenzofuran	3.46E-12	173.3	11	N
17093	8907002186	41.4973643	-88.294909	CT000001	P	1,2,3,4,7,8-hexachlorodibenzofuran	3.86E-12	173.3	11	N
17093	8907002186	41.4973643	-88.294909	CT000001	P	1,2,3,7,8,9-hexachlorodibenzofuran	6.15E-13	173.3	11	N
17093	8907002186	41.4973643	-88.294909	CT000001	P	2,3,4,6,7,8-hexachlorodibenzofuran	2.53E-12	173.3	11	N
17093	8907002186	41.4973643	-88.294909	CT000001	P	1,2,3,4,6,7,8-heptachlorodibenzofuran	1.63E-12	173.3	11	N
17093	8907002186	41.4973643	-88.294909	CT000001	P	1,2,3,4,7,8-hexachlorodibenzo-p-dioxin	3.28E-13	173.3	11	N
17093	8907002186	41.4973643	-88.294909	CT000001	P	1,2,3,7,8-pentachlorodibenzofuran	3.53E-12	173.3	11	N
17093	8907002186	41.4973643	-88.294909	CT000001	P	indeno[1,2,3-c,d]pyrene	2.25E-11	173.3	11	N
...	...	...	...	...	...	...	...	...	...	...

Table 70 Note: The All Outer Receptor file tends to be a very large file, especially if you chose to model with the default maximum distance for your modeling domain of 50 kilometers and a default (discrete / inner) modeling distance of 3 kilometers. Deposition flux is not calculated for the outer modeling domain represented by the All Outer Receptor file, so these columns will not appear in this file even if you chose to model deposition. Receptor Type (not shown above) is also provided in this output: C for census block, P for populated user or alternate receptor, B for boundary receptor, M for monitor, S for school.

**Table 71. Sample All Polar Receptors HEM Output file (facility-specific, abbreviated)**

Source ID	Emission type	Pollutant	Conc (ug/m <sup>3</sup> )	Distance (m)	Angle (from north)	Sector	Ring number	Elevation (m)	Latitude	Longitude	Overlap	Wet deposition (g/m <sup>2</sup> /yr)	Dry deposition (g/m <sup>2</sup> /yr)
CT000001	P	2,3,4,7,8-pentachlorodibenzofuran	1.61E-11	100	0	1	1	196	41.49089612	-88.27001629	N	2.21E-12	3.69E-12
CT000001	P	1,2,3,6,7,8-hexachlorodibenzo-p-dioxin	1.04E-12	100	0	1	1	196	41.49089612	-88.27001629	N	1.43E-13	2.39E-13
CT000001	P	1,2,3,7,8-pentachlorodibenzo-p-dioxin	1.11E-12	100	0	1	1	196	41.49089612	-88.27001629	N	1.52E-13	2.55E-13
CT000001	P	1,2,3,6,7,8-hexachlorodibenzofuran	1.00E-11	100	0	1	1	196	41.49089612	-88.27001629	N	1.37E-12	2.30E-12
CT000001	P	1,2,3,4,7,8-hexachlorodibenzofuran	1.12E-11	100	0	1	1	196	41.49089612	-88.27001629	N	1.53E-12	2.56E-12
CT000001	P	1,2,3,7,8,9-hexachlorodibenzofuran	1.78E-12	100	0	1	1	196	41.49089612	-88.27001629	N	2.44E-13	4.08E-13
CT000001	P	2,3,4,6,7,8-hexachlorodibenzofuran	7.31E-12	100	0	1	1	196	41.49089612	-88.27001629	N	1.00E-12	1.68E-12
CT000001	P	1,2,3,4,6,7,8-heptachlorodibenzofuran	4.73E-12	100	0	1	1	196	41.49089612	-88.27001629	N	6.48E-13	1.08E-12
CT000001	P	1,2,3,4,7,8-hexachlorodibenzo-p-dioxin	9.49E-13	100	0	1	1	196	41.49089612	-88.27001629	N	1.30E-13	2.18E-13
CT000001	P	1,2,3,7,8-pentachlorodibenzofuran	1.02E-11	100	0	1	1	196	41.49089612	-88.27001629	N	1.40E-12	2.34E-12
CT000001	P	indeno[1,2,3-c,d]pyrene	6.51E-11	100	0	1	1	196	41.49089612	-88.27001629	N	8.91E-12	1.49E-11
CT000001	P	1,2,3,4,6,7,8-heptachlorodibenzo-p-dioxin	1.21E-12	100	0	1	1	196	41.49089612	-88.27001629	N	1.66E-13	2.79E-13
CT000001	P	2,3,4,7,8-pentachlorodibenzofuran	1.41E-11	500	0	1	2	196	41.49449822	-88.27008666	N	4.31E-12	3.08E-12
CT000001	P	1,2,3,6,7,8-hexachlorodibenzo-p-dioxin	9.17E-13	500	0	1	2	196	41.49449822	-88.27008666	N	2.79E-13	2.00E-13
CT000001	P	1,2,3,7,8-pentachlorodibenzo-p-dioxin	9.76E-13	500	0	1	2	196	41.49449822	-88.27008666	N	2.97E-13	2.13E-13
CT000001	P	1,2,3,6,7,8-hexachlorodibenzofuran	8.80E-12	500	0	1	2	196	41.49449822	-88.27008666	N	2.68E-12	1.92E-12
CT000001	P	1,2,3,4,7,8-hexachlorodibenzofuran	9.81E-12	500	0	1	2	196	41.49449822	-88.27008666	N	2.99E-12	2.14E-12
CT000001	P	1,2,3,7,8,9-hexachlorodibenzofuran	1.56E-12	500	0	1	2	196	41.49449822	-88.27008666	N	4.76E-13	3.41E-13
CT000001	P	2,3,4,6,7,8-hexachlorodibenzofuran	6.42E-12	500	0	1	2	196	41.49449822	-88.27008666	N	1.96E-12	1.40E-12
CT000001	P	1,2,3,4,6,7,8-heptachlorodibenzofuran	4.15E-12	500	0	1	2	196	41.49449822	-88.27008666	N	1.27E-12	9.06E-13
CT000001	P	1,2,3,4,7,8-hexachlorodibenzo-p-dioxin	8.34E-13	500	0	1	2	196	41.49449822	-88.27008666	N	2.54E-13	1.82E-13
CT000001	P	1,2,3,7,8-pentachlorodibenzofuran	8.97E-12	500	0	1	2	196	41.49449822	-88.27008666	N	2.73E-12	1.96E-12

Source ID	Emission type	Pollutant	Conc (ug/m <sup>3</sup> )	Distance (m)	Angle (from north)	Sector	Ring number	Elevation (m)	Latitude	Longitude	Overlap	Wet deposition (g/m <sup>2</sup> /yr)	Dry deposition (g/m <sup>2</sup> /yr)
CT000001	P	indeno[1,2,3-c,d]pyrene	5.72E-11	500	0	1	2	196	41.49449822	-88.27008666	N	1.74E-11	1.25E-11
CT000001	P	1,2,3,4,6,7,8-heptachlorodibenzo-p-dioxin	1.07E-12	500	0	1	2	196	41.49449822	-88.27008666	N	3.25E-13	2.33E-13
...	...	...	...	...	...	...	...	...	...	...	...	...	...

Table 71 Note: The Dry deposition and Wet deposition flux units will be in g/m<sup>2</sup>/yr if you modeled with annual averages, or in g/m<sup>2</sup> if you modeled with period averages. These columns will be blank if you did not choose to model deposition in your Facility List Options file.

Figure 29. Sample AERMOD.inp file (facility-specific, abbreviated)

```
aermod.inp - Notepad
File Edit Format View Help
CO STARTING
CO TITLEONE Fac1-NC
CO TITLETWO Combined particle and vapor-phase emissions
CO MODELOPT CONC ALPHA BETA ELEV
CO URBANOPT 347602.0
CO AVERTIME 1 PERIOD
CO POLLUTID UNITHAP
CO RUNORNOT RUN
CO FINISHED

SO STARTING
SO ELEVUNIT METERS
SO LOCATION CT000001 POINT 690956 3974986 92
SO SRCPARAM CT000001 1000 50.292 322.04 21.06275 2.819
SO URBANSRC CT000001
SO BUILDHGT CT000001 26.0 26.0 26.0 26.0 26.0 26.0 26.0 26.0 26.0 26.0 26.0 26.0 26.0 26.0 26.0 26.0 26.0 26.0 26.0 26.0 :
SO BUILDWID CT000001 111.07 107.16 100.0 115.85 128.17 136.6 140.88 140.88 136.6 128.17 115.85 100.0 107.16 111.07 111.6 108.74 108
SO BUILDLEN CT000001 128.17 115.85 100.0 107.16 111.07 111.6 108.74 108.74 111.6 111.07 107.16 100.0 115.85 128.17 136.6 140.88 140
SO XBADJ CT000001 -93.97 -98.48 -100.0 -107.16 -111.07 -111.6 -108.74 -108.74 -111.6 -111.07 -107.16 -100.0 -98.48 -93.97 -86.6
SO YBADJ CT000001 55.54 53.58 50.0 40.56 29.88 18.3 6.16 -6.16 -18.3 -29.88 -40.56 -50.0 -53.58 -55.54 -55.8 -54.37 -54.37 -55.8
SO LOCATION CV000001 POINTCAP 690817 3975122 92
SO SRCPARAM CV000001 1000 60.0 350.0 0.005 1.8
SO URBANSRC CV000001
SO LOCATION HV000001 POINTHOR 690561 3975207 92
SO SRCPARAM HV000001 1000 45.0 300.0 0.006 3.0
SO URBANSRC HV000001
SO LOCATION FU000001 AREA 690957 3974943 92
SO SRCPARAM FU000001 0.1 2.0 100.0 100.0 45.0 0.0
SO URBANSRC FU000001
SO LOCATION SR000001 VOLUME 690991 3974996 92
SO SRCPARAM SR000001 1000 10.0 10.0 10.0
SO URBANSRC SR000001
SO LOCATION RW000001 LINE 690560 3975117 690751 3975163 92
SO SRCPARAM RW000001 0.0678675172 3.0 75.0 3.0
SO URBANSRC RW000001
Ln 1, Col 1 100% Windows (CRLF) UTF-8
```

Figure 29 Note: If particle and vapor phase emissions are modeled separately (e.g., when modeling deposition/depletion), then two aermod.inp files will be provided in the facility folder: an aermod\_P.inp file for particle phase emissions and an aermod\_V.inp file for vapor phase emissions.

**Figure 30. Sample AERMOD.out file (facility-specific, abbreviated)**

```

aermod.out - Notepad
File Edit Format View Help
CO STARTING
CO TITLEONE Fac1-NC
CO TITLETWO Combined particle and vapor-phase emissions
CO MODELOPT CONC ALPHA BETA ELEV
CO URBANOPT 347602.0
CO AVERTIME 1 PERIOD
CO POLLUTID UNITHAP
CO RUNORNOT RUN
CO FINISHED

SO STARTING
SO ELEVUNIT METERS
SO LOCATION CT000001 POINT 690956 3974986 92
SO SRCPARAM CT000001 1000 50.292 322.04 21.06275 2.819
SO URBANSRC CT000001
SO BUILDHGT CT000001 26.0 26.0 26.0 26.0 26.0 26.0 26.0 26.0 26.0 26.0 26.0 26.0 26.0 26.0 26.0 26.0 26.0 26.0 26.0 26.0
SO BUILDWID CT000001 111.07 107.16 100.0 115.85 128.17 136.6 140.88 140.88 136.6 128.17 115.85 100.0 107.16 111.07 111.6 108.74 108
SO BUILDLN CT000001 128.17 115.85 100.0 107.16 111.07 111.6 108.74 108.74 111.6 111.07 107.16 100.0 115.85 128.17 136.6 140.88 140
SO XBADJ CT000001 -93.97 -98.48 -100.0 -107.16 -111.07 -111.6 -108.74 -108.74 -111.6 -111.07 -107.16 -100.0 -98.48 -93.97 -86.6
SO YBADJ CT000001 55.54 53.58 50.0 40.56 29.88 18.3 6.16 -6.16 -18.3 -29.88 -40.56 -50.0 -53.58 -55.54 -55.8 -54.37 -54.37 -55.8
SO LOCATION CV000001 POINTCAP 690817 3975122 92
SO SRCPARAM CV000001 1000 60.0 350.0 0.005 1.8
SO URBANSRC CV000001
SO LOCATION HV000001 POINTHOR 690561 3975207 92
SO SRCPARAM HV000001 1000 45.0 300.0 0.006 3.0
SO URBANSRC HV000001
SO LOCATION FU000001 AREA 690957 3974943 92
SO SRCPARAM FU000001 0.1 2.0 100.0 100.0 45.0 0.0
SO URBANSRC FU000001
SO LOCATION SR000001 VOLUME 690991 3974996 92
SO SRCPARAM SR000001 1000 10.0 10.0 10.0
SO URBANSRC SR000001
SO LOCATION RW000001 LINE 690560 3975117 690751 3975163 92
SO SRCPARAM RW000001 0.0678675172 3.0 75.0 3.0
SO URBANSRC RW000001

```

Figure 30 Note: If particle and vapor phase emissions are modeled separately (e.g., when modeling deposition/depletion), then two aermod.out files will be provided in the facility folder: an aermod\_P.out file for particle phase emissions and an aermod\_V.out file for vapor phase emissions. Deposition fluxes (Dry Depo and Wet Depo) will be provided with depletion applied to concentrations, if modeled.

Figure 31. Sample plotfile.plt output file (facility-specific, abbreviated)

```

plotfile.plt - Notepad
File Edit Format View Help
* AERMOD ( 19191): Fac1-NC 08/25/20
* AERMET ( 19191): 12:00:45
* MODELING OPTIONS USED: NonDEFAULT CONC ELEV ALPHA URBAN ADJ_U* BUOYLINE
* PLOT FILE OF PERIOD VALUES AVERAGED ACROSS 0 YEARS FOR SOURCE GROUP: CT000001
* FOR A TOTAL OF 329 RECEPTORS.
* FORMAT: (2(1X,F13.5),1X,E13.6,3(1X,F8.2),2X,A6,2X,A8,2X,I8.8,2X,A8)
* X Y AVERAGE CONC ZELEV ZHILL ZFLAG AVE GRP NUM HRS NET ID
*
688085.00000 3975161.00000 0.253092E+02 100.00 100.00 0.00 PERIOD CT000001 00003326
688431.00000 3974590.00000 0.297584E+02 89.00 89.00 0.00 PERIOD CT000001 00003326
688074.00000 3974564.00000 0.275790E+02 96.00 96.00 0.00 PERIOD CT000001 00003326
688329.00000 3973976.00000 0.301464E+02 87.00 87.00 0.00 PERIOD CT000001 00003326
688603.00000 3974075.00000 0.311166E+02 81.00 81.00 0.00 PERIOD CT000001 00003326
689200.00000 3973740.00000 0.356151E+02 84.00 84.00 0.00 PERIOD CT000001 00003326
688986.00000 3973544.00000 0.331389E+02 86.00 86.00 0.00 PERIOD CT000001 00003326
688843.00000 3975073.00000 0.302065E+02 87.00 87.00 0.00 PERIOD CT000001 00003326
688627.00000 3975147.00000 0.292191E+02 94.00 94.00 0.00 PERIOD CT000001 00003326
688703.00000 3974777.00000 0.307262E+02 87.00 87.00 0.00 PERIOD CT000001 00003326
688794.00000 3974637.00000 0.319091E+02 86.00 86.00 0.00 PERIOD CT000001 00003326
688857.00000 3974368.00000 0.336242E+02 88.00 88.00 0.00 PERIOD CT000001 00003326
688897.00000 3974590.00000 0.336846E+02 89.00 89.00 0.00 PERIOD CT000001 00003326
688987.00000 3974348.00000 0.358162E+02 91.00 91.00 0.00 PERIOD CT000001 00003326
688771.00000 3973458.00000 0.318658E+02 87.00 87.00 0.00 PERIOD CT000001 00003326
688844.00000 3973490.00000 0.327004E+02 89.00 89.00 0.00 PERIOD CT000001 00003326
688649.00000 3973298.00000 0.299506E+02 85.00 85.00 0.00 PERIOD CT000001 00003326
688548.00000 3973225.00000 0.288798E+02 83.00 83.00 0.00 PERIOD CT000001 00003326
688950.00000 3972883.00000 0.298544E+02 79.00 79.00 0.00 PERIOD CT000001 00003326
689303.00000 3973138.00000 0.338950E+02 81.00 81.00 0.00 PERIOD CT000001 00003326
689577.00000 3972790.00000 0.358756E+02 74.00 74.00 0.00 PERIOD CT000001 00003326
689172.00000 3972686.00000 0.330014E+02 84.00 84.00 0.00 PERIOD CT000001 00003326
689054.00000 3972778.00000 0.316748E+02 84.00 84.00 0.00 PERIOD CT000001 00003326
689351.00000 3972699.00000 0.339758E+02 77.00 77.00 0.00 PERIOD CT000001 00003326
688985.00000 3973950.00000 0.367440E+02 92.00 92.00 0.00 PERIOD CT000001 00003326
690232.00000 3977482.00000 0.245790E+02 82.00 82.00 0.00 PERIOD CT000001 00003326
689973.00000 3977269.00000 0.233639E+02 88.00 88.00 0.00 PERIOD CT000001 00003326

```

Figure 31 Note: If particle and vapor phase emissions are modeled separately (e.g., when modeling deposition/depletion), then these concentrations will be provided based on particle phase emissions in a plotfile\_p.plt file and in a plotfile\_v.plt file for vapor phase emissions. Deposition fluxes (Dry Depo and Wet Depo) will be provided with depletion applied to concentrations, if modeled. (Although this figure shows AERMOD 19191, HEM5.0 includes AERMOD 24142.)

**Figure 32. Sample maxhour.plt output file (optional facility-specific, abbreviated)**

```

maxhour.plt - Notepad
File Edit Format View Help
* AERMOD ( 19191): Fac1-NC                                08/25/20
* AERMET ( 19191): Combined particle and vapor-phase emissions 12:00:45
* MODELING OPTIONS USED: NonDEFAULT CONC ELEV ALPHA URBAN ADJ_U* BUOYLINE
* PLOT FILE OF HIGH 87TH HIGH 1-HR VALUES FOR SOURCE GROUP: CT000001
* FOR A TOTAL OF 329 RECEPTORS.
* FORMAT: (2(1X,F13.5),1X,E13.6,3(1X,F8.2),3X,A5,2X,A8,2X,A5,5X,A8,2X,I8)
* X Y AVERAGE CONC ZELEV ZHILL ZFLAG AVE GRP RANK NET ID DATE(CONC)
*
688085.00000 3975161.00000 0.284562E+03 100.00 100.00 0.00 1-HR CT000001 87TH 19032801
688431.00000 3974590.00000 0.316115E+03 89.00 89.00 0.00 1-HR CT000001 87TH 19030220
688074.00000 3974564.00000 0.301197E+03 96.00 96.00 0.00 1-HR CT000001 87TH 19021915
688329.00000 3973976.00000 0.329636E+03 87.00 87.00 0.00 1-HR CT000001 87TH 19022215
688603.00000 3974075.00000 0.329503E+03 81.00 81.00 0.00 1-HR CT000001 87TH 19060919
689200.00000 3973740.00000 0.406146E+03 84.00 84.00 0.00 1-HR CT000001 87TH 19030908
688986.00000 3973544.00000 0.375320E+03 86.00 86.00 0.00 1-HR CT000001 87TH 19060911
688843.00000 3975073.00000 0.336322E+03 87.00 87.00 0.00 1-HR CT000001 87TH 19052105
688627.00000 3975147.00000 0.325032E+03 94.00 94.00 0.00 1-HR CT000001 87TH 19060814
688703.00000 3974777.00000 0.314162E+03 87.00 87.00 0.00 1-HR CT000001 87TH 19040119
688794.00000 3974637.00000 0.335495E+03 86.00 86.00 0.00 1-HR CT000001 87TH 19021214
688857.00000 3974368.00000 0.370621E+03 88.00 88.00 0.00 1-HR CT000001 87TH 19041011
688897.00000 3974590.00000 0.364171E+03 89.00 89.00 0.00 1-HR CT000001 87TH 19021710
688987.00000 3974348.00000 0.385640E+03 91.00 91.00 0.00 1-HR CT000001 87TH 19052724

```

Figure 32 Note: The Maxhour plot file will be produced if you opted to model acute concentrations in your Facility List Options file. If particle and vapor phase emissions are modeled separately (e.g., when modeling deposition/depletion), then these acute concentrations will be provided based on particle phase emissions in a maxhour\_p.plt file and for vapor phase emissions in an maxhour\_v.plt file. (Although this figure shows AERMOD 19191, HEM5.0 includes AERMOD 24142.)

**Table 72. Sample Input Selection Options HEM Output file (facility-specific, abbreviated)**

Facility ID	Aermod Title2	Emissions Phase	Rural / Urban	Deposition (YN)	Depletion (YN)	Deposition Type (particle/vapor)	Depletion Type (particle/vapor)	Elevation (YN)	Acute Hours	Acute Multiplier	Building Downwash (YN)	User Receptors (YN)	Max Modeling Distance	Discrete Modeling Distance	Overlap Distance	Number of Polar Rings	Number of Polar Radials	Acute (YN)	First Ring Distance	...
Fac1-NC	CO TITLETW O Combined particle and vapor-phase emissions			N	N	NO/NO	NO/NO	Y	1	10	Y	Y	50000	3000	30	13	16	Y	565	...

Table 72 Note: The above Input Selection Options files do not show all information provided; the actual file contains 34 fields (columns) providing chosen modeling run options.

**Table 73. Sample Acute Maximum Concentrations HEM Output file (optional facility specific, abbreviated)**

Pollutant	Conc (ug/m <sup>3</sup> )	Conc sci (ug/m <sup>3</sup> )	Aegl_1 1hr (mg/m <sup>3</sup> )	...	Acute Rel (mg/m <sup>3</sup> )	Pop	Distance (m)	Angle (from north)	Elevation (m)	Hill Hght (m)	Fips	Block	Utm easting	Utm northing	Latitude	Longitude	Receptor type	Notes	
1,3-butadiene	64.172	6.4e+01	1500	...	0	0	565	90	92	92	na	na	691471	3975205	35.90242	-78.87832	PG	Polar	
Acetaldehyde	14.339	1.4e+01	81	...	0.47	0	459	233	90	90	U0000	0000UR CPT1	35	3974934	35.90016	-78.88875	P	Discrete	
acrolein	100.37	1.0e+02	0.069	...	0.0025	0	459	233	90	90	U0000	0000UR CPT1	35	3974934	35.90016	-78.88875	P	Discrete	
arsenic compounds	69.242	6.9e+01	0	...	0.0002	0	565	180	92	92	na	na	690906	3974640	35.89744	-78.88471	PG	Polar	
benzene	29.947	3.0e+01	170	...	0	0	565	90	92	92	na	na	691471	3975205	35.90242	-78.87832	PG	Polar	
bis(2-ethylhexyl)-pht-halate	1839.11	1.8e+03	0	...	0	0	565	180	92	92	na	na	690906	3974640	35.89744	-78.88471	PG	Polar	
cadmium compounds	7.4528	7.5e+00	0.1	...	0	0	565	180	92	92	na	na	690906	3974640	35.89744	-78.88471	PG	Polar	
chloroform	0.4092	4.1e-01	0	...	0.15	0	565	67	92	92	na	na	691428	3975421	35.90438	-78.87874	PG	Polar	
chromium (iii) compounds	39.581	4.0e+01	0	...	0	0	565	180	92	92	na	na	690906	3974640	35.89744	-78.88471	PG	Polar	
chromium (vi) compounds	0.0395	4.0e-02	0	...	0	0	565	180	92	92	na	na	690906	3974640	35.89744	-78.88471	PG	Polar	
cumene	1.0267	1.0e+00	250	...	0	0	565	90	92	92	na	na	691471	3975205	35.90242	-78.87832	PG	Polar	
...	...	...	...	...	...	...	...	...	...	...	...	...	...	...	...	...	...	...	...

Table 73 Note: The Acute Maximum Concentrations (acute\_chem\_max) file will be produced if you opted to model acute concentrations in your Facility List Options file. The above sample file is abbreviated; the actual file contains five acute benchmark columns, but only the Aegl\_1hr and Rel columns are shown.

**Table 74. Sample Acute Populated Concentrations HEM Output file (optional facility-specific, abbreviated)**

Pollutant	Conc (ug/m <sup>3</sup> )	Conc sci (ug/m <sup>3</sup> )	Aegl_1 1hr (mg/m <sup>3</sup> )	...	Acute Rel (mg/m <sup>3</sup> )	Pop	Distance (m)	Angle (from north)	Elevation (m)	Hill Hght (m)	Fips	Block	Utm easting	Utm northing	Latitude	Longitude	Receptor type	Notes	
1,3-butadiene	10.224	1.0e+01	1500	...	0	219	1124	191	85	85	37063	0020272057	690684	3974103	35.89265	-78.8873	C	Discrete	
Acetaldehyde	9.996	1.00+01	81	...	0.47	7	383	301	97	97	37063	0020272047	690578	3975403	35.90438	-78.88816	C	Discrete	
acrolein	69.972	7.0e+01	0.069	...	0.0025	7	383	301	97	97	37063	0020272047	690578	3975403	35.90438	-78.88816	C	Discrete	
arsenic compounds	60.794	6.1e+01	0	...	0.0002	2	492	220	90	90	37063	0020272056	690588	3974829	35.89921	-78.88819	C	Discrete	
benzene	4.771	4.8e+00	170	...	0	219	1124	191	85	85	37063	0020272057	690684	3974103	35.89265	-78.8873	C	Discrete	
bis(2-ethylhexyl)-phthalate	942.976	9.4e+02	0	...	0	2	492	220	90	90	37063	0020272056	690588	3974829	35.89921	-78.88819	C	Discrete	
cadmium compounds	6.546	6.5e+00	0.1	...	0	2	492	220	90	90	37063	0020272056	690588	3974829	35.89921	-78.88819	C	Discrete	
chloroform	0.058	5.8e-02	0	...	0.15	2	4329	48	117	117	37063	0018091060	694160	3978061	35.92762	-78.84785	C	Interpolated	
chromium (iii) compounds	35.868	3.6e+01	0	...	0	2	492	220	90	90	37063	0020272056	690588	3974829	35.89921	-78.88819	C	Discrete	
chromium (vi) compounds	0.0358	3.60-02	0	...	0	2	492	220	90	90	37063	0020272056	690588	3974829	35.89921	-78.88819	C	Discrete	
cumene	0.163	1.6e-01	250	...	0	219	1124	191	85	85	37063	0020272057	690684	3974103	35.89265	-78.8873	C	Discrete	
...	...	...	...	...	...	...	...	...	...	...	...	...	...	...	...	...	...	...	...

Table 74 Note: The Acute Populated Concentrations (acute\_chem\_pop) file will be produced if you opted to model acute concentrations in your Facility List Options file. The above sample file is abbreviated; the actual file contains five acute benchmark columns, but only the Aegl\_1hr and Rel columns are shown.

**Table 75. Sample Acute Breakdown HEM Output file (optional facility-specific)**

Pollutant	Source ID	Emission type	Max conc at populated receptor (ug/m <sup>3</sup> )	Is max populated receptor interpolated? (Y/N)	Max conc at any receptor (ug/m <sup>3</sup> )	Is max conc at any receptor interpolated? (Y/N)
1,2,3,4,6,7,8,9-octachlorodibenzo-p-dioxin	FU000001	C	6.816696-07	N	1.3295E-06	N
1,2,3,4,6,7,8,9-octachlorodibenzofuran	FU000001	C	7.04392E-08	N	1.3738E-07	N
1,2,3,4,6,7,8-heptachlorodibenzo-p-dioxin	CT000001	C	3.112916-09	N	2.0383E-09	N
1,2,3,4,6,7,8-heptachlorodibenzo-p-dioxin	CV000001	C	1.87004E-08	N	1.1675E-08	N
1,2,3,4,6,7,8-heptachlorodibenzo-p-dioxin	HV000001	C	8.13071E-09	N	2.569E-08	N
1,2,3,4,6,7,8-heptachlorodibenzofuran	CT000001	C	1.23623E-08	N	8.0945E-09	N
1,2,3,4,6,7,8-heptachlorodibenzofuran	CV000001	C	7.42649E-08	N	4.6364E-08	N
1,2,3,4,6,7,8-heptachlorodibenzofuran	HV000001	C	3.228946-08	N	1.0202E-07	N
1,2,3,4,7,8,9-heptachlorodibenzofuran	FU000001	C	9.429766-08	N	1.8391E-07	N
1,2,3,4,7,8-hexachlorodibenzo-p-dioxin	CT000001	C	2.54693E-09	N	1.6677E-09	N
1,2,3,4,7,8-hexachlorodibenzo-p-dioxin	CV000001	C	1.53004E-08	N	9.552E-09	N
1,2,3,4,7,8-hexachlorodibenzo-p-dioxin	HV000001	C	6.6524E-09	N	2.1019E-08	N
1,2,3,4,7,8-hexachlorodibenzofuran	CT000001	C	2.96397E-08	N	1.9407E-08	N
1,2,3,4,7,8-hexachlorodibenzofuran	CV000001	C	1.780576-07	N	1.1116E-07	N
1,2,3,4,7,8-hexachlorodibenzofuran	HV000001	C	7.74168E-08	N	2.446E-07	N
1,2,3,4,7,8-hexachlorodibenzofuran	RV000003	C	3.945836-09	N	1.2858E-09	N
1,2,3,6,7,8-hexachlorodibenzo-p-dioxin	CT000001	C	2.710776-09	N	1.77496-09	N
1,2,3,6,7,8-hexachlorodibenzo-p-dioxin	CV000001	C	1.62846E-08	N	1.0166E-08	N
1,2,3,6,7,8-hexachlorodibenzo-p-dioxin	HV000001	C	7.08033E-09	N	2.2371E-08	N
1,2,3,6,7,8-hexachlorodibenzo-p-dioxin	RV000002	C	5.67075E-10	N	5.9953E-11	N
1,2,3,6,7,8-hexachlorodibenzofuran	CT000001	C	2.66608E-08	N	1.7457E-08	N
1,2,3,6,7,8-hexachlorodibenzofuran	CV000001	C	1.601626-07	N	9.9989E-08	N
1,2,3,6,7,8-hexachlorodibenzofuran	HV000001	C	6.96362E-08	N	2.2002E-07	N
1,2,3,6,7,8-hexachlorodibenzofuran	RV000003	C	3.549276-09	N	1.1565E-09	N
...	...	...	...	...	...	...

Table 75 Note: The Acute Breakdown file will be produced if you opted to model acute concentrations in your Facility List Options file.

**Table 76. Sample Facility Max Risk and HI HEM Output file (for run group, abbreviated)**

Facil_id	mx_can_rsk	can_rsk_int-erpltd	can_rcpt_type	can_la_titude	can_lo- ngitude	can_b lk	Respira- tory_hi	[59 TOSHI columns]	pop_ over- lp	Inci- dence	metname	km_to_ metstation	fac_center _latitude	fac_center _longitude	rural_ urban
Fac1- NC	0.000617	N	Census block	35.899 0848	-78.8880	98010 01074	0.677049	...	0	0.047682	NC13722_ 2019.SFC	9.2712	35.9025311	-78.884577	U
Fac2- IL	9.00146 E-07	N	Census block	41.479 7356	-88.2618	89070 02218	0.03653	...	0	4.581E- 06	IL04808_2 019.SFC	35.6838	41.49	-88.27	R
...	...	...	...	...	...	...	...	...	...	...	...	...	...	...	...

Table 76 Note: The Facility Max Risk and HI file covers the entire run group with one row of output per facility. The above sample file is abbreviated; there are 59 additional columns not shown pertaining to all 14 TOSHI values and locations.

**Table 77. Sample Facility Cancer Risk Exposure HEM Output file (for run group)**

Facil_id	latitude	longitude	Number people exposed to >= 1 in 1,000 risk	Number people exposed to >= 1 in 10,000 risk	Number people exposed to >= 1 in 100,000 risk	Number people exposed to >= 1 in 1,000,000 risk	Number people exposed to >= 1 in 10,000,000 risk
Fac1-NC	35.90253	-78.8845	0	435	48998	800221	1545731
Fac2-IL	41.49	-88.27	0	0	0	0	296
...	...	...	...	...	...	...	...

**Table 78. Sample Facility TOSHI Exposure HEM Output file (for run group)**

Facility ID	Number people exposed to > 1 Respira- tory HI	Number people exposed to > 1 Liver HI	Number people exposed to > 1 Neurolo- gical HI	Number people exposed to > 1 Develop- mental HI	Number people exposed to >1 Repro- ductive HI	Number people exposed to >1 Kidney HI	Number people exposed to >1 Ocular HI	Number people exposed to > 1 Endocri- nological HI	Number people exposed to > 1 Hematol- ogical HI	Number people exposed to > 1 Immuno- logical HI	Number people exposed to > 1 Skeletal HI	Number people exposed to > 1 Spleen HI	Number people exposed to > 1 Thyroid HI	Number people exposed to > 1 Whole Body HI
Fac1-NC	0	0	0	435	0	0	0	0	0	0	0	0	0	0
Fac2-IL	0	0	0	0	0	0	0	0	0	0	0	0	0	0
...	...	...	...	...	...	...	...	...	...	...	...	...	...	...

**Figure 33. Sample All Facility Source Locations Image (for run group)**

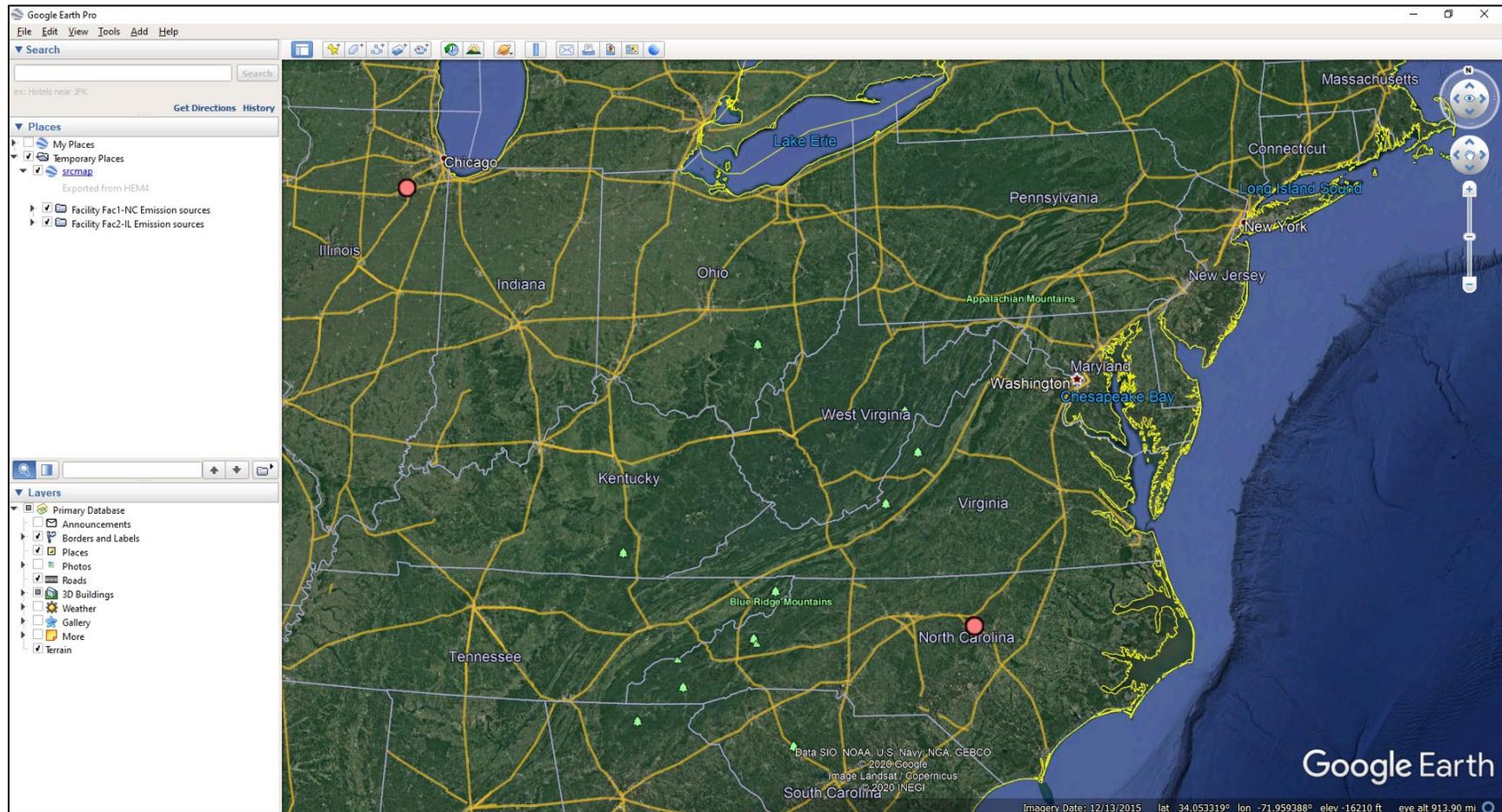


Figure 33 Note: The All Facility Source Locations Google Earth™ image depicts the two sample facilities modeled in this run group – located in Illinois and North Carolina – on a map. On the actual map image, you can zoom in to see the individual sources at each facility in more detail.

**Figure 34. Sample HEM Log Output file (for run group, abbreviated)**

## 13. Appendix B: Demographic Assessment Calculations

The overall methodology and Census data used by HEM's Demographic Assessment module are discussed in Section 8.1 of this guide. This Appendix provides additional detail on the calculation methods HEM uses to produce the Demographic Assessment results described in Sections 8.2 and 8.3 of this guide.

As summarized in Table 57 of Section 8.1, U.S. Census-based demographic data is available at the block group level and tract level. However, HEM-AERMOD computes risk data at the finer census block level. When a user chooses to model with U.S. Census receptors, HEM models the cancer risk and noncancer "risk" (hazard index, HI) at a point near the geographic center of each census block called the block centroid. HEM's risk estimates are assumed to apply to all individuals residing in the census block.

Each U.S. Census block is designated by a 15-digit code which includes identifiers for the block group, tract and county in which the block is located. The first five digits designate the county, followed by six digits to designate the tract, one digit to designate the block group, and three digits to designate the block. The Demographic Assessment module uses these identification codes to link the HEM modeling results for each census block to the appropriate American Community Survey (ACS) census block group and tract demographic statistics (US Census Bureau, 2023b, 2024a, 2024b). This linking allows HEM to estimate the distribution of cancer and noncancer risks for different demographic categories including race/ethnicity, age, household income relative to the poverty level, high school educational attainment, household language (limited English-speaking), and disability.

The demographic characteristics of the population potentially impacted by emissions from facilities in your run group are determined by applying the characteristics of a census block group or tract to the HEM modeled census block populations located within that block group or tract. Specifically, the block group percentage of people of different races/ethnicities, the block group percentage in different age groups, the block group percentage in low income categories (below the poverty level and below twice the poverty level), the block group percentage of adults without a high school diploma, the block group percentage that are living in limited English speaking households, and the tract percentage of people with one or more disabilities are presumed to also describe each census block located within that block group or tract.

For comparison, the nationwide demographic percentages are computed from the Census' ACS five-year averages for 2018-2022 (US Census Bureau, 2023b). The denominator for these nationwide percentages uses the total nationwide population, which is likewise computed from the 2018-2022 ACS and determined by summing the total population of all census block groups and tracts. Note: HEM's Demographic Assessment module also produces state and county level demographic statistics for comparison, as discussed in Section 8.

Section B.1 describes the calculation method used to estimate the total population exposed to different risk levels. Sections B.2 through B.6 describe calculation methods used to compute risks for racial/ethnic, age, education level, income level (relative to poverty level), limited English speaking, and disability demographic categories. Section B.7 describes the gap-filling approach used by HEM's Demographic Assessment module when block group statistics are not available for a given block.

## B.1 Total Population Risks

HEM calculates (cancer and noncancer) risk distributions for the total population using a block-by-block accumulation of people at various risk levels. The Demographic Assessment module identifies a set of bins reflecting the level of risk and then assigns the population of each block to the appropriate risk bin based on HEM's modeled risk level in the block. The numbers of people in each risk bin are then added together for all modeled census blocks in the run group using Equation (16):

$$H(R_{ab}) = \sum_i^{(R_a \leq R_i < R_b)} [N(i)] \quad (16)$$

where:

- $H(R_{ab})$  is the population count for risk bin  $R_{ab}$ , which is between  $R_a$  and  $R_b$
- $R_i$  is the modeled risk level in block "i" (cancer or noncancer)
- $\sum_i^{(R_a \leq R_i < R_b)}$  refers to the summation over all blocks i where  $R_i$  falls in bin  $R_{ab}$ , between  $R_a$  and  $R_b$
- $N(i)$  is the number of people in block i

The average risk for the total population is then calculated using Equation (17):

$$A(s) = \frac{\sum_i [N(i) \times R_i]}{\sum_i [N(i)]} \quad (17)$$

where:

- $A(s)$  is the average risk for the population in the modeling domain (cancer or noncancer), population weighted
- $\sum_i$  refers to the summation over all blocks "i" modeled for the run group
- $N(i), R_i$  are defined under Equation 16

These risk bins, populations within each risk bin and population-weighted average risk results are shown in the outputs produced by HEM's Demographic Assessment module, for each facility and for the run group as a whole.

**Note:** The average risk (cancer or noncancer) is less than the maximum risk because the average risk takes into account risk levels at all populated block receptors for the entire modeled domain of the run group, whereas the maximum risk occurs at an individual populated receptor (that receptor with the highest modeled risk level). The average risk statistic encompasses higher risk levels (generally closer into facility emissions) as well as lower risk locations (generally farther away in the domain). HEM's Demographic Assessment module reports the average risk for the total population as well as separately for each demographic group described below.

## B.2 Race, Ethnicity and Age

Table B03002 (Hispanic or Latino origin by race, as noted in Table 57 of Section 8.1) of the ACS data (US Census Bureau, 2023b, 2024a, 2024b) provides race/ethnicity statistics for each

census block group nationwide. Table B01001 provides age statistics for the population by ranges (in years) for each census block group nationwide. For each modeled census block, HEM’s Demographic Assessment module estimates the race/ethnicity (White, Black, American Indian and Alaskan Native, Asian, Multiracial/Other, or Hispanic/Latino) and age range (0-17, 18-64 and ≥65 years) for that block, based on demographic information provided at the block group level, using Equation (18):

$$N(s, b/bg) = N(t, b/bg) \times P(s, bg)/100 \quad (18)$$

where:

- N(s,b/bg) is the number of people in racial/ethnic or age subgroup “s”, in census block “b” of block group “bg”
- N(t,b/bg) is the total number of people in census block “b” of block group “bg”
- P(s,bg) is the percentage of people in racial/ethnic or age subgroup “s”, in census block group “bg”

The number of people in each racial/ethnic and age category is calculated using Equation (18), summed over all blocks that fall within the specified radius of each facility. Equation (16) in Section B.1 is then used to generate cancer and noncancer risk distributions based on the block-level results, and Equation (17) in Section B.1 is used to compute the average cancer and noncancer risk for people in each racial/ethnic or age subgroup.

### B.3 Level of Education

Table B15002 (educational attainment, as noted in Table 57 of Section 8.1) of the ACS (US Census Bureau, 2023b, 2024a, 2024b) provides education attainment statistics for each census block group nationwide. For each modeled census block, HEM’s Demographic Assessment module estimates the number of people 25-years and older without a high school diploma, based on demographic information provided at the block group level, using Equation (19):

$$N(nhs, b/bg) = N(t, b/bg) \times P(nhs, bg)/100 \quad (19)$$

where:

- N(nhs,b/bg) is the number of people 25-years and older without a high school diploma “nhs”, in census block “b” of block group “bg”
- N(t,b/bg) is the number of people 25-years and older in census block “b” of block group “bg”
- P(nhs,bg) is the percentage of people 25-years and older without a high school diploma “nhs”, in census block group “bg”

The number of people 25-years and older without a high school diploma is calculated using Equation (19), summed over all blocks that fall within the specified radius of each facility. Equation (16) in Section B.1 is then used to generate cancer and noncancer risk distributions based on the block-level results, and Equation (17) in Section B.1 is used to compute the average cancer and noncancer risk for adults without a high school diploma.

## B.4 Low Income Level

Table C17002 (ratio of income to poverty level, as noted in Table 57 of Section 8.1) of the ACS (US Census Bureau, 2023b, 2024a, 2024b) estimates the numbers of individuals within a census block group who live in households where the household income is below the poverty line, and below various multiples of the poverty line. HEM's Demographic Assessment module calculates two low-income statistics based on the fractions of (1) individuals living in households earning incomes below the poverty level and (2) individuals living in households earning incomes below two times the poverty level. For each modeled census block, HEM's Demographic Assessment module estimates the block's household income level, based on demographic information provided at the block group level, using Equation (20):

$$N(hi, b/bg) = N(t, b/bg) \times P(hi, bg)/100 \quad (20)$$

where "hi" indicates household income, whether below the poverty level or below two times the poverty level, depending on the income statistic relative to the poverty level, and:

- N(hi,b/bg) is the number of people living in low-income households "hi" relative to the poverty level, in census block "b" of block group "bg"
- N(t,b/bg) is the total number of people in census block "b" of block group "bg"
- P(hi,bg) is the percentage of people living in low-income households "hi" relative to the poverty level, among the population for which poverty status is known, in census block group "bg"

The numbers of people living in households earning (1) below the poverty level and (2) below two times the poverty level are calculated using Equation (2), summed over all blocks that fall within the specified radius of each facility. Equation (16) in Section B.1 is then used to generate cancer and noncancer risk distributions based on the block-level results, and Equation (17) in Section B.1 is used to compute the average cancer and noncancer risk for people living in low-income households.

## B.5 Limited English Speaking Households

Limited English speaking households are households that may need English-language assistance and are defined in the ACS as a household "in which no member 14 years old and over (1) speaks only English at home or (2) speaks a language other than English at home and speaks English 'Very well' " (i.e., households that have difficulty with English) (US Census Bureau, 2022a, p. 52, 2024c). The previous term for this ACS demographic was "Linguistic Isolation". Table C16002 (household language, as noted in Table 57 of Section 8.1) of the ACS (US Census Bureau, 2023b, 2024a, 2024b) provides the number of limited English speaking households in each block group. For each modeled census block, HEM's Demographic Assessment module estimates the number of people living in limited English speaking households, based on demographic information provided at the block group level, using Equation (21):

$$N(le, b/bg) = N(t, b/bg) \times P(le, bg)/100 \quad (21)$$

where:

- $N(l_e, b/bg)$  is the number of people living in limited English speaking households “ $l_e$ ”, in census block “ $b$ ” of block group “ $bg$ ”
- $N(t, b/bg)$  is the total number of people in census block “ $b$ ” of block group “ $bg$ ”
- $P(l_e, bg)$  is the percentage of limited English speaking households “ $l_e$ ”, in census block group “ $bg$ ”

The number of people living in limited English speaking households is calculated using Equation (21), summed over all blocks that fall within the specified radius of each facility. Equation (16) in Section B.1 is then used to generate cancer and noncancer risk distributions based on the block-level results, and Equation (17) in Section B.1 is used to compute the average cancer and noncancer risk for people living in limited English speaking households.

## B.6 Disability

The demographic percentages for people with one or more disabilities are based on Census ACS surveys at the tract level and include people who report having one or more of six disabilities: hearing difficulty, vision difficulty, cognitive difficulty, ambulatory difficulty, self-care difficulty, and independent living difficulty (US Census Bureau, 2022a, pp. 64-66, 2024a, 2024b). Table B99181 of the ACS (Disability, as noted in Table 57 of Section 8.1) provides the number of civilian non-institutionalized people (i.e., all U.S. civilians not residing in institutional group quarters facilities such as correctional institutions, juvenile facilities, skilled nursing facilities, and other long-term care living arrangements) living with one or more disabilities (US Census Bureau, 2022a). For each modeled census block, HEM’s Demographic Assessment module estimates the number of people living with one or more disabilities, based on demographic information provided at the tract level, using Equation (22):

$$N(di, b/T) = N(t, b/T) \times P(di, T)/100 \quad (22)$$

where:

- $N(di, b/T)$  is the number of people living with one or more disability “ $di$ ”, in census block “ $b$ ” of tract “ $T$ ”
- $N(t, b/T)$  is the total number of people in census block “ $b$ ” of tract “ $T$ ”
- $P(di, T)$  is the percentage of people in the census tract who were identified in the ACS survey as living with one or disabilities “ $di$ ”, in tract “ $T$ ”

The number of people living with one or more disabilities is calculated using Equation (22), summed over all blocks that fall within the specified radius of each facility. Equation (16) in Section B.1 is then used to generate cancer and noncancer risk distributions based on the block-level results, and Equation (17) in Section B.1 is used to compute the average cancer and noncancer risk for people living with one or more disabilities.

## B.7 Demographic Defaults

Block and block group designations used in the Census may be modified to accommodate population growth in some U.S. regions. As a result, certain blocks modeled in HEM, which are based on the last Decennial Census, may not map to the block group designations used in the

latest five-year ACS survey. In addition, some statistics may not be reported in the ACS for every block group. Race, ethnicity, and age statistics are generally reported for all block groups. However, low income, limited English speaking households, and low educational attainment statistics are not available for some block groups.

In these cases, HEM's Demographic Assessment module computes default estimates for the missing demographic statistics based on the average statistics for the tract in which the block is located. If no tract-level data are available, demographic statistics are estimated based on the statistics of the nearest (non-zero population) block group neighbor to the unmatched block location. This gap-filling exercise is performed separately for each type of demographic data. That is, in the case where some categories of data are available (for instance, race, age and ethnicity) and others are not available (educational attainment, low income, or limited English speaking households), HEM's Demographic Assessment module only computes defaults for the categories of data that are missing.

Note: Disability is only available at the tract level and does not need defaulting for the 2018-2022 ACS, because disability data is available for all tracts. However, if defaulting were needed for future ACS versions, the county average would be used.

The tract level defaults are computed using weighted averages based on all the other block groups in the tract for which data are available. Tract level defaults are calculated for race, ethnicity, and age subgroups using Equation (23):

$$P(s, T) = \frac{\{\sum P(s, bg/T) \times N(t, bg)\}}{\{\sum N(t, bg)\}} \quad (23)$$

where:

- $P(s, T)$  is the percentage of people in race, ethnicity, or age subgroup "s", in tract "T"
- $\sum$  refers to the summation over all census block groups in tract "T" for which data are available
- $P(s, bg/T)$  is the percentage of people in race, ethnicity, or age subgroup "s", in census block group "bg" of tract "T"
- $N(t, bg)$  is the total number of people in census block group "bg"

Defaults for educational attainment, low income, and limited English speaking households are calculated in a similar fashion, except that the population weighting term N is replaced by the population over age 25, the population for which poverty status is known, and the number of households, respectively.

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