US EPA Information Collection Rule

Base Analysis Document:
Membrane Studies

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2. Introduction

The *Base Analysis Document: Membrane Studies* is part of the documentation package for the *ICR Treatment Study Database*. The term "base analysis" refers to the review, analysis and reduction of the raw data from each study to generate a standard set of data elements that are consistent across all membrane studies. For the majority of users, the output from the base analysis will be more relevant and useful than the raw data. Furthermore, the standard data elements developed during the base analysis can be managed in a relational database which provides the user with a platform for more sophisticated analyses. For users that are interested in the raw data, the reviewed *Data Collection Spreadsheets* can be accessed through the *Treatment Study Data Library* module of the database (USEPA, 2000).

The *ICR Treatment Study Database* is a relational database designed to manage and organize the complex data sets generate by the 99 treatment studies conducted under the ICR. The raw data from these studies is managed in the *Treatment Study Data Library*, while the results from the base analysis are managed in either the *Membrane Data Module* or the *GAC Data Module*. These modules are described in more detail in the *User's Guide* for this database (USEPA, 2000).

The *Membrane and GAC Data Modules* are extremely powerful tools designed to support more sophisticated analyses by allowing users to sort and query the base analysis results in a variety of ways. These modules also perform calculations based on user defined breakthrough criteria, for GAC studies, or based on user defined blended water quality goals for membrane studies. To use this tool to its full potential, it is important to understand the assumptions and methodology used to conduct the base analysis.

The purpose of this document is to describe the base analysis approach used for membrane treatment studies. Section 3 provides background on the membrane treatment studies, while Section 4 presents an overview of the analysis. Section 5 describes the review processes used to identify and correct erroneous data. The remaining sections, 6 through 9, present the details of the base analysis for membrane studies.

3. Background

Thirty-six of the 99 studies conducted under the ICR, evaluated membrane technology. Membrane treatment studies were conducted at bench-, pilot-, or full-scale according to one of the five procedures described below (USEPA, 1996a):

- The rapid bench-scale membrane test (RBSMT) used a tangential-flow cell with a 24 in^2 sheet of membrane material. A flow-through system with concentrate recycle was used so that the system could be operated at high recoveries, while still meeting the hydraulic constraints of the membrane. The standard experimental design for RBSMT studies included the evaluation of two membranes over four quarters of one year. Each membrane was evaluated at four recoveries (30%, 50%, 70% and 90%) during each quarter of testing.
- The quarterly single-element bench-scale test (SEBST) used a single spiral-wound element, typically 4 or 2.5 inches in diameter by 40 inches in length. Due to the significant volume requirements of a 4" by 40" or 2.5" by 40" element, testing had to be performed on-site. Similar to the RBSMT, the SEBST system used concentrate recycle to achieve high recoveries, but during SEBST studies, only a single recovery of 75% was evaluated. The standard experimental design for SEBST studies included the evaluation of two membranes over four quarters of one year.
- The long-term single-element bench-scale test (LT-SEBST) used the same system and operating conditions as the SEBST procedure. However, during LT-SEBST studies a single membrane was evaluated under continuous operation over a one-year period.
- The pilot-scale testing protocol used multiple spiral-wound elements designed in a staged array. Either 2-stage or 3-stage pilot systems were used during ICR testing, with 2-stage systems designed as a 2-1 array and 3-stage systems designed as a 3-2-1 or a 2-1-1 array. Pilot systems used either 8 inch by 40 inch or 4 inch by 40 inch elements, although a few studies did use 2.5 inch diameter elements in the third stage. Pilot studies typically evaluated a single membrane type over a one-year period, although some studies did evaluate two or three different membranes. The system was typically operated at a recovery of 75%; however, recoveries as low as 48% and as high as 93% were evaluated in some cases.
- Full-scale studies are similar to pilot-scale studies with respect to system design and sampling requirements; however, all full-scale systems were designed using 8 inch by 40 inch elements and the system recovery was typically around 85%.

The distribution of the 36 membrane studies by protocol and source water type is shown in Table 3-1. Nineteen studies were conducted on ground water sources and 17 on surface water sources. The 36 membrane studies included 19 bench-scale studies, 14 pilot-scale studies and three full-scale studies. Thirteen of the bench-scale studies were conducted using the RBSMT procedure, while the remaining bench-scale studies include two quarterly and four long-term SEBST studies.

Table 3-1. Distribution of ICR membrane treatment studies

Study Protocol	Total	Surface Water	Groundwater
RBSMT	13	6	7
SEBST	2	1	1
LT-SEBST	4	4	0
Pilot-Scale	14	6	8
Full-Scale	3	0	3

The different protocols used to evaluate membrane technology during the ICR impact the type and quality of information provided by these studies. In general, as the scale of the system used in the study increases, the applicability of the results to full-scale performance improves (Allgeier, 1997a; Bergman and Lozier, 1993). Furthermore, as the duration of the study increases, estimates of sustained performance improve. Table 3-2 summarizes the scale and duration for the various protocols and describes how these differences among the testing procedures affect data analysis.

Table 3-2. Scale and duration of ICR membrane treatment study protocols

Protocol	Scale	Duration
RBSMT	SMALL: 24 in^2 membrane area. Small membrane area necessitates use of concentrate recycle. Water quality evaluated at recoveries of 30%, 50%, 70% and 90% is not directly applicable to full-scale.	SHORT: 1 to 2 weeks. The short duration results in poor estimates of sustained membrane performance. Extrapolation of productivity data is required.
SEBST	MEDIUM: 27 to 90 ft^2 membrane area. Use of a single element necessitates use of concentrate recycle. Water quality evaluated at a recovery of 75% is not directly applicable to full-scale.	MEDIUM: 4 to 6 weeks. Duration may be long enough to obtain a rough estimate of sustained performance. Extrapolation of productivity data may be necessary.
LT-SEBST	MEDIUM: 27 to 90 ft^2 membrane area. Use of a single element necessitates use of concentrate recycle. Water quality evaluated at a recovery of 75% is not directly applicable to full-scale.	LONG: 6 to 12 months. Duration is typically long enough to obtain good estimates of sustained performance.
Pilot-Scale	LARGE: 700 to 3600 ft^2 membrane area. System designed as a staged array and typically operated without concentrate recycle. Results are typically applicable to full-scale.	LONG: 6 to 12 months. Duration is typically long enough to obtain good estimates of sustained performance.
Full-Scale	FULL: 75,000 to 134,000 ft^2 membrane area. Water quality evaluated from either a 2- or 3-stage array in a full-scale system.	LONG: 6 to 12 months. Excellent estimates of sustained performance.

4. Overview of Data Analysis

The membrane base analysis included an evaluation of water quality and productivity data. The objective of this analysis was to assess the ability of a membrane to produce water that meets specific treatment objectives and to produce water at an acceptable rate without excessive cleaning requirements. The membrane base analysis was designed to reduce the large amounts of raw data from each study to standard data elements that could be used to evaluate water quality or productivity across all membrane studies.

Over the course of a membrane study, a significant amount of feed, permeate and concentrate water quality data was collected. This data demonstrated the ability of nanofiltration to remove various contaminants as conditions changed over the course of the study, e.g., changes in feed water quality, operating conditions, pretreatment, etc. However, the permeate and concentrate water quality data generated from the membrane studies were also impacted by differences in the study protocols as discussed in Section 3. The use of concentrate recycle and different recoveries among the various protocols had the most significant impact on water quality.

During the base analysis, the impact of study protocol and operating conditions on permeate and concentrate water quality was accounted for through a modeling approach. The Differential Water Quality Model was used to calculate estimates of permeate and concentrate water quality from a full-scale membrane array using the same membrane that was evaluated during the study. Input to this model included a set of design assumptions for the full-scale array, influent water quality data from the study, and mass transfer coefficients for each water quality parameter that were derived from the experimental permeate water quality data. The model consists of a mathematical representation of the full-scale array that was solved using a differential analysis. The details of this analysis and the Differential Water Quality Model are described in Section 8.

The productivity analysis summarized the large amount of flow and pressure data collected over the course of a study to develop a few parameters that effectively summarize membrane productivity. Specifically, these productivity parameters include the rate of specific flux decline, cleaning interval, cleaning efficiency, sustained flux and sustained specific flux. The specific flux was used as a key indicator of membrane productivity during the base analysis. The specific flux is the flow of water through a membrane that is normalized with respect to area, temperature and pressure. Time plots of the specific flux were used to evaluate the rate at which specific flux decreased due to membrane fouling. The rate of specific flux decline was then used to determine the cleaning interval required to maintain productivity at or above 85% of the baseline value. The cleaning efficiency was calculated after each cleaning event. The sustained flux and sustained specific flux were evaluated over periods of stable system operation, and these sustained parameters are intended to provide an estimate of long-term membrane performance. The details of the productivity analysis are described in Section 9.

5. Data Review

In order to ensure that the data used in this analysis was complete and accurate, the following review process was implemented: 1.) the raw data was reviewed upon receipt from the utility; 2.) the data was reviewed to identify outliers prior to analysis; 3.) the results of the base analysis were reviewed; and 4.) the data uploaded to the database was reviewed. Errors were identified and corrected through this multi-tiered review approach, minimizing the propagation of errors and greatly improving the accuracy of the information in the database. The following section describes each of these review processes.

5.1. Review of Raw Study Data

Utilities reported the data from their studies using standard *Data Collection Spreadsheets*, thus the data from all studies using the same testing protocol was submitted in the same format (USEPA, 1997). This facilitated the development of a spreadsheet tool that allowed the following checks to be performed on the raw data:

- Verify that all required data was submitted.
- Verify that the data was reported in the proper tables in the *Data Collection Spreadsheets.*
- Verify that all calculations in the *Data Collection Spreadsheets* were performed correctly. Specific calculation checks include pressure, recovery, cross-flow velocity, flux and specific flux as well as THM and HAA class sums.
- Review the reported test conditions for the simulated distribution system (SDS) procedure. Utilities were asked to verify SDS tests with reported conditions that were inconsistent with chlorination chemistry or that varied greatly from the target conditions. In cases where it was verified that the SDS test was not performed correctly, all disinfection byproduct (DBP) data associated with that test was rejected and not used in subsequent analyses. Furthermore, all DBP data associated with any SDS test for which a chlorine residual was reported below the minimum reporting level (MRL) was rejected.
- Feed, permeate and concentrate water quality data was reviewed as time series plots to help identify possible errors. Utilities were asked to verify data that was flagged as potential outlier data during this review.
- The relative values of permeate, feed and concentrate concentrations were compared to determine if the expected trend of permeate concentration < feed concentration < concentrate concentration was observed. Utilities were asked to verify data that did not follow this trend.
- Mass balance closure errors were calculated from the measured feed, permeate and concentrate concentrations. Utilities were asked to verify mass balance closure errors greater than 20%.
- For RBSMT studies, permeate and concentrate water quality was plotted as a function of recovery to determine if the data followed the expected trend of increasing permeate and concentrate concentrations with increasing recovery. Utilities were asked to verify data that did not follow this trend.
- Pressure, flow, flux and specific flux data was reviewed as time series plots to help identify possible errors. Utilities were asked to verify data that was flagged during this review.

- The temporal occurrence of cleaning events was verified.
- For pilot- and full-scale studies, flow and pressure balances were calculated. Utilities were asked to verify data with flow or pressure balance closure errors greater than 10%.

These reviews generated checklists that were sent to the utility responsible for the study. The utility was asked to supply missing information and verify possible errors. The range of problems identified during this review varied greatly over the 36 membrane studies. The review of some studies identified only a few minor problems, while other studies required multiple reviews to correct all deficiencies and verify all questionable data. During this process, many problems were corrected that would have otherwise gone undetected during subsequent review and analysis.

5.2. Review of Study Data for Outliers

After the utilities made corrections to their raw data, the *Data Collection Spreadsheets* were finalized and electronically protected. However, in cases where utilities did not have a justification for removing questionable data, i.e., there were no known QC failures or experimental errors to justify removal of the data, outlier data still remained in the finalized spreadsheets. The second step of the review process focused on the identification and removal of these outlier data.

A spreadsheet tool, very similar to the spreadsheet developed for review of the raw data was used during the outlier review. The spreadsheet generated graphical and statistical summaries of the data showing the variability of each parameter around the mean. This allowed outlier data to be quickly identified and removed from subsequent analysis.

During this review, only extreme outliers that would significantly skew the analysis were removed. Due to the variety of factors that affect outlier determination, such as the variability of the entire data set, a single outlier identification process could not be used for all cases. However, the following guidelines were used during the process:

- Productivity data points that deviated significantly from the trend of the time-series plot of the entire data set were considered outliers. In many cases, outlier data could be traced back to erroneous flow or pressure readings.
- Influent water quality data that deviated by more than three standard deviations from the mean was considered as potential outlier data.
- Permeate concentrations were typically too low to assess outliers directly. Thus, rejection data was used to identify outlier permeate data. Typically, permeate data associated with rejections that deviated by more than 10% from the average rejection value were considered as potential outlier data.

A summary of the issues identified during the raw data and outlier reviews and a count of the outliers identified and removed prior to analysis are documented for each study in the *Graphical Summary File* in the *Treatment Study Data Library* (USEPA, 2000).

5.3. Review of Base Analysis Results

Upon completion of the membrane study base analysis, the results were reviewed with respect to accuracy and reasonableness. To ensure accuracy, the data extractions from the *Data Collection Spreadsheets* that were used in the base analysis were compared with the source data. If discrepancies were found, the data extractions were corrected and the base analysis was repeated. An expert review of the base analysis output was performed to verify that the results were reasonable. During this expert review, the results of the base analysis were evaluated in the context of the expected performance of a given membrane treating water of a certain quality. DBP concentrations formed upon chlorination of the feed and permeate water were assessed with respect to the chlorination conditions and precursor levels in the waters. Finally, the results of the base analysis were compared with the results of any analyses reported by the utility or consultant that conducted the study. Any major discrepancies were documented in the *Graphical Summary File* in the *Treatment Study Data Library* (USEPA, 2000).

5.4. Review of Data Uploaded to the Database

The results of the base analysis were uploaded to the *ICR Treatment Study Database*. To ensure the accuracy of the upload process, the results in the database table were cross-checked against the upload files generated during the base analysis process. Spreadsheet tools were developed to assist in this review and resulted in a direct verification of over 80% of the data uploaded to the database. The remaining 20% of data that could not be directly verified was spot checked at a frequency of 10%.

6. Treatment Study Run Determination

One of the primary objectives of the base analysis was to reduce the large, complex data sets from each treatment study to data and information that could be managed in a database structure. During the base analysis, it was important to strike a balance between summarizing the data and maintaining important details in the raw data. These details are reflected in the variability observed over the course of a study, including changes in feed water quality, permeate water quality, system operation, chlorination conditions, or membrane type. To capture the impact of these changes on process performance, an expert analysis was conducted to divide each membrane study into smaller units, referred to as treatment study runs. Each treatment study run was assigned a corresponding treatment study run identification number (TSRunID).

A treatment study run is a period of operation in which the feed and permeate water quality is relatively stable. The permeate water quality can be affected by several factors such as membrane type, feed water quality, operating conditions and chlorination conditions. All of these factors were considered when dividing studies into treatment study runs.

Studies that were conducted quarterly were designed in a manner that predefines the treatment study runs. In general, each quarterly experiment for each membrane evaluated defines a treatment study run. During RBSMT and quarterly SEBST studies, two membranes were typically evaluated over four quarters of a one-year period, resulting in eight runs per study. Some RBSMT studies deviated from this standard experimental design. For example, there were a few RBSMT studies that evaluated four membranes over two quarters, but this variation still produced eight treatment study runs.

Studies that were conducted on a continuous basis, including pilot-scale, full-scale and LT-SEBST studies, were divided into treatment study runs based on changes in water quality, and those factors that impact permeate water quality. Specifically, the following guidelines were used to identify treatment study runs for long-term studies:

1. *Change in permeate water quality.* Significant changes in permeate water quality, especially the DBP precursors (TOC, UV and bromide), were used to define treatment study runs.
2. *Change in feed water quality.* Significant changes in feed water quality, especially the DBP precursors (TOC, UV and bromide), were used to define treatment study runs.
3. *Changes in SDS chlorination conditions*. During most long-term studies, the SDS conditions were varied to match actual distribution system conditions, with SDS incubation temperature experiencing the widest fluctuation. When significant changes in SDS conditions were made, a new treatment study run was defined.
4. *Changes in membrane type*. Long-term studies typically evaluated only a single membrane type; however, some studies evaluated additional membranes. A new treatment study run was always defined for each new membrane tested.
5. *Membrane replacement*. During some studies, severe fouling or membrane damage necessitated the replacement of one or more elements. If this resulted in a significant

change in system performance, especially with respect to the rejection characteristics of the membrane, then a new treatment study run was defined.

6. *Changes in pretreatment*. In many studies, pretreatment processes were varied in an attempt to minimize membrane fouling. During studies in which modification to pretreatment resulted in changes in feed or permeate water quality, a new treatment study run was defined.
7. *Changes in operating conditions*. Some studies varied operating conditions such as flux and recovery, and these changes can impact permeate water quality. However, during the actual analysis process, there were very few instances in which the changes in operating conditions impacted permeate water quality to the point that it was necessary to define a new treatment study run.

The treatment study run designations were critical elements of the base analysis since they defined the bounds over which data was analyzed and summarized. In the *Treatment Study Database*, the TSRunID is the field that links all of the data from a specific treatment study run, i.e., the TSRunID is the primary key in most database tables. The following sections summarize the analyses conducted on the membrane study data, and unless noted otherwise, all analyses were conducted on data within a given TSRunID.

7. Data Summaries for Membrane Studies

7.1. Summary of Influent Water Quality

A statistical summary of the influent water quality data was generated for each TSRunID, including the average, standard deviation, and 25th, 50th and 75th percentiles for each parameter. If "null" records are displayed for an influent water quality parameter, either the parameter was not measured during the study, or the data for that parameter was removed during one of the reviews discussed in Section 5.

Statistics for the following influent water quality parameters are included in the Influent Water Quality table of the database: temperature, pH, alkalinity, total dissolved solids, total hardness, calcium hardness, ammonia, bromide, TOC, UV, TSUVA, SDS-chlorine demand, SDS-TOX, SDS-THM4, SDS-HAA5, SDS-HAA6, SDS-HAA9, SDS-CHCl3, SDS-BDCM, SDS-DBCM, SDS-CHBr3, SDS-MCAA, SDS-DCAA, SDS-TCAA, SDS-MBAA, SDS-DBAA, SDS-BCAA, SDS-TBAA, SDS-CDBAA, and SDS-DCBAA.

7.2. Summary of SDS Conditions

A statistical summary of the SDS chlorination conditions was generated for each TSRunID, including the average, standard deviation, and 25th, 50th and 75th percentiles for each parameter. If "null" records are displayed for a SDS parameter, either the parameter was not measured during the study, or the data for that parameter was removed during one of the reviews discussed in Section 5.

Statistics for the following SDS parameters are included in the Simulated Distribution System Conditions table of the database: SDS incubation time, SDS incubation temperature, SDS pH and SDS free chlorine residual.

The statistics reported in the database were calculated from all feed and permeate SDS conditions reported during a specific TSRunID. The feed and permeate SDS data were combined in this manner since the same target SDS conditions were used for both feed and permeate samples.

Utilities were asked to report the measured chlorination conditions for each SDS test that was conducted; however, some utilities did not have actual SDS available and reported the target SDS conditions instead. In the database, target SDS conditions will have a standard deviation equal to 0.00. However, the converse is not necessarily true: a standard deviation of 0.00 does not necessarily imply that target conditions were reported. For example, the use of a temperature incubator may allow all SDS tests to be conducted at the same temperature within the precision of temperature measurements.

7.3. Summary of Membrane System Operating Conditions

A statistical summary of the system operating conditions was generated for each TSRunID, including the average, standard deviation, and 25th, 50th and 75th percentiles for each parameter. If "null" records are displayed for an operating parameter, either the parameter was not measured

during the study, or the data for that parameter was removed during one of the reviews discussed in Section 5.

Statistics for the following system operating parameters are included in the Membrane System Operating Conditions table of the database: system recovery, cross-flow velocity, recycle ratio, pH of the system feed, pH of the system concentrate, feed TDS rejection and bulk TDS rejection. Stage operating conditions for pilot- and full-scale studies are not reported in the database.

7.4. Summary of Membrane Pretreatment Process Information

Detailed information for the pretreatment processes used prior to nanofiltration was provided in the *Data Collection Spreadsheets.* However, standard nomenclature and abbreviations were not used, and this would limit a user's ability to query pretreatment information across studies in a meaningful manner. To correct this deficiency, the pretreatment data for each TSRunID was summarized using standard nomenclature.

The first step of this process was the extraction of the raw pretreatment information from the *Data Collection Spreadsheets.* The raw data was analyzed to determine standard process names, process chemicals, and dosing units for each process. Typically, the detailed process description was not modified during this analysis. A standard pretreatment code was also assigned to the entire pretreatment process train used during each TSRunID. For example, the pretreatment code "CONV" was used as an abbreviation for conventional treatment: the combination of coagulation, flocculation, sedimentation and filtration processes.

Once the pretreatment information was standardized, the process name, process description, chemical name, chemical dose, chemical dose units and pretreatment code were uploaded to the Pretreatment Information table of the database. A concatenated (combined) version of the pretreatment information was also generated and uploaded to the Membrane Study Design table of the database.

7.5. Summary of Field QA/QC Data

During the treatment studies, utilities were required to collect and analyze field duplicate samples for all measured parameters. For each pair of field duplicate data (i.e., the primary and duplicate values), a relative percent error (RPE_FDup) was calculated according to Equation 7-1:

$$RPE\_FDup = (|C_1 - C_2| / C_1) \times 100\% \qquad \text{Equation 7-1}$$

where C_1 is the concentration of the primary sample and C_2 is the concentration of the duplicate sample.

RPEs for field duplicates were only calculated when values for both the primary and duplicate samples were reported and detected above the MRL. If the primary, duplicate or both samples were below the MRL, then the RPE_FDup was not calculated for the data set.

A statistical summary of the field duplicate RPE data was generated for each water quality parameter for each study. The statistical summary includes the count, average, standard deviation, and 25th, 50th and 75th percentiles for each parameter. A record for a given parameter in a study may be "null" for any one of the following reasons: 1) the parameter was not measured during the study; 2) data for that parameter was removed during the review process; 3) duplicate analyses were not performed for that parameter; or 4) no values were measured above the MRL for that parameter.

The statistics reported in the database were calculated from all feed, permeate and concentrate field duplicate RPE data collected for a given water quality parameter. Unlike other parameters that are summarized over a TSRunID, the field duplicate RPE data is summarized over the entire study.

Statistics for RPE field duplicate data are included in the Field Duplicate QA/QC Data table of the database for the following water quality parameters: alkalinity, ammonia, bromide, calcium hardness, HAA5, HAA6, HAA9, pH, SDS-BCAA, SDS-BDCM, SDS-CDBAA, SDS-CHBr3, SDS-CHCl3, SDS-Cl2 Residual, SDS-DBAA, SDS-DBCM, SDS-DCAA, SDS-DCBAA, SDS-MBAA, SDS-MCAA, SDS-TBAA, SDS-TCAA, SDS-TOX, TDS, temperature, THM4, TOC, total hardness, turbidity and UV.

7.6. Summary of Analytical QA/QC Data

Laboratories performing analyses in support of the ICR treatment studies were required to perform QC analyses on many of the parameters monitored during the studies (USEPA, 1996b). Specifically, laboratories were required to analyze analytical duplicates, laboratory fortified matrix spike samples, and performance evaluation (PE) samples. Analytical duplicates were performed by conducting primary and duplicate analyses on a single sample, and calculating the relative percent error (RPE_ADup) according to Equation 7-2:

$$RPE\_ADup = (|C_1 - C_2| / C_{Avg}) \times 100\% \qquad \text{Equation 7-2}$$

where C_1 is the result from the primary analysis, C_2 is the result from the duplicate analysis, and C_{Avg} is the average of C_1 and C_2.

Laboratory fortified matrix spikes were conducted by adding a know quantity of the method analyte to a sample and measuring the concentrations of the analyte in both the fortified and unfortified samples. The difference between the concentrations of these two samples is the measured fortifying concentration. The percent recovery for laboratory fortified matrix spike samples (PR_LMS) was calculated according to Equation 7-3:

$$PR\_LMS = (C_M / C_T) \times 100\% \qquad \text{Equation 7-3}$$

where C_M is the measured fortifying concentration and C_T is the true fortifying concentration.

PE samples were supplied by a third party (typically USEPA for the ICR treatment studies), and the concentration of these samples was unknown to the laboratory. The PE samples were analyzed, and the measured concentration was reported to the third party. The percent recovery for the PE samples (PR_PE) was calculated according to Equation 7-4:

$$PR\_PE = (C_M / C_T) \times 100\% \qquad \text{Equation 7-4}$$

where C_M is the measured concentration of the PE sample and C_T is the true concentration of the PE sample.

Values for all of these QA/QC parameters were only calculated when the analyte was measured above the MRL. Results below the MRL typically only occurred for analytical duplicates, and if the primary, duplicate or both samples were below the MRL, then the RPE_ADup was not calculated for the data set.

Laboratories reported a statistical summary for each QA/QC parameter for each analyte that was measured. Normally, the QA/QC information was summarized over each individual study that the laboratory supported. However, four laboratories, CA013, FL029, OR001, and VA001, reported statistics summarizing the QA/QC data over all studies that the laboratory supported.

For each study, the QA/QC data for a specific water quality parameter is associated with one laboratory, one analytical method and one MRL. When more than one laboratory, method or MRL was used for an analyte during a study, multiple sets of QA/QC data are reported for that analyte.

The statistical summary includes the count, average, standard deviation, and 25^{th}, 50^{th} and 75^{th} percentiles for each QA/QC parameter. A record for a given parameter in a study may be "null" for any one of the following reasons: 1) the parameter was not measured during the study; 2) the QA/QC analysis was not performed for that parameter; 3) the QA/QC data was not available for that parameter, or 4) no values were measured above the MRL for that parameter. Additionally, percentiles were not reported for records in which the count was less than six.

Statistics for QA/QC data are included in the database for the following water quality parameters: bromide, HAA5, HAA6, HAA9, SDS-BCAA, SDS-BDCM, SDS-CDBAA, SDS-CHBr3, SDS-CHCl3, SDS-DBAA, SDS-DBCM, SDS-DCAA, SDS-DCBAA, SDS-MBAA, SDS-MCAA, SDS-TBAA, SDS-TCAA, SDS-TOX, THM4, TOC, and UV.

8. Water Quality Analysis

8.1. Overview of the Differential Water Quality Model

As discussed in Section 3 there are important differences among the protocols used to evaluate membrane technology under the ICR, which impact the permeate and concentrate water quality observed during these studies. Specifically, the range of recoveries and the use of concentrate recycle in some protocols complicated the direct comparison of permeate and concentrate water quality across studies. Furthermore, the water qualities from these studies do not necessarily reflect the permeate and concentrate water quality for a full-scale system where high recoveries are achieved through staging. To address these issues, a modeling approach was developed.

The Differential Water Quality Model was used with the study results to develop permeate and concentrate water quality data that is both comparable across studies and representative of full-scale performance. Conceptually, this model is a mathematical representation of a full-scale membrane array that is used to solve for equivalent, full-scale permeate and concentrate concentrations. Since flows, pressures and concentrations are constantly changing within the full-scale array, it was necessary to divide the array into a series of differential elements that are small enough such that conditions within each element are essentially constant. Equations describing this series of differential elements were solved over the length of the entire array to develop estimates of permeate and concentrate water quality from the system as well as individual stages. A detailed description of the Differential Water Quality Model is presented in the following sub-sections. Table 8-1 lists the nomenclature used in this model and throughout this section.

Table 8-1. Nomenclature used in the Differential Water Quality Model

Parameter	Definition
$(C_B)_i$	Concentration of a solute in bulk solution in differential element i
$(C_E)_i$	Concentration of a solute in the effluent stream from differential element i
C_F	Concentration of a solute in the feed stream to the model membrane array
$(C_I)_i$	Concentration of a solute in the influent stream to differential element i
(C_p)_avg	Mass transfer coefficient for sieving
$(C_p)_i$	Concentration of a solute in the permeate stream from differential element i
$(C_p)_{Stage\text{-}n}$	Concentration of a solute in the permeate stream from stage n
$(C_p)_{System}$	Concentration of a solute in the permeate stream from the membrane system
DE	Differential element of length Δx and width W_n in the model membrane array
F_S	Solute flux across the membrane
F_W	Water flux across the membrane
$(F_W)_i$	Water flux across the membrane in differential element i

$(M_S)_i$	Mass flow rate of a solute in the permeate stream from differential element i
$\Sigma(M_S)_{Stage\text{-}n}$	Mass flow rate of a solute in the permeate stream from stage n
$\Sigma(M_S)_{System}$	Mass flow rate of a solute in the permeate stream from the membrane system
$(NDP)_i$	Net driving pressure across the membrane in differential element i
P	Mass transfer coefficient for diffusion
P_F	Pressure of the feed stream entering the model membrane array
$(P)_i$	Feed-side pressure in differential element i
$P_{p\text{-}n}$	Permeate back-pressure in stage n
ΔP_n	Unit pressure drop per foot of membrane in stage n
$\#PV_n$	Number of parallel pressure vessels in stage n
$(Q_E)_i$	Effluent flow from differential element i
Q_F	Flow rate of the feed stream entering the model membrane array
$(Q_I)_i$	Influent flow to differential element i
$(\Delta Q_p)_i$	Permeate flow from differential element i
$\Sigma(Q_p)_i$	Cumulative permeate flow from all differential elements up to position $(x)_i$
$\Sigma(Q_p)_{Stage\text{-}n}$	Permeate flow from stage n
$\Sigma(Q_p)_{System}$	Permeate flow from the membrane system
$(R)_i$	Cumulative recovery from all differential elements up to position $(x)_i$
$(R_B)_i$	Rejection calculated relative to the bulk concentration in differential element i
$(R_B)_{Stage\text{-}n}$	Average of the bulk rejections for all differential elements in stage n
$(R_B)_{System}$	Average of the bulk rejections for all differential elements in the system
$(R_F)_i$	Rejection calculated relative to the feed concentration in differential element i
$(R_F)_{Stage\text{-}n}$	Feed rejection based on the permeate concentration from stage n
$(R_F)_{System}$	Feed rejection based on the permeate concentration from the system
SF	Average specific flux for a specific membrane and TSRunID
SF_T	Specific flux normalized to an average seasonal temperature
#S	Number of membrane sheets in an 8" by 40" element
T	Average seasonal temperature for a specific TSRunID
T_{norm}	Temperature to which SF data was normalized (average yearly temperature)

W	Mass transfer coefficient for convection
W_n	Width of a differential element in stage n
W_S	Width of a single membrane sheet in an 8" by 40" element
$(x)_i$	Position of the differential element along the axial direction of the array
Δx	Length of a differential element in the model membrane array
$(\Delta\pi)_i$	Osmotic pressure differential across the membrane in differential element i

8.2. Full-Scale Array Design for the Differential Water Quality Model

The first step of this approach was the development of a conceptual design for a full-scale array. Figure 8-1 shows the 3-stage array that was used in the model. This array consists of six 8" x 40" elements per pressure vessel with three pressure vessels in the first stage, two in the second stage and one in the third stage. The standard design assumptions for this array are listed in Table 8-2.

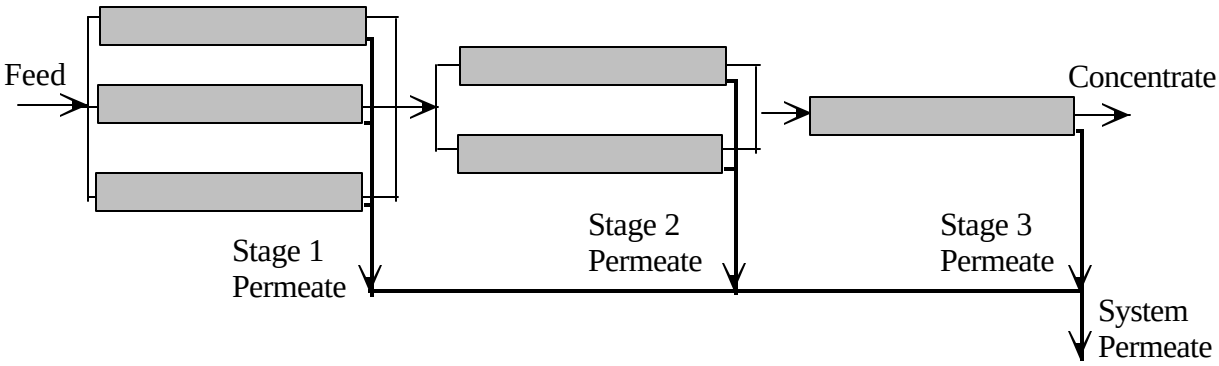

Figure 8-1. Schematic of the 3-stage Array used in the Differential Water Quality Model

Table 8-2 list a system recovery of 85% as a standard design parameter in the Differential Water Quality Model for all studies. This recovery was selected to represent a typical recovery that could be achieved in a nanofiltration array; however, the actual recovery that a system could achieve will depend on site-specific factors such as pretreatment, influent water quality and treatment objectives.

Two values are listed for the average permeate water flux in Table 8-2: 10 and 15 gallons per day per square foot of membrane area (gfd). A flux of 15 gfd was used for ground water studies, while a flux of 10 gfd was used for surface water studies. These flux values represent the average flux for each stage in the system, but higher and lower flux values occurred at the beginning and end of each stage, respectively. Permeate back-pressure on the individual stages was used to balance the fluxes and achieve the same average flux for each stage as well as provide 10 psi of pressure at the manifold for the combined permeate stream from the system.

Table 8-2. Full-scale array design assumptions for the Differential Water Quality Model

Design Parameter	Design Value
Configuration	3-stage array
Number of Stages	3
Number of pressure vessels in stage 1	3
Number of pressure vessels in stage 2	2
Number of pressure vessels in stage 3	1
Number of elements per pressure vessel	6
Element size	8" x 40"
Sheet length (ft)	2.8
System recovery (%)	85
Average permeate water flux (gfd)	10 (SW), 15 (GW)
ΔP for stage 1 (psi/ft)	2.2
ΔP for stage 2 (psi/ft)	1.2
ΔP for stage 3 (psi/ft)	1.2
P_p for system (psi)	10

To account for pressure losses in the system, a pressure loss per foot of membrane was assumed. Table 8-2 shows the assumed pressure loss, ΔP, for each stage. A higher pressure loss term was used for the first stage to account for the higher flows and pressures in that stage relative to stages 2 and 3. These pressure loss terms include pressure losses through the elements as well as losses due to manifold piping between stages. In an actual system, these manifold piping losses would occur between stages, but the model used a simplification and incorporated all pressure losses into a single pressure loss term.

Table 8-3 shows the range of design values for parameters that are specific to the membrane evaluated during the a TSRunID. These membrane specific design parameters include: membrane area, number of sheets per element, sheet width, minimum and maximum flow rates, and the specific flux. The sustained specific flux determined during the productivity analysis (discussed in Section 9) was used in the Differential Water Quality Model. To account for the impact of temperature variations on membrane productivity, the average sustained specific flux was normalized to the average temperature for the season in which the TSRunID was conducted.

Table 8-3. Range of values for study specific design parameters used in the Differential Water Quality Model

Parameter	Range of Design Values
Area of single element (ft^2)	330 - 400
Number of sheets per element	32 - 36
Sheet width (ft)	3.5 - 4.0
Minimum flow rate per element (gpd)	21,000 - 39,000
Maximum flow rate per element (gpd)	47,000 - 85,000
Specific Flux (gfd/psi)	0.073 - 0.494

8.3. Solute Mass Transfer Models used during Water Quality Analysis

To predict permeate and concentrate water quality from the Differential Water Quality Model, it was necessary to use a solute mass transfer model that describes the manner in which solutes are rejected by the membrane barrier. During the base analysis of the membrane studies, three solute mass transfer models were considered: diffusion, convection and sieving. The equations that describe these models are shown in Table 8-4.

Table 8-4. Solute mass transfer models used in the Differential Water Quality Model

Model	Relationship	Coefficient	Recovery **8**	Flux **8**
Diffusion	$F_S = P \times (C_B - C_p)$	$P = (F_W \times C_p) / (C_B - C_p)$	R_F **9**; R_B **!**	R_F **8**; R_B **8**
Convection	$F_S = W \times F_W \times C_B$	$W = (C_p / C_B)$	R_F **9**; R_B **!**	R_F **!**; R_B **!**
Sieving	$F_S = F_W \times C_p$	$(C_p)\_avg$ = constant	R_F **!**; R_B **8**	R_F **!**; R_B **!**

Note: = **8** *increase;* **9** *= decrease; – = no change*

A diffusion model assumes that the concentration gradient across the membrane is the driving force for mass transfer. The permeation coefficient, *P*, relates the solute flux to the concentration gradient and can be calculated from the measured flux, permeate concentration and bulk concentration.

A convection model assumes that the solute is transported across the membrane with the bulk solution, and that the pressure gradient is the driving force for solute permeation. The convective hindrance factor, *W*, is a relative measure of the transport of a solute compared to transport of the bulk solution, and can be calculated from the measured permeate and bulk concentrations.

A sieving model assumes that solutes are rejected solely on the basis of size exclusion. A component that is rejected by sieving will have a constant permeate concentration independent of operation or influent concentration. The sieving coefficient is simply the average of the measured permeate concentrations.

The mass transfer coefficient for each of these models was calculated for each set of data collected over the study using paired data, e.g., feed/permeate pairs. The diffusion, convection and sieving coefficients for each water quality parameter were averaged over each TSRunID in a study.

In order to apply the Differential Water Quality model, it was necessary to select an appropriate mass transfer model for each water quality parameter and TSRunID. This was accomplished through an expert analysis of the raw permeate and feed water quality data and operational data in a TSRunID. During this analysis, the impact of recovery on permeate water quality was assessed through the RBSMT recovery experiments and the stage data from pilot- and full-scale studies. As shown in Table 8-4, the three mass transfer models respond differently to changes in recovery and flux. Both diffusion and convection models predict changes in the feed rejection with changes in recovery, but only the diffusion model is sensitive to changes in flux. The sieving model predicts no change in feed rejection with changing recovery or flux; however, bulk rejection is predicted to increase with increasing recovery. These trends were used to develop the following guidelines for selecting an appropriate permeation model:

1. A sieving model was typically selected for water quality parameters with permeate concentrations that did not change with recovery.
2. A sieving model was typically selected for water quality parameters with permeate concentrations that were not detected above the minimum reporting level.
3. In a few cases, the measured permeate concentrations of bromide, alkalinity, ammonia and some brominated DBPs were slightly higher than the corresponding feed concentrations. In these cases, a sieving model was selected.
4. When the permeate concentration of a specific parameter was found to be sensitive to recovery, either a diffusion or a convection model was selected. Typically, the flux data from the treatment studies was not sufficient to make a determination between diffusion or convection, so other guidelines were used to select between these two models.
5. When selecting between diffusion and convection models, the predicted permeate and concentrate concentrations for these two models were compared to each other and to the raw water quality data to determine which model produced the expected trends.
6. When diffusion and convection models both produced acceptable results for inorganic parameters, diffusion was selected over convection since diffusion is a more widely accepted permeation model for inorganic solutes.
7. A secondary criteria used to select between convection and diffusion was maintaining consistency with respect to the permeation models selected for groups of parameters. For example, if a convection model was selected for THM4, and both convection and diffusion gave acceptable results for the THM species, convection would be selected for the species to maintain consistency.

8.4. Differential Water Quality Model Calculations

The Differential Water Quality Model mathematically divides the full-scale array described in Section 8.2 into a series of differential elements along the axial direction of the array (i.e., in the direction of feed flow). A schematic of a differential element is shown in Figure 8-2. The length of the differential element was selected to be small enough, 0.1 feet, such that the flows, pressures and concentration in each differential element could be treated as constant values.

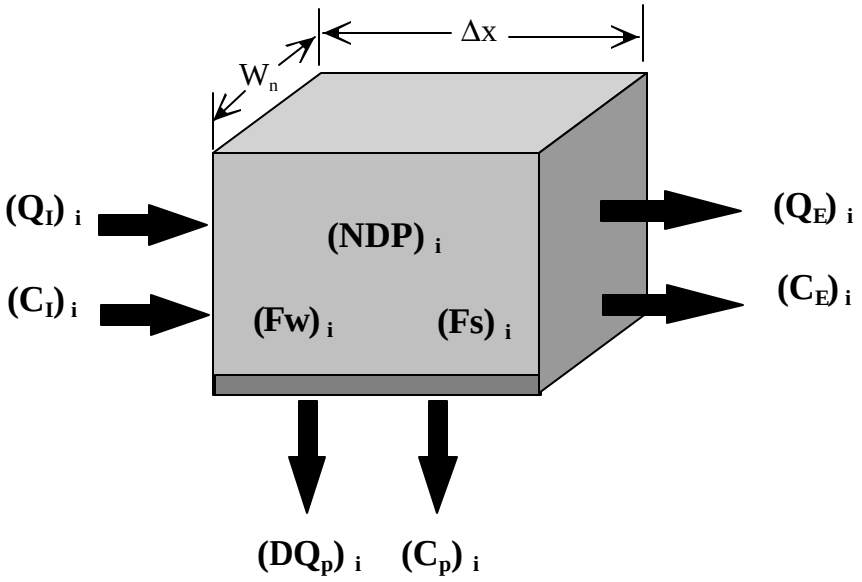

Figure 8-2. Schematic of a differential element used in the Differential Water Quality Model

Mass balance and continuity relationships were used to calculate the concentrations, flows and pressures in each differential element of the model array; however, an iterative solution is required since the parameters are interrelated. The equations and initial conditions for the Differential Water Quality Model are listed in Table 8-5. Once the effluent conditions from a differential element were determined through these iterative calculations, they became the influent conditions to the following differential element. The equations for each differential element were solved in this manner for the entire array, yielding flows, concentrations and pressures for the system and individual stages.

Equation 8-9 was used to calculate the feed side pressure at any location $(x)_i$ in the array. The influent or concentrate pressure for the system is equal to the pressure in the differential element at the beginning or end of the system, respectively, and the influent or concentrate pressure for an individual stage are determined in a similar manner. The permeate back-pressure for a stage was selected to balance the fluxes across the three stages. The minimum permeate back-pressure for a stage was set at 10 psi to provide a system permeate pressure of 10 psi. The average permeate back-pressure for the system was determined from a flow-weighted average of the back-pressures for each stage.

Table 8-5. Initial conditions and equations for the Differential Water Quality Model

EQ #	Parameter	Initial Condition	General Equation
8-1	$(x)_i$	$(x)_1 = \Delta x$	$(x)_i = (x)_{i-1} + \Delta x$
8-2	Δx	Same as general EQ	$\Delta x = 0.1$
8-3	W_n	Same as general EQ	$W_n = W_S \times \#S \times \#PV_n$
8-4	$(Q_I)_i$	$(Q_I)_1 = Q_F$	$(Q_I)_i = (Q_E)_{i-1}$
8-5	$(\Delta Q_p)_i$	$(\Delta Q_p)_1 = (F_W)_i \times W_n \times (x)_1$	$(\Delta Q_p)_i = (F_W)_i \times W_n \times \Delta x$
8-6	$\Sigma(Q_p)_i$	$\Sigma(Q_p)_1 = (\Delta Q_p)_1$	$\Sigma(Q_p)_i = (\Delta Q_p)_i + \Sigma(Q_p)_{i-1}$
8-7	$(Q_E)_i$	Same as General Equation	$(Q_E)_i = (Q_I)_i - (\Delta Q_p)_i$
8-8	$(R)_i$	Same as General Equation	$(R)_i = \Sigma(Q_p)_i / Q_F$
8-9	$(P)_i$	$(P)_1 = P_F$	$(P)_i = (P)_{i-1} - (½ \times \Delta x \times \Delta P_n)$
8-10	$(\Delta\pi)_i$	Same as general EQ	$(\Delta\pi)_i = 0.01 \times [(TDS_B)_i - (TDS_p)_i]$
8-11	$(NDP)_i$	Same as general EQ	$(NDP)_i = (P)_i - (\Delta\pi)_i - P_{p-n}$
8-12	SF_T	Same as general EQ	$SF_T = SF \times 1.03\text{^}(T - T_{norm})$
8-13	$(F_W)_i$	Same as general EQ	$(F_W)_i = SF_T \times (NDP)_i$
8-14	$(C_I)_i$	$(C_I)_1 = C_F$	$(C_I)_i = (C_E)_{i-1}$
8-15	$(C_p)_i$	Same as general EQ	Diffusion: $(C_p)_i = [(C_B)_i \times P] / [(F_W)_i + P]$ Convection: $(C_p)_i = (C_B)_i \times W$ Sieving: $(C_p)_i = (C_p)\_avg$
8-16	$(C_E)_i$	Same as general EQ	$(C_E)_i = [(Q_I)_i \times (C_I)_i - (\Delta Q_p)_i \times (C_p)_i] / [(Q_E)_i]$
8-17	$(C_B)_i$	Same as general EQ	$(C_B)_i = ½ \times ((C_I)_i + (C_E)_i)$
8-18	$(R_F)_i$	Same as general EQ	$(R_F)_i = [(C_F - (C_p)_i) / C_F] \times 100\%$
8-19	$(R_B)_i$	Same as general EQ	$(R_B)_i = [((C_B)_i - (C_p)_i) / (C_B)_i] \times 100\%$
8-20	$(M_S)_i$	Same as general EQ	$(M_S)_i = (\Delta Q_p)_i \times (C_p)_i$
8-21	$(C_p)_{System}$	NA	$(C_p)_{System} = \Sigma(M_S)_{System} / \Sigma(Q_p)_{System}$
8-22	$(C_p)_{Stage-n}$	NA	$(C_p)_{Stage-n} = \Sigma(M_S)_{Stage-n} / \Sigma(Q_p)_{Stage-n}$
8-23	$(R_F)_{System}$	NA	$(R_F)_{System} = [(C_F - (C_p)_{System}) / C_F] \times 100\%$
8-24	$(R_F)_{Stage-n}$	NA	$(R_F)_{Stage-n} = [(C_F - (C_p)_{Stage-n}) / C_F] \times 100\%$
8-25	$(R_B)_{System}$	NA	Arithmetic average of $(R_B)_i$ over the system
8-26	$(R_B)_{Stage-n}$	NA	Arithmetic average of $(R_B)_i$ over stage n

The feed and concentrate flow rates for the system are determined in the same manner as the feed and concentrate pressures. The permeate flow rate from the system or a stage was determined

from Equation 8-6 which calculates the cumulative permeate flow rate at position $(x)_i$ in the array. The permeate flow rate from the system is the cumulative permeate flow for the entire array. The permeate flow rate from a stage was calculated as the difference between the cumulative flow at the end of that stage and the permeate flow rate from any preceding stages. For example, the permeate flow rate from stage 3 is equal to the cumulative permeate flow rate at the end of stage 3 minus the permeate flow rates from stages 1 and 2.

The concentrate concentration from the system or a stage was determined from Equation 8-16 which calculates the effluent concentration from a differential element at position $(x)_i$. The concentrate concentration for the system is equal to the concentrate concentration from the final differential element in the system. Similarly, the concentrate concentration from a stage is equal to the concentrate concentration from the final differential element in that stage.

The permeate concentration from the system was calculated using Equations 8-20 and 8-21. Equation 8-20 calculates the mass flow rate of a solute from a differential element, and Equation 8-21 sums these mass flow rates over the entire system and divides by the system permeate flow to determine the permeate concentration from the system. Permeate concentrations from a stage are calculated in a similar manner using Equations 8-20 and 8-22.

Feed and bulk rejections were calculated for the system and stages using Equations 8-23 through 8-26. The feed rejection for the system or a stage was calculated from the feed concentration and the permeate concentration from the system or stage, respectively. The bulk rejection for the system is calculated as the average of the bulk rejections for the differential elements over the entire array. The bulk rejection for a stage is calculated in a similar manner.

8.5. Feed/Permeate Blending Calculations

In many cases, the permeate water quality from a nanofiltration process will exceed the treatment objective, and a portion of the feed stream can bypass the nanofiltration process and blend with the permeate stream while still meeting the treatment objective. The practice of feed/permeate blending has several benefits including reduced capital and operating costs, increased product water stability, and reduced post-treatment requirements.

The *Membrane Module* of the database contains an interface that allows a user to calculate blended water quality for a specified treatment objective. The algorithm used to calculated the blended water quality is based on a mass balance that relates the blended concentration to the proportion of feed and permeate flows in the blended water. The blending algorithm is as follows:

1. The user enters a concentration for the target water quality parameter (C_T).
2. The average feed concentration (C_F) and predicted permeate concentration (C_p) for the target water quality parameter are used to compute the blend ratio:

$$r_{blend} = (Q_p/Q_T) = (C_F - C_T) / (C_F - C_p) \qquad \text{Equation 8-27}$$

where: r_{blend} is the minimum blend ratio; Q_T is the total flow (i.e., permeate plus by-passed feed); Q_p is the minimum permeate flow required to meet the treatment objective.

3. The calculated blend ratio is used to compute the blended concentration (C_{blend}) of other water quality parameters:

$$C_{blend} = (1 - r_{blend}) \times C_F + r_{blend} \times C_p \qquad \text{Equation 8-28}$$

The value of the blend ratio only has physical significance in the range from zero to one, inclusive. A blend ratio of zero results in a blended concentration that is equal to the feed concentration while a blend ratio of one results in a blended concentration that is equal to the permeate concentration.

A blend ratio of zero will occur under one of two scenarios. First, if the feed concentration is less than the target concentration then nanofiltration is not required to meet the treatment objective. Under the second scenario, the permeate concentration is greater than the feed concentration. In this case, nanofiltration considered to be an inappropriate technology to meet the target treatment objective. This latter scenario is unlikely but possible.

A blend ratio of one will occur when the permeate concentration is greater than or equal to the target concentration. In this case, complete treatment by nanofiltration cannot meet the treatment objective.

Only some parameters are considered during blending analysis: alkalinity, ammonia, bromide, calcium hardness, SDS-Chlorine demand, SDS-HAA5, SDS-HAA6, SDS-HAA9, SDS-THM4, SDS-TOX, TOC, total dissolved solids, total hardness and UV. The parameters that are not considered during blending analysis include all SDS-THM and SDS-HAA species. The decision not to include the THM and HAA species in the blending calculations is based on the results of a study demonstrating that the mass balance model does not always result in accurate predictions for DBP species (Gusses, et al., 1999).

8.6. Pressure Estimates from the Differential Water Quality Model

As discussed in Section 8.4, the Differential Water Quality Model was used to calculate feed-side pressures throughout the full-scale array. By evaluating the feed-side pressure at specific points through a full-scale array, estimates of the feed and concentrate pressures were generated for the system and the individual stages. These predicted pressures are based on the 3-stage array design assumptions discussed in Section 8.2, as well as study specific factors such as the specific flux and temperature. The Differential Water Quality Model used the sustained specific flux generated during the productivity analysis for a given study to calculate the system and stage pressures. Equation 8-12 was used to normalize the specific flux to the average temperature over a given TSRunID resulting in predicted pressures that reflect seasonal changes in temperature. In summary, the predicted pressures are specific to the membrane, operating conditions and temperature evaluated over a TSRunID, but the pressures have been scaled up to a full-scale array.

The pressure data generated for each TSRunID is summarized in Table 8-6. This data was uploaded to the database along with the output from the productivity analysis discussed in Section 9. A distinction should be made between these predicted pressures, which are generated from the Differential Water Quality Model, and the other productivity parameters which are derived from a direct analysis of the raw productivity data.

Table 8-6. Predicted pressures calculated from the Differential Water Quality Model

Pressure	Description
Influent pressure	Influent pressures were calculated from the Differential Water Quality Model for the system, stage 1, stage 2 and stage 3.
Concentrate pressure	Concentrate pressures were calculated from the Differential Water Quality Model for the system, stage 1, stage 2 and stage 3.
Permeate pressure	Permeate pressure for the individual stages were selected by the analyst to balance the flux from each stage. The system permeate pressure is a flow-weighted average of the stage permeate pressures.
Osmotic pressure	Osmotic pressures were calculated from TDS concentrations predicted by the Differential Water Quality Model for the system, stage 1, stage 2 and stage 3.

8.7. Water Quality Data Uploaded to the Treatment Study Database

Four database tables are populated with results from the base analysis of the water quality data. These tables contain the predicted permeate concentrations, predicted concentrate concentrations, solute mass transfer coefficients used in the Differential Water Quality Model and the configuration of the full-scale array used in the Differential Water Quality Model. Tables 8-7 through 8-10 summarize the fields uploaded to each of these tables.

Table 8-7. Fields uploaded to the Predicted Permeate Water Quality table of the database

Field Name	Description
Stg_Num	Abbreviation used to indicate whether the data is associated with the system or a stage: 0 = system, 1 = stage 1, 2 = stage 2, and 3 = stage 3.
Temp_P (^{o}C)	Temperature of the permeate stream over the TSRunID for the system or an individual stage as indicated by the Stg_Num.
pH_P	pH of the permeate stream over the TSRunID for the system or an individual stage as indicated by the Stg_Num.
Turb_P (NTU)	Turbidity of the permeate stream over the TSRunID for the system or an individual stage as indicated by the Stg_Num.
Alk_P (mg/L CaCO3)	Predicted alkalinity of the permeate stream over the TSRunID for the system or an individual stage as indicated by the Stg_Num.

TDS_P (mg/L)	Predicted TDS in the permeate stream over the TSRunID for the system or an individual stage as indicated by the Stg_Num.
TH_P (mg/L CaCO3)	Predicted total hardness in the permeate stream over the TSRunID for the system or an individual stage as indicated by the Stg_Num.
CaH_P (mg/L CaCO3)	Predicted calcium hardness in the permeate stream over the TSRunID for the system or an individual stage as indicated by the Stg_Num.
NH3_P (mg NH3-N/L)	Predicted ammonia in the permeate stream over the TSRunID for the system or an individual stage as indicated by the Stg_Num.
Br_P (µg/L)	Predicted bromide in the permeate stream over the TSRunID for the system or an individual stage as indicated by the Stg_Num.
TOC_P (mg/L)	Predicted TOC in the permeate stream over the TSRunID for the system or an individual stage as indicated by the Stg_Num.
Br-TOC_P (µg/mg)	Predicted bromide-to-TOC ratio in the permeate stream over the TSRunID for the system or an individual stage as indicated by the Stg_Num.
UV_P (1/cm)	Predicted UV in the permeate stream over the TSRunID for the system or an individual stage as indicated by the Stg_Num.
TSUVA_P (L/(mg*m))	Predicted total specific UV absorbance in the permeate stream over the TSRunID for the system or an individual stage as indicated by the Stg_Num.
Cl2D_P (mg/L)	Predicted chlorine demand in the permeate stream over the TSRunID for the system or an individual stage as indicated by the Stg_Num.
TOX_P (µg Cl/L)	Predicted total organic halide in the permeate stream over the TSRunID for the system or an individual stage as indicated by the Stg_Num.
THM4_P (µg/L)	Predicted trihalomethane sum (4) in the permeate stream over the TSRunID for the system or an individual stage as indicated by the Stg_Num.
HAA5_P (µg/L)	Predicted haloacetic acid sum (5) in the permeate stream over the TSRunID for the system or an individual stage as indicated by the Stg_Num.
HAA6_P (µg/L)	Predicted haloacetic acid sum (6) in the permeate stream over the TSRunID for the system or an individual stage as indicated by the Stg_Num.
HAA9_P (µg/L)	Predicted haloacetic acid sum (9) in the permeate stream over the TSRunID for the system or an individual stage as indicated by the Stg_Num.
CHCl3_P (µg/L)	Predicted chloroform in the permeate stream over the TSRunID for the system or an individual stage as indicated by the Stg_Num.

BDCM_P (µg/L)	Predicted bromodichloromethane in the permeate stream over the TSRunID for the system or an individual stage as indicated by the Stg_Num.
DBCM_P (µg/L)	Predicted dibromochlormethane in the permeate stream over the TSRunID for the system or an individual stage as indicated by the Stg_Num.
CHBr3_P (µg/L)	Predicted bromoform in the permeate stream over the TSRunID for the system or an individual stage as indicated by the Stg_Num.
MCAA_P (µg/L)	Predicted monochloroacetic acid in the permeate stream over the TSRunID for the system or an individual stage as indicated by the Stg_Num.
DCAA_P (µg/L)	Predicted dichloroacetic acid in the permeate stream over the TSRunID for the system or an individual stage as indicated by the Stg_Num.
TCAA_P (µg/L)	Predicted trichloroacetic acid in the permeate stream over the TSRunID for the system or an individual stage as indicated by the Stg_Num.
MBAA_P (µg/L)	Predicted monobromoacetic acid in the permeate stream over the TSRunID for the system or an individual stage as indicated by the Stg_Num.
DBAA_P (µg/L)	Predicted dibromoacetic acid in the permeate stream over the TSRunID for the system or an individual stage as indicated by the Stg_Num.
BCAA_P (µg/L)	Predicted bromochloroacetic acid in the permeate stream over the TSRunID for the system or an individual stage as indicated by the Stg_Num.
TBAA_P (µg/L)	Predicted tribromoacetic acid in the permeate stream over the TSRunID for the system or an individual stage as indicated by the Stg_Num.
CDBAA_P (µg/L)	Predicted chlorodibromoacetic acid in the permeate stream over the TSRunID for the system or an individual stage as indicated by Stg_Num.
DCBAA_P (µg/L)	Predicted dichlorobromoacetic acid in the permeate stream over the TSRunID for the system or an individual stage as indicated by Stg_Num.

Table 8-8. Fields uploaded to the Predicted Concentrate Water Quality table of the database

Field Name	Description
Stg_Num	Abbreviation used to indicate whether the data is associated with the system or a stage: 0 = system, 1 = stage 1, 2 = stage 2, and 3 = stage 3.
Temp_C (°C)	Temperature of the concentrate stream over the TSRunID for the system or an individual stage as indicated by the Stg_Num.
pH_C	pH of the concentrate stream over the TSRunID for the system or an individual stage as indicated by the Stg_Num.
Turb_C (NTU)	Turbidity of the concentrate stream over the TSRunID for the system or an individual stage as indicated by the Stg_Num.
Alk_C (mg/L CaCO3)	Predicted alkalinity of the concentrate stream over the TSRunID for the system or an individual stage as indicated by the Stg_Num.
TDS_C (mg/L)	Predicted TDS in the concentrate stream over the TSRunID for the system or an individual stage as indicated by the Stg_Num.
TH_C (mg/L CaCO3)	Predicted total hardness in the concentrate stream over the TSRunID for the system or an individual stage as indicated by the Stg_Num.
CaH_C (mg/L CaCO3)	Predicted calcium hardness in the concentrate stream over the TSRunID for the system or an individual stage as indicated by the Stg_Num.
NH3_C (mg NH3-N/L)	Predicted ammonia in the concentrate stream over the TSRunID for the system or an individual stage as indicated by the Stg_Num.
Br_C (µg/L)	Predicted bromide in the concentrate stream over the TSRunID for the system or an individual stage as indicated by the Stg_Num.
TOC_C (mg/L)	Predicted TOC in the concentrate stream over the TSRunID for the system or an individual stage as indicated by the Stg_Num.
UV_C (1/cm)	Predicted UV in the concentrate stream over the TSRunID for the system or an individual stage as indicated by the Stg_Num.
TSUVA_C (L/(mg*m))	Predicted total specific UV absorbance in the concentrate stream over the TSRunID for the system or an individual stage as indicated by the Stg_Num.
Cl2D_C (mg/L)	Predicted chlorine demand in the concentrate stream over the TSRunID for the system or an individual stage as indicated by the Stg_Num.

Every TSRunID has a predicted permeate concentration for each parameter listed in Table 8-7 that was measured during the TSRunID. Similarly, there is a predicted concentrate concentration for

each parameter listed in Table 8-8. Since the Differential Water Quality Model does not rely on concentrate concentrations to predict water quality, there are predicted concentrate concentrations for parameters that were not measured in the concentrate stream during the study.

Permeate and concentrate concentrations were predicted for the system as well as the three individual stages in the model full-scale array. Only one set of permeate and concentrate concentrations was calculated for each parameter over each TSRunID. These concentrations are based on the average influent concentration and average mass transfer coefficient over the TSRunID; thus, these predicted values represent a central tendency for permeate and concentrate water quality from a full-scale array.

Table 8-9. Fields uploaded to the Model Coefficients table of the database

Field Name	Description
Stg_Num	Abbreviation used to indicate whether the data is associated with the system or a stage. MTC data is only reported for the system (Stg_Num = 0).
WQParam	Water quality parameter for which the model coefficient data is reported.
MTC_Type	The type of the mass transfer coefficient used in the Differential Water Quality model: convection, diffusion, or sieving.
MTC_Unit	The units for the mass transfer coefficient: no units for convection, gfd for diffusion and units of the parameter for sieving.
MTC_Value	The average value of the mass transfer coefficient.
MTC_Var	Variability around the average mass transfer coefficient value (measured as the standard deviation around the mean).

The Model Coefficients table of the database contains information about the mass transfer coefficients used in the Differential Water Quality Model. Table 8-9 lists the fields that are included in this database table. For each water quality parameter modeled, the table reports the type, units, value and variability for the mass transfer coefficient used in the Differential Water Quality Model is reported. The Stg_Num field is included in this table, but is always equal to "0" since a single MTC value was used to predict stage and system water quality for each parameter and TSRunID.

Table 8-10. Fields uploaded to the Full-Scale Array Configuration table of the database

Field Name	Description
Stg_Num	Abbreviation used to indicate whether the data is associated with the system or a stage: 0 = system, 1 = stage 1, 2 = stage 2, and 3 = stage 3.
NFSize	The size of the membrane element used in the Differential Water Quality Model. The element size is always 8x40.
A_elm (ft2)	The area of the 8x40 element used in the Differential Water Quality Model. The area is specific to the membrane evaluated during the TSRunID.
A_s (ft2)	The membrane area of the system or an individual stage as indicated by the Stg_Num. This membrane area is based on the A_elm and N_elm used in the Differential Water Quality Model.
N_elm	The number of 8x40 elements in the system or stage as indicated by the Stg_Num. The number of elements is always 18 in stage 1, 12 in stage 2, 6 in stage 3 and 36 in the system.
N_PV	The number of pressure vessels in the system or stage as indicated by the Stg_Num. The number of pressure vessels is always 3 in stage 1, 2 in stage 2, 1 in stage 3 and 6 in the system.
R (%)	The recovery for the system or a stage as indicated by the Stg_Num. The recovery for the stages varies, but the system recovery is always 85%.

Some of the design assumptions used for the full-scale array are reported in the Full-Scale Array Configuration table of the database. The fields included in this table are listed in Table 8-10 and include the size and area of an element, the membrane area in the system/stage, the number of elements in the system/stage, the number of pressure vessels in the system/stage, and the recovery of the system/stage. As indicated in Table 8-10, the NFSize, N_elm, and N_PV are constant across all TSRunIDs. Additionally, the system recovery was held constant at 85% for all TSRunIDs.

9. Productivity Analysis

9.1. Overview of Productivity Analysis

The objective of the productivity analysis was to reduce the large amount of flow and pressure data from each study to a few key indicators of membrane productivity. Specifically, these productivity parameters include the sustained flux, sustained specific flux, rate of specific flux decline, the cleaning interval and the cleaning efficiency. Also, as discussed in Section 8.6, estimates of the influent, concentrate, permeate and osmotic pressures were derived from the Differential Water Quality Model.

The following approach was used to develop this productivity information from the raw membrane study data. First, the productivity data for an entire study was divided into operational cycles that were bounded by two consecutive cleaning events. The rate of specific flux decline, cleaning interval and cleaning efficiency were then computed for each operational cycle. The cycle-by-cycle productivity data was used in conjunction with pretreatment and operational data to determine the period of stable performance for that study. The period of stable performance is defined as a period over which pretreatment and system operation is relatively stable. Finally, the sustained productivity data was calculated from the results of the cycle-by-cycle analysis over the period of stable performance. A list of the nomenclature used in the productivity analysis is shown in Table 9-1, and a detailed description of the analysis is presented in this section.

9.2. Cycle-by-Cycle Productivity Analysis

Over the course of a membrane treatment study, temporal data including flow, pressure and temperature were collected. These parameters were used to calculate the temperature-normalized specific flux (SF_{Norm}), which was the primary parameter for productivity analysis. This parameter is normalized with respect to membrane area, net driving pressure and temperature; thus, temporal changes in the SF_{Norm} can be attributed to a decline in productivity due to membrane fouling.

The first step of the productivity analysis was the calculation of the temperature-normalized specific flux from the raw data using the equations listed in Table 9-2. The net driving pressure was calculated using Equations 9-1 and 9-2. The flux was calculated from the permeate flow rate, membrane area and Equation 9-3. The specific flux was calculated according to Equation 9-4, and was normalized to an average temperature using Equation 9-5.

The chemical cleaning events performed during the study were identified and used to establish the operational cycles in the study. Operational cycles were bounded by two consecutive cleaning events, except for the first operational cycle which was bounded by the start of the study and the first cleaning event. The temperature-normalized specific flux data was plotted as a function of operating time and divided into operational cycles, as shown in Figure 9-1.

Table 9-1. Nomenclature used in the productivity analysis

Parameter	Definition
NDP	Average net driving pressure across the membrane (psi)
P_I	Influent pressure (psi)
P_C	Concentrate pressure (psi)
P_p	Permeate back-pressure (psi)
$\Delta\pi$	Osmotic pressure differential across the membrane (psi)
TDS_I	Influent total dissolved solids concentration (mg/L)
TDS_C	Concentrate total dissolved solids concentration (mg/L)
TDS_p	Permeate total dissolved solids concentration (mg/L)
F_W	Water flux across the membrane (gfd)
Qp	Permeate flow rate (gpd)
A	Membrane area (ft^2)
SF	Specific flux (gfd/psi)
SF_{Norm}	Specific flux normalized to the average yearly temperature (gfd/psi)
T_{Meas}	Temperature measurement corresponding with flow and pressure readings (^oC)
T_{Norm}	Average yearly temperature used to normalize specific flux data (^oC)
$(SF_{Norm})_B$	Baseline specific flux in an operational cycle (gfd/psi)
$(SF_{Norm})_F$	Final specific flux in an operational cycle (gfd/psi)
$(SF_{Norm})_{Cln}$	Specific flux after a cleaning event in an operational cycle (gfd/psi)
$\Delta SF/\Delta t$	Time rate of specific flux decline (gfd/psi/day)

Table 9-2. Equations used during cycle-by-cycle productivity analysis

EQ #	Parameter	General Equation
9-1	NDP	$NDP = (P_I + P_C)/2 - \Delta\pi - P_p$
9-2	$\Delta\pi$	$\Delta\pi = 0.01 \times ((TDS_I + TDS_C)/2 - TDS_p)$
9-3	F_W	$F_W = Q_p / A$
9-4	SF	$SF = F_W / NDP$
9-5	SF_{Norm}	$SF_{Norm} = SF \times 1.03\text{^}(T_{Norm} - T_{Meas})$
9-6	CI	$CI = (0.15 \times (SF_{Norm})_B) / (\Delta SF/\Delta t)$
9-7	CE	$CE = ((SF_{Norm})_{Cln} - (SF_{Norm})_F) / ((SF_{Norm})_B - (SF_{Norm})_F) \times 100\%$

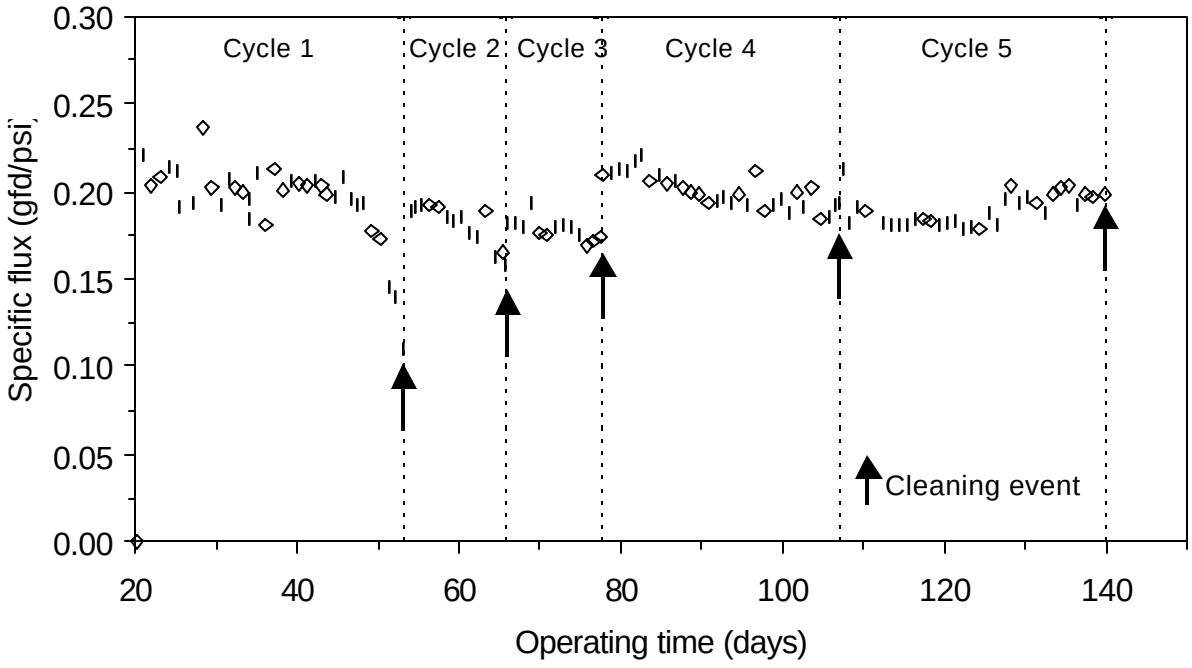

Figure 9-1. Specific flux decline plot divided into operational cycles

Figure 9-2 shows an example of a specific flux plot for a single operational cycle and the key points on the curve that were used in the productivity analysis. The baseline specific flux (SF_B) served as the reference point for productivity data analysis over a cycle. For cases in which the specific flux curve was linear over the entire cycle, the first point in the cycle was defined as the baseline specific flux. However, in many cases the specific flux curve exhibited a sharp initial decline that occurred after a cleaning event, as shown in Figure 9-2. This rapid initial decline typically occurred over a short period of time and was not considered representative of typical performance. Therefore, the data from this period of rapid initial decline was excluded from analysis by defining the baseline specific flux at the start of the linear portion of the specific flux curve. A final specific flux (SF_F) was also defined for each operational cycle and typically occurred immediately before the cleaning event that defined the end of a cycle.

The time rate of specific flux decline ($\Delta SF/\Delta t$) was calculated as the slope of the data between the baseline and final specific flux values. The rate of specific flux decline was used in Equation 9-6 to project the cleaning interval. This equation assumes that a cleaning event would be triggered by a 15% decline in the temperature-normalized specific flux relative to the baseline value.

An important consideration with respect to the interpretation of the rate of specific flux decline and the cleaning interval is the sensitivity of these parameters to the selection of the baseline value. Since the rate of specific flux decline was typically a very small value, a small change in the baseline specific flux could have a significant impact on the rate of specific flux decline and the cleaning interval.

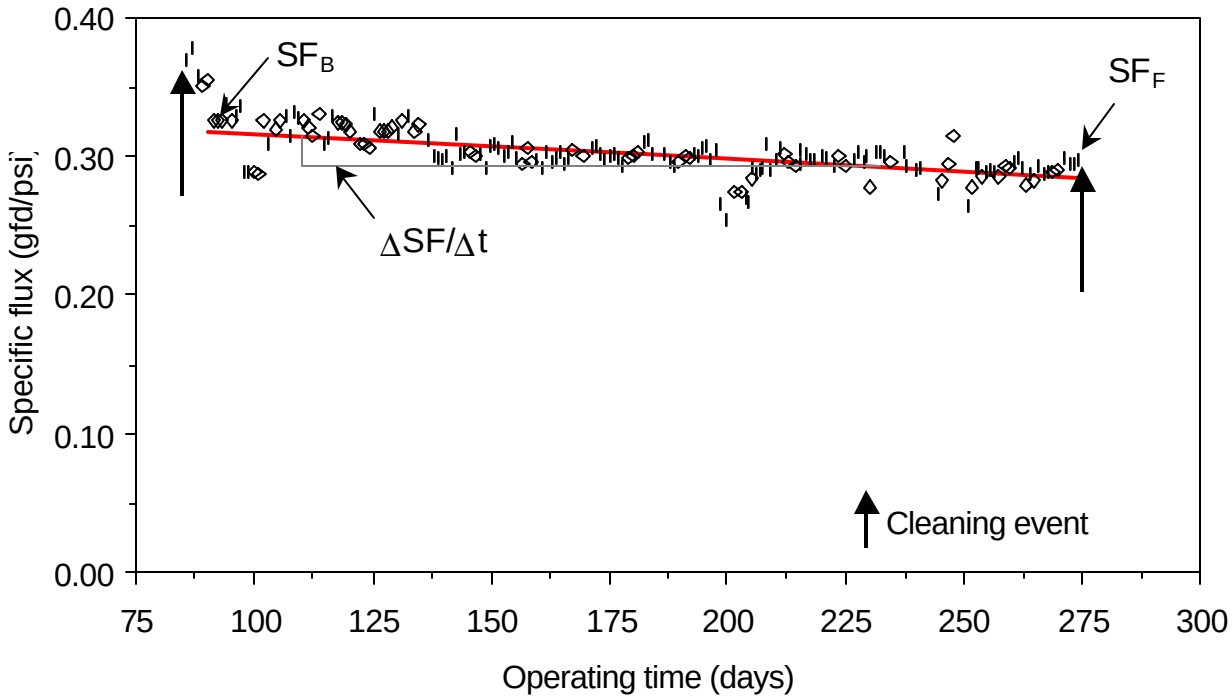

Figure 9-2. Specific flux decline plot for a single operational cycle

The cleaning efficiency was calculated during the cycle-by-cycle productivity analysis according to Equation 9-7. This parameter is defined as the ratio of the specific flux recovered after cleaning to the specific flux lost over the operational cycle and is expressed as a percentage. Typically, the calculated cleaning efficiency varied between 0% and 100% as expected; however, in a few cases the calculated value was outside of this range. Negative cleaning intervals were adjusted to 0% and cleaning intervals greater than 100% were adjusted to 100%.

The results of this productivity analysis typically agreed well with the results of analyses conducted by the utilities and consultants that conducted these studies; however, a productivity analysis conducted under a set of assumptions different than those used in this analysis could yield different results.

9.3. Defining a Period of Stable Performance for Productivity

After completing the cycle-by-cycle productivity analysis, an expert analysis was conducted to identify a period of stable performance. For the purpose of this analysis, stable performance was defined as a period over which system operation, pretreatment, influent water quality and the rate of productivity decline remained relatively stable. During the start-up phase of many studies, there were instances of severe membrane fouling that are not representative of sustained performance, and data collected over these periods was not included in the period of stable

performance. Figure 9-3 shows the period of stable performance, and the initial fouling events that were excluded from this period, for an example study.

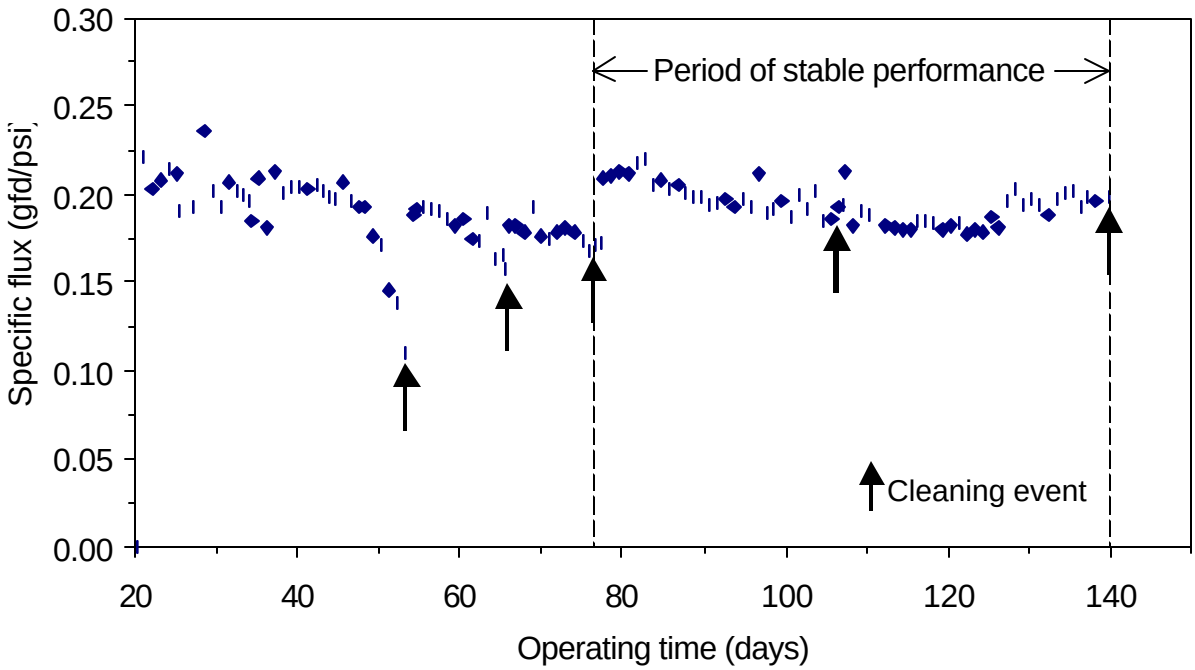

Figure 9-3. Period of stable performance for an example study

The period of stable performance was identified through an analysis of the cycle-by-cycle productivity data, pretreatment data, operational data and influent water quality data. In the example shown in Figure 9-3, a significant change in pretreatment was made after 75 days of operation resulting in improved membrane performance; thus, this change was used to identify the beginning of the period of stable performance.

Only one period of stable performance was defined for each membrane evaluated during each study. This is different from the analysis of water quality data which was summarized over treatment study runs. In the *Treatment Study Database*, the productivity data for a given membrane and TSID is duplicated for all TSRunIDs in that study.

9.4. Productivity Analysis over Period of Stable Performance

Once the period of stable performance was identified, the productivity data from the operational cycles within that period were summarized to estimate sustained productivity. Table 9-3 lists the sustained productivity information summarized over the period of stable performance.

Table 9-3. Productivity data summarized over the period of stable performance

Parameter	Methodology
Sustained flux over the period of stable performance	Average of all flux values within the period of stable performance
Sustained specific flux over the period of stable performance	Average of all specific flux values within the period of stable performance
Rate of specific flux decline over the period of stable performance	Average of the slopes of the specific flux curves from each cycle in the period of stable performance
Cleaning interval over the period of stable performance	Average of the cleaning intervals from each cycle in the period of stable performance
Cleaning efficiency over the period of stable performance	Average of the cleaning efficiencies from each cycle in the period of stable performance

9.5. Productivity Data Uploaded to the Treatment Study Database

Table 9-4 summarizes the fields uploaded to the Productivity Table of the database. These fields include the sustained productivity parameters described in Section 9.4 as well as the pressure estimates derived from the Differential Water Quality Model as described in Section 8.6.

All studies have values for the sustained productivity parameters for the system, including: SF_decline, CI, ClnEff, FwTemp_sustn, and SF_sustn. In addition to the system productivity information, pilot- and full-scale studies will also have values for the sustained productivity parameters for individual stages. A study using a 2-stage system will have sustained productivity data for 2 stages and a study using a 3-stage system will have data for 3 stages. Since these sustained productivity parameters are calculated over the period of stable performance for a given TSID and membrane, the values of the parameters are constant for all TSRunIDs within a study.

Table 9-4 also contains pressure estimates predicted from the Differential Water Quality Model, specifically: P_I_Prdct, P_C_Prdct, P_P_Prdct, and P_O_Prdct. Since these predictions are based on the 3-stage array design used in the Differential Water Quality Model, all studies have predicted pressures for the system as well as for stages 1, 2 and 3. These pressure estimates also vary for different TSRunIDs to reflect the impact of changes in influent temperature on the pressure required to achieve an average flux of 10 gfd for surface waters and 15 gfd for ground waters in each stage of the Differential Water Quality Model array.

Table 9-5 summarizes the sustained productivity data and predicted pressure data for different membrane protocols used in the ICR.

Table 9-4. Fields uploaded to the Productivity Data table of the database

Field Name	Description
Stg_Num	Abbreviation used to indicate whether the data is associated with the system or a stage: 0 = system, 1 = stage 1, 2 = stage 2, and 3 = stage 3.
SF_decline (gfd/psi/day)	The rate of specific flux decline over the period of stable performance for the system or an individual stage as indicated by the Stg_Num. Both the average and the standard deviation are reported.
CI (day)	The cleaning interval over the period of stable performance for the system or an individual stage as indicated by the Stg_Num. Both the average and the standard deviation are reported.
ClnEff (%)	The cleaning efficiency over the period of stable performance for the system or an individual stage as indicated by the Stg_Num. Both the average and the standard deviation are reported.
FwTemp_sustn (gfd)	The sustained, temperature-normalized flux over the period of stable performance for the system or an individual stage as indicated by the Stg_Num. Both the average and the standard deviation are reported.
SF_sustn (gfd/psi)	The sustained, temperature-normalized specific flux over the period of stable performance for the system or an individual stage as indicated by the Stg_Num. Both the average and the standard deviation are reported.
P_I_Prdct (psi)	The influent pressure predicted by the Differential Water Quality Model for the system or an individual stage as indicated by the Stg_Num
P_C_Prdct (psi)	The concentrate pressure predicted by the Differential Water Quality Model for the system or an individual stage as indicated by the Stg_Num
P_P_Prdct (psi)	The permeate pressure predicted by the Differential Water Quality Model for the system or an individual stage as indicated by the Stg_Num
P_O_Prdct (psi)	The osmotic pressure predicted by the Differential Water Quality Model for the system or an individual stage as indicated by the Stg_Num

Table 9-5. Sustained productivity and predicted pressure data for various study protocols

Protocol	Sustained Productivity Data	Predicted Pressure Data
RBSMT, SEBST & LTSEBST	• One set of values per study and per membrane. • Data is repeated for each TSRunID. • System data only.	• One set of values per TSRunID. • Pressures vary with seasonal changes in temperature. • System and stage 1, 2, 3 data.
2-Stage Pilot & 2-Stage Array	• One set of values per study and per membrane. • Data is repeated for each TSRunID. • System and stage 1, 2 data.	• One set of values per TSRunID. • Pressures vary with seasonal changes in temperature. • System and stage 1, 2, 3 data.
3-Stage Pilot & 3-Stage Array	• One set of values per study and per membrane. • Data is repeated for each TSRunID. • System and stage 1, 2, 3 data.	• One set of values per TSRunID. • Pressures vary with seasonal changes in temperature. • System and stage 1, 2, 3 data.

9.6. Limitations of Productivity Data from Various Study Protocols

Sustained productivity estimates were developed and reported for all membrane studies conducted under the ICR; however, the applicability of these estimates to full-scale performance varies significantly for the different protocols. In general, the applicability of these productivity estimates to full-scale performance improves with increasing study scale, i.e., applicability of study results is poorest for RBSMT studies and best for full-scale studies. Table 9-6 presents a qualitative assessment of full-scale applicability of productivity data generated by the various membrane study protocols.

The assessment provided in Table 9-6 should be viewed as general guidelines since the quality of productivity estimates varies from study to study. The RBSMT protocol used in the ICR typically does not provide a good estimate of the sustained rate of specific flux decline and the cleaning interval since these studies were not run for a sufficient duration to obtain an accurate estimate of the slope of the specific flux decline curve (Allgeier, et al., 1997b). However, the RBSMT does provide a reasonable estimate of the initial specific flux and cleaning interval. The single element studies provide reasonable estimates of the rate of specific flux decline and cleaning interval, with the data from the long-term studies generally being superior to the data from the quarterly SEBST studies. The pilot-scale studies provide productivity data that is generally considered directly applicable to full-scale performance. The pressure estimates for all study protocols were derived from the Differential Water Quality Model and are considered fair to excellent estimates of the pressure requirements for a full-scale system under the design assumptions listed in Section 8.2.

Table 9-6. Qualitative assessment of productivity data from various study protocols

Productivity Parameter	Scale of Study			
	RBSMT	***SEBST***	***Pilot-Scale***	***Full-Scale***
SF_sustn	Fair	Good	Excellent	Excellent
SF_decline	Poor	Good	Excellent	Excellent
CI	Poor	Good	Excellent	Excellent
ClnEff	Fair	Fair	Good	Excellent
Pressures	Fair	Fair	Good	Excellent

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