

## D. APPENDIX: R-PLOT GENERATION

To provide an aid in the Risk Characterization section, NMFS developed a plot (referred to as a ‘Risk-plot’ or ‘R-plot’) displaying the various sources of data (i.e. exposure, response, and use) available as part of the consultation (e.g. EPA’s BEs and risk assessments and NMFS’s analyses). The R-plots are generated using the R programming language:

R Core Team (2017). R: A language and environment for statistical computing. R Foundation for Statistical Computing, Vienna, Austria. URL <https://www.R-project.org/>.

This Appendix consists of several sections with information on the R-plot process:

- **R-plot Process Overview:** An overview of the R-plot process
- **Example R-plot:** An example of an R-plot
- **Files:** A list of the files used by the R-plot process
- **Format of R-plot data file:** Description of the format of a R-plot data table

### R-plot Process Overview

The following is a brief overview of the R-plot process. The overview assumes an understanding of the data and some knowledge of the R programming environment. The data displayed on the R-plots comes from several sources. A summary of the sources is detailed here:

- 1) Toxicity information for a species gathered from the available literature. For sublethal endpoints, such as growth, this is typically a range of LOECs or EC25s across the available studies. For endpoints such as mortality, this is can be a range of percent mortalities using an LC50 and slope chosen based on a species sensitivity distribution.
- 2) Data on the overlaps of species range and critical habitat (e.g. a list of HUC-12s) and the uses of the pesticide (e.g. the Vegetable and Ground Fruit UDL). This information is from GIS analyses provided to NMFS by EPA (EPA 2017a; 2017b; 2017c).
- 3) Exposure estimates generated using existing data for each crop and use category (e.g. lettuce crop within the Vegetable and Ground Fruit use category). See Chapter 11 for details of generating EECs for the a.i.s associated with this Biological Opinion. For example, the Pesticide Water Calculator (PWC) can be used to generate thirty years of EECs for each HUC-2 and aquatic bin. For the R-plot process the resulting EECs for each use can be summarized as the distribution of annual peak EECs (e.g. median and range).

The user collects all the data into a single table as either a csv file or an Excel worksheet. Additional information in the table specifies how the data is plotted and any additional annotations (see **Format of R-plot data file** below). The R code then uses the information in the table to into a single plot. An example of an R-plot is shown in **Example R-plot**. The plot consists of five parts.

- 1) The upper portion displays the toxicity information in terms of the effects concentrations (e.g. ppb). This consists of multiple rows of endpoints each with a set of labeled markers.

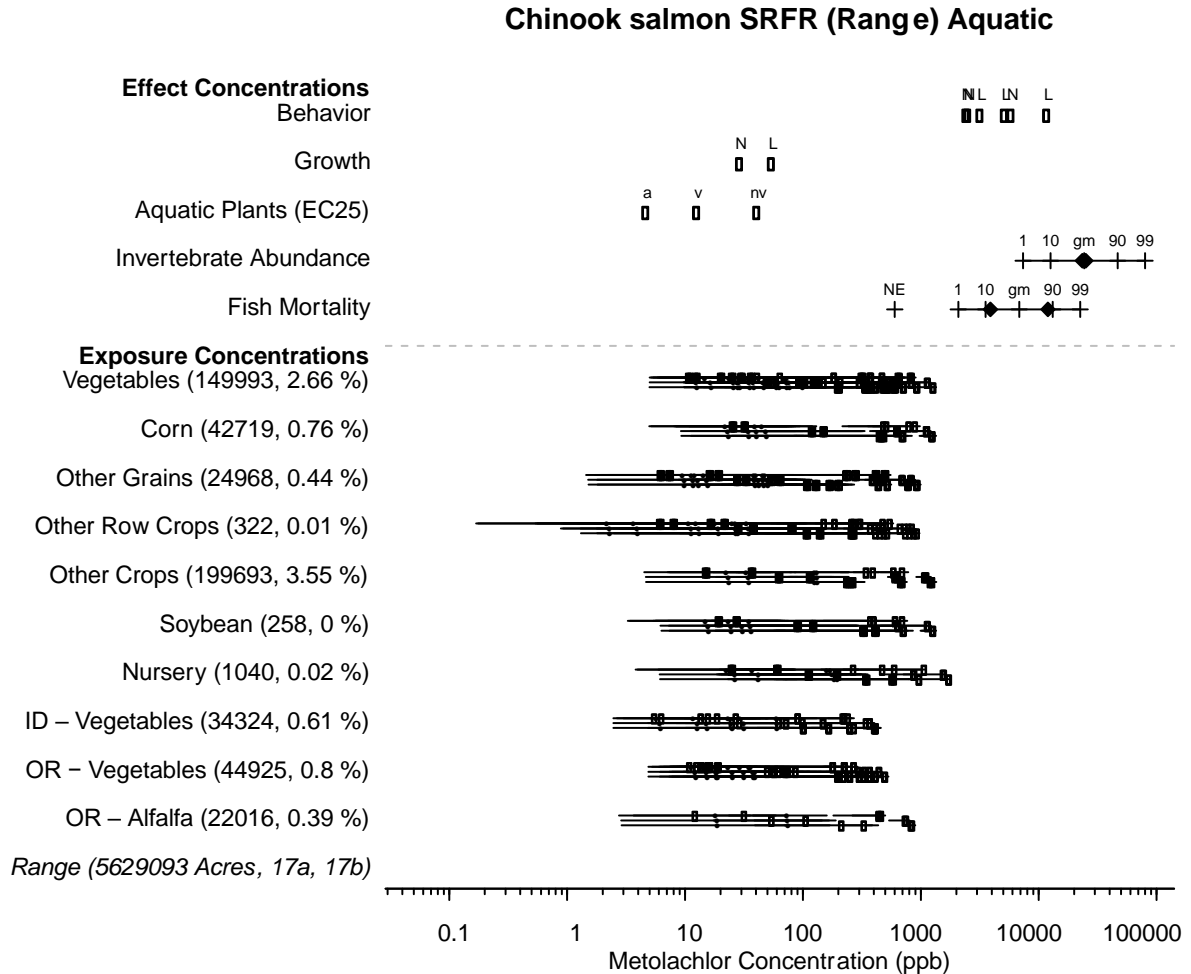
The meaning of each marker is up to the user (e.g. a LOEC, percent morality, etc.). The markers are positioned along the concentration axis below.

- 2) The center of the plot displays all the EEC data associated with the selected chemical and relevant scenarios that produce the potential exposure concentrations. Typically, for each crop (e.g. lettuce) of a use category (e.g. Corn) there will be a point for each averaging period and each aquatic bin (for aquatic R-plots) or exposure model and application method (for terrestrial R-plots). For aquatic EECs, each point represents the median peak annual EEC for several averaging periods (1-day, 4-day, and 21-day as different sub-rows in this example) and aquatic bins (bins 0, 2, and 7 as different symbols in this example) for a specific PWC scenario (a separate row in this example). For EECs based on the PWC, error bars around the point can indicate the 5% and 95%tile of the distribution of thirty years of data. The EEC data is positioned using the same concentration axis as the toxicity data to allow direct comparison of exposure and effects.
- 3) The left side of the plot (i.e. the left Y-axis labels) lists the use categories associated with the species range or habitat. The portion of the species range or habitat associated with each use category is denoted in the parentheses (the area of the use category within the range or habitat in acres and as a percent of the species total acres).

Generating an R-plot involves building a table with the desired information either as a csv file or the second worksheet in an Excel file. The table provides all the information needed to generate an R-plot using the R script *Rplotting2A.R*. NMFS used two additional R scripts (*ExtractYearlyPkEECsB.R* and *AggregateEECs.R*) to gather aquatic EEC data from the files generated by PWC batch runs (e.g. the \*.zts and \*.daily.csv files) into a single file that can form part of the R-plot data table. Some information on the table format is described below and examples are provided in Appendix E. An R-plot is generated by running *Rplotting2A.R* and specifying the desired table as the input.

### Example R-plot

Example of an aquatic R-plot. This R-plot is the result of using *Chinook salmon SRFR (Range)* *Aquatic\_Rdata.csv* as the data file input when running the *Rplotting2A.R* R Script.



## Files

Annotated list of files associated with running the R-plot process. These files are provided as part of Appendix E. The first four are R Script files that need to be in the same directory. Additional files listed are supporting files and examples of data files that can serve as inputs for the R-plot process.

### R Scripts

*Rplotting2A.R*

Main R code run generate an R-plot  
Uses a csv or Excel file as input  
Can generates a pdf as output

*ExtractYearlyPkEECsB.R*

R code run to collect data from a folder of PWC batch runs  
Creates a single file with yearly peak EECs for all uses  
e.g. *Metolachlor\_PWC\_Runs\_eec.csv*

*AggregateEECs.R*

R code used to summarize all years of EECs for each use  
Uses the output of *ExtractYearlyPkEECsB.R*  
Creates a single file with means and ranges of EECs  
e.g. *Metolachlor\_PWC\_Runs\_eec.csv\_aggregated.csv*

*AqEECsFunctionsB.R*

Utility functions needed by other R Scripts

### Other files

*useList.df*

R dataframe with crosswalk of crops (PWC) and uses (UDL)

*Chloropicrin\_Rplot\_112720.xlsx*

Excel data files used in the R-plot process

*Metolachlor\_Rplot\_010921.xlsx*

Various Worksheets in the file gather information

*Telone\_Rplot\_010921.xlsx*

The second worksheet is the input for *Rplotting2A.R*

*Chinook salmon SRFR (Range) Aquatic\_Rdata.csv*

Example of a csv file formatted for input to the R-plot process  
Used as input for *Rplotting2A.R*

### Format of R-plot data file

The R-plot generated by *Rplotting2A.R* is based on information present in a file selected when the R code is run. The information is in a table that can be either a csv file or the second Worksheet in an Excel file. The table provides all the information used by the R script to generate the R-plot. Each row specifies an element in the figure. Rows can be added to the spreadsheet. Order of elements does not matter (i.e. *row* does not need to be in increasing order). Blank rows in the spreadsheet are allowed. For Excel files, values in a cell can be a formula (i.e. the result of a calculation and/or from another worksheet). The data needed in the table is described below. An example csv file (*Chinook salmon SRFR (Range) Aquatic\_Rdata.csv*) is provided in Appendix E. Excel files used for the Biological Opinion are also included in Appendix E.

Cells in Bold or Italics need to remain the same.	
<b>plot title</b>	Text in the cell below specifies the plot title at the top.
<b>plot axis</b>	Text in the cell below specifies the X-axis title.
<b>plot labels</b>	The columns below specify the labels along the Y-axis. Rows can be added as desired.
<i>label</i>	Specifies the text to use to label the row in the figure
<i>row</i>	Specifies the row where the label should be located. Numbers start from the X-axis and work upwards.
<i>font</i>	Options include 1 for regular, 2 for bold, and 3 for italic.
<b>plot data</b>	The columns below specify all the components within the plot. Each row specifies one component.
<i>row</i>	Specifies the row where the component should be located. Numbers start from the X-axis and work upwards. Ignored for a vertical line.
<i>type</i>	The component type; p for a point, v for a vertical line, or h for a horizontal line.
<i>conc</i>	Specifies the concentration (initial X position) associated with the component.
<i>end</i>	Species the end of the component. For a horizontal line this is the end concentration. For a vertical line this can be the row where the line ends. Ignored for a point.
<i>note</i>	The text to use to annotate the component.
<i>pch</i>	The point style. R has many options; e.g. 21 is a filled circle and 22 is a filled square.
<i>cex</i>	The point size relative to the default (i.e. 1).
<i>bg</i>	The fill color for a point. Numerous colors can be specified by name (e.g. "blue").
<i>col</i>	The color for the line or point border.
<i>lty</i>	The line type; e.g. 1 for solid or 2 for dashed. R has additional options.
<i>lwd</i>	The line width.
<i>comment</i>	For user comments. Not part of the plot.