

Guide to Using R for Analyses Performed in the Delta Mercury Control Program Review

R & RStudio

The R Analyses used in the DMCP Review were confirmed to run with RStudio version 2023.06.0 build 421 using R version 4.2.2. Using earlier or later versions may result in code errors.

Required Packages

The R Analyses used in the DMCP Review require the following packages and was confirmed to run using the specified versions. Using earlier or later versions may result in code errors.

- actuar (version 3.3-0)
- DT (version 0.24)
- fitdistrplus (version 1.1-8)
- ggbeeswarm (version 0.7.2)
- janitor (version 2.1.0)
- kableExtra (version 1.3.4)
- mgcv (version 1.8-41)
- NADA (version 1.6-1.1)
- plotly (version 4.10.0)
- readxl (version 1.4.3)
- shiny (version 1.7.2)
- tidyverse (version 2.0.0)
 - tidyr (version 1.3.1)
 - dplyr (version 1.1.4)
 - ggplot2 (version 3.5.1)
- writexl (version 1.5.0)

Project File

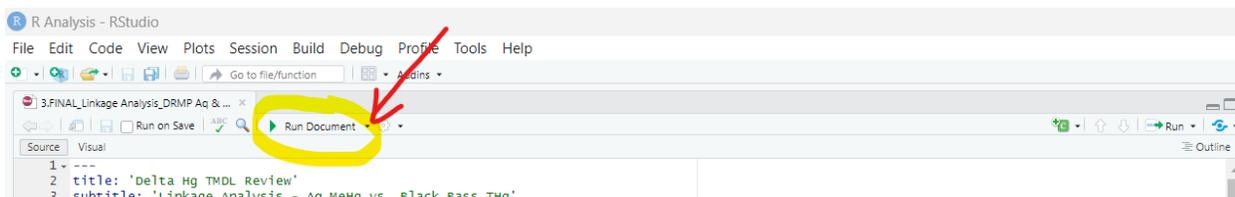
Extracting the “DMCP Review R Analysis.zip” file will create a project folder called “R Analysis”. This parent folder contains all the data excel files and R scripts used for the scientific portion of the DMCP Review. To start the DMCP Review R Analysis project workspace, open the R project file called “Reeval_DMCP Analyses.Rproj” (located in the “R Analysis” folder) in RStudio.

How to Run “.R” and “.RMD” files

After “Reeval_DMCP Analyses.Rproj” is open in RStudio, R scripts (see Table of Contents below) can be accessed from within the “Files” pane of RStudio. Double clicking an R script opens it in RStudio’s Source pane. To run “.R” files, click “Source” as indicated below.



To Run “.RMD” files, click “Run Document” or “Knit”. Both are located in the area indicated below.



R Script Outputs

Outputs from the data compilation R scripts are saved in the same directory of the script that created the output. Other scripts save outputs in a subfolder called “output” located in the script’s directory.

R Scripts

Table of Contents

Function Scripts

The following scripts contain functions written by Board staff to help with various aspects of the analysis.

Parent Folder: [R Analysis/R Functions](#)

- [function_AqFishSamplePairing.R](#)
- [function_AqSampleFishModelPairing.R](#)
- [function_predictionModelPlot.R](#)
- [function_predictionModels.R](#)
- [function_randomSampleLinkage.R](#)
- [function_TLG_CompositeWeighted_AvgHg.R](#)
- [function_TLG_CompositeWeighted_AvgHg_TissueOptns.R](#)
- [functions_estimate NDDNQ values.R](#)
- [functions_QA data.R](#)
- [ggplot_force_panelsizes.R](#)
- [ggplot_theme_border.R](#)

Data Compilation Scripts

The following scripts are used to format and compile data from different sources.

Aqueous Data

Parent Folder: [R Analysis/Reeval_Impl_Goals_Linkage_Analysis/Data/Aqueous](#)

- [1_Merging Aqueous Data.R](#)
- [2_Prep Aq Data for GIS Scoping.R](#)
- [3_Demarc Aq Data to Delta TMDL.R](#)
- [4_Filter for Delta Aq Data.R](#)
- [5_QA Aq Data.R](#)
- [6_Remove Repeated Aq Data.R](#)
- [AmericanRiver_format-to-ceden.R](#)
- [App_L_MeHg_format-to-ceden.RI](#)

- App_L_THg_format-to-ceden.R
- CALFED2003-1a_format_to_ceden.R
- CEDENAqSed_format-to-ceden.R
- DeltaSED_format-to-ceden.R
- DRMP_format-to-ceden.R
- DWR_format-to-ceden.R
- DWRMeHg_format-to-ceden.R
- R5AQ & SNIP - Test for Hidden Repeated Data due to wrong Analyte Name.R
- R5AQ_format-to-ceden.R
- R5SED_format-to-ceden.R
- SNIP_format-to-ceden.R
- USGS_format-to-ceden.R
- WQP_aq_sed_format-to-ceden.R

Parent Folder: [R Analysis/Reeval_Impl_Goals_Linkage_Analysis/Data/DRMP FY16-19](#)

- DRMP_merging Aq_Sed Data.R

Fish Data

Parent Folder: [R Analysis/Reeval_Impl_Goals_Linkage_Analysis/Data/Fish](#)

- 1_Merging Fish Data.R
- 2_Prep Fish Data for GIS Scoping.R
- 3_Demarc Fish Data to Delta TMDL.R
- 4_Filter for Delta Fish Data.R
- 5_QA Fish Data.R
- 6_Remove Repeated Fish Data.R
- AppK_Fish MeHg_format-to-ceden.R
- CEDENFish_format-to-ceden.R
- DRMP_2016_CEDENfish_format-to-ceden.R
- DRMP_2017_2019_Fish_format-to-ceden.R
- MasterFish_format-to-ceden.R
- SNIP_FISH_format-to-ceden.R
- USGSFISH_format-to-ceden.R
- WQP_FISH_format-to-ceden.R

Parent Folder: [R Analysis/Reeval_Impl_Goals_Linkage_Analysis/Data/DRMP FY16-19](#)

- DRMP_merging Fish Data.R

Black Bass Implementation Goal Scripts

The following scripts evaluate the data analysis options considered by Board staff to develop the proposed black bass implementation goal.

Parent Folder: [R Analysis/Reeval_Impl_Goals_Linkage_Analysis/eval1_TLG Eval & BB Impl Goal](#)

- 1.TEST TLG 1998-2019 & BB 2000-2019_pooled vs wt avg.Rmd
- 2.TEST TLG & BB_wt avg_year ranges.Rmd
- 3.FINAL Impl Goal_TLG 2002-2019 & BB 2002-2019_wt avg.Rmd

Aqueous Methylmercury Implementation Goal Scripts

The following scripts evaluate the data analysis options considered by Board staff to develop the proposed aqueous methylmercury implementation goal.

Parent Folder: [R Analysis/Reeval_Impl_Goals_Linkage_Analysis/eval2_Linkage & Aq Impl Goal](#)

- 1.TEST_Linkage Analysis_Aq & BB_Year Pairings.Rmd
- 2.FINAL_Margin of Safety Analysis_DRMP Aq & BB 2016-2019.R
- 3.FINAL_Linkage Analysis_DRMP Aq & BB 2016-2019.Rmd

Source Analysis Scripts

The following scripts were used to evaluate methylmercury source loads and losses.

Parent Folder: [R Analysis/Reeval_Source_Analysis/Source Data/](#)

- 01_Tributaries/01_Tributaries.Rmd
- 01_Tributaries/Flow/01_Tributaries_FRE_Flow.Rmd
- 01_Tributaries/Flow/01_Tributaries_MRS_Flow.Rmd
- 01_Tributaries/Flow/01_Tributaries_RCS_Flow.Rmd
- 01_Tributaries/Flow/Incomplete Datasets/CacheCr Inflow Annual Vol Distrib Eval.R
- 01_Tributaries/Flow/Incomplete Datasets/CCSB Outflow Annual Vol Distrib Eval.R
- 01_Tributaries/Flow/Incomplete Datasets/CCSB Weir Annual Vol Distrib Eval.R
- 01_Tributaries/Flow/Incomplete Datasets/Fremont Weir Annual Vol Distrib Eval.R
- 02b_Nontidal Wetlands/02b_Nontidal Wetlands.Rmd
- 03a_Municipal WWTPs (NPDES)/03a_WWTP MeHg Annual Loads.Rmd
- 03a_Municipal WWTPs (NPDES)/Data/03.0_NPDES_eSMR MeHg Data Fix Check.Rmd
- 03a_Municipal WWTPs (NPDES)/Data/03.1_WWTP Flow Data Prep & Eval.Rmd
- 03a_Municipal WWTPs (NPDES)/Data/03.1_WWTP MeHg Data Prep & Eval.Rmd
- 04_Ag/04_Agricultural Return Flows.Rmd
- 05_Urban Runoff/05_Urban MS4 Ph2 MeHg Median Conc.Rmd
- 05_Urban Runoff/05_Urban Runoff.Rmd

Parent Folder: [R Analysis/Reeval_Source_Analysis/Loss Data/](#)

- 01_SF Bay/01_SF Bay.Rmd
- 02_Southern CA/02_Southern CA.Rmd
- 04_Tidal Wetlands/04_Tidal Wetlands.Rmd

Allocation Scripts

The following scripts were used to evaluate methylmercury reductions and allocations.

Parent Folder: [R Analysis/Reeval_Allocations/](#)

- 01_Aq MeHg Reductions/1_Allocations_PercentReduction.Rmd
- 03_NPDES WWTP WLAs/NPDES Allocations & WWTP Projected Growth.Rmd
- 04_Percent Allocations/Gross Flux Calculations/Gross Flux Calculations.Rmd
- 04_Percent Allocations/NPDES Allocation Comparison_final.Rmd