About

This document includes plots requested by Bureau of Reclamation for the "Track-a-Cohort" page in development on SacPAS: Central Valley Prediction & Assessment of Salmon website developed and maintained by Columbia Basin Research, University of Washington.

All code used to develop this quarto webpage are available via the Columbia Basin Research GitHub repository: Columbia-Basin-Research-CBR and can be used in total or individual plots can be generated using the code provided.

How to use:

- To view the code used to generate individual plots, navigate to the `R` folder within the repository or run the following code in the terminal `Rscript R/SCRIPT_NAME.R.` Each file includes the necessary information to load the data and directs user to which libraries are needed to run the script.

- To access the final individual plots (.png), navigate to the `docs/www/` folder within the repository. The rendered plots are available in respective species folders, `TAC_SPECIES_figures_files>figure-html`.

- To view the final data used to generate the plots, navigate to the `data` folder within the repository. Raw data that supports the data for generating plots and/or tables are available in the `data-raw` folder and can all be updated at once using the `R/update_data.R` script. Alternatively, the data will be prompted to update with each new build of the quarto webpage.

- To render the complete quarto webpage locally, download the repository to `R` and run the code `make` in the terminal, or clicking `Build` in the panel tabs within your R environment. Once complete, navigate to the `docs/` folder where you'll find the rendered webpage: `index.html`. Open in browser to view the complete webpage.

Please direct general questions to: web@cbr.washington.edu