

# 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](mailto:web@cbr.washington.edu)