

# Salmon contaminant workflow

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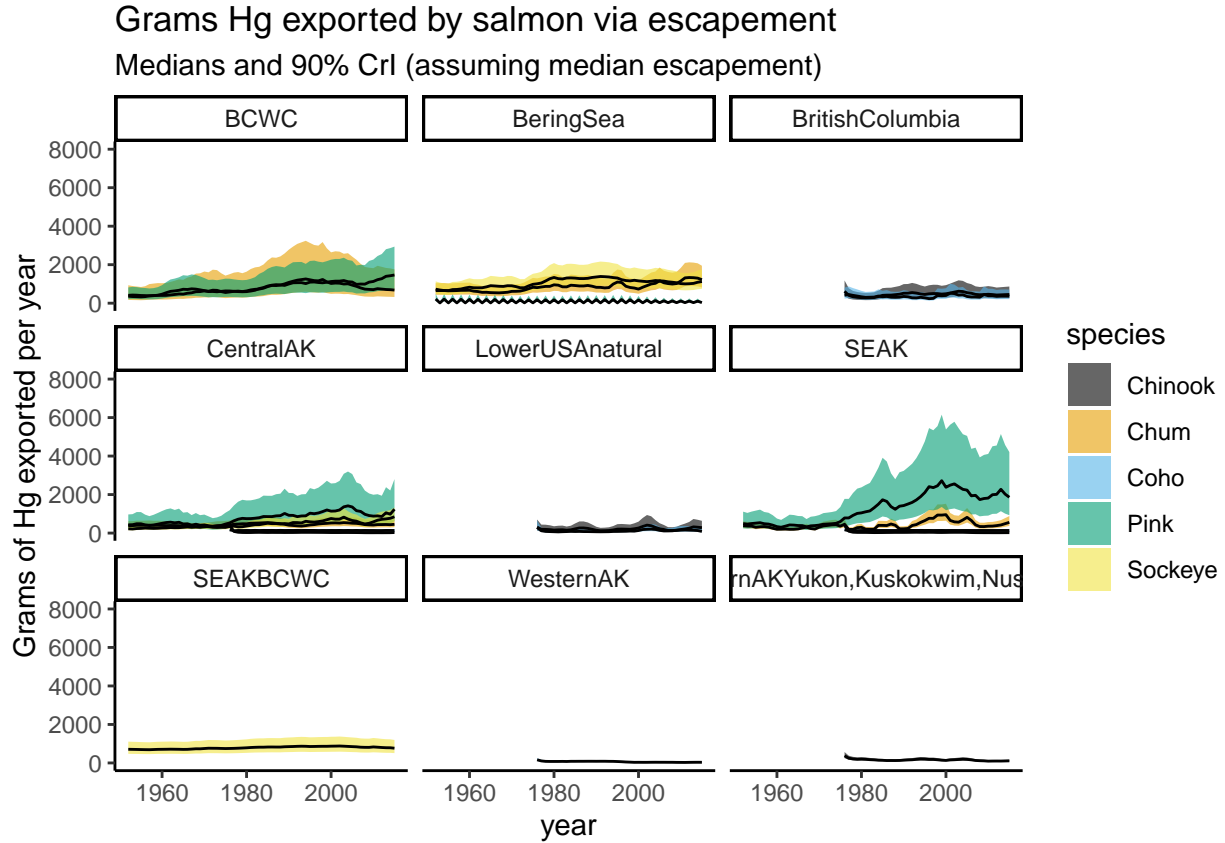


Figure 1: Estimate of mercury exported in migrating salmon among species and regions.

## What we've got so far

Fig. 1 shows the current model estimate of mercury flux in salmon. It is derived from two models. First, we modeled salmon population sizes using separate Bayesian state-space models for each combination of species and location using data from Ruggerone et al. (2018) (Figure 2). Second, we modeled the concentrations of mercury (ng/kg ww) in salmon among regions using data compiled from literature estimates using a Bayesian generalized linear model with a Gamma likelihood (Figure 3). We then converted concentrations per kg to concentrations per individual by multiplying the model results (i.e. posterior) by the mean mass of an individual fish.

To combine estimates from the two models, we multiplied the posterior distribution of mercury concentrations by three scenarios of salmon population sizes - low, median, and high. These corresponded to the 12.5, 50,

and 88.5 quantiles of the posterior for each species by location combination. Only the 50% quantile is shown in Fig. 1.

