## Survival of Migrating Salmon Smolts in Large Rivers With and Without Dams

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## S. 3 Tests of Statistical Significance for Figure 3.

To calculate the average survival and $95 \%$ confidence interval for Fraser R Chinook and steelhead shown in Fig. 3 we used the following Monte Carlo procedure: For the $\mathrm{j}=1, \ldots, \mathrm{~J}$ annual survival estimates available for each species (for example, $\mathrm{J}_{\text {Chinook }}=6$; $\mathrm{J}_{\text {Steelhead }}=7$ in the Thompson), we calculated the average of J survival estimates by drawing from component normalized binomial distributions $\mathrm{S}_{\mathrm{j}} \sim \frac{1}{N_{j}^{*}} \mathrm{~B}\left(\bar{S}_{\mathrm{j}}, N_{j}^{*}\right)$ that describe the expected probability density function of each survival observation. This was repeated 10,000 times to provide a set of results, each describing the outcome from calculating the average across J observations, with the individual survival observations weighted by their relative uncertainty.

Here $\mathrm{S}_{\mathrm{j}} \sim \frac{1}{N_{j}^{*}} \mathrm{~B}\left(\bar{S}_{\mathrm{j}}, N_{j}^{*}\right)$ is the normalized binomial distribution for the $\mathrm{j}^{\text {th }}$ observation of survival with observed survival proportion $\bar{S}_{\mathrm{j}}$ and sample size $N_{j}^{*}$ (the latter parameter determines the fatness of the tails). The set of $M=10,000$ survival estimates was used to calculate the average and the interval defining the upper and lower 2.5 percentiles of the distribution. Here $\bar{S}_{\mathrm{j}}$ is the observed survival for the $\mathrm{j}^{\text {th }}$ group calculated from the CJS model, but we replace the number of fish released, $\mathrm{N}_{\mathrm{j}}$, by $N_{j}^{*}$, where $N_{j}^{*}$ is that value of N that will generate the variance on S estimated by the CJS model. (We use the fact that the standard error on a proportion $\mathrm{S}_{\mathrm{j}}$ defined by a binomial distribution can be written as
$\mathrm{SE}\left(\mathrm{S}_{\mathrm{j}}\right)=\sqrt{\frac{S_{j}\left(1-S_{j}\right)}{N}}$; knowing $\mathrm{S}_{\mathrm{j}}$ and its standard error, we can solve for the value of $N_{j}^{*}$
that yields this standard error using the binomial distribution, which is $N_{j}^{*}=\frac{S_{j}\left(1-S_{j}\right)}{S E\left(S_{j}\right)^{2}}$.
This is a large sample Gaussian approximation to the binomial appropriate when $\mathrm{SN} \geq 5$, which is true for all of the annual estimates). This approach was taken because the variance of $S$ when the detection efficiency of the array is unknown is greater than if the detection efficiency is known. In general, this is a conservative test for our purposes because $\mathrm{N}^{*}<\mathrm{N}$, and results in sampling from a fatter-tailed distribution. A similar calculation was done to calculate the mean $\& 95 \%$ confidence interval on the average survival estimates reported for the three sections of the Columbia River reported in Fig. 3.

To compare whether survival estimates for Thompson-Fraser fish are different from survival estimates for smolts in the Columbia R , we used a similar procedure, based on calculating the statistical distribution of the difference between pairs of survival estimates for the two rivers. For each of the three Columbia R groups (up-river (impounded), lower-river, or entire river), we calculated a separate set of 10,000 survival estimates formed by averaging over the set of $\mathrm{j}=1, \ldots, \mathrm{~J}$ observations, $\mathrm{S}_{\mathrm{j}} \sim \frac{1}{N_{j}^{*}} \mathrm{~B}\left(\bar{S}_{j}, \mathrm{~N}_{\mathrm{j}}{ }^{*}\right)$, available, and where the $\mathrm{N}_{\mathrm{j}}{ }^{*}$ values are those needed to yield the reported standard errors on the survival estimates. A separate set of 10,000 survival estimates were drawn using the Fraser R parameters, and the pair-wise set of differences was calculated. If there is no difference in survival between the two rivers, then the difference between these pair-wise
values should be zero on average. We accepted the hypothesis of no difference in survival if the $95 \%$ confidence interval on these pair-wise differences included zero. We ran all experiments multiple times to ensure that the conclusions were stable across repeated runs.

