

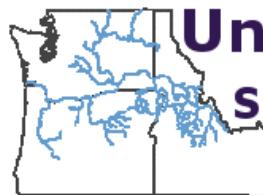
# Salmon Insider

Spring 2007  
Columbia Basin Research Newsletter



University of Washington  
School of Aquatic & Fishery  
Sciences  
Columbia Basin Research  
1325 Fourth Avenue, Suite 1820  
Seattle, Washington 98101-2509

newsletter@cbr.washington.edu  
[www.cbr.washington.edu](http://www.cbr.washington.edu)

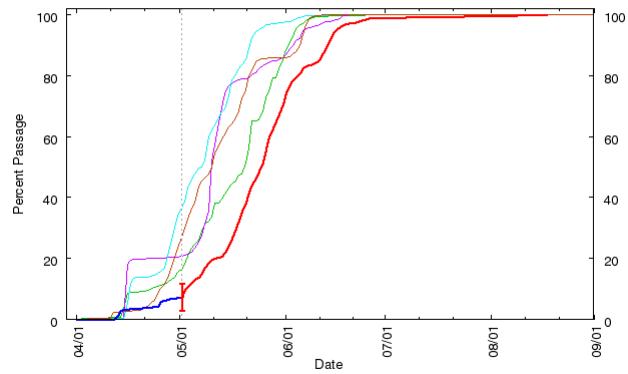


## University of Washington School of Aquatic & Fishery Sciences Columbia Basin Research

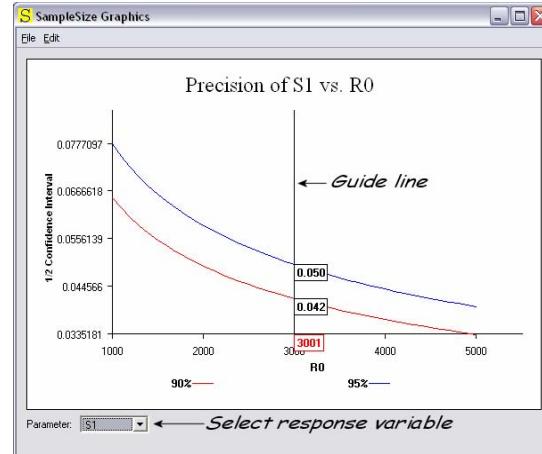
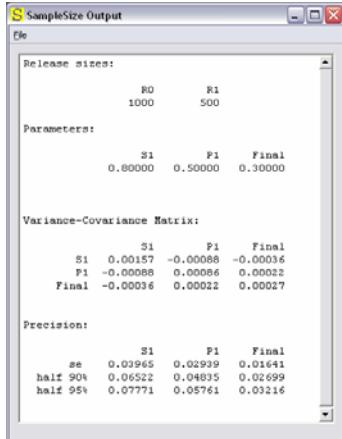
Columbia Basin Research (CBR) is a scientific research group at the University of Washington, School of Aquatic & Fishery Sciences. We investigate salmon biology and survival in the Columbia and Snake river basins. We provide user-friendly data analysis and modeling tools, and maintain DART, an interactive secondary database, for the fisheries community and the general public.

### Inside . . .

#### Inseason Forecasts for Salmonid Migration



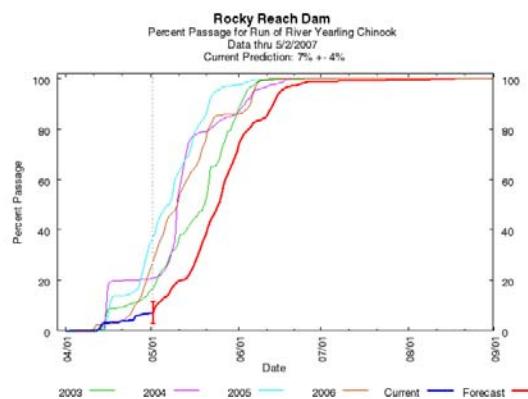
#### Program SampleSize for the Design of Survival Studies



## Inseason Forecasts for Salmonid Migration

In April, we began the 2007 predictions of run-timing and arrival distributions of salmonid juvenile outmigrations and adult returns at monitoring sites along the Columbia/Snake rivers. We distribute the predictions on the [Inseason Forecasts](#) website.

Predictions of the current status of the runs are updated daily throughout the migration season, April through October, incorporating "real time" observed data from the Pacific States Marine Fisheries Commission, Fish Passage Center, US Army Corps of Engineers, and Chelan County PUD. Predictions can be viewed with or without historical data and in a variety of different graphical formats (see Fig. 1 for an example).



**Fig. 1.** Percent passage of run-of-river yearling Chinook salmon at Rocky Reach Dam as of 5/1/2007. Prediction in red; current status in dark blue (lower left-hand corner.) Data from Chelan County PUD. Forecast category: [Smolt Passage \(Chelan\)](#). Click on figure for updated prediction and information.

The smolt inseason forecasts utilize two separate programs to generate downstream passage distributions: [RealTime](#) and COMPASS (implemented in 2007). The COMprehensive PASSage

(COMPASS) model, a juvenile fish passage model, was derived from the Columbia River Salmon Passage (CRISP) model and is in development by NOAA Fisheries, along with other federal, state, and tribal agencies, and the University of Washington. Additional information on COMPASS will be provided in a future issue.

In addition to passage distributions, predictions of inriver seasonal survival from dam to dam for specific PIT-tagged salmonid stocks is generated using COMPASS, based on parameter values and stock calibration provided by NOAA Fisheries.

**Table 1.** Predicted Composite Yearling Chinook In-River Survivals as of 5/1/2007. Forecast category: [Smolt Passage \(PIT Tag\)](#). Click for [updated prediction](#) and information.

	LGS	LMN	IHR	MCN	JDA	TDA	BON
LWG	0.90	0.79	0.72	0.64	0.53	0.47	0.43
LGS		0.88	0.81	0.71	0.59	0.52	0.48
LMN			0.92	0.81	0.68	0.59	0.55
IHR				0.88	0.74	0.64	0.59
MCN					0.84	0.73	0.68
JDA						0.87	0.81
TDA							0.92

Predictions for juvenile ESUs (Evolutionarily Significant Units) as well as spring and fall Chinook salmon, sockeye salmon, and steelhead passage, adult salmonid passage, and water quality are available for hydroelectric projects in the Snake and Columbia rivers. Please refer to the [Stock Map and Information](#) web page for more details.

See <http://www.cbr.washington.edu/crisprt/>.

## Program SampleSize for the Design of Survival Studies

We frequently receive requests at CBR for assistance with calculating sample sizes for survival studies. Researchers will request help with calculating the number of tags required to ensure precision levels are met on their survival estimates. To meet this need, Program [SampleSize](#) was developed and presented on the internet to help investigators estimate release sizes for their study ([www.cbr.washington.edu/paramest/samplesize](http://www.cbr.washington.edu/paramest/samplesize)). This program, though originally designed for PIT-tag survival studies, also translates well to any release-recapture study, including those using acoustic- or radio-tags.

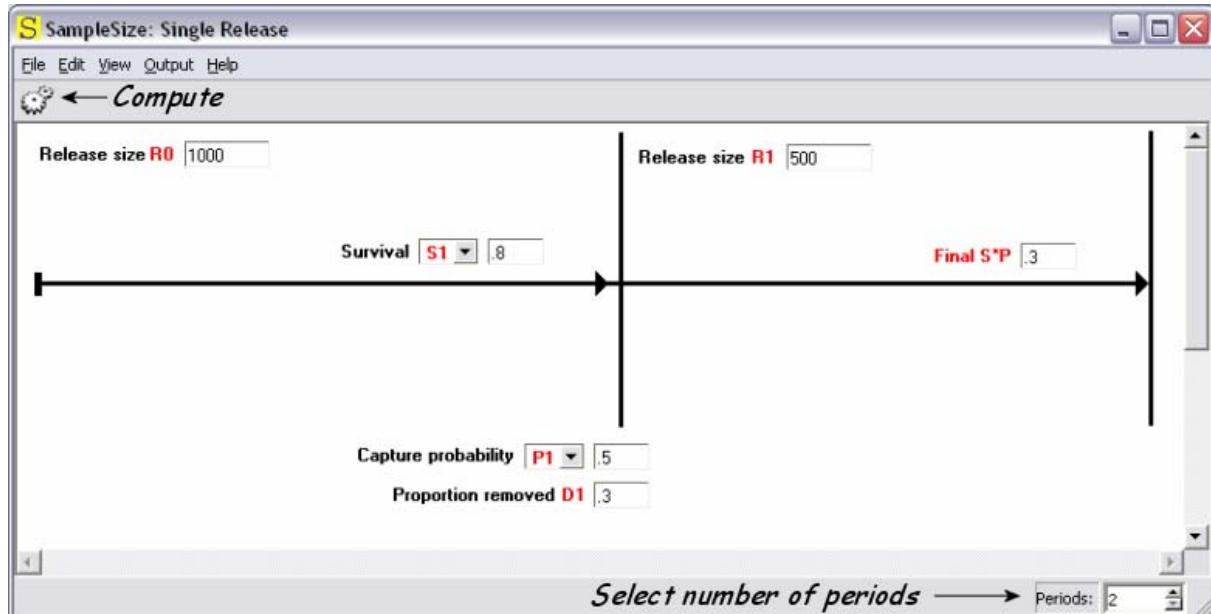
Four types of studies are supported by Program SampleSize:

1. Single release-recapture studies.
2. Paired release-recapture studies.

3. Transport-inriver studies.
4. Balloon-tag passage survival studies.

Figure 2 (below) shows the user dialog window for a single-release study. The user enters the number of detection periods (or sites) in the box in the lower right corner of the window, and the diagram adjusts accordingly. The user must specify values for the release size for each release/sampling occasion ( $R_n$ ), the anticipated survival probability ( $S_n$ ), the capture probability ( $P_n$ ), and the proportion removed ( $D_n$ ).

For the last sampling occasion, the user enters the combined probability of survival and detection, since they are not separately estimable. The anticipated probabilities are typically based on historical data or, if necessary, the user's best guess.

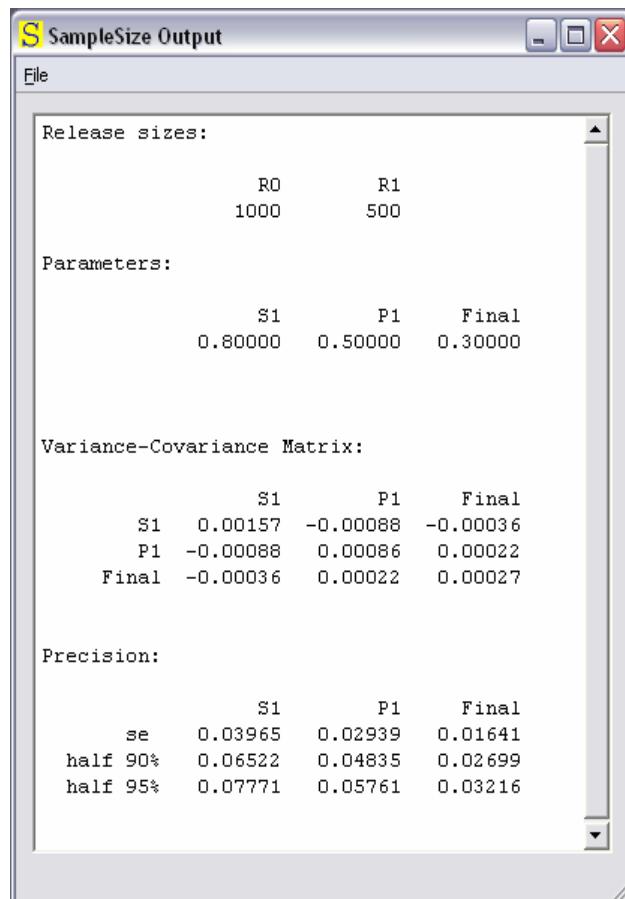


**Fig. 2.** SampleSize dialog for a single-release study.

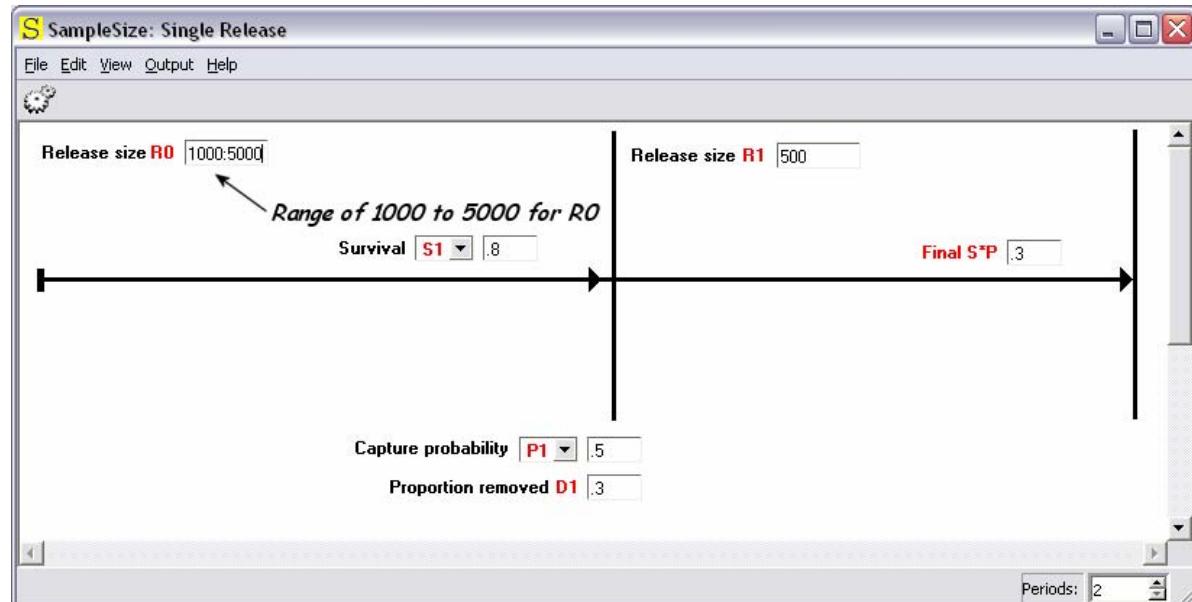
## Program SampleSize (cont.)

The user must enter values for each parameter and release size. If the user enters a single value in each entry and presses the compute button, a text window appears, as shown in Fig. 3 (right). The program predicts a standard error for  $S_1$  of 0.03965 or a 95% confidence interval half-width of 0.07771.

Another option is to enter a range of values for any one (and only one) of the probabilities or the release sizes using the format *minimum value:maximum value*. Figure 4 (below) is similar to Figure 2, except that a range of 1000 to 5000 has been entered for the initial release size.



**Fig. 3.** Output for a single-release study with no range specified.



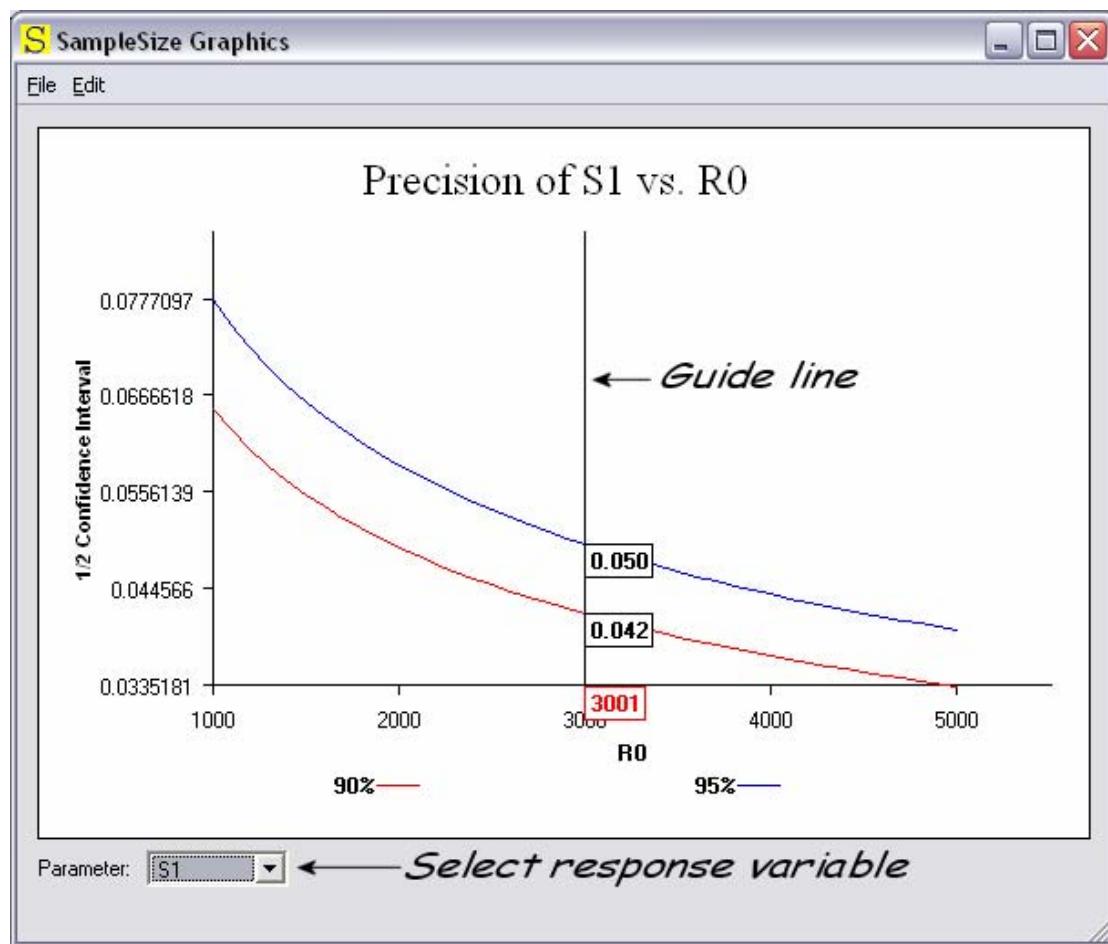
**Fig. 4.** Main SampleSize dialog for a single release,  $R0$  specified as a range of values

## Program SampleSize (cont.)

When the compute button is pressed, a graph is produced (Fig. 5) of release size vs. parameter precision, instead of the previous SampleSize output page (Fig. 3) with text and numbers. This graph shows one-half of a 90% (red) and 95% (blue) confidence interval for the each parameter (response variable) against the specified release size range on the X-axis.

In addition, this graph is interactive. The user may select the

parameter for which precision is being calculated (Fig. 5, lower left corner). Clicking the mouse anywhere inside the graph causes the vertical guide line to appear along with the X-value, the 90% value, and the 95% value at the guide line. The user can use the mouse to drag the guide line along the graph. In this case, the guide line shows that for an initial release size of 3001, a 90% confidence interval for  $S1$  is 0.042 and a 95% confidence interval is  $0.8 \pm 0.05$ .

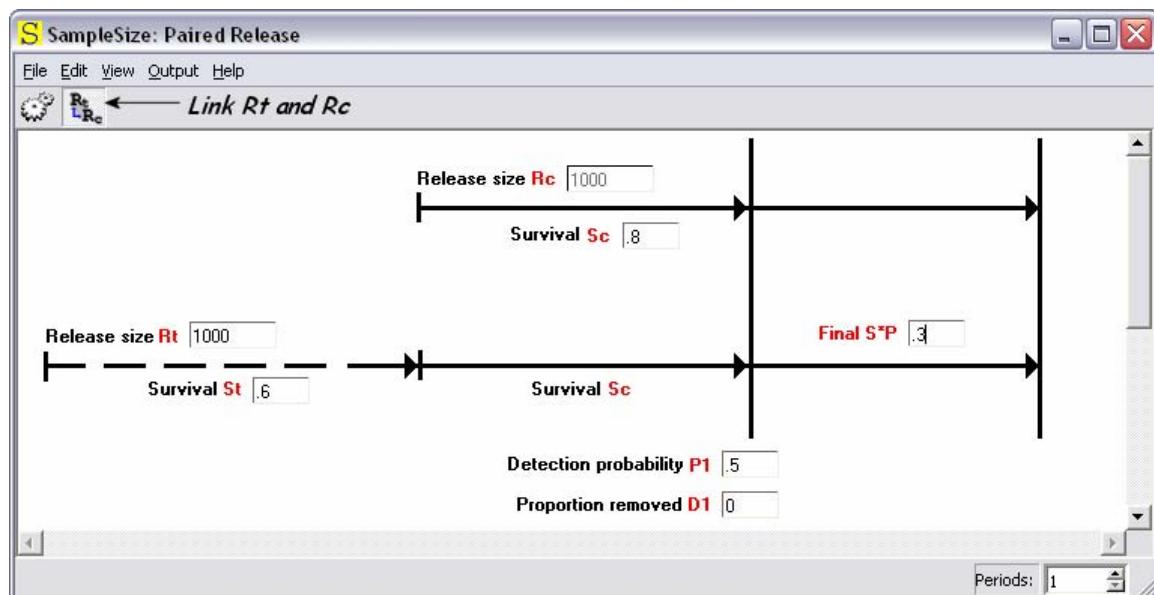


**Fig. 5.** Graph for a single-release study with  $R0$  specified as the range of values. Red indicates 90% confidence intervals and blue, 95% confidence intervals.

## Program SampleSize (cont.)

Figure 6 (below) displays the SampleSize dialog for a paired-release study. It is similar to the single-release study dialog (Fig. 2), and the process for entering values and ranges of values is same.

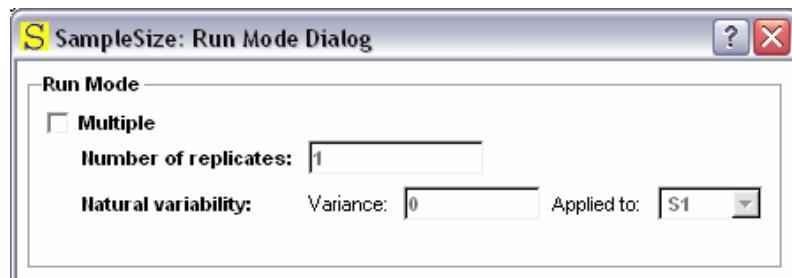
treatment effect. As shown in Fig. 6, there is an additional button to allow the treatment and control release sizes to be equal. If depressed, the  $R_c$  release is forced to have the same value as  $R_t$ .



**Fig. 6.** SampleSize dialog for a paired-release study.

For a paired-release study, there is a control release ( $R_c$ ) and a treatment release ( $R_t$ ). The control release is assumed to have the survival probability  $S_c$  from release to the first re-sampling occasion, and the treatment release is assumed to have the survival probability of  $S_c * S_t$ , where  $S_t$  represents the

For the single- and paired-release studies, an additional window appears as shown in Fig. 7. This allows the sample size calculations to be adjusted for the natural variability between replicate releases. If the "Multiple" box is selected, the user must specify the number of replicates and an estimate for the amount of natural variability expected.

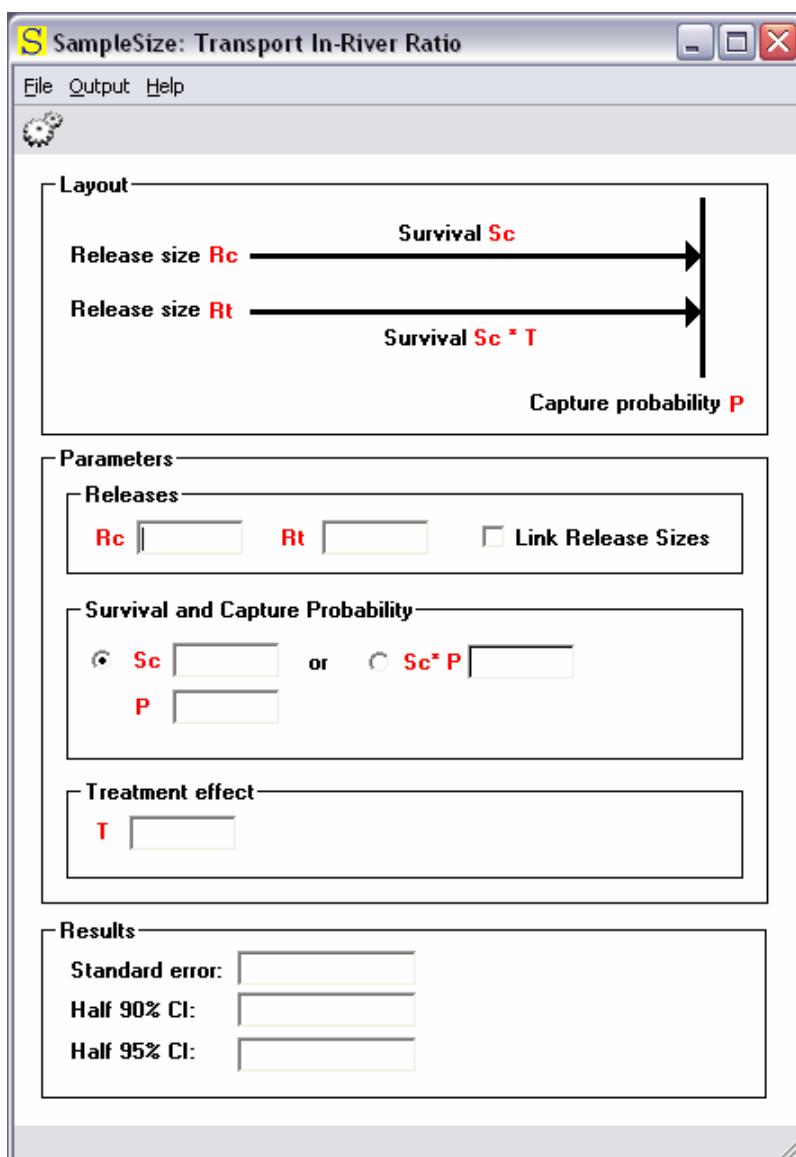


**Fig. 7.** Dialog for natural variability among replicate releases.

## Program SampleSize (cont.)

Figure 8 (below) shows the SampleSize dialog window for transport-inriver ratio studies. The process is fundamentally the same as previously described, with parameters specific to the type of study. The transport-inriver ratio study is a special case of the paired release-recapture

study (Fig. 6) in that only one detection site is used. Both release groups consequently experience the same basic survival ( $S_c$ ) and capture probabilities ( $P$ ), but the treatment release ( $R_t$ ) is expected to have an additional multiplicative effect ( $T$ ) applied to it (i.e., transportation).



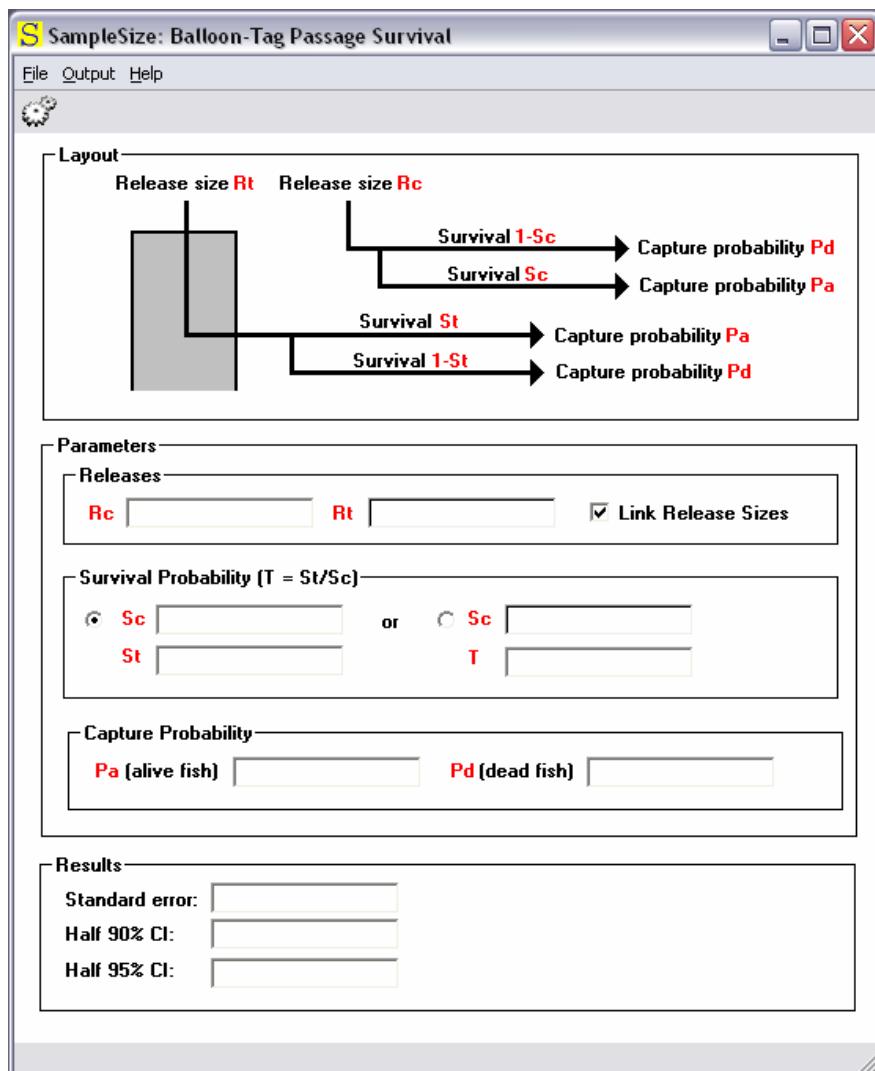
**Fig. 8.** SampleSize dialog for a transport-inriver study.

## Program SampleSize (cont.)

Figure 9 (below) shows the SampleSize dialog for balloon-tag passage survival studies. This model is appropriate in balloon-tag passage survival studies where capture probabilities may differ between those fish that are alive after passage ( $P_a$ ) and those that have suffered mortality ( $P_d$ ). Capture probabilities are expected to be the same regardless of the route

taken—depending only on the status of the fish.

In addition to assisting investigators better prepare their study, this tool enables exploration of alternative “what-if” scenarios. The latest version of the software and the current user’s manual are available at the CBR website: [SampleSize](#) or [www.cbr.washington.edu/paramest/samplesize](http://www.cbr.washington.edu/paramest/samplesize).



**Fig. 9.** SampleSize dialog for a balloon-tag passage survival study.