Tributary Survival SampleSize MANUAL

STATISTICAL ANALYSIS OF JUVENILE PIT-TAG DETECTIONS IN TRIBUTARIES

COLUMBIA BASIN RESEARCH

SCHOOL OF AQUATIC AND FISHERY SCIENCES

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Program Tributary Survival SampleSize

for Estimating Survival in Tributaries

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Table of Contents

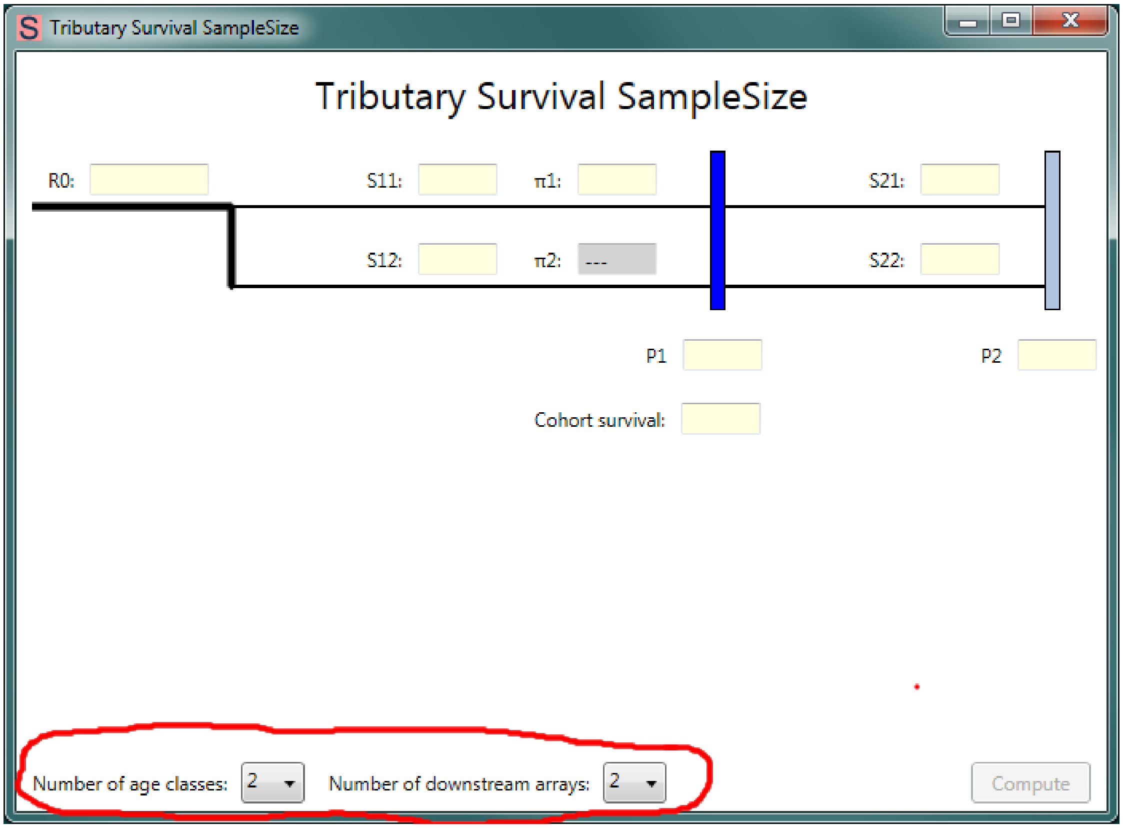
Chapter 1: Overview

Studies have shown that many juvenile salmon and steelhead stay upstream in the tributaries one or more years before migrating downstream, and traditional release-recapture models are not valid for analyzing these data. This was the motivation behind the development of Program TribPit, available on the Columbia Basin Research Tributary Survival SampleSize page. The details of the model are explained in the TribPit User's Manual available at the same website.

The Program Tributary Survival SampleSize was developed to allow project managers to calculate the required sample sizes for studies in the tributaries to achieve a required precision of cohort survival at the first detection site.

Chapter 2: Study Configuration

When the Tributary Survival SampleSize program is started, a splash screen is displayed. It will go away in about five seconds, or the user can simply click on it to dismiss it. The user then sees the data entry dialog as shown in Figure 1.

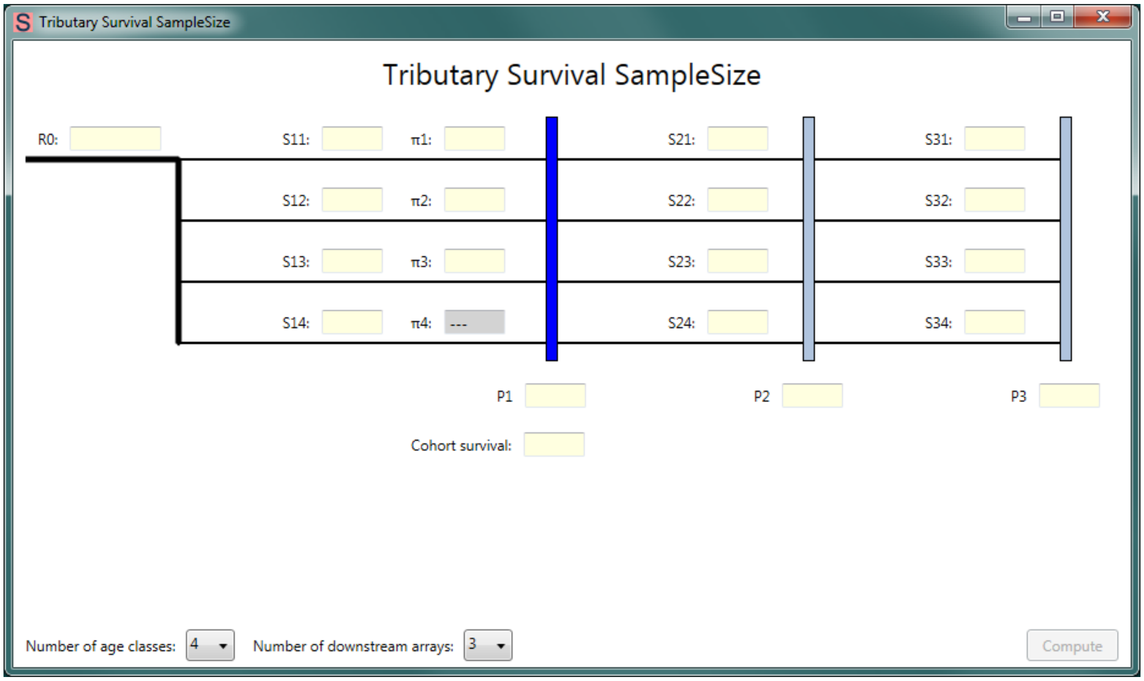


Number of age classes: 2

Number of downstream arrays: 2

Figure 1. Data entry dialog when user starts the Tributary Survival SampleSize program.

At the bottom of the dialog are two user controls (circled in red in Figure 1), allowing the user to set (1) the number of age classes, and (2) the number of downstream arrays. The number of age classes can be set between 2 and 9, and the number of downstream arrays can be either 2 or 3. At initial startup, the number of age classes is 2 and the number of downstream arrays is set to 2. When the user changes the number of age classes and/or number of downstream arrays, the diagram immediately changes to reflect the new configuration. For example, see below in Figure 2.



Number of age classes: 4

Number of downstream arrays: 3

Figure 2. Data entry dialog with 4 age classes and 3 downstream array.

Notice that now there are three detection sites rather than two. The first detection site is highlighted in dark blue—it is the site for which cohort survivals are being estimated. The subsequent downstream sites are in a lighter shade of blue.

Chapter 3: Data Entry

The user enters data for the sample size calculation in the text boxes with a light-yellow background. The values to be entered are:

Parameter **Definition**

R_0 = release size, either a single value or a range of values as explained below.

S_{1j} = estimated survival probability for the first reach for age class *j* (*j* being a number between 1 and the number of age classes). Survival probability must be between 0 and 1.

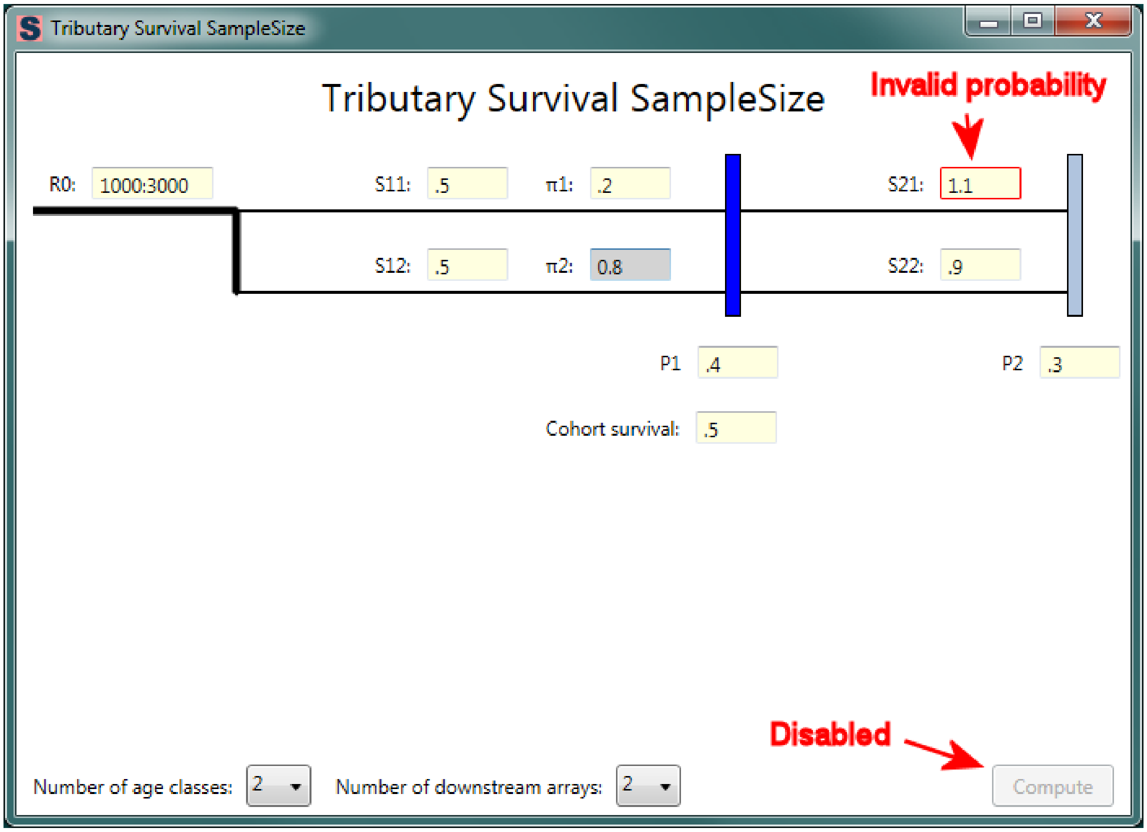
π_j = estimated proportion of individuals of age class *j* that survive to the first detection site. The proportion must be between 0 and 1. In addition, all the proportions must sum to 1. Notice that the final proportion is in gray. The user does not enter a value for the final proportion; it is automatically set to 1 minus the sum of the other proportions.

S_{ij} = estimated survival probability for the downstream sites. For three downstream arrays, the user enters estimates for S_{2j} and S_{3j}; for two downstream arrays, only values for S_{2j} are required. The survival probabilities must be between 0 and 1.

P_i = estimated detection probability for site *i*, between 0 and 1.

Cohort survival = estimated overall cohort survival for the first detection site, between 0 and 1.

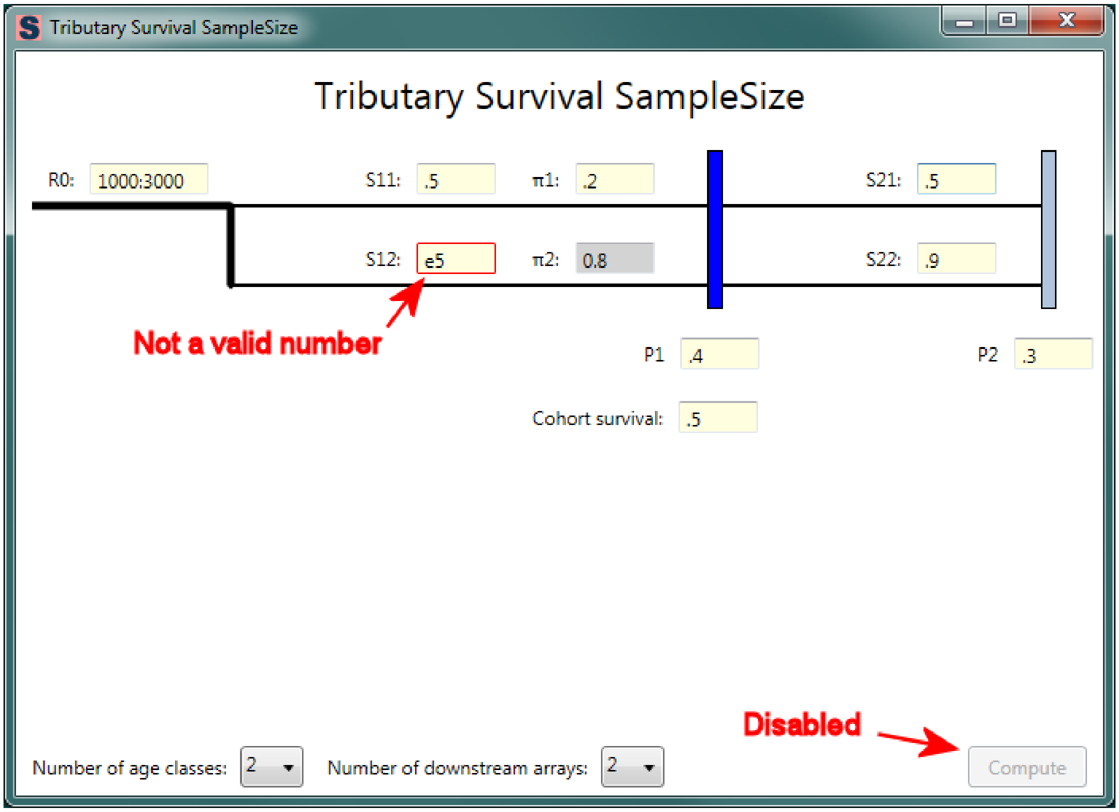
The “Compute” button at the bottom left is grayed out (disabled) when the program is started. It is only enabled when there is a valid entry in each user input. When user input is invalid, the text box with the invalid input is outlined in red. In Figure 3, the user entered “1.1” for the survival in reach 2, age class 1. The text box is outlined in red, and the compute button is disabled.



R0: 1000:3000
S11: .5
π1: .2
S21: 1.1
S12: .5
π2: 0.8
S22: .9
P1 .4
P2 .3
Cohort survival: .5
Number of age classes: 2
Number of downstream arrays: 2

Figure 3. Data entry dialog with an invalid value for a survival probability.

In Figure 4, an invalid number has been entered; hence, the compute button is disabled.



R0: 1000:3000

S11: .5

π1: .2

S21: .5

S12: e5

π2: 0.8

S22: .9

P1 .4

P2 .3

Cohort survival: .5

Number of age classes: 2

Number of downstream arrays: 2

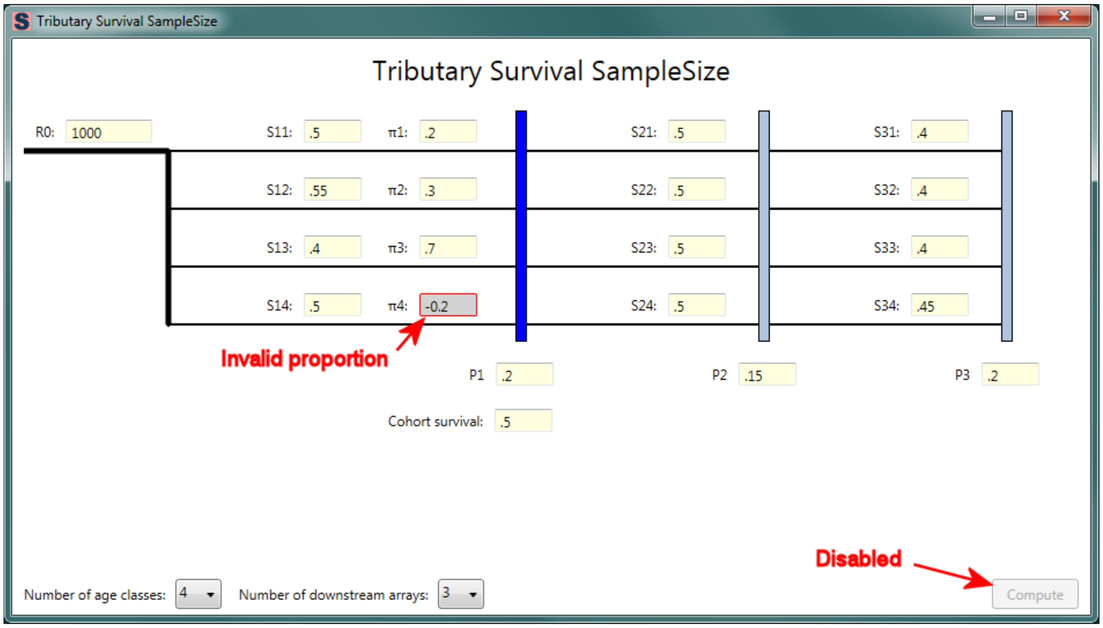
Not a valid number

Disabled

Figure 4. Data entry dialog with an invalid number.

Entering the Proportions

The proportions (π_j) represent the number of age class *j* that survive to the first detection site. The proportion for the final age class is in gray because it is not a user input; it is calculated automatically so that the sum of all the proportions is 1.0. Thus, not only must the proportions be between 0 and 1, but they must sum to 1.0. In Figure 5, the user has entered proportions between 0 and 1 for the first three age class, but they sum to 1.2, causing the final proportion to be set to -1.2.



R0: 1000

S11: .5 π1: .2 S21: .5 S31: .4

S12: .55 π2: .3 S22: .5 S32: .4

S13: .4 π3: .7 S23: .5 S33: .4

S14: .5 π4: -0.2 S24: .5 S34: .45

P1 .2 P2 .15 P3 .2

Cohort survival: .5

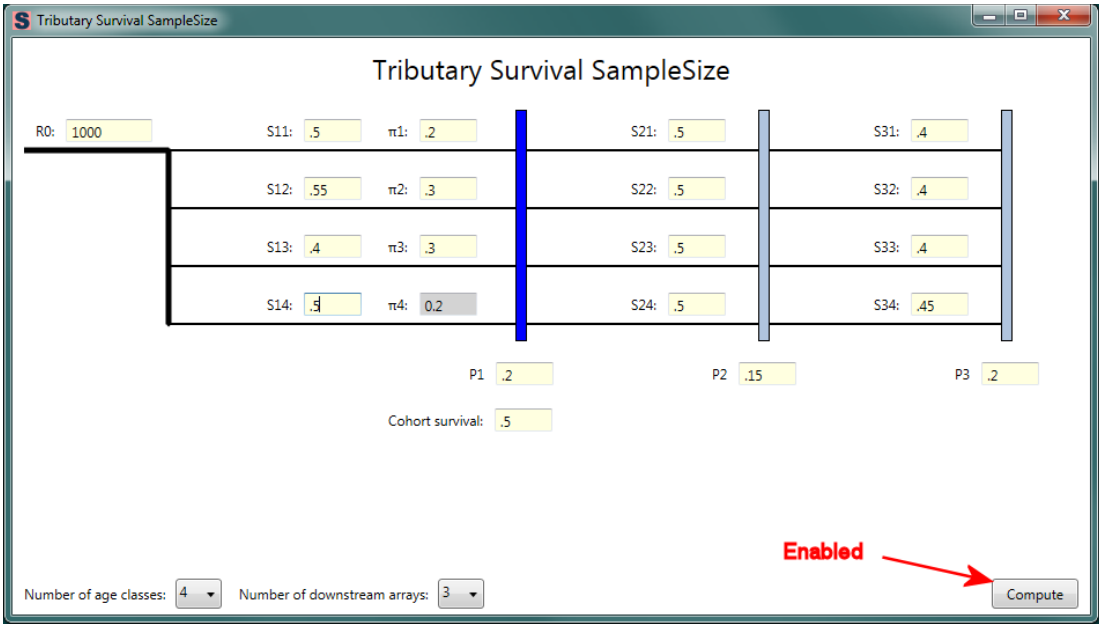
Number of age classes: 4 Number of downstream arrays: 3

Invalid proportion

Disabled

Figure 5. Data entry dialog with invalid proportions.

Figure 6 shows an example with all entries valid and the compute button enabled.



R0: 1000

S11: .5 π1: .2 S21: .5 S31: .4

S12: .55 π2: .3 S22: .5 S32: .4

S13: .4 π3: .3 S23: .5 S33: .4

S14: .5 π4: 0.2 S24: .5 S34: .45

P1 .2 P2 .15 P3 .2

Cohort survival: .5

Number of age classes: 4 Number of downstream arrays: 3

Enabled

Figure 6. Data entry dialog with all entries valid and the Compute button enabled.

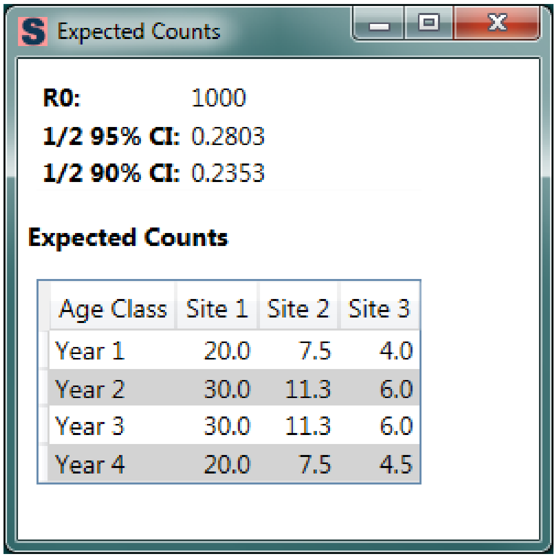
Chapter 4: Compute Function

When the user presses the Compute button, one of two actions will be performed: (1) If a single value for the release size (R_0) is entered, a table of expected counts is shown; (2) if a range is entered for R_0, a plot of ½ confidence intervals as a function of the release size is shown.

Single Value for the Release Size

If the user enters a single value for the release size, a table will be produced as shown in Figure 7. The first three lines are:

1. The entered release size,
2. ½ of a 95% confidence interval,
3. ½ of a 90% confidence interval.



R0: 1000
1/2 95% CI: 0.2803
1/2 90% CI: 0.2353

Expected Counts

Age Class	Site 1	Site 2	Site 3
Year 1	20.0	7.5	4.0
Year 2	30.0	11.3	6.0
Year 3	30.0	11.3	6.0
Year 4	20.0	7.5	4.5

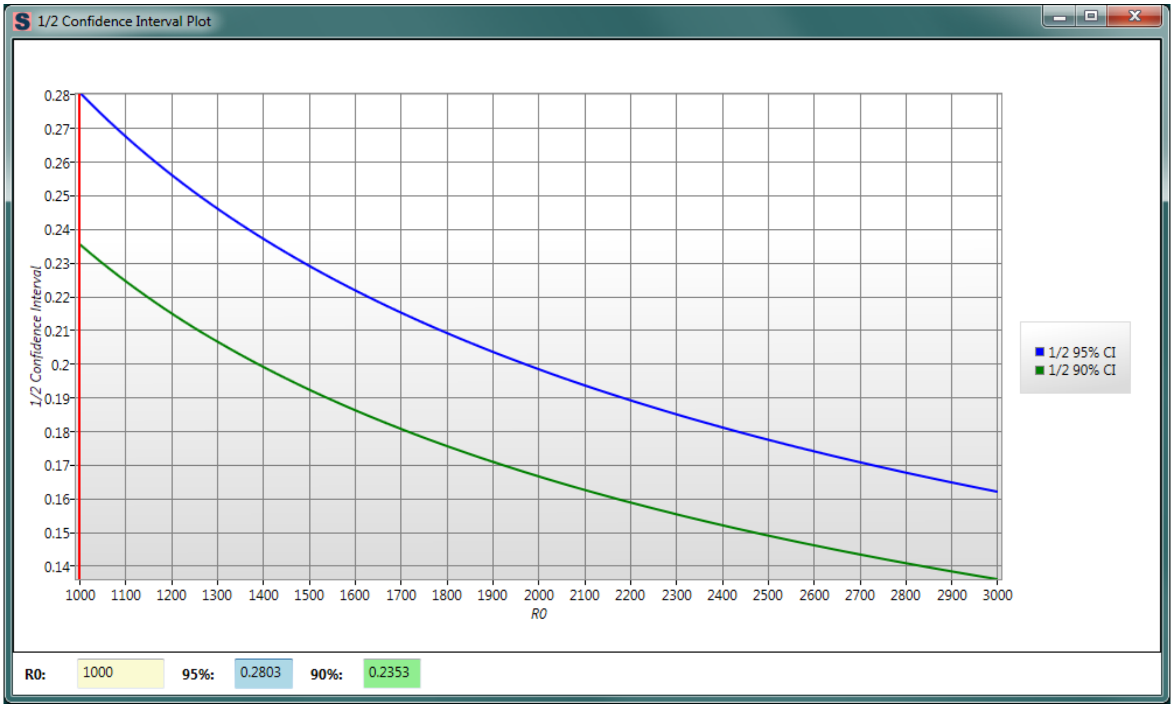
Figure 7. Table produced when a single value is entered for the release size.

In the example shown in Figure 7, if the user had entered, say, 0.55 for the cohort survival, a 95% confidence interval would be 0.55 ± 0.2803, and a 90% confidence interval would be 0.55 ± 0.2353.

The second part of the table shows the expected counts for each age class and site based on the user inputs.

Range of Values for the Release Size

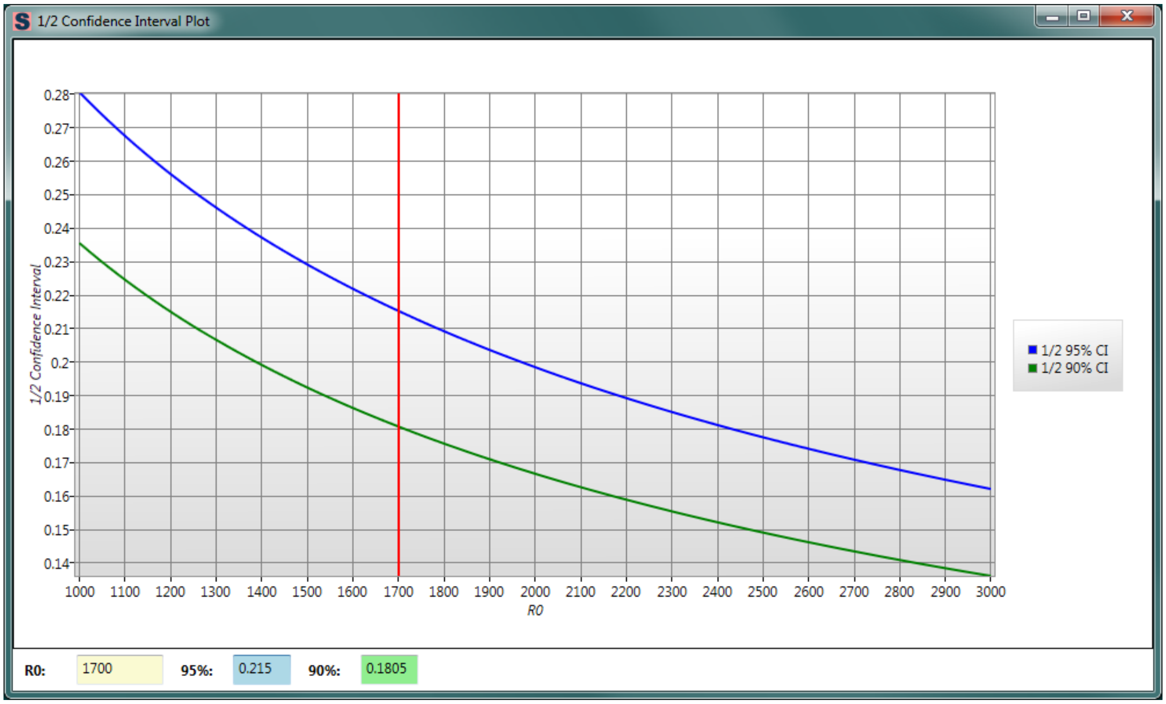
The user has the option of entering a range of values for R_0 in the form “min:max.” For example, in Figure 4, the user specified a range of values from 1,000 to 3,000 for R_0. When the user presses the Compute button for a range of values for the release size, a plot appears as shown in Figure 8. The X axis is the release size R_0, and the Y axis is the corresponding values for the confidence intervals. The 95% confidence interval is represented by the blue line, and the 90% confidence interval is represented by the green line.



R0: 1000 **95%:** 0.2803 **90%:** 0.2353

Figure 8. Plot for a range of values for the release size.

When the plot first appears, a vertical red line is positioned at the left side at the minimum release size. When the user left clicks on the plot, the line will move to the mouse position. The user can then drag the red “tracker” line by holding the left mouse button and moving the mouse. The text boxes at the bottom of the plot show the release size (R_0), ½ of a 95% confidence interval (blue background), and ½ of 90% confidence interval (green background) corresponding to the current position of the red tracking line. In Figure 9, the user has positioned the red tracking line at a release size of 1700. If the cohort survival is 0.55, then a 95% confidence interval for R_0 = 1700 would be 0.55 ± 0.215, and a 90% confidence interval would be 0.55 ± 0.1805.



R0: 1700 **95%:** 0.215 **90%:** 0.1805

Figure 9. Plot for a range of values with the red tracking line positioned at R_0 = 1700.

Alternately, the user can edit the value in the R_0 text box directly, causing the red tracking line to move to the specified value.

Appendix: Calculations

Calculate the Migration Proportions

Parameter **Definition**

S = cohort survival to three first detection site,

S_{ij} = reach survival to site i, age class j,

P_i = detection probability at site i,

π_j = proportion of those reaching the first detection site in year j,

R_0 = number released, and

K = number of age classes.

Calculate θ_j = probability of migrating in year j. Let $\tau_j = \theta_j S_{ij}$.

$$S = \sum_{k=1}^{K} \theta_k S_{1k} = \sum_{k=1}^{K} \tau_k \tag{1}$$

$$\pi_j = \frac{\tau_j}{\sum_{k=1}^{K} \tau_k}. \tag{2}$$

Equations (1) and (2) can be written for 2 age classes:

$$\begin{bmatrix} \pi_1 - 1 & \pi_1 \\ 1 & 1 \end{bmatrix} \begin{bmatrix} \tau_1 \\ \tau_2 \end{bmatrix} = \begin{bmatrix} 0 \\ S \end{bmatrix}.$$

For 3 age classes:

$$\begin{bmatrix} \pi_1 - 1 & \pi_1 & \pi_1 \\ \pi_2 & \pi_2 - 1 & \pi_2 \\ 1 & 1 & 1 \end{bmatrix} \begin{bmatrix} \tau_1 \\ \tau_2 \\ \tau_3 \end{bmatrix} = \begin{bmatrix} 0 \\ 0 \\ S \end{bmatrix}.$$

In general

$$M\vec{\tau} = \vec{y}$$

$$\vec{\tau} = M^{-1}\vec{y},$$

so

$$\theta_j = \frac{\tau_j}{S_{1j}}.$$

Calculate the Variance of $\widehat{S}$

$$\hat{S} = \frac{n_1}{\hat{P}_1 R_0},$$

where n_1 = number detected at the first detection site.

$$E(n_1) = R_0 p_1 \sum_{k=1}^{K} \theta_k S_{1k}$$

$$\mathrm{Var}(\hat{S}) = \mathrm{Var}\left[E\left(\hat{S}\middle|p_1\right)\right] + E\left[\mathrm{Var}\left(\hat{S}\middle|p_1\right)\right]$$

$$E\left(\hat{S}\middle|p_1\right) = \frac{n_1}{\hat{p}_1 R_0}$$

$$\mathrm{Var}\left[E\left(\hat{S}\middle|p_1\right)\right] = \tfrac{n_1^2}{R_0^2}\mathrm{Var}\left(\tfrac{1}{p_1}\right).$$

Using the delta method

$$\mathrm{Var}\left(\frac{1}{\hat{p}_1}\right) = \frac{1}{p_1^4} Var(\hat{p}_1)$$

$$\mathrm{Var}\left[E\left(\hat{S}\middle|\hat{p}_1\right)\right] = \frac{n_1^2}{R_0^2 p_1^4} \mathrm{Var}(\hat{p}_1)$$

$$\mathrm{Var}\left(\hat{S}\middle|p_1\right) = \frac{1}{\hat{p}_1^2 R_0^2} \mathrm{Var}(n_1)$$

$$\mathrm{Var}\left(\hat{S}\middle|p_1\right) = \frac{1}{\hat{p}_1^2 R_0^2} \cdot R_0 \cdot p(n_1) \cdot \left(1 - p(n_1)\right)$$

$$\mathrm{Var}\left(\hat{S}\middle|p_1\right) = \frac{1}{\hat{p}_1^2 R_0} \cdot p_1 \hat{S}\left(1 - p_1 \hat{S}\right)$$

$$E\left[\mathrm{Var}\left(\hat{S}\middle|p\right)\right] = \frac{\hat{S}}{\hat{p}_1 R_1}\left(1 - \hat{p}_1 \hat{S}\right)$$

$$\mathrm{Var}\left(\hat{S}\right) = \frac{n_1^2}{R_0^2 \hat{p}_1^4} \mathrm{Var}(\hat{p}_1) + \frac{\hat{S}}{\hat{p}_1 R_0}\left(1 - \hat{p}_1 \hat{S}\right).$$

Substituting $E(n_1)$ for n_1

$$\mathrm{Var}\left(\hat{S}\right) = \frac{R_0^2 \hat{p}_1^2 \hat{S}^2}{R_0^2 \hat{p}_1^4} \mathrm{Var}(\hat{p}_1) + \frac{\hat{S}}{\hat{p}_1 R_0}\left(1 - \hat{p}_1 \hat{S}\right)$$

$$\mathrm{Var}\left(\hat{S}\right) = \frac{\hat{S}^2}{\hat{p}_1^2} \mathrm{Var}(\hat{p}) + \frac{\hat{S}}{\hat{p}_1 R_0}\left(1 - \hat{p}_1 \hat{S}\right).$$

Calculate the variance of $\hat{p}_1$

$\hat{p}_1$ can be written as

$$\hat{p}_1 = \frac{n_{11}}{n_{11} + n_{01}}.$$

Using the delta method

$$\mathrm{Var}(\hat{p}_1) = \frac{(n_{11}n_{01})^2}{(n_{11}+n_{01})^4}\left[\frac{\mathrm{Var}(n_{11})}{n_{11}^2} + \frac{\mathrm{Var}(n_{01})^2}{n_{01}^2} + \frac{2\mathrm{Cov}(n_{11}, n_{01})}{n_{11}n_{01}}\right]$$

$$\mathrm{Var}(n_{11}) = R_0 p(n_{11})\big(1 - p(n_{11})\big)$$

$$\mathrm{Var}(n_{01}) = R_0 p(n_{01})\big(1 - p(n_{01})\big)$$

$$\mathrm{Cov}(n_{11}, n_{01}) = -R_0 p(n_{11}) p(n_{01})\,.$$

Substitute in expected values for n_{11}, n_{01}.

For two downstream arrays:

$$E(n_{11}) = R_0 p_1 p_2 \sum_{k=1}^{K} \theta_k S_{1k} S_{2k}$$

$$E(n_{01}) = R_0 (1 - p_1) p_2 \sum_{k=1}^{K} \theta_k S_{1k} S_{2k}$$

For three downstream arrays:

$$E(n_{11}) = R_0 p_1 \sum_{k=1}^{K} \theta_k S_{1k} S_{2k} \,(p_2 + p_3 S_{3k} - p_2 p_3 S_{3k})$$

$$E(n_{01}) = R_0 (1 - p_1) \textstyle\sum_{k=1}^{K} \theta_k S_{1k} S_{2k} \,(p_2 + p_3 S_{3k} - p_2 p_3 S_{3k}).$$

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