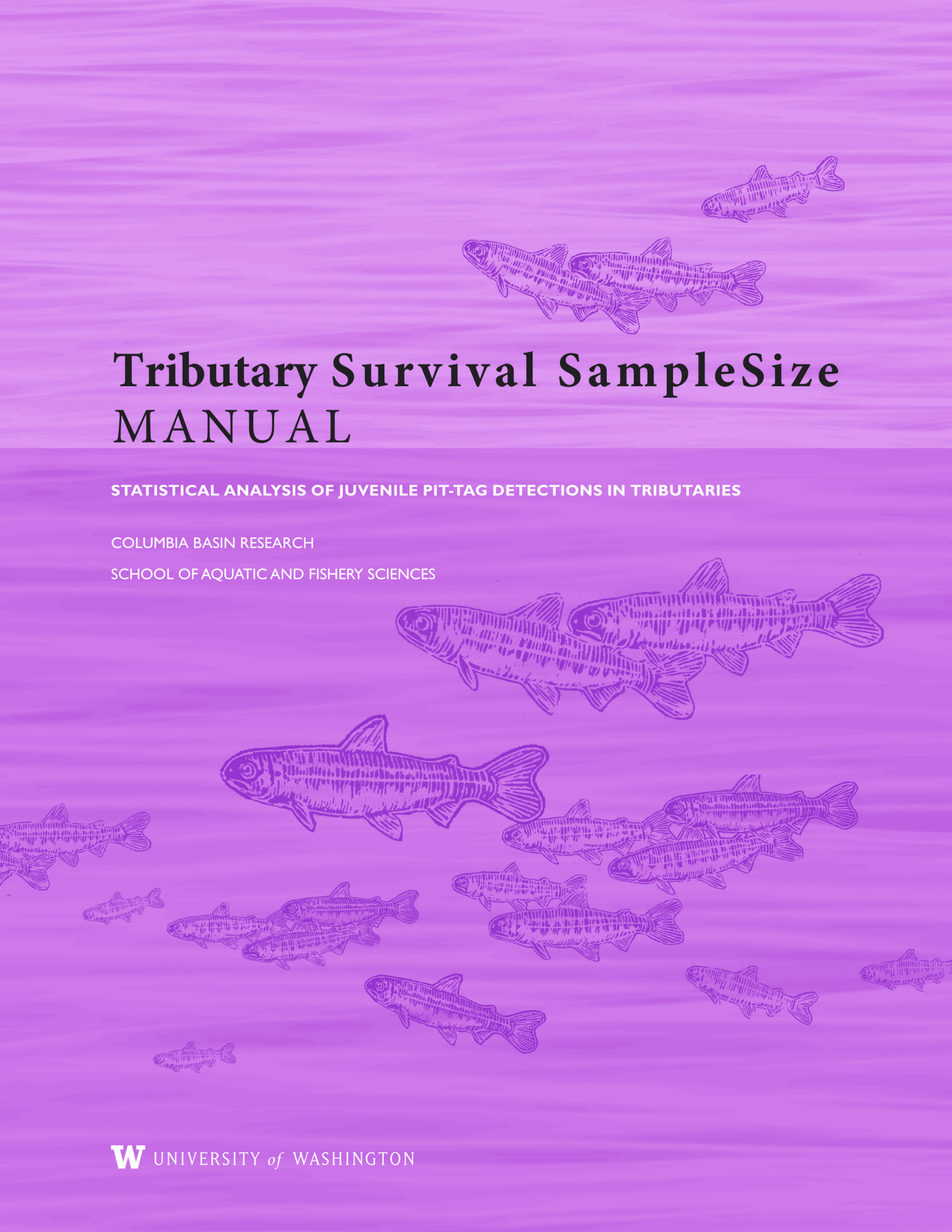


The background of the cover features several stylized, hand-drawn illustrations of juvenile fish, likely trout or salmon, swimming in various directions. The drawings are in a simple, sketchy style with visible scales and fins. They are scattered across the page, with some larger fish in the center and smaller ones towards the edges.

Tributary Survival SampleSize MANUAL

STATISTICAL ANALYSIS OF JUVENILE PIT-TAG DETECTIONS IN TRIBUTARIES

COLUMBIA BASIN RESEARCH

SCHOOL OF AQUATIC AND FISHERY SCIENCES

Program TribPit SampleSize

for Estimating Survival in Tributaries

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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 at www.cbr.washington.edu/analysis/apps/TribPit. The details of the model are explained in the TribPit User's Manual available at the same website.

The Program TribPit 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.

The screenshot shows the 'Tributary Survival SampleSize' data entry dialog. The window has a title bar with the program name and standard Windows controls. The main area contains a diagram of a river with a dam. Upstream of the dam are two sampling points, S11 and S12, with input fields for their respective values. A vertical blue line represents the dam. Downstream of the dam are two more sampling points, S21 and S22, also with input fields. Below the diagram are input fields for P1, P2, and Cohort survival. At the bottom of the dialog, there are two dropdown menus: 'Number of age classes' and 'Number of downstream arrays', both set to 2. A 'Compute' button is located in the bottom right corner.

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.

The screenshot shows a software window titled "Tributary Survival SampleSize". Inside, there is a diagram representing a river system with four age classes (rows) and three downstream arrays (columns). The first column is labeled "R0:" and the subsequent columns are labeled "S11:", "S12:", "S13:", "S14:" for the first array; "π1:", "π2:", "π3:", "π4:" for the second array; "S21:", "S22:", "S23:", "S24:" for the third array; and "S31:", "S32:", "S33:", "S34:" for the fourth array. Each cell contains a text input field. A thick dark blue vertical line is positioned between the second and third columns, and a lighter blue vertical line is between the third and fourth columns. Below the grid, there are three input fields labeled "P1", "P2", and "P3", and a "Cohort survival:" label with an input field. At the bottom left, there are two dropdown menus: "Number of age classes:" set to 4 and "Number of downstream arrays:" set to 3. A "Compute" button is located at the bottom right.

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:

R_0	The release size, either a single value or a range of values as explained below.
S_{1j}	The estimated survival probability for the first reach for age class j (j being a number between 1 and the number of age classes). The survival probability must be between 0 and 1.
π_j	The 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}	The 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	The estimated detection probability for site i , between 0 and 1.
Cohort survival	The 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.

The screenshot shows the "Tributary Survival SampleSize" dialog box. The title bar includes a red 'S' icon and the text "Tributary Survival SampleSize". The main area contains a diagram of a river reach with two age classes (1 and 2) and two downstream arrays (S11, S12 and S21, S22). The inputs are as follows:

Parameter	Value
R0:	1000:3000
S11:	.5
π_1 :	.2
S21:	1.1
S12:	.5
π_2 :	0.8
S22:	.9
P1:	.4
P2:	.3
Cohort survival:	.5

At the bottom, there are two dropdown menus: "Number of age classes:" set to 2 and "Number of downstream arrays:" set to 2. The "Compute" button is grayed out and labeled "Disabled" with a red arrow pointing to it. A red arrow also points to the S21 input box, which is outlined in red and labeled "Invalid probability".

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.

The screenshot shows a software window titled "Tributary Survival SampleSize". Inside, there is a diagram of a river with two detection sites. The input fields are as follows:

Field	Value
R0:	1000:3000
S11:	.5
π_1 :	.2
S21:	.5
S12:	e5
π_2 :	0.8
S22:	.9
P1:	.4
P2:	.3
Cohort survival:	.5

At the bottom, there are two dropdown menus: "Number of age classes:" set to 2 and "Number of downstream arrays:" set to 2. The "Compute" button is disabled, indicated by a red arrow and the text "Disabled". A red arrow also points to the "S12:" field with the text "Not a valid number".

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.

The screenshot shows the 'Tributary Survival SampleSize' dialog box. It features a hierarchical tree structure with nodes R0, S11-S14, S21-S24, S31-S34, P1-P3, and Cohort survival. The 'm4' field under S14 is highlighted in red with the text 'Invalid proportion' and a red arrow pointing to it. The 'Compute' button at the bottom right is disabled, indicated by a red arrow and the text 'Disabled'. The 'Number of age classes' is set to 4 and 'Number of downstream arrays' is set to 3.

Node	Value
R0	1000
S11	.5
π 1	.2
S12	.55
π 2	.3
S13	.4
π 3	.7
S14	.5
π 4	.0.2
S21	.5
S22	.5
S23	.5
S24	.5
S31	.4
S32	.4
S33	.4
S34	.45
P1	.2
P2	.15
P3	.2
Cohort survival	.5

Figure 5. Data entry dialog with invalid proportions

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

The screenshot shows the 'Tributary Survival SampleSize' dialog box with all entries valid. The 'm4' field under S14 is now 0.2 (without a decimal point) and is no longer highlighted. The 'Compute' button at the bottom right is now enabled, indicated by a red arrow and the text 'Enabled'. The 'Number of age classes' is set to 4 and 'Number of downstream arrays' is set to 3.

Node	Value
R0	1000
S11	.5
π 1	.2
S12	.55
π 2	.3
S13	.4
π 3	.3
S14	.5
π 4	0.2
S21	.5
S22	.5
S23	.5
S24	.5
S31	.4
S32	.4
S33	.4
S34	.45
P1	.2
P2	.15
P3	.2
Cohort survival	.5

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

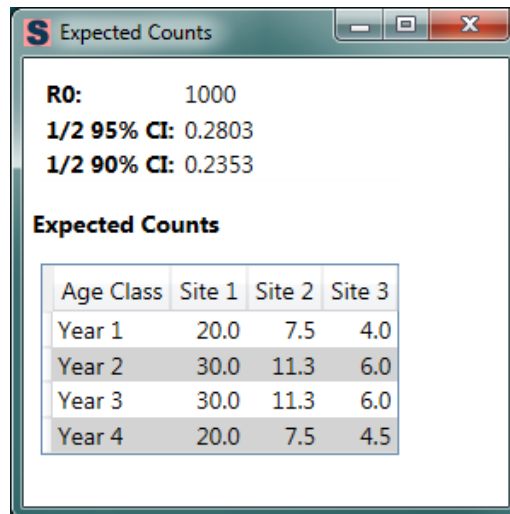
Chapter 4: Compute Function

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 $\frac{1}{2}$ 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. $\frac{1}{2}$ of a 95% confidence interval,
3. $\frac{1}{2}$ of a 90% confidence interval.



The screenshot shows a window titled "Expected Counts" with a blue header bar. Inside, the following text is displayed:

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

Below this text is a section titled "Expected Counts" containing a table with 4 rows and 4 columns. The columns are labeled "Age Class", "Site 1", "Site 2", and "Site 3". The rows are labeled "Year 1", "Year 2", "Year 3", and "Year 4".

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.

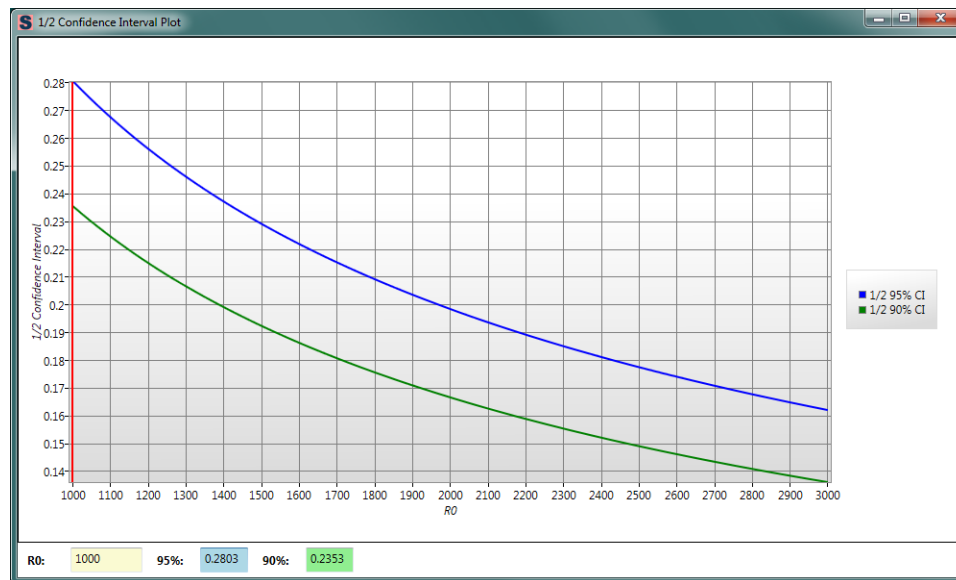


Figure 8. Plot for a range of values for the release size

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), $\frac{1}{2}$ of a 95% confidence interval (blue background), and $\frac{1}{2}$ 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 .

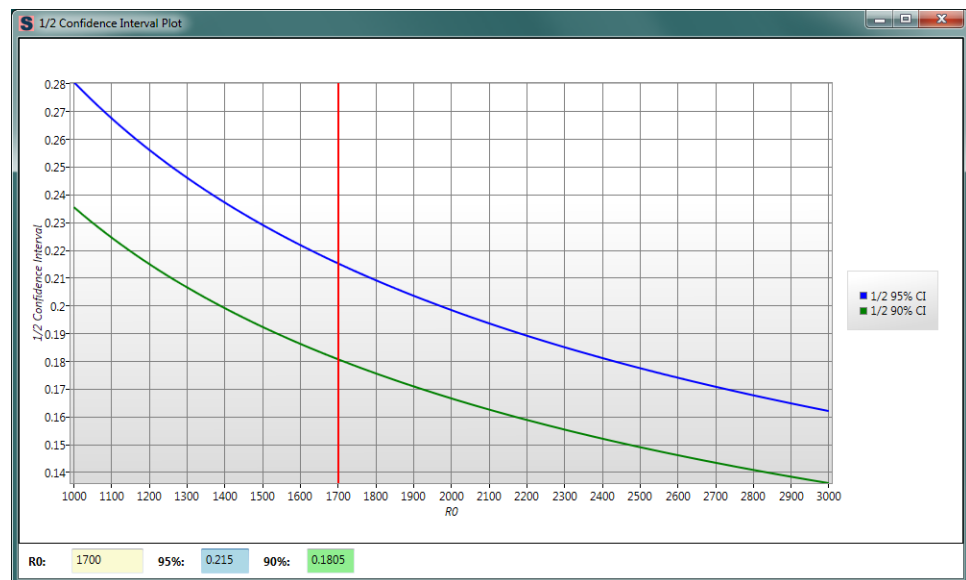


Figure 9. Plot for a range of values with the red tracking line positioned at $R_0 = 1700$

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

S = cohort survival to the 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

K = number of age classes

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

$$S = \sum_{k=1}^K \theta_k S_{1k} = \sum_{k=1}^K \tau_k \quad (1)$$

$$\pi_j = \frac{\tau_j}{\sum_{k=1}^K \tau_k} \quad (2)$$

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 $\hat{S}$

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

where n_1 = number detected at the first detection site.

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

$$\text{Var}(\hat{S}) = \text{Var}[E(\hat{S}|p_1)] + E[\text{Var}(\hat{S}|p_1)]$$

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

$$\text{Var}[E(\hat{S}|p_1)] = \frac{n_1^2}{R_0^2} \text{Var}\left(\frac{1}{p_1}\right)$$

Using the delta method

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

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

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

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

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

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

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

Substituting $E(n_1)$ for n_1

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

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

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

$$\begin{aligned} \text{Var}(\hat{p}_1) = \frac{(n_{11}n_{01})^2}{(n_{11} + n_{01})^4} & \left[\frac{\text{Var}(n_{11})}{n_{11}^2} + \frac{\text{Var}(n_{01})^2}{n_{01}^2} \right. \\ & \left. + \frac{2\text{Cov}(n_{11}, n_{01})}{n_{11}n_{01}} \right] \end{aligned}$$

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

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

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

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:

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

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

