



ATLAS 1.9 USER'S MANUAL

ACTIVE TAG LIFE ADJUSTED SURVIVAL

COLUMBIA BASIN RESEARCH

SCHOOL OF AQUATIC AND FISHERY SCIENCES

UNIVERSITY OF WASHINGTON

Program ATLAS 1.12

Active Tag Life Adjusted Survival

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Chapter 1 — Introduction

Program ATLAS was developed to analyze the survival of smolts migrating downstream in the Columbia River Basin using acoustic- and radio-tagging data. Active tagging technologies allow increased flexibility in designing survival studies but also introduces the problem of tag failure. Tag failure can be the result of mechanical or battery failure and cannot be distinguished from mortality in release-recapture studies. Therefore, the perceived survival estimates (the probability of a fish and tag being “alive”) must be adjusted for the probability of tag failure to obtain an unbiased survival estimate.

Program ATLAS has five modes of operation corresponding to five study designs:

1. **Single Release,**
2. **Paired Release,**
3. **Virtual/Paired Release,**
4. **Virtual Release with Dead Fish Correction (ViRDcT) – full, and**
5. **Virtual Release with Dead Fish Correction (ViRDcT) – reduced.**

Chapter 2 describes the ATLAS user interface. Chapter 3 describes how to perform analyses with Program ATLAS as it pertains to all study designs. See Chapter 4 for details on the Single-release mode, Chapter 5 for the paired-release mode, Chapter 6 for the virtual/paired-release mode, Chapter 7 for the full Virtual Release with Dead Fish Correction (ViRDcT) mode, and Chapter 8 for the reduced ViRDcT mode.

This manual describes Program ATLAS version 1.12. The latest version of the software, along with a .pdf copy of this manual, is available on the Columbia Basin Research website [on the Columbia Basin Research ATLAS page](#).

Chapter 2 — ATLAS User Interface

When running Program ATLAS for the first time, an initial splash screen appears followed by the initial dialog for study design selection as shown in Figure 2.1. To skip this window on subsequent runs, uncheck the check box in the lower right corner of the dialog. The ability to change the default study design is still available under the **Edit** menu at the top of the main window.

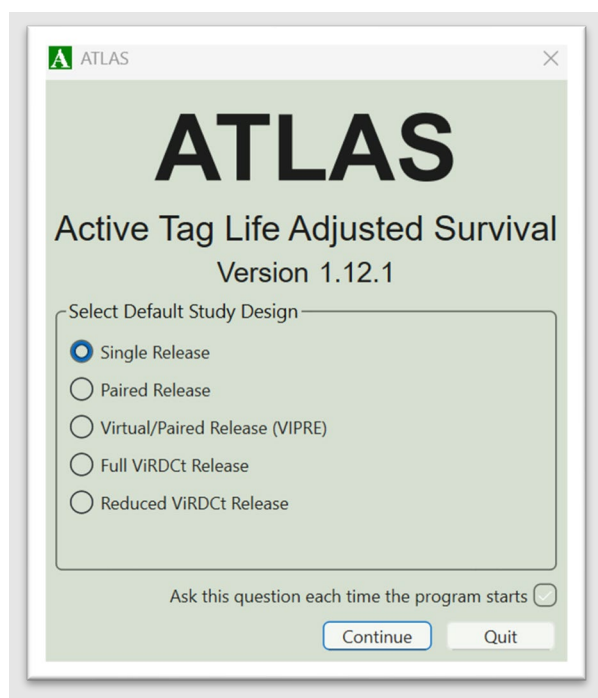


Figure 2.1: Initial dialog for study design selection.

Once the desired study design is selected, press the **Continue** button to open the main window. Figure 2.2 shows Program ATLAS upon initial startup in **Single Release** mode.

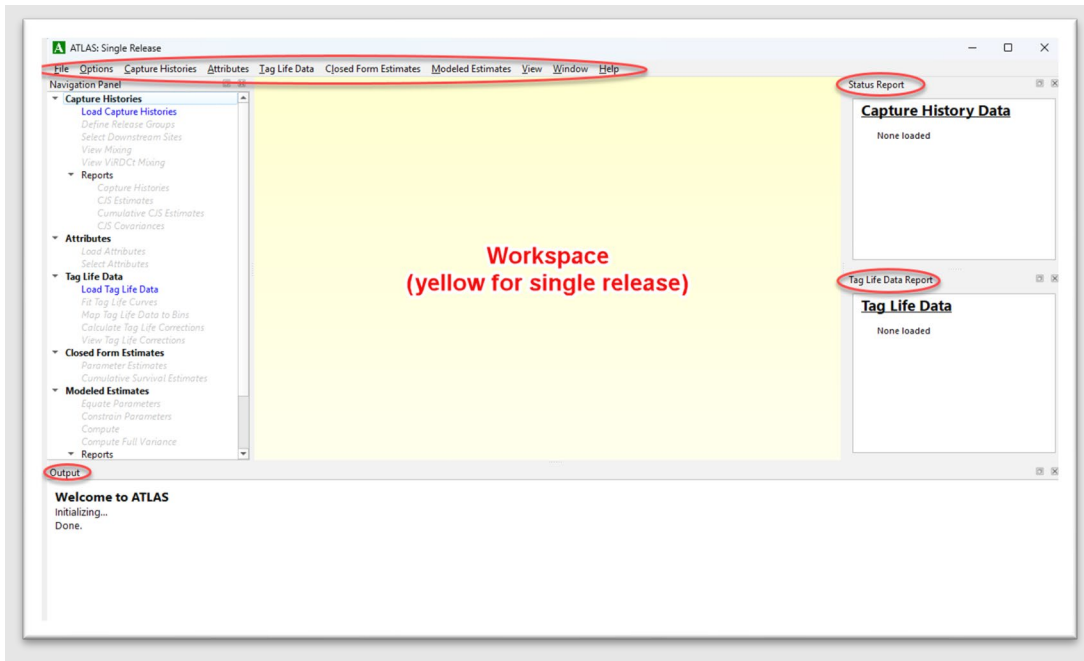


Figure 2.2: Program ATLAS at initial startup in single-release mode.

The main window (for all study designs) consists of the following components:

- The **ATLAS Menu** (i.e., the system of drop-down menus) provides alternative access to the commands on the navigation panel as well as many general setting commands for the ATLAS program.
- The **Navigation Panel** on the left side is a hierarchical list of available actions for the user to take. Actions not currently available are grayed out. An action is initiated by double clicking on it.
- The **Status Report Panel** on the right side gives the current program state. At initial startup, it simply shows that there are no capture history data loaded.
- The **Tag Life Data Report** below the status report panel shows which tag-life data have been loaded, the tag-life curve associated with each tag-life data, and the truncation count for each.

- The **Output** along the bottom is where status messages, warnings, and errors are reported as actions are performed.
- The **Workspace** with the colored background is where all subsequent reports and dialogs appear.

Any of the above (except the Workspace) can be hidden by clicking the “close window” (**X**) icon on the right of their respective title bars or via the **View** menu. They can also be unhidden via the **View** menu. Figure 2.2 shows the default positions of the main window components. The positions can be changed by dragging their title bars to a new position on the window or dragging them completely outside of the Program ATLAS window.

As shown in Figure 2.2 there is a system of drop-down menus across the top of the ATLAS main window. All the menu commands echo those available via the **Navigation Panel** and are described in later sections. Others are available only via the **ATLAS Menu**; these are described in this section.

Accessibility features: The **ATLAS Menu** provides navigation through ATLAS’s features and modeling process using the keyboard rather than the mouse. Access a specific menu or option using the “alt” key combined with the letter indicated for the selection. Navigate within menu and reports using the arrow keys or the tab key. Check boxes can be selected using the keyboard by tabbing until the check box is highlighted and then clicking the space bar.

2.1 File Menu

The **File** menu is shown in Figure 2.3. The top section echoes file-related commands available on the navigation panel. At the bottom the **Exit** command causes the ATLAS program to exit. The middle section contains commands for saving and printing reports and graphs. They are available only when a plot or report is being displayed. These commands are described as follows:

- **Save As** saves the current report or graph to a selected output file. Reports are saved in Rich Text Format (.rtf), and graphs are saved in Portable Network Graphics format (.png). For the .png files, the dimensions of the output can be specified via the **Settings** dialog (Section 2.2.1.1).
- **Print Preview** simply gives a preview of the output.
- **Print** prints the current report or graph to the selected printer.
- **Exit** leaves the program.

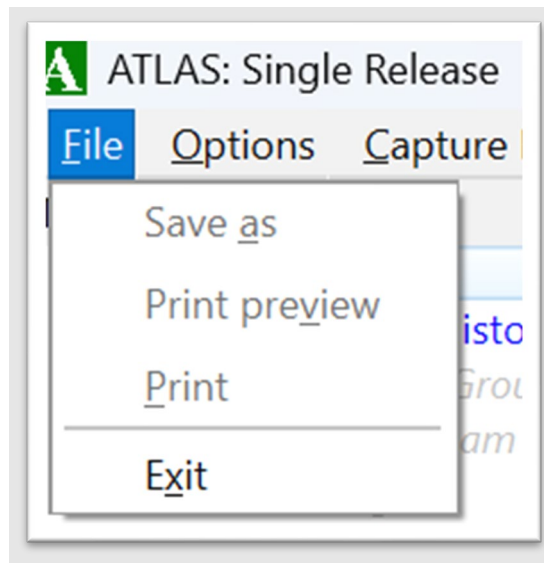


Figure 2.3: The **File** menu.

2.2 Options Menu

The Options menu is shown in Figure 2.4.

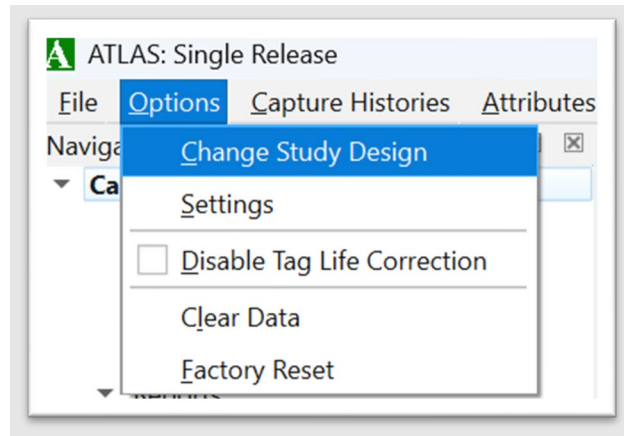


Figure 2.4: The **Edit** menu.

- **Change Study Design** allows the user to switch from one study design (single-release, paired-release, virtual/paired-release, full ViRDCT, reduced ViRDCT) to another. When selected, ATLAS will prompt for the desired study design. Changing the study design will cause all loaded data and current settings to be lost.
- **Settings** is described below in Section 2.2.1.
- **Disable Tag Life Correction** is a checkable item that allows the user to disable tag-life corrections. This allows the user to analyze mark-recapture data that did not use active tags or do not have data available from a tag-life study for use in estimating tag-life corrections.
- **Clear Data** removes all currently loaded data (capture history and tag-life data) from ATLAS.
- **Factory Reset** removes all currently loaded data and changes all settings to the initial settings that came with the program.

2.2.1 Settings

When the Settings option is selected from the Edit menu, the Settings dialog

appears with three main tabs available: (1) **Reports**, (2) **Graphics**, (3) **Bootstrapping**, (4) **Capture Histories**, and (5) **Optimizer**.

2.2.1.1 Reports Settings

Figure 2.5 shows the **Settings** dialog with the **Reports** tab selected. This option allows the user to change the level of precision displayed in all reports. The precision for the point estimates is editable separately from the precision for the standard error estimates.

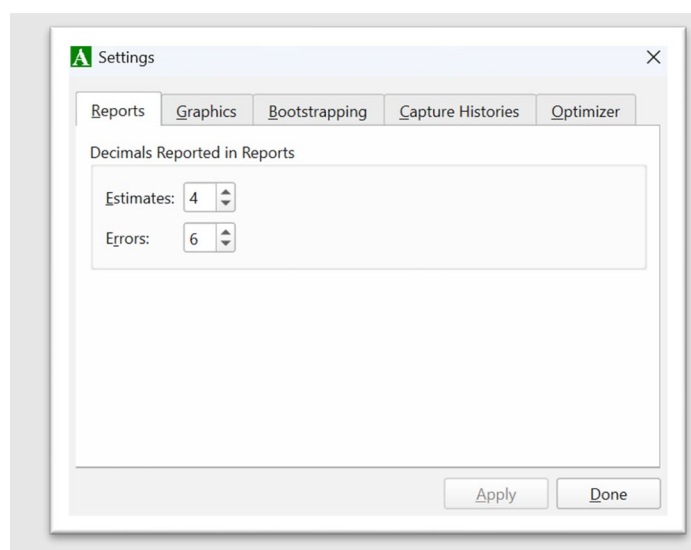


Figure 2.5: The **Reports** dialog under **Settings**.

2.2.1.2 Graphics Settings

Figure 2.6 shows the **Settings** dialog with the **Graphics** tab selected. This allows the user to change the size of any graphs saved with the **Save As** command and is set via a desired pixel size.

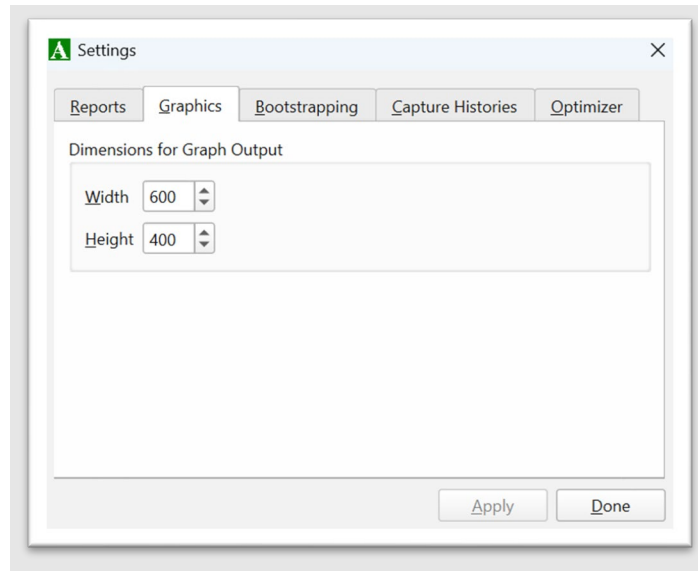


Figure 2.6: The **Graphics** dialog under **Settings**.

2.2.1.3 Bootstrapping Settings

The **Bootstrapping** tab (Figure 2.7) allows the user to set the number of bootstrap iterations for both the tag-life bootstrapping and the full variance bootstrapping (Section 3.3.3, Appendix B.2.1). The default and recommended value for both is 1000. The user is also given the option of changing these settings when performing the actual bootstrapping.

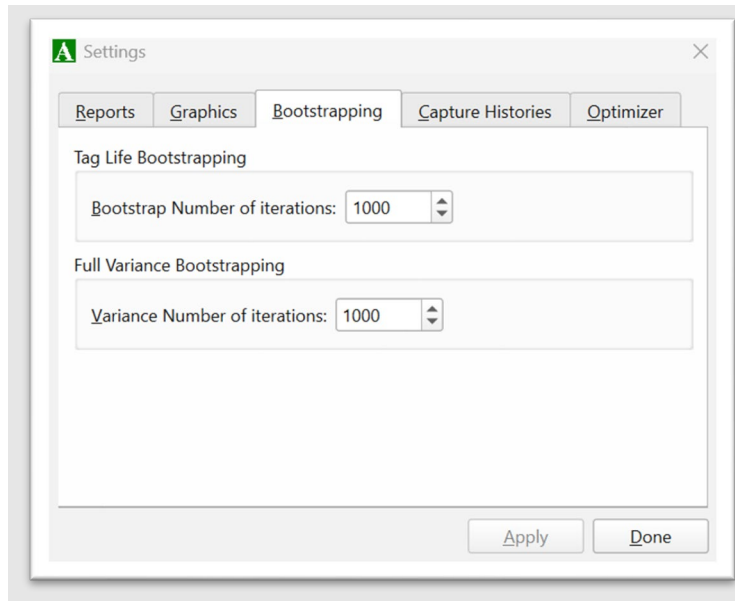


Figure 2.7: The **Bootstrapping** dialog under **Settings**.

2.2.1.4 Capture Histories Settings

Figure 2.9 shows the **Capture Histories** tab of the **Settings** dialog. The only choice in this **Settings** tab is listed under the **Capture History Report** and includes a checkbox to **Exclude captures histories with zero counts** from any analysis if the user wishes to do so. Clicking this box affects only the capture histories that are reported in the **Capture History Report**; all capture histories, including those with zero counts, are used to fit the model.

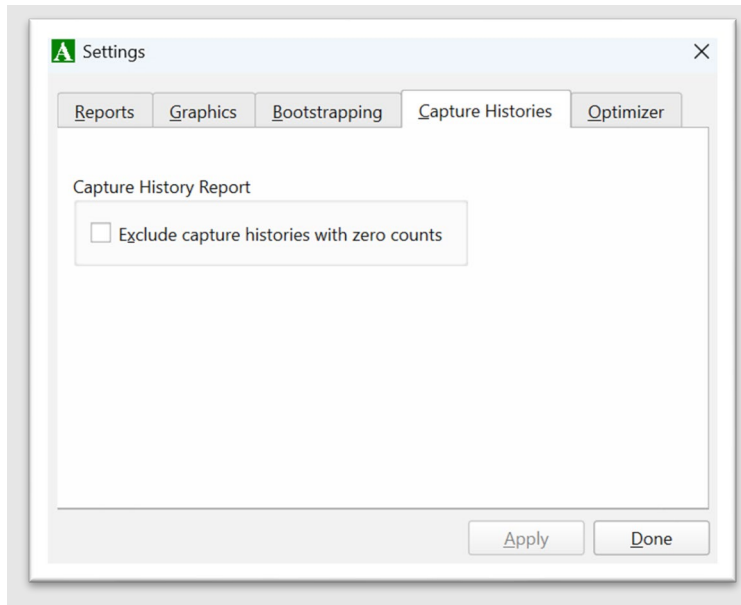


Figure 2.8: The **Capture Histories** dialog under **Settings**.

2.2.1.3 Optimizer Settings

Figure 2.9 shows the **Optimizer** dialog. **Optimizer** is used to numerically maximize the likelihood and thus calculate the parameter estimates, as described in Appendix B. Four optimizers are available:

1. **Fletcher**,
2. **Quasi-Newton (FBSG)**,
3. **Direction Set (Powell's)**, and
4. **Simplex**.

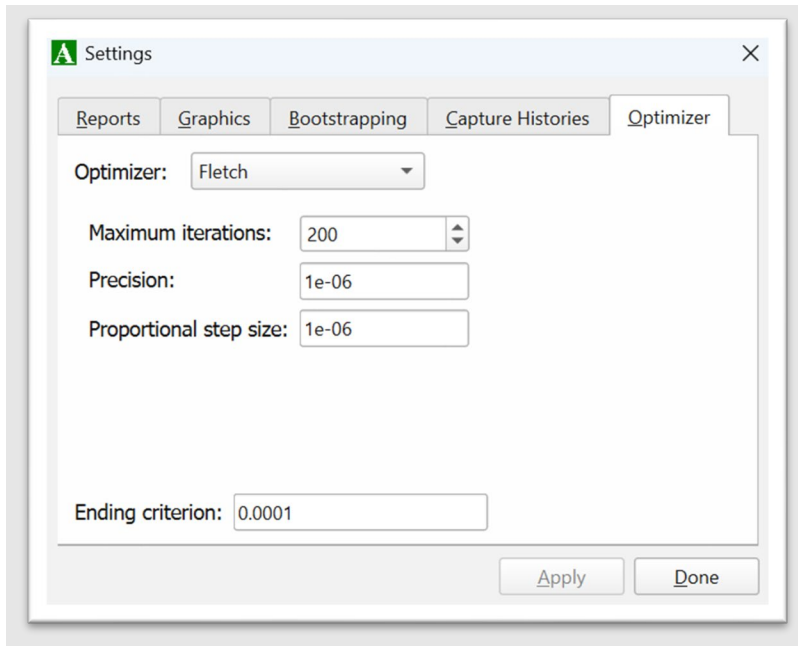


Figure 2.9: The **Optimizer** dialog under **Settings**.

Experience suggests that **Fletch**, which is a quasi-Newton optimizer, is the best choice in ATLAS. More information about the others can be found in Press et al. (2007).

2.3 Captures Histories, Attributes, Tag Life Data, Closed Form Estimates, and Modeled Estimates Menus

Figure 2.10 shows the **ATLAS Menu** and corresponding actions available in the **Navigation Panel**. These two operational routes allow users to navigate by either mouse or keyboard commands. These **Atlas Menu** options are defined further in this manual in the sections listed below and are as follows:

- **Capture Histories (alt-c)** contains all the functions under **Capture Histories** in the **Navigation Panel**:
 - **Load Capture Histories** (Section 3.1),
 - **Define Release Groups** (Section 3.1.1),

- **Select Downstream Sites** (Section 3.1.3),
- **View Mixing** (Section 3.1.2),
- **View ViRDCt Mixing** (Section 3.1.2), and
- **Reports** (Section 3.1.4).
- **Attributes (alt-a)** mimics the **Navigation Panel** functions and allows for loading in an optional attributes file (**Load Attributes**, Section 3.2) and then selecting pertinent attribute values for analysis (**Select Attributes**, Section 3.2).
- **Tag Life Data (alt-t)** matches the functionality found on the **Navigation Panel** and includes:
 - **Load Tag Life Data** (Section 3.3),
 - **Fit Tag Life Curves** (Section 3.3.1),
 - **Map Tag Life Data to Bins** (Section 3.3.2),
 - **Calculate Tag Life Corrections** (Section 3.3.3), and
 - **View Tag Life Corrections** (Section 3.3.4).
- **Closed Form Estimates (alt-l)** mimics the **Navigation Panel** and includes **Parameter Estimates** and **Cumulative Survival Estimates** (Section 3.4.1).
- **Modeled Estimates (alt-m)** contains all functionality of its **Navigation Panel** twin, including:
 - **Equate Parameters** (Section 3.4.2.1),
 - **Constrain Parameters** (Section 3.4.2.2),
 - **Compute** (Section 3.4.2),
 - **Compute Full Variance** (Section 3.4.3), and
 - **Reports** (Section 3.4.4), including:
 - **Parameter Estimates**,
 - **Cumulative Estimates**,
 - **Survival Covariance**, and

- **Generate Reports.**

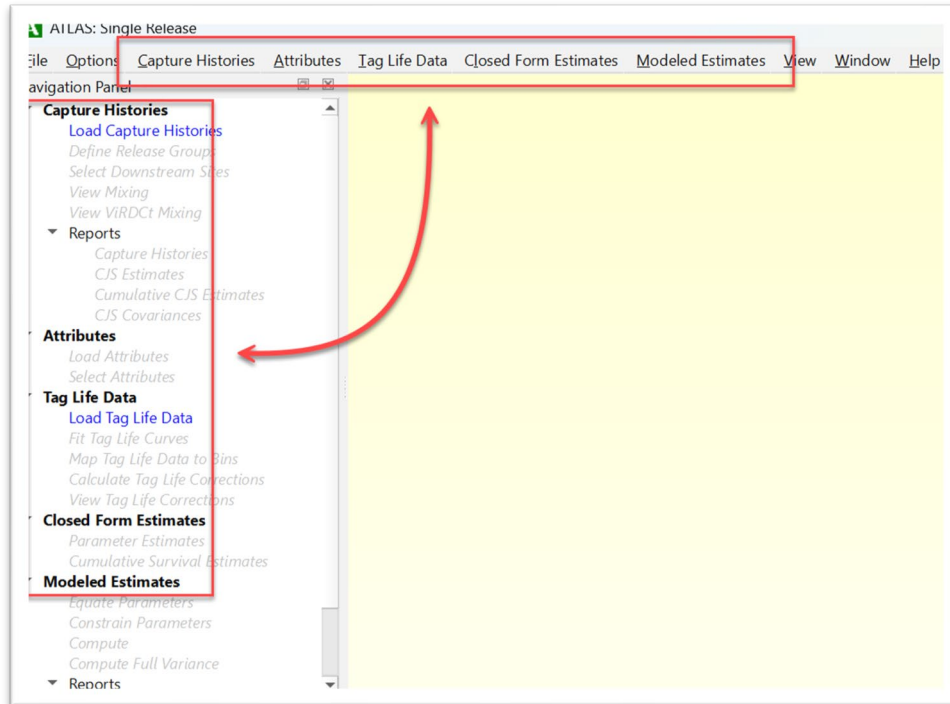


Figure 2.10: The **ATLAS Menu** and corresponding actions available in the **Navigation Panel**.

2.4 View, Window, and Help Menu Settings

Figure 2.11 shows the **View** menu. It simply allows the user to display or hide various components of the ATLAS main dialog, as described above, by checking or unchecking the associated entry.

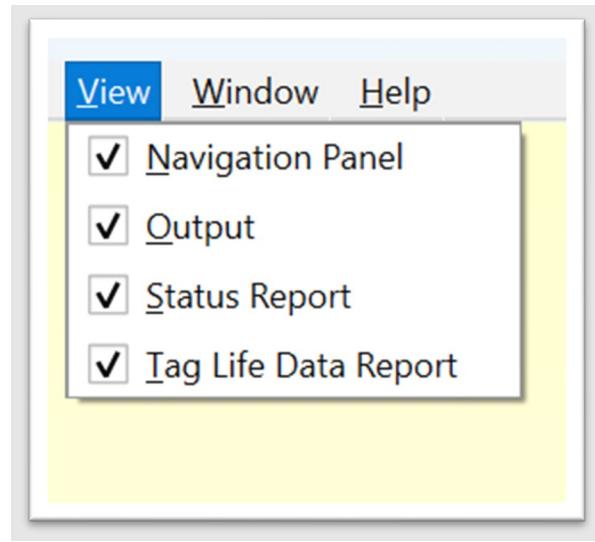


Figure 2.11: The **View** menu.

Figure 2.12 shows the **Window** menu. This menu allows users to either **Tile Windows**, **Cascade Windows**, or **Close All** open windows. **Tile Windows** arranges all generated windows in non-overlapping grids to fill the screen space. **Cascade Windows** stacks windows diagonally, showing only their title bars to reduce clutter while keeping them easily accessible. Choosing **Close All** will close all previously generated windows.

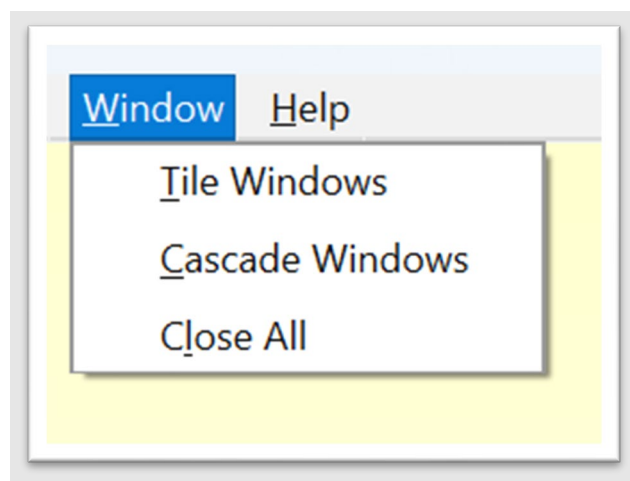


Figure 2.12: The **Window** menu.

Figure 2.13 shows the **Help** menu, where users can find a brief **About** dialog, **Check for Updates**, or **Configure Updates**.

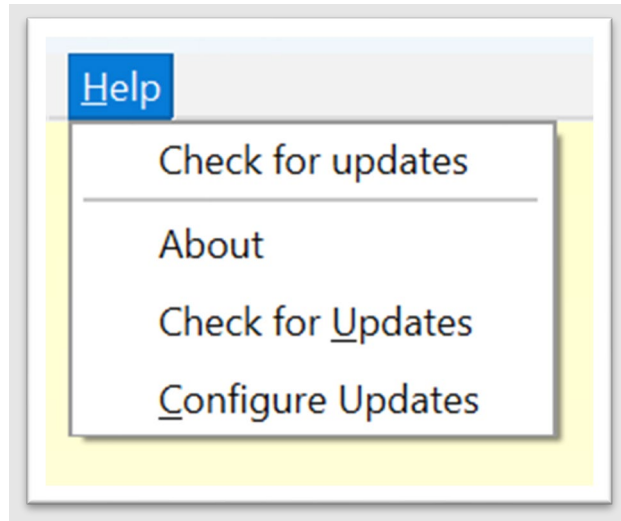


Figure 2.13: The **Help** menu.

Chapter 3 — Analysis with ATLAS

At initial startup, the only actions available on the **Navigation Panel** are **Load Capture History Data** under the **Capture History Data** heading, and **Load Tag Life Data** under the **Tag Life Data** heading. Capture history data are required to do any analysis, and tag-life data are required if taking into account tag failure. Optionally, after the tag-life data are loaded, the user can load an attribute group file that allows analysis of subsets of the capture history data.

The five main sections under the navigation panel are as follows:

- **Capture Histories** (Section 3.1) is for loading and examining the capture history data, and for configuring the sites and releases to be used in the analysis,
- **Attributes** (Section 3.2) defines one or more attributes (e.g., tagger, tag lot) and assigns tag codes to attribute values that can be selected or deselected in the analysis,
- **Tag Life Data** (Section 3.3) allows the user to load the tag-life data, fit the tag-life curves, and estimate the resulting tag-life corrections, and
- **Closed Form Estimates** (Section 3.4.1) and **Modeled Estimates** (Section 3.4.2) are where the survival probabilities are estimated.

3.1 Capture Histories

The capture history data file contains the detection history for each tagged individual in each release group in the study. Details of this file are given in Appendix A.1—it is typically created by [the TagPro utility app available on the Columbia Basin Research website](#). In order to load the capture history data, double click on **Load Capture History Data** on the **Navigation Panel** and select the capture history data file to be loaded.

3.1.1 Define Release Groups

ATLAS distinguishes between the idea of a “release” and that of a “release group.” A release consists of tagged individuals released from the same site at about the same time and is designated within the capture history data file by grouping tags together under a user-specified release name. A release group, on the other hand, defines the collection of tags to be modeled using common survival and detection probabilities in the relevant release-recapture model during analysis. Each study design, other than the single-release study design, uses multiple release groups. Additionally, some study designs allow multiple releases to be grouped together to define the release group used in analysis. All releases included in a single-release group will be used to estimate a common set of survival and detection probabilities. The use of the release group structure in ATLAS allows users to pool individual releases from within the program, without having to rename them in the input data file.

Once the capture history data file has been loaded into ATLAS, the individual releases are listed in the **Status Report** window under **Releases**. The types of release groups allowed are determined by the selected study design and consist of either individual releases or else pooled releases. Clicking on **Define Release Groups** opens a window to allow the user to select to which release group an individual release will be assigned. This enables creating larger release groups from within ATLAS or reassignment of a group if the default selection is not correct. The specifics of the Define Release Groups dialog are described in Sections 4.2 and 4.3 for single-release studies, Section 5.1 for paired-release studies, Section 6.1 for virtual/paired-release studies, and Sections 7.1 and 8.1 for ViRDCT studies.

3.1.2 View Mixing and View ViRDCT Mixing

The **View Mixing** action is applicable to the paired-release and virtual/paired-release study designs. Section 5.3 discusses the **View Mixing** function for a paired-release study design and 6.3 for a virtual/paired-release study design. The **View**

Mixing function is not applicable to the ViRDcT study designs because the downstream release is extended throughout the study.

The **View ViRDcT Mixing** action is available only for the Full ViRDcT or Reduced ViRDcT study designs. Discussion of the **View ViRDcT Mixing** function is available in Section 7.2 for the full ViRDcT study design. The mixing plot for the reduced ViRDcT design is similar.

3.1.3 Select Downstream Sites

Select the **Select Downstream Sites** action to bring up the **Active Sites** dialog. The **Active Sites** dialog for a single-release study is shown in Figure 3.1. Note that the first two sites are listed as **Required**. This is because a minimum of two downstream sites are required for a single-release study; the number of required downstream sites is a function of the study design. In the data for Figure 3.1, there are four optional sites downstream for a total of six sites. By default, the check boxes for the optional sites are selected, meaning they will be included in the analysis. If a user deselects a site, all sites downstream of the site will be deselected as well and will not be included in analysis. Conversely, if a user selects an unselected site, all upstream sites are selected as well. Note that the **Apply** button must be pressed for any changes to take effect. In Figure 3.1, only the first two of the four optional sites are selected; this defines the data set used in the rest of this chapter.

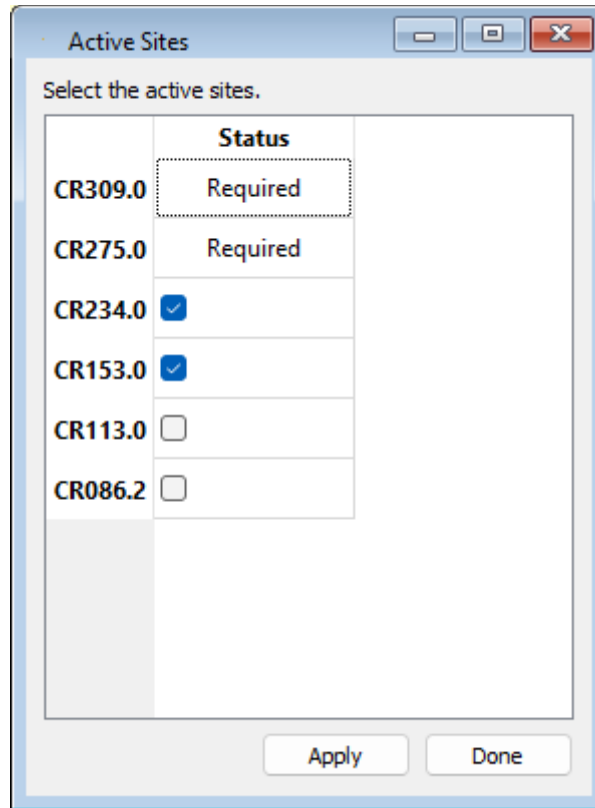


Figure 3.1: Active Sites selection dialog for a single-release study with six downstream sites, four of which are used in modeling.

3.1.4 Reports

The following reports are available under **Reports** in **Capture Histories** on the **Navigation Panel** once the capture history data file has been loaded:

- **Capture History Report,**
- **Cormack-Jolly-Seber (CJS) Report,**
- **CJS Cumulative Survival Report** (single release only), and
- **CJS Survival Covariance Report** (single release only).

3.1.4.1 Capture History Report

An example of a **Capture History Report** is shown in Figure 3.2. A capture history is a symbolic representation of the detection history of an individual fish: “1”

indicates detection without removal at a site, “0” indicates no detection, and “2” indicates detection and removal (i.e., the tag’s detection data are censored at this event to remove detections that should no longer be included in the study, for example after known removal, physical rehandling, etc.). The capture history reads from left to right with the first field representing the most upstream site and the final field representing the most downstream site. In the example in Figure 3.2, six fish in the “Roosevelt Chinook” release have a capture history of “1 1 0 1,” meaning that they were detected at the first two sites, not detected at the third downstream site, and detected again at the final downstream site.

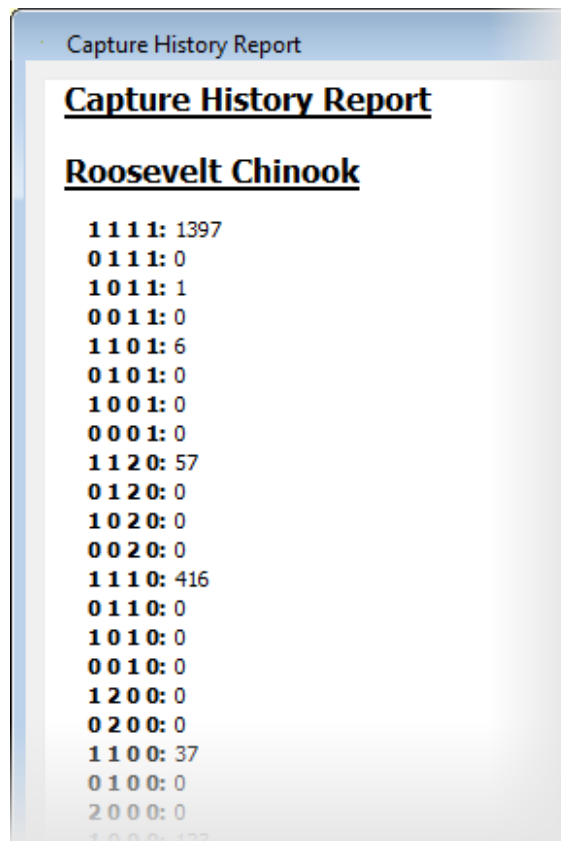


Figure 3.2: A portion of a **Capture History Report**.

If there are six or fewer downstream sites, all possible capture histories are included in the capture history report; for seven or more sites, only capture histories that were observed in the given release are included.

3.1.4.2 CJS Report

Figure 3.3 shows a **Cormack-Jolly-Seber (CJS) Report** for a study with one release named “Roosevelt Chinook.” There is one line per release in both the survival estimates table and the capture estimates table. The derivation of the survival estimates and the capture estimates can be found in Burnham et al. (1987).

The **Survival Estimates** in the **CJS Report** are only perceived survival estimates. They are not corrected for tag failure and thus represent the combined probability of fish survival and tag survival.

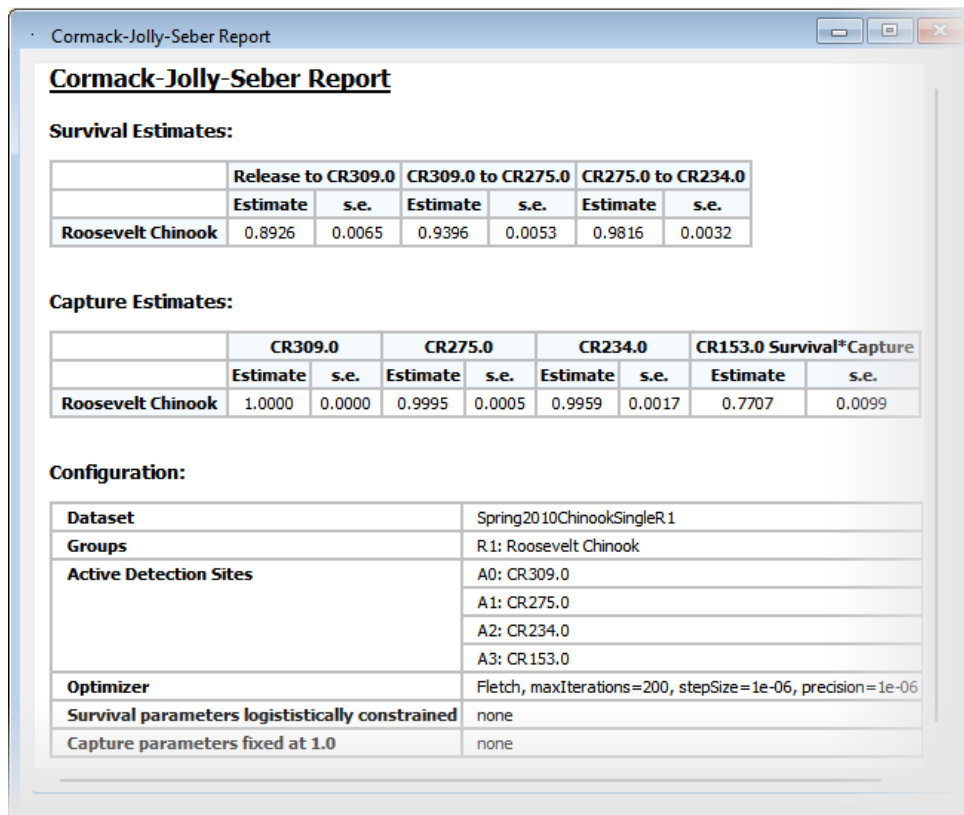


Figure 3.3: Cormack-Jolly-Seber Report for a single-release study.

3.1.4.3 Cormack-Jolly-Seber Survival Cumulative Report

The **CJS Cumulative Survival Report**, available in single-release mode only, gives the cumulative survival estimate to each site. Figure 3.4 shows the **CJS**

Cumulative Survival Report for the same capture history data as in Figure 3.3. The survival from release to the first site is the same in each report; the survival from release to the second site in Figure 3.4 is the product of the survival probabilities in Figure 3.3: $0.8926 \times 0.9396 = 0.8387$.

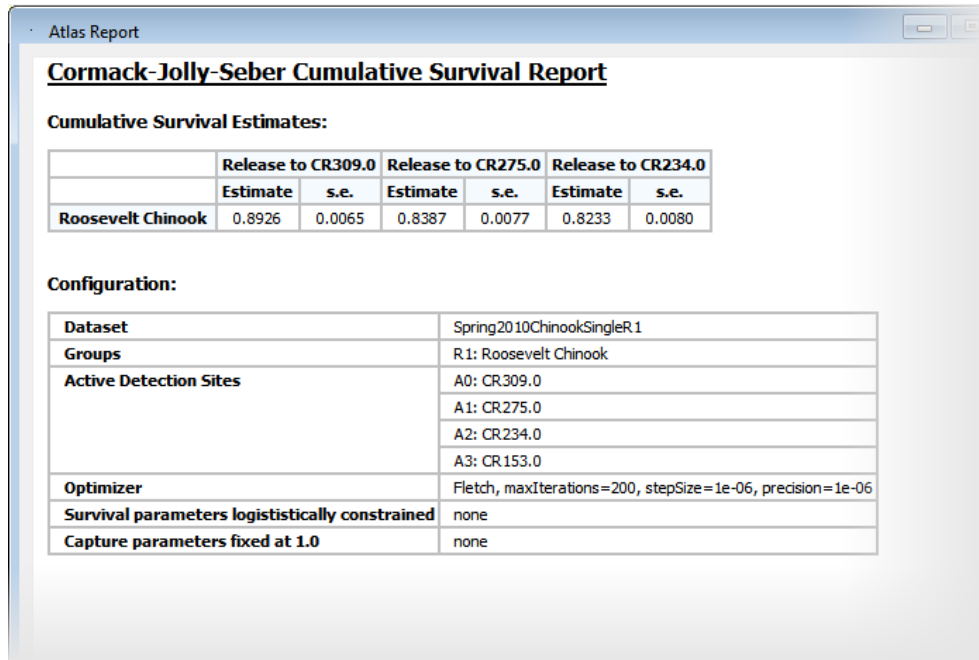


Figure 3.4: Cormack-Jolly-Seber Cumulative Survival Report for a single-release study.

3.1.4.4 CJS Survival Covariance Report

The covariance matrix for the CJS survival estimates, available in single-release mode only, allows the user to calculate the variance of a function of the survival estimates. The values are reported in full precision via the **CJS Covariance Report**, and the user can readily copy and paste the table into a spreadsheet. An example is shown in Figure 3.5.

CJS Survival Covariance Report			
	R1 S1	R1 S2	R1 S3
R1 S1	0.000041996219128	0.0000000000000000	0.0000000000000000
R1 S2	0.0000000000000000	0.000027853797213	-0.0000000005066124
R1 S3	0.0000000000000000	-0.0000000005066124	0.000010081072525

Key

R1 S1	Roosevelt Chinook, Release to CR309.0
R1 S2	Roosevelt Chinook, CR309.0 to CR275.0
R1 S3	Roosevelt Chinook, CR275.0 to CR234.0

Figure 3.5: CJS Survival Covariance Report.

3.2 Attributes

ATLAS 1.12 allows the user to load an optional attribute group file, providing the analysis of a subset of the data. The details of the attribute group file are given in Appendix A.2.

Once the attribute group file is loaded, the user can double click on **Select Attributes** on the navigation panel to bring up the **Attribute Group Selection** dialog as shown in Figure 3.6. If multiple attributes are present (i.e., such as release size or time, each in a separate column), the user can select the attribute of interest at the bottom of the dialog as shown in Figure 3.6. By default, all attribute values are selected. When a subset of the attributes is selected, all further analysis will use only the tags that have the selected attribute values. If a combination of attributes is desired (e.g., large size at release combined with morning release time), a separate column in the attributes file will be required that assigns a unique code to the possible factor combinations.

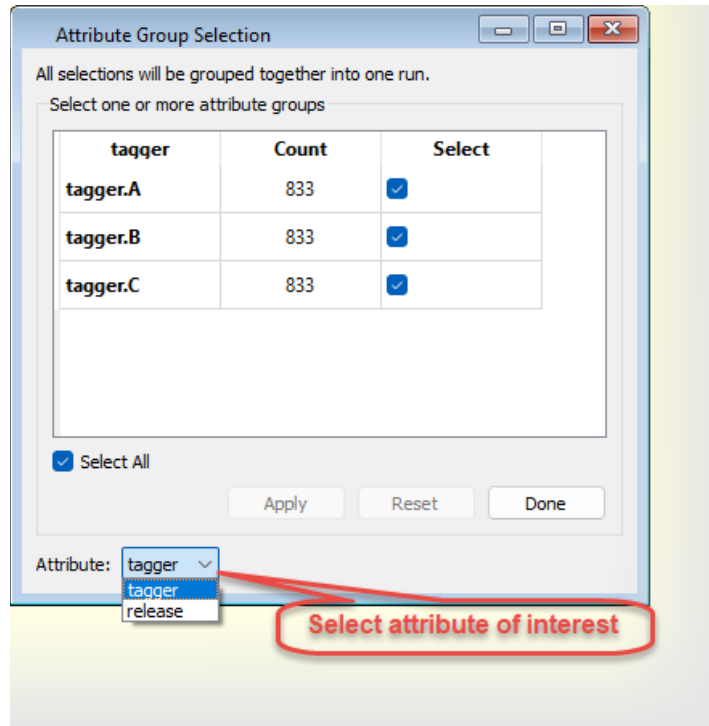


Figure 3.6: Attribute Group Selection dialog for an attribute file with two attributes.

3.3 Tag Life Data

In order to obtain independent estimates of the tag-life correction probabilities, a representative sample of tags from the study must be set aside and the failure time of each tag must be recorded. These failure times are recorded in the tag-life data file as described in Appendix A.3. ATLAS 1.12 allows for the use of multiple tag-life files.

Multiple tag-life files may be necessary when multiple tag bins are used with different failure time curves or when tags are released under differing protocols. For example, multiple tag-life files would be necessary for a paired-release study if all tags were activated at the same time for the upper and lower releases but tags in the lower release were held longer before release than tags in the upper release; this would provide more opportunity to observe a tag failure for the lower release tags and result in a different tag-failure model. To load tag-life data, double click on

Load Tag Life Data and select the desired tag-life data file. Repeat for each tag-life data file to be loaded. Figure 3.7 shows the navigation panel after two tag-life data files have been loaded.

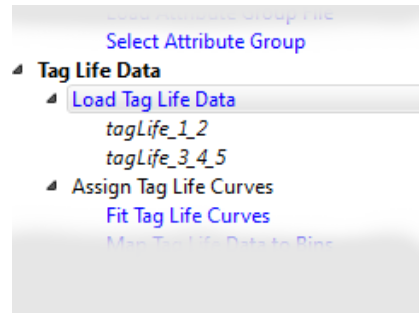


Figure 3.7: Navigation Panel after loading two tag-life files.

3.3.1 Fit Tag-life Curves

In order to estimate the tag corrections, the form of the failure time model (**Tag Life Function**) must be selected to model the tag failure for each tag-life file. Program ATLAS provides four types of failure time models to choose from:

1. the **Non-Parametric** estimator, also known as the Kaplan-Meier estimator (Kaplan and Meier 1958),
2. the **Weibull 2-parameter** distribution,
3. the **Weibull 3-parameter** distribution, or
4. the **Vitality** survival function (Li and Anderson, 2009, see also [the Vitality Model page on the Columbia Basin Research site](#)).

When the user selects the **Fit Tag Life Curve** action, the **Tag Life** dialog opens as shown in Figure 3.8. The points on the plot represent the data from the tag-life data file (Appendix A.3); the X-axis is time in days, and the Y-axis is the proportion of tags still functioning at a given time. At the bottom of the dialog shown in Figure 3.8, the user first selects the current **Tag Life Dataset** of interest and then selects the type of failure time model (**Tag Life Function**) to model the tag failure for that dataset. Once selected, ATLAS immediately estimates the parameters for the tag-life curve and plots the

resulting curve in red, allowing the user to review the model fit and select the failure curve that best fits the tag-life data. Figure 3.8 shows the vitality survival function fitted to the tag-life dataset named “tagLife_data.” The user must click **Apply** to finalize the tag life function selection.

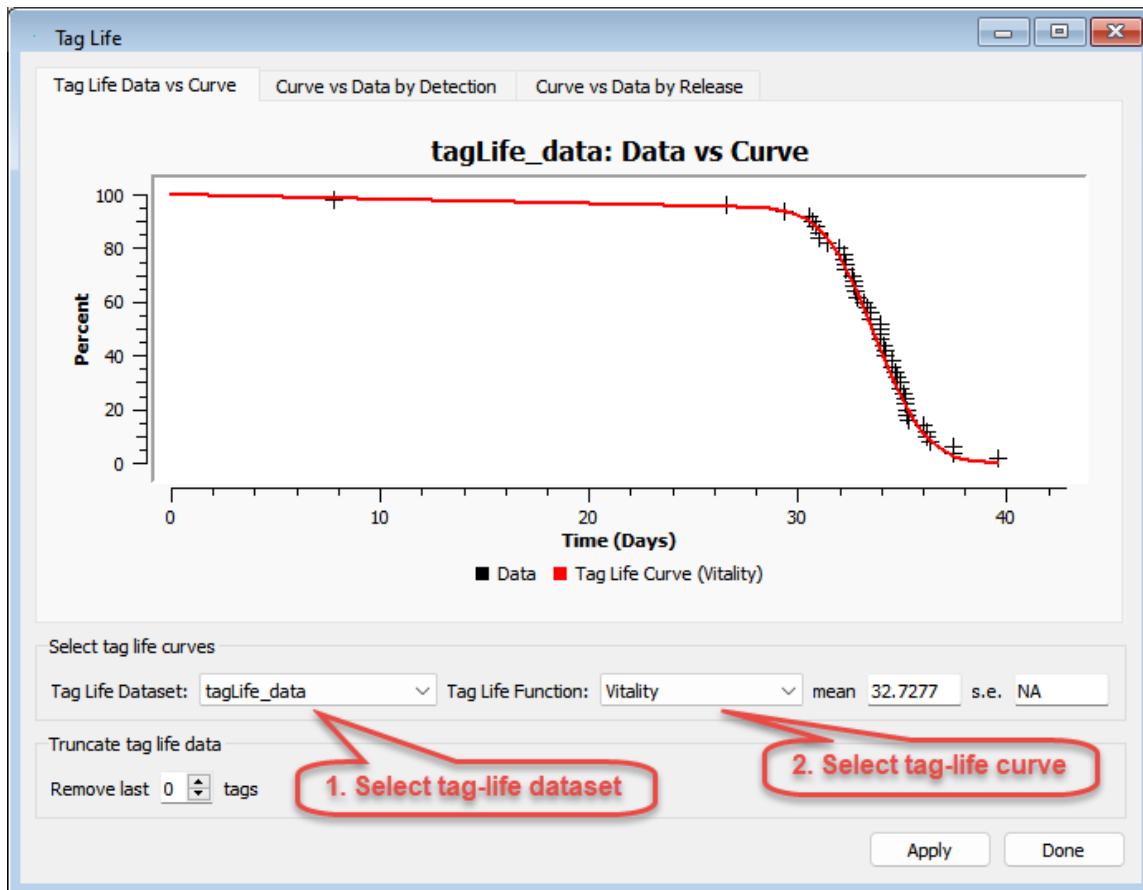


Figure 3.8: Tag Life selection dialog.

Along the top of the Tag Life dialog are three tabs. The first one, **Tag Life Data vs Curve**, is the default when the **Fit Tag Life Curve** action is initiated, because selecting the **Tag Life Function** is always the first step (Figure 3.8). Once the appropriate function has been selected, the user may select either the **Curve vs Data by Detection** tab or the **Curve vs Data by Release** tab. Both these tabs allow the user to view the arrival timing of individuals as a function of the selected tag-life curve.

3.3.1.1 Curve vs Data by Detection

Figure 3.9 shows the Tag Life dialog with the **Curve vs Data by Detection** tab selected. It allows the user to select a detection site of interest for the currently selected tag-life dataset. The plot will show the arrival timing distribution for all releases that were released upstream of the selected site superimposed on the selected tag-life curve. If a given release arrives at a site beyond the range of the tag-life curve, the user may want to consider excluding the release from analysis.

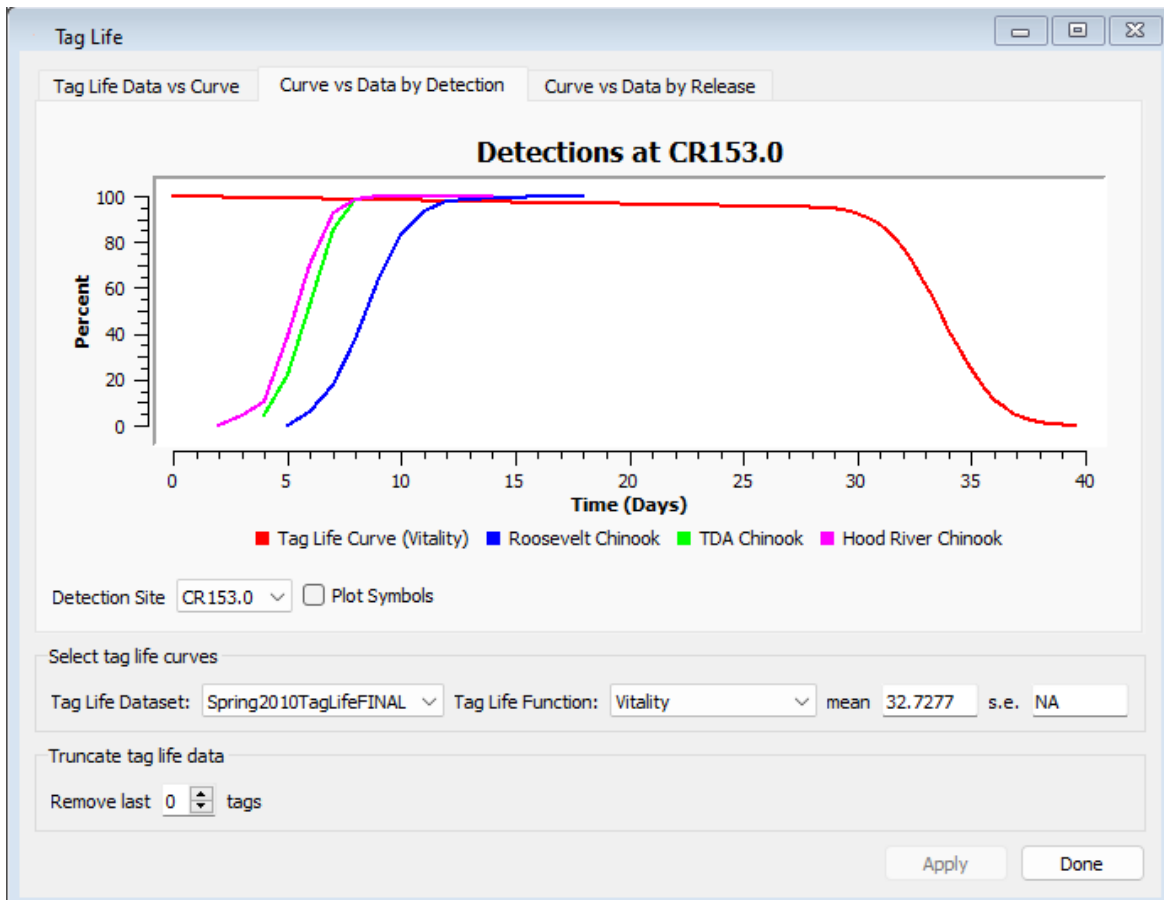


Figure 3.9: Tag-life curve with arrival time distributions at a selected site.

3.3.1.2 Curve vs Data by Release

Figure 3.10 shows the left portion of the **Tag Life** dialog with the **Curve vs Data by Release** tab selected. On this tab, the user selects the release group of interest and the plot shows the arrival distribution for that release group at all

downstream detection sites. If a selected release arrives too far down the tag-life curve, the user may need to consider either excluding the release from analysis or excluding the relevant detection site, along with all sites further downstream.

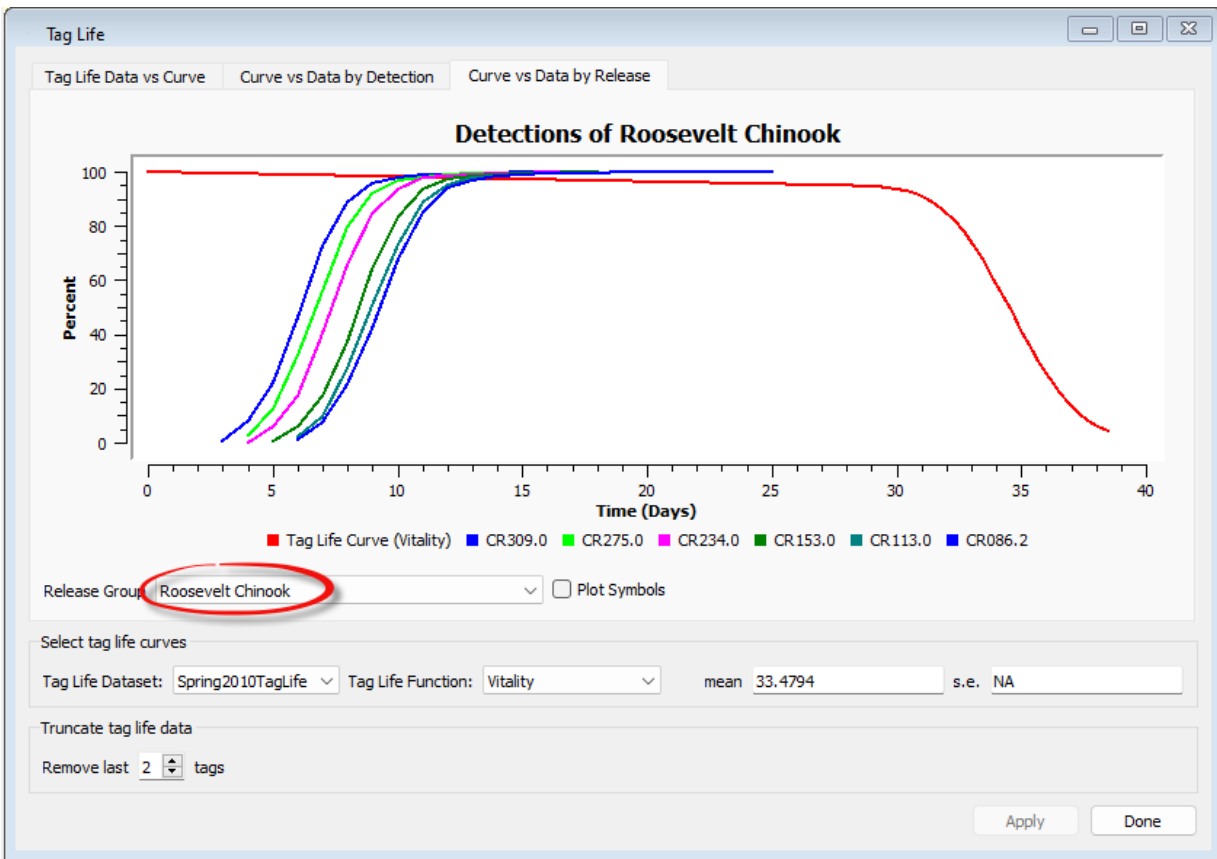


Figure 3.10: Tag-life curve with arrival time distributions for a selected release group.

3.3.1.3 Truncating Tag-Life Data

In a well-designed study, the tag detections will occur well before the majority of tag failures used to fit the tag-life curve, falling on the flat area of the curve rather than toward the tail of the curve (see Figure 3.9 and Figure 3.10). In some cases, outlier tags in the tag-life study may exert undue influence on the parameter estimation for the tag-life curve, resulting in a biased prediction of tag survival at the times of tag detection. This happens when some tags in the tag-life study last much longer than the rest. Figure 3.11 shows simulated tag-life data with two outliers that failed more than 20 days

after the previous tags failed. Although no fish were detected at this tail end of the curve, the outliers may strongly affect estimation of the tag-life curve and thus the tag-life corrections. The user has the option of removing the outliers from being considered in estimating the tag-life curve parameters. Figure 3.12 shows the same simulated data with the last two tags removed. Notice how much better the estimated curve fits the data.

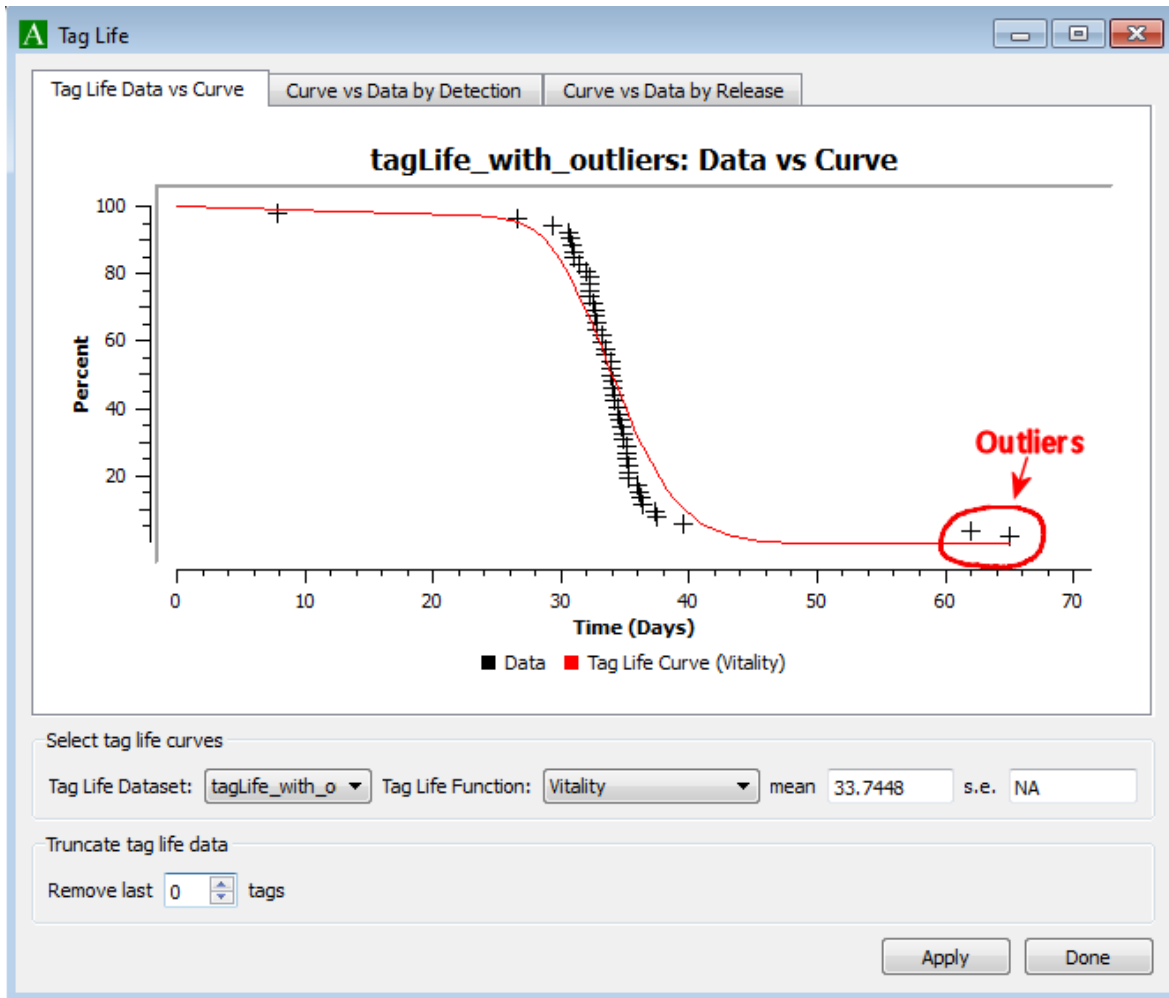


Figure 3.11: Tag-life curve with simulated data with outliers.

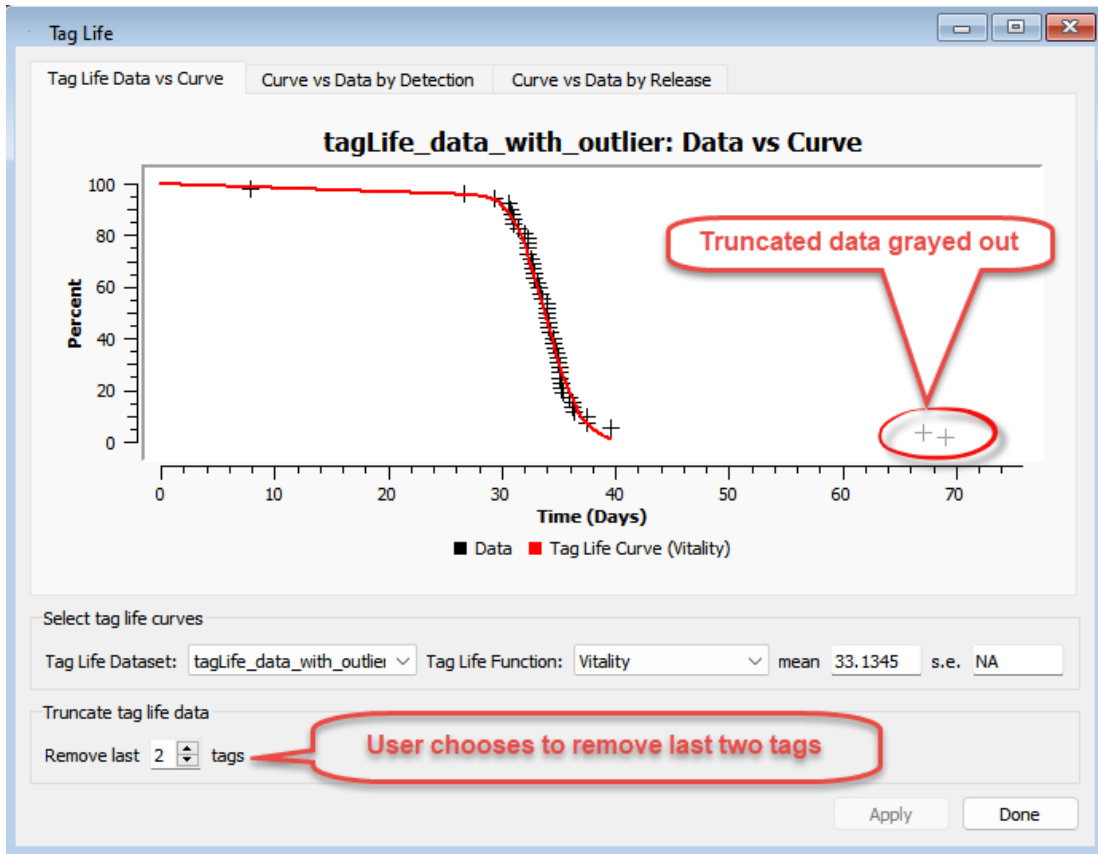


Figure 3.12: Tag-life curve after outliers have been excluded from the truncated analysis.

3.3.2 Map Tag Life Data to Bins

Sometimes it is necessary to use different tag corrections for different groups of tags in the study. For example, if the tags came from more than one manufacturing lot, then it may be necessary to use a separate tag-life curve for each manufacturing lot. In these cases, the user must provide unique tag-life datasets for each manufacturing lot and tell ATLAS which tag-life datasets should be used for fitting each tag-life curve by assigning tag-life datasets to bins, and the ATLAS capture history file must identify the appropriate bin for each tag released. The TagPro utility can be used to assign tag codes to bins. Within ATLAS, the user must then map each bin to a tag-life dataset. This is done by double clicking on **Map Tag Life Data to Bins**, which brings up the **Map Tag Life Data to Bins** dialog. In the example in Figure 3.13, there are two tag bins for the tags used in this

study as identified in the capture history data file. The user has loaded two tag-life datasets: “tagLife_1” and “tagLife_2.” The user has associated the tag-life curve for tagLife_1 to bin 1, and the tag-life curve for tagLife_2 to bin 2. All tags in a single tag-life dataset must be assigned to the same bin, and more than one tag-life dataset can be mapped to the same bin. All bins must be assigned a tag-life dataset.

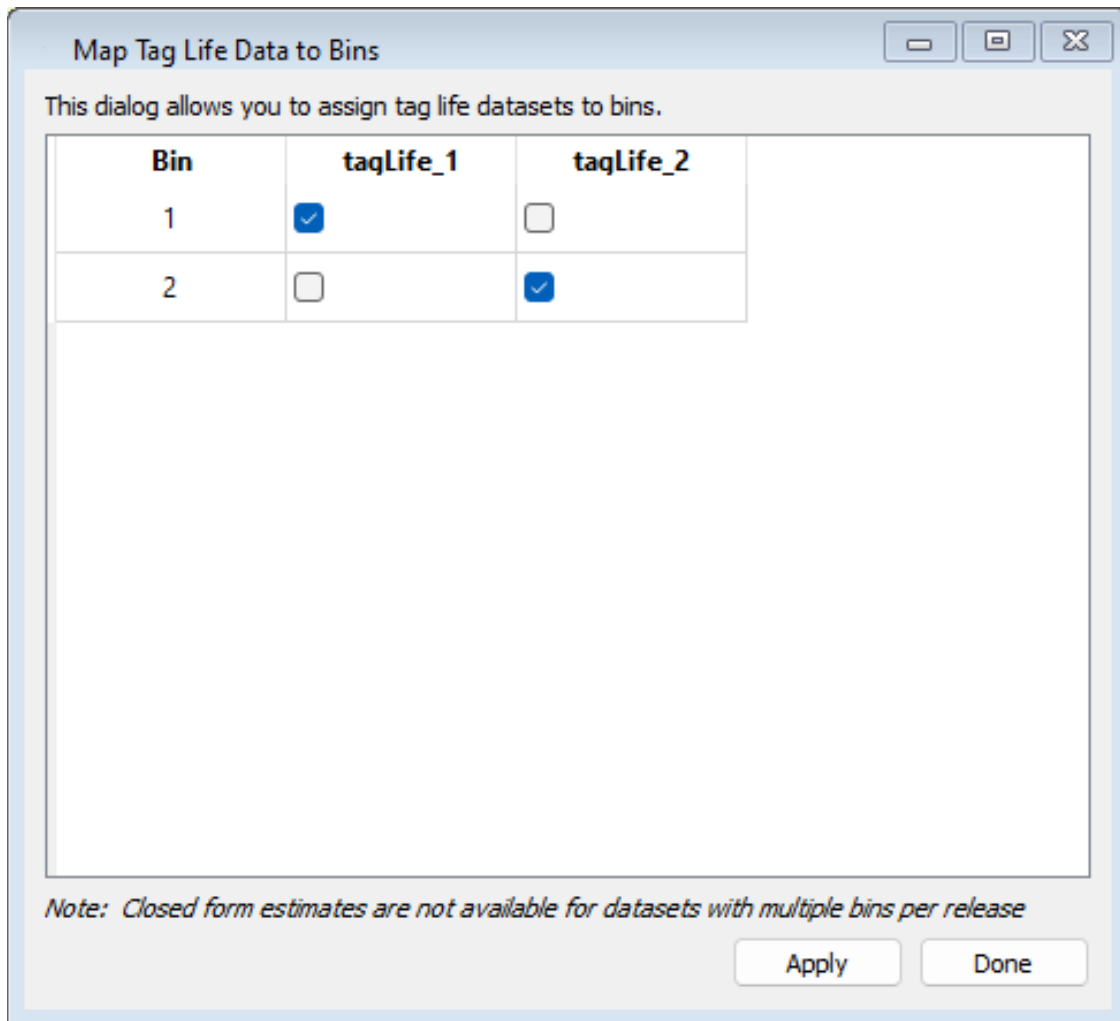


Figure 3.13: Dialog for mapping tag-life curves to tag bins.

There may be reasons for dividing the tags into multiple bins other than manufacturing lots. For example, if there was a significantly longer time between tag activation and release for some tags than for others, it may be desirable to put the tags with the longer hold times in a separate bin.

Although a given release may consist of tags from multiple bins, thus requiring separate tag-life correction estimates, all tagged fish from the release are assumed to share the same survival and detection probabilities. In other words, unique tag-life corrections are estimated for each bin, but the survival and capture parameter estimates apply to an entire release group.

3.3.3 Calculate Tag Correction Table

After selecting the tag-life curve, and mapping tag bins to tag-life curves if necessary, the user can then estimate the tag-life corrections by double clicking on **Calculate Tag Life Corrections**. The user will then be asked to enter the number of iterations for the bootstrapping process. The default is 1000, which is the recommended value. Increasing the number of iterations increases the precision of the variance estimates but also increases the time it takes to perform the bootstrapping process. The details of the bootstrapping are given in Appendix B.2.1.

In some instances, especially with the ViRDCT models, the data may be too sparse to calculate the tag-life correction variances. In that case, the **Compute Full Variance** option will not be available. Instead, the variances will be based only on the inverse Hessian and will be underestimated.

3.3.4 View Tag Life Correction Table

After the probabilities of a tag being active at the downstream detection sites have been calculated, the user may double click on the **View Tag Corrections** to view the tag-life correction estimates. Figure 3.14 shows a portion of a **Tag Correction Report** for the virtual/paired-release study design using a common tag-life curve applied across all releases.

Tag Correction Report

Detection Site Key:

A0: CR309.0
A1: CR275.0
A2: CR234.0
A3: CR153.0
A4: CR113.0
A5: CR086.2

Release			Detection Sites					
Group	Site	Bin	A0	A1*	A2*	A3*	A4*	A
V1	Roosevelt Chinook	1	0.9875 (0.006083)	0.9990 (0.000516)	0.9978 (0.001097)	0.9960 (0.002060)	0.9951 (0.002436)	0.9945 (0.002810)
R2	TDA Chinook	1	--	--	0.9901 (0.004854)	0.9881 (0.005990)	0.9874 (0.006239)	0.9867 (0.006588)
R3	Hood River Chinook	1	--	--	0.9910 (0.004407)	0.9891 (0.005522)	0.9881 (0.005863)	0.9876 (0.006201)

** For V1 only, probabilities are conditional on tag being active at A0.
 For R2 and R3, the tag-life probabilities are unconditional.*

Tag Life Dataset: Spring2010TagLifeFINAL

Fit Curve: Vitality
Log-Likelihood: -321.8102
Bootstrap iterations: 1000

Parameters:

r: 0.0296301 (0.00026652)

Figure 3.14: Example of a Tag Correction Report table for a virtual/paired-release study.

3.4 Analysis: Closed Form Estimates and Modeled Estimates

Program ATLAS provides two methods for estimating survival parameters corrected for tag life: (1) closed-form estimates, available under **Closed Form Estimates** and (2) **Modeled Estimates** on the **Navigation Panel**. Only the modeled estimates are available for the full ViRDCT study design.

3.4.1 Closed Form Estimates

Figure 3.15 shows the top portion of the **Closed Form Parameter Report** for a single-release study. It is structured the same as the **CJS Report** (Section 3.1.4.2) but it differs in that the survival estimates are corrected for tag life; the reported survival estimates are the CJS estimates divided by the tag correction.

Note that all estimates and standard errors under the **Capture Detail** section of the report are the same as those on the **CJS Report**.

Closed Form Parameter Report

Survival Detail:

	Release to CR309.0		CR309.0 to CR275.0		CR275.0 to CR234.0	
	Estimate	s.e.	Estimate	s.e.	Estimate	s.e.
Roosevelt Chinook	0.9045	0.008270	0.9407	0.012108	0.9828	0.012728

Capture Detail:

	CR309.0		CR275.0		CR234.0		CR153.0 Survival*Capture	
	Estimate	s.e.	Estimate	s.e.	Estimate	s.e.	Estimate	s.e.
Roosevelt Chinook	1.0000	0.000000	0.9995	0.000533	0.9959	0.001688	0.7707	0.009871

Note: The standard errors do not include variation from the tag life estimation.

Configuration:

Dataset	Spring2010ChinookTriple
Tag Life Curves	Bin 1 / Spring2010TagLife: Vitality
Groups	R1: Roosevelt Chinook
Active Detection Sites	A0: CR309.0
	A1: CR275.0
	A2: CR234.0
	A3: CR153.0
Optimizer	Fletcher, maxIterations=200, stepSize=1e-06, precision=1e-06
Survival parameters logistically constrained	none
Capture parameters fixed at 1.0	none

Figure 3.15: Example of a **Closed Form Parameter Report** for a single-release study.

For the paired-release study design and the virtual/paired-release study design, the **Closed Form Parameter Report** will also report the paired-release survival estimate or estimated dam passage survival, respectively (Sections 5.4 and 6.4). The **Closed Form Parameter Report** is not available for the full ViRDcT study design. See Appendix B.2.1 for details on calculating the estimates and the corresponding standard errors.

For a single-release study design, a **Closed Form Cumulative Survival Report** is available as well and is analogous to the **CJS Cumulative Survival Report** (Section 3.1.4.3).

Note that the **Closed Form Parameter Report** is not available if any of the

releases has more than one bin associated with it. Also, for the single-release model and the reduced ViRDCt model, the **Closed Form Parameter Report** is not available if there is more than one upstream release

3.4.2 Modeled Survival Estimates

Although the **Closed Form Parameter Report** adjusts the survival probabilities for tag failure, the standard errors reported on the **Closed Form Parameter Report** represent only the variance from the release-recapture model and omit the portion of the variance that arises from the tag-life model. Additionally, the **Closed Form Parameter Report** does not allow the user to either equate parameters across release groups or constrain survival and detection probabilities, both of which may be necessary either to calculate appropriate parameter estimates or to attain the optimal precision. Finally, the **Closed Form Parameter Report** is not available for some study designs, such as the full ViRDCt study design. The actions under the **Modeled Estimates** address these issues.

Under **Modeled Estimates**, Program ATLAS uses numerical optimization to calculate the Maximum Likelihood Estimates (MLE) of the model parameters. For the single release, paired release, and virtual/paired-release study design, Program ATLAS models each release (including virtual releases) with a single-release likelihood as described in Appendix B.2.1; for the ViRDCt study design, Program ATLAS models the live and dead releases with a joint-release likelihood as described in Appendices B.2.4 and B.2.5. These likelihood models incorporate the tag-life corrections treated as known constants within the likelihood function. Once the tag corrections have been computed, the user may simply double click on the **Compute** action on the navigation panel to compute the maximum likelihood estimates. The output of the optimizer is displayed in the output window, an **Estimation Complete** message will appear, and the **Parameter Estimates** report will be available on the navigation panel. The **Compute** action performs two steps via numerical methods:

1. Estimate the parameters
2. Estimate the covariance matrix and thus the standard errors of the parameters

Either of these steps can fail due to sparse data or due to survival or capture probabilities at or above 1.0. In order to deal with this, the user may have to constrain parameters as explained in Section 3.4.2.2.

3.4.2.1 Equate Parameters Across Releases

The closed-form estimates (Section 3.4.1) assume that each release group in a study design has unique parameters. The same is true of the modeled estimates if the default settings are used when Compute is performed. Given the fact that study designs with multiple release groups are designed so that the release groups encounter the same conditions downstream, this approach may be overly conservative. The **Equate Parameters Across Releases** action via **Equate Parameters** on the **Navigation Panel** allows the user to have Program ATLAS assume common survival and detection probabilities across releases. Reducing the number of parameters in the model may increase the precision of the resulting survival estimates.

Figure 3.16 shows the **Equate Parameters Across Releases** dialog for a paired-release study. Selecting a check box tells Program ATLAS to assume a common parameter across releases for survival or detection at the particular site or for the final product.

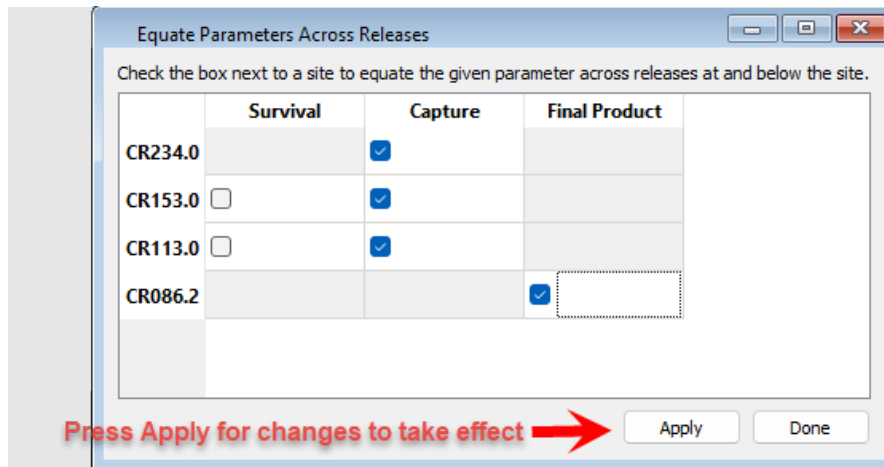


Figure 3.16: Equate Parameters Across Releases dialog for a paired-release study.

Selecting a site for survival or detection causes all downstream sites to be selected as well; conversely, deselecting a site causes all upstream sites to be deselected as well. The parameters that can be equated vary for each study design; hence, the **Equate Parameters Across Releases** dialog will look different for each study design.

In Figure 3.16, the user has chosen to equate all detection parameters across releases and equate the final product parameter across releases. The **Apply** button must be pressed for these selections to take effect the next time **Compute** is pressed.

Figure 3.17 shows the **Modeled Parameter Report** from a paired-release study with no parameters equated across releases. Figure 3.18 shows the parameter report with the detection and lambda parameters equated across releases for the same data. The parameter reports show both the maximized log-likelihood values and the number of parameters in the model, allowing the user to perform a Likelihood Ratio Test (LRT) to test whether or not it is valid to equate the parameters. The LRT statistic in this example is $2(-39.7235 - (-40.7096)) = 1.9723$. The degrees of freedom are the difference in the number of parameters ($14 - 10 = 4$). The P-value for a $\chi^2 = 1.9723$ with 4 degrees of

freedom is 0.74, indicating that the parameters can be equated across the two releases. Using an LRT in this way to test the validity of equating parameters can be done with any study design (except for a single-release study with only one release).

Modeled Parameter Report

Estimates:

Log Likelihood: -39.7235

Num Parameters: 14

AIC: 107.447

Paired Survival:

	Estimate	s.e.
Paired Survival:	0.9757	0.008075

Survival Detail for Fitted Model:

	Release to CR234.0		CR234.0 to CR153.0		CR153.0 to CR113.0	
	Estimate	s.e.	Estimate	s.e.	Estimate	s.e.
TDA Chinook	0.9715	0.006933	0.9435	0.008587	1.0009	0.002578
Hood River Chinook	0.9957	0.004173	0.9564	0.007648	0.9974	0.003880

Capture Detail for Fitted Model:

	CR234.0		CR153.0		CR113.0		CR086.2 Survival*Capture	
	Estimate	s.e.	Estimate	s.e.	Estimate	s.e.	Estimate	s.e.
TDA Chinook	0.9944	0.002770	0.8022	0.014865	0.9354	0.009421	0.9457	0.008779
Hood River Chinook	0.9973	0.001886	0.7968	0.014763	0.9268	0.009864	0.9341	0.009475

*Note: All standard errors are based on **only** the inverse Hessian.
For full standard errors on the survival estimates, perform the "Estimate Full Variance" action.*

Configuration:

Figure 3.17: Modeled Parameter Report with default configuration of no parameters equated across releases for a paired-release study.

Modeled Parameter Report

Estimates:

Log Likelihood: -40.7096

Num Parameters: 10

AIC: 101.419

Paired Survival:

	Estimate	s.e.
Paired Survival:	0.9755	0.008072

Survival Detail for Fitted Model:

	Release to CR234.0		CR234.0 to CR153.0		CR153.0 to CR113.0	
	Estimate	s.e.	Estimate	s.e.	Estimate	s.e.
TDA Chinook	0.9714	0.006932	0.9436	0.008575	1.0015	0.002543
Hood River Chinook	0.9958	0.004174	0.9563	0.007655	0.9968	0.003788

Capture Detail for Fitted Model:

	CR234.0		CR153.0		CR113.0		CR086.2 Survival*Capture	
	Estimate	s.e.	Estimate	s.e.	Estimate	s.e.	Estimate	s.e.
TDA Chinook	0.9959	0.001664	0.7995	0.010476	0.9311	0.006825	0.9398	0.006468
Hood River Chinook	0.9959	0.001664	0.7995	0.010476	0.9311	0.006825	0.9398	0.006468

*Note: All standard errors are based on **only** the inverse Hessian.*

For full standard errors on the survival estimates, perform the "Estimate Full Variance" action.

Configuration:

Figure 3.18: Modeled Parameter Report with the capture and lambda parameters equated across releases for a paired-release study.

3.4.2.2 Constrain Parameters

Numerical optimization algorithms require initial seeds for the parameters to be estimated. Program ATLAS uses the CJS estimates as seeds for the parameters, and it is possible for these estimates to be at or above 1.0. Because of the nature of the likelihood function, this can cause the numerical optimizer to be unable to estimate the parameters. The **Constrain Parameters** action allows the user to constrain the problematic parameters in order to estimate the remaining parameters and the covariance matrix.

Survival parameters and detection parameters are constrained in different ways. Detection parameters may be treated as constants set to 1.0 rather than parameters to be estimated, and survival parameters may be constrained using the *logit* function

$$S = \frac{\exp(S_0)}{1 - \exp(S_0)} \quad (3.1)$$

where S_0 is the parameter to be estimated and S is the resulting survival estimate. This allows S_0 to be any real number while constraining S to be between 0.0 and 1.0.

Figure 3.19 shows the output window after double clicking the **Compute** action on the navigation panel with data from a single-release study design (the same error message will appear as an error dialog as well). Note that Program ATLAS was able to estimate the point estimates but not the covariance matrix, thus no results are available. A look at the CJS estimates in Figure 3.20 shows that the survival estimate in the first reach is greater than 1.0, which may be the source of the problem. Figure 3.21 shows the **Constrain Parameters** dialog for the same data with the Survival tab selected and the initial survival parameter (Release to CR275.0) constrained via the logistic function. The rows represent detection sites, and the columns represent releases. The CJS estimates are displayed for each release and site. The **Apply** button must be pushed for the specified constraints to take effect.

Once the survival parameter has been constrained, the **Compute** action is selected again, and Figure 3.22 shows the resulting parameter report with the initial survival parameter at 1.0.

```

Scanning Spring2010TagLife.csv...
Loading file Spring2010TagLife.csv...
Updating...
Done.
Updating...
Done.
Updating...
Done.
Estimating parameters...
Calculation canceled.
Covariance matrix estimation error: "Singular Hessian in calculating covariance matrix"

```

Figure 3.19: Output window showing covariance estimation error (in red) after the Compute action.

Cormack-Jolly-Seber Report

Survival Estimates:

	Release to CR275.0		CR275.0 to CR234.0		CR234.0 to CR153.0		CR153.0 to CR113.0	
	Estimate	s.e.	Estimate	s.e.	Estimate	s.e.	Estimate	s.e.
Hood River Chinook	1.0006	0.000199	0.9858	0.004300	0.9544	0.007632	0.9965	0.003876

Capture Estimates:

	CR275.0		CR234.0		CR153.0		CR113.0	
	Estimate	s.e.	Estimate	s.e.	Estimate	s.e.	Estimate	s.e.
Hood River Chinook	0.9606	0.006943	0.9973	0.001886	0.7968	0.014763	0.9268	0.009876

Configuration:

Dataset	Spring2010ChinookPaired
Tag Life Curves	Bin 1 / Spring2010TagLife: Weibull3
Groups	R1: Hood River Chinook
Active Detection Sites	A0: CR275.0 A1: CR234.0 A2: CR153.0 A3: CR113.0

Figure 3.20: CJS estimates with a survival probability greater than 1.0.

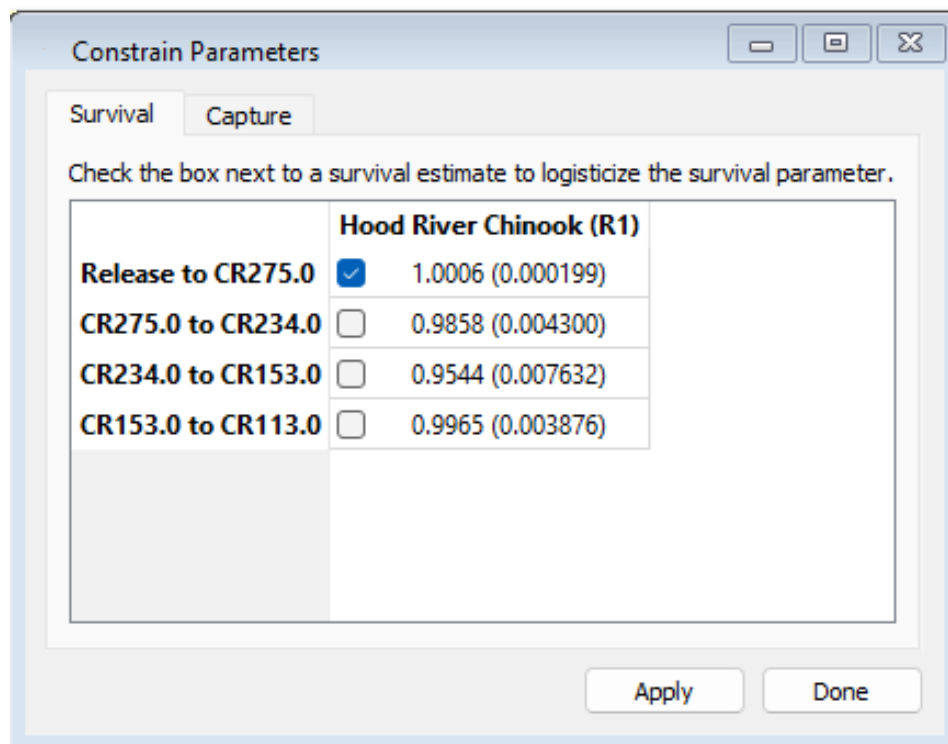


Figure 3.21: Constraining the survival parameter with the logistic function.

Modeled Parameter Report

Estimates:

Log Likelihood: -37.4286

Num Parameters: 9

AIC: 92.8571

Survival Detail for Fitted Model:

	Release to CR275.0		CR275.0 to CR234.0		CR234.0 to CR153.0		CR153.0 to CR113.0	
	Estimate	s.e.	Estimate	s.e.	Estimate	s.e.	Estimate	s.e.
Hood River Chinook	1.0000	0.000239	0.9863	0.004134	0.9564	0.007648	0.9974	0.003880

Capture Detail for Fitted Model:

	CR275.0		CR234.0		CR153.0		CR113.0		CR086.2 Survival*Capture	
	Estimate	s.e.	Estimate	s.e.	Estimate	s.e.	Estimate	s.e.	Estimate	s.e.
Hood River Chinook	0.9611	0.006849	0.9973	0.001886	0.7968	0.014763	0.9268	0.009864	0.9341	0.009475

Note: All standard errors are based on **only** the inverse Hessian.

For full standard errors on the survival estimates, perform the "Estimate Full Variance" action.

Configuration:

Dataset	Spring2010ChinookPaired
Tag Life Curves	Bin 1 / Spring2010TagLife: Vitality
Groups	R1: Hood River Chinook
Active Detection Sites	A0: CR275.0 A1: CR234.0 A2: CR153.0 A3: CR113.0 A4: CR086.2
Optimizer	Fletcher, maxIterations=200, stepSize=1e-06, precision=1e-06
Number of Variance Bootstrap Iterations	NA
Survival parameters logistically constrained	R1_Release to CR275.0
Capture parameters fixed at 1.0	none

Figure 3.22: Modeled Parameter Report after constraining the survival probability with the logistic function. Compare to Figure 3.20.

3.4.3 Compute Full Variance

Once the **Compute** action has been performed and the MLEs calculated, the **Modeled Parameter Report** is available as shown in Figure 3.22. However, near the bottom of the Parameter Report will be the phrase "Note: all standard errors are based on **only** the inverse Hessian." The Hessian is the matrix of second derivatives. Under maximum likelihood theory, the inverse of the Hessian is the covariance matrix from which the standard error estimates are derived. This covariance matrix is based on the likelihood model. The likelihood model necessarily assumes that tag corrections are known without error and does not incorporate the standard errors of the tag corrections as reported in the Tag

Correction Report. Thus, standard errors that are based only on the inverse Hessian will underestimate the true standard errors.

In order to estimate the full variance of the survival estimates that takes into account the variance of the tag corrections, bootstrapping must be performed. The details of the bootstrapping are given in Appendix B.2.1. The **Compute Full Variance** action will bring up a dialog asking the user for the number of bootstrap iterations. A higher number of iterations will improve the estimate of variance but will also take longer to compute. The default is 1,000 bootstrap iterations.

Once the **Compute Full Variance** action has completed, the **Modeled Parameter Report** will be updated as shown in Figure 3.23 to reflect the full standard errors for all survival parameters (the standard errors for the detection and product probabilities remain unchanged).

Modeled Parameter Report

Estimates:

Log Likelihood: -37.4286
 Num Parameters: 9
 AIC: 92.8571

Survival Detail for Fitted Model:

	Release to CR275.0		CR275.0 to CR234.0		CR234.0 to CR153.0		CR153.0 to CR113.0	
	Estimate	s.e.†	Estimate	s.e.†	Estimate	s.e.†	Estimate	s.e.†
Hood River Chinook	1.0000	0.000239	0.9863	0.004134	0.9564	0.007730	0.9974	0.003920

Capture Detail for Fitted Model:

	CR275.0		CR234.0		CR153.0		CR113.0		CR086.2 Survival*Capture	
	Estimate	s.e.*	Estimate	s.e.*	Estimate	s.e.*	Estimate	s.e.*	Estimate	s.e.*
Hood River Chinook	0.9611	0.006849	0.9973	0.001886	0.7968	0.014763	0.9268	0.009864	0.9341	0.009475

Notes:

* Standard error is based on only the inverse Hessian.
 † Standard error is based on bootstrapping.

Configuration:

Dataset	Spring2010ChinookPaired
Tag Life Curves	Bin 1 / Spring2010TagLife: Vitality
Groups	R1: Hood River Chinook
Active Detection Sites	A0: CR275.0 A1: CR234.0 A2: CR153.0 A3: CR113.0 A4: CR086.2
Optimizer	Fletcher, maxIterations=200, stepSize=1e-06, precision=1e-06
Number of Variance Bootstrap Iterations	1000
Survival parameters logistically constrained	R1_Release to CR275.0
Capture parameters fixed at 1.0	none

Figure 3.23: Parameter Report after Estimate Full Variance action.

3.4.4 Reports

Under the **Reports** section of the Modeled Estimates heading, three reports are available: (1) **Parameter Estimates**, (2) **Cumulative Survival**, and (3) **Survival Covariance**. The **Modeled Parameter Estimates** report has already been shown in the previous discussion (e.g., Figure 3.22 and Figure 3.23). The **Modeled Cumulative Survival Report** (Figure 3.24) and the **Modeled Survival Covariance Report** (Figure 3.25) are available only for a single-release study. Each report reflects the adjustments for tag-life corrections in the point estimates of

survival and any modeling actions performed. If the user has not previously performed the **Compute Full Variance** action, then the standard errors in these reports reflect only the uncertainty from the release-recapture data as represented by the inverse Hessian. After the user has performed the **Compute Full Variance** action, the standard errors also reflect the uncertainty from the tag-life corrections from bootstrapping. However, the covariance report will continue to be based only on the inverse Hessian (Figure 3.25).

A portion of a **Modeled Cumulative Survival Report** is shown in Figure 3.24. It is analogous to the **CJS Cumulative Survival Report** (Section 3.1.4.3) in that it shows survival estimates from release to each site.

A portion of the **Modeled Survival Covariance Report** is shown in Figure 3.25. As with the **CJS Survival Covariance Report** (Section 3.1.4.4), the values are reported in full precision and may be copied and pasted to a spreadsheet for custom variance calculations.

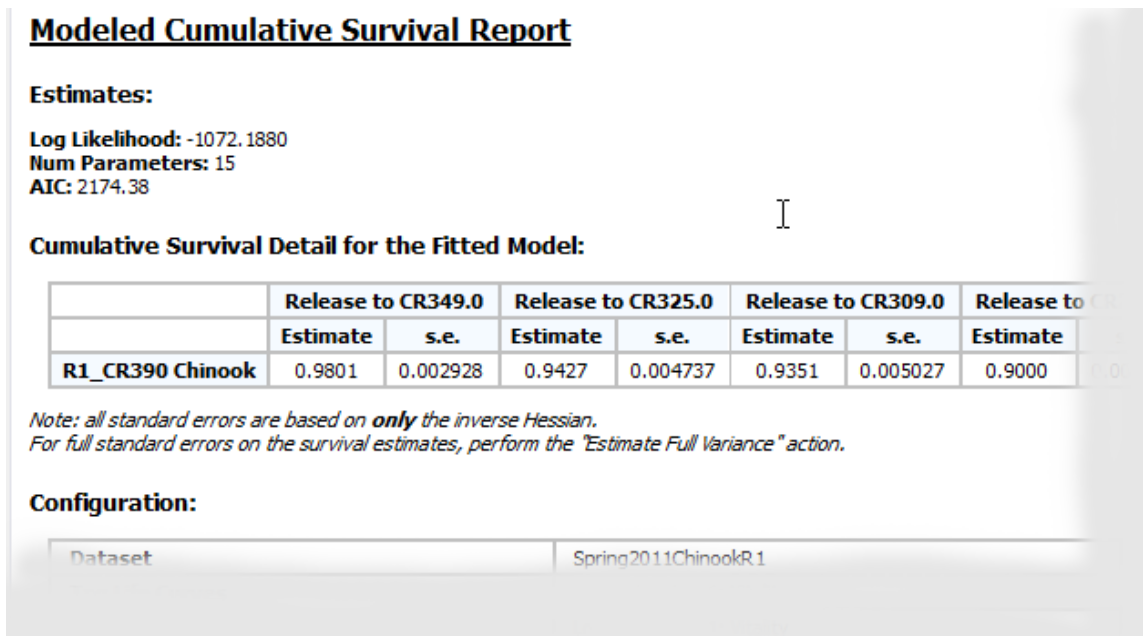


Figure 3.24: A portion of a **Modeled Cumulative Survival Report** for a single-release study before selecting **Compute Full Variance**.

Modeled Survival Covariance Report

	R1 S1	R1 S2	R1 S3	R1 S4
R1 S1	0.000008571990075	-0.000000013060758	0.000000000000015	0.000000000000029
R1 S2	-0.000000013060758	0.000015132743028	-0.000000060094631	0.000000000000003
R1 S3	0.000000000000015	-0.000000060094631	0.000003716125535	-0.000000178000960
R1 S4	0.000000000000029	0.000000000000003	-0.000000178000960	0.00001693830555
R1 S5	-0.000000000000004	-0.0000000000000376	-0.000000000000098	-0.000001176962393
R1 S6	-0.000000000000013	0.0000000000000564	0.000000000000124	0.0000000000007159
R1 S7	-0.000000000000001	-0.0000000000000232	-0.000000000000151	0.0000000000003652

Note: all variances are based on **only** the inverse Hessian.

Key

R1 S1	R1_CR.390 Chinook, Release to CR.349.0
R1 S2	R1_CR.390 Chinook, CR.349.0 to CR.325.0
R1 S3	R1_CR.390 Chinook, CR.325.0 to CR.309.0
R1 S4	R1_CR.390 Chinook, CR.309.0 to CR.275.0
R1 S5	R1_CR.390 Chinook, CR.275.0 to CR.234.0
R1 S6	R1_CR.390 Chinook, CR.234.0 to CR.161.0
R1 S7	R1_CR.390 Chinook, CR.161.0 to CR.113.0

Figure 3.25: A portion of a **Modeled Survival Covariance Report** for a single-release study.

Chapter 4 — Single-release Study

Design

This chapter presents details unique to analyzing data from the single-release study design. Analysis elements that are common to all study designs are described in Chapter 3.

A single-release study consists of a single release group with multiple downstream detection sites. It may be either an actual single-release study with the release group consisting of a single release as illustrated in Figure 4.1 or a virtual single-release study with a single virtual release composed of fish from multiple upstream releases as illustrated in Figure 4.2. Single-release survival can be estimated when multiple releases are available in the capture history by selecting each release group one at a time.

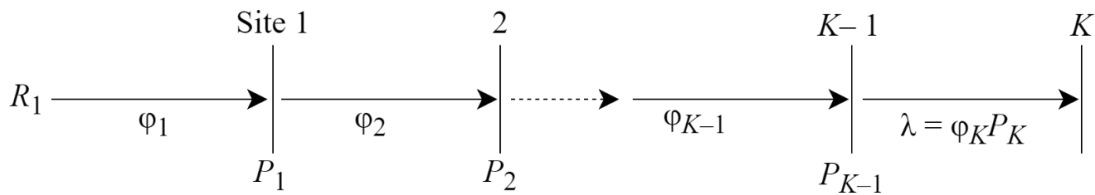


Figure 4.1: Actual single-release study with K detection sites.

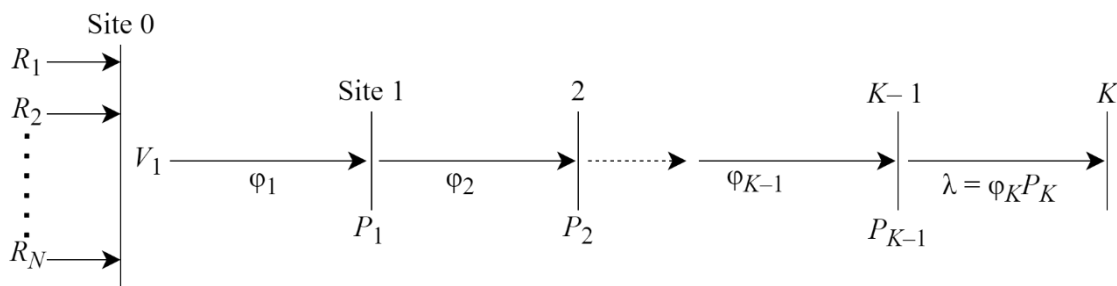


Figure 4.2: Virtual single-release study with K detection sites.

4.1 Load Capture History Data

When the user loads a capture history file in single-release mode, the dialog shown in Figure 4.3 appears, forcing the user to select the type of single-release study.

Upon selecting the single-release study type and pressing the **Next** button, the user must next select which releases in the dataset to include in the analysis. If the user selected an **Actual** single-release study, only one release group can be selected, as demonstrated in Figure 4.4; if a **Virtual** single-release study was selected, one or more release groups can be selected to form the virtual release.

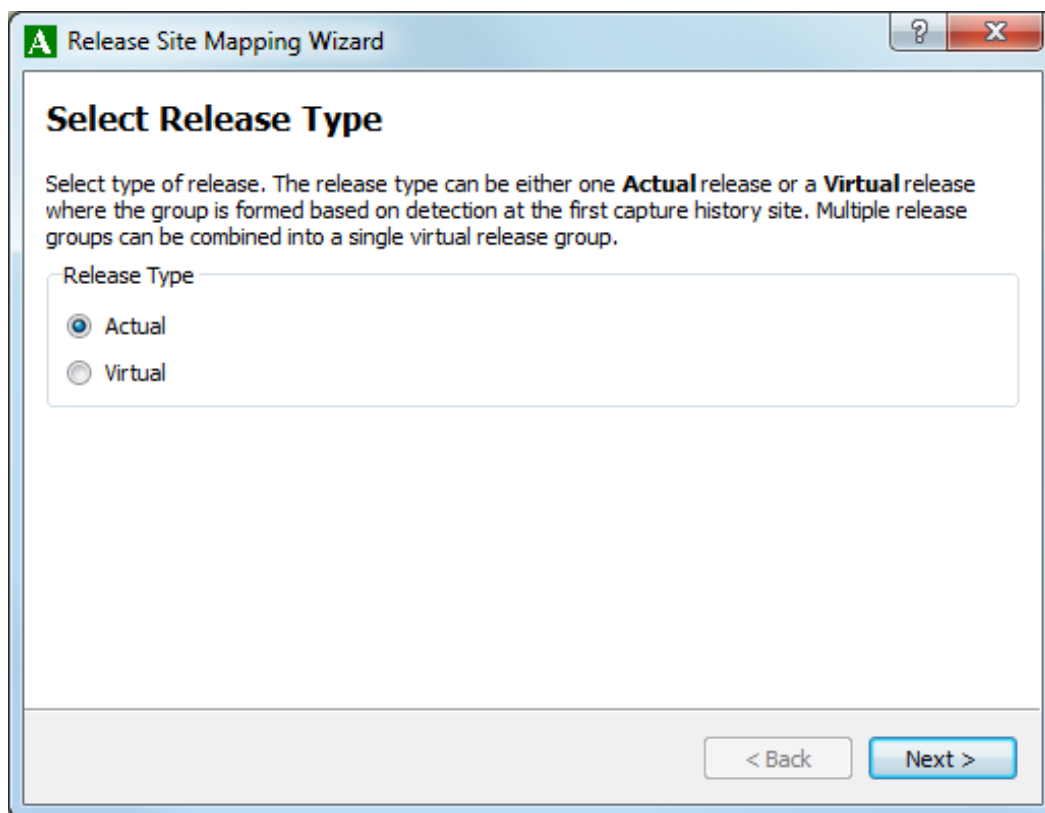


Figure 4.3: Select Release Type dialog in single-release mode.

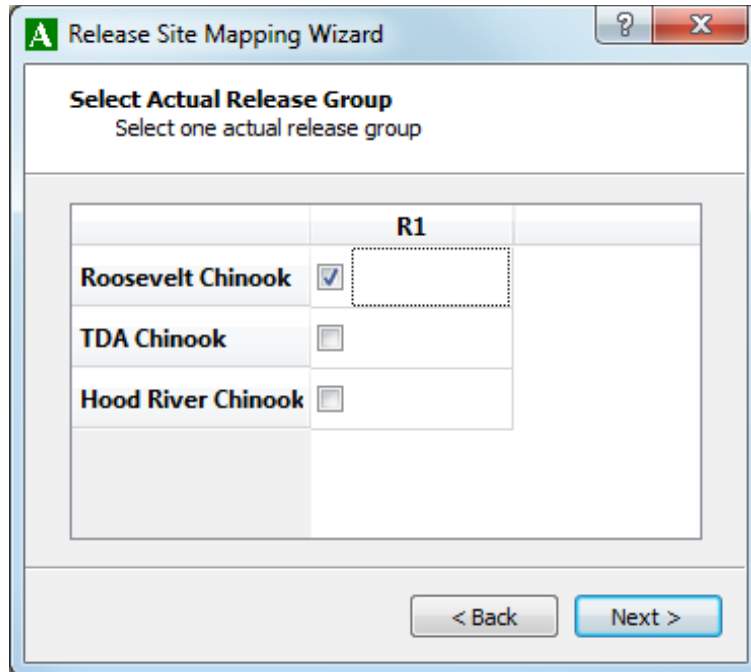


Figure 4.4: Dialog for **Selecting Actual Release Group(s)** to be used in single-release study.

The **Next** button brings up the review dialog as shown in Figure 4.5. The user can then select **Finish** or **Back**. As the dialog points out, the user can select **Define Release Groups** after the fact to change the setup.

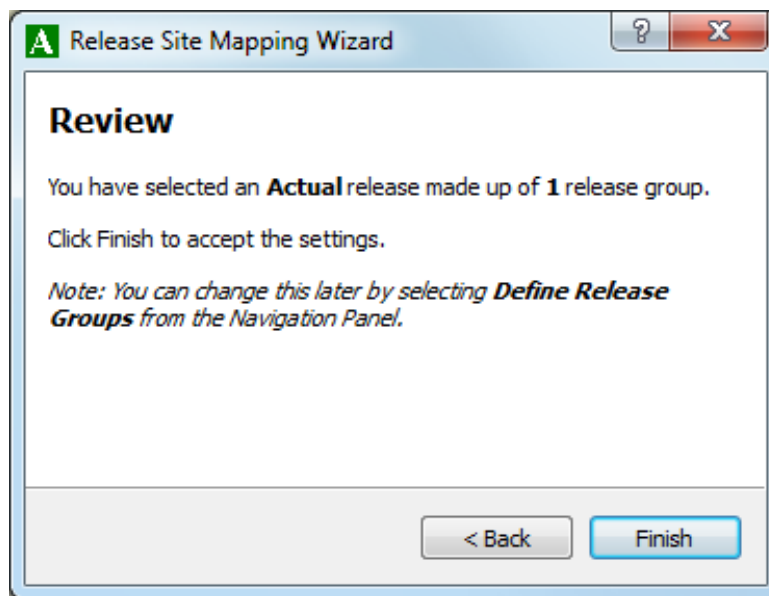
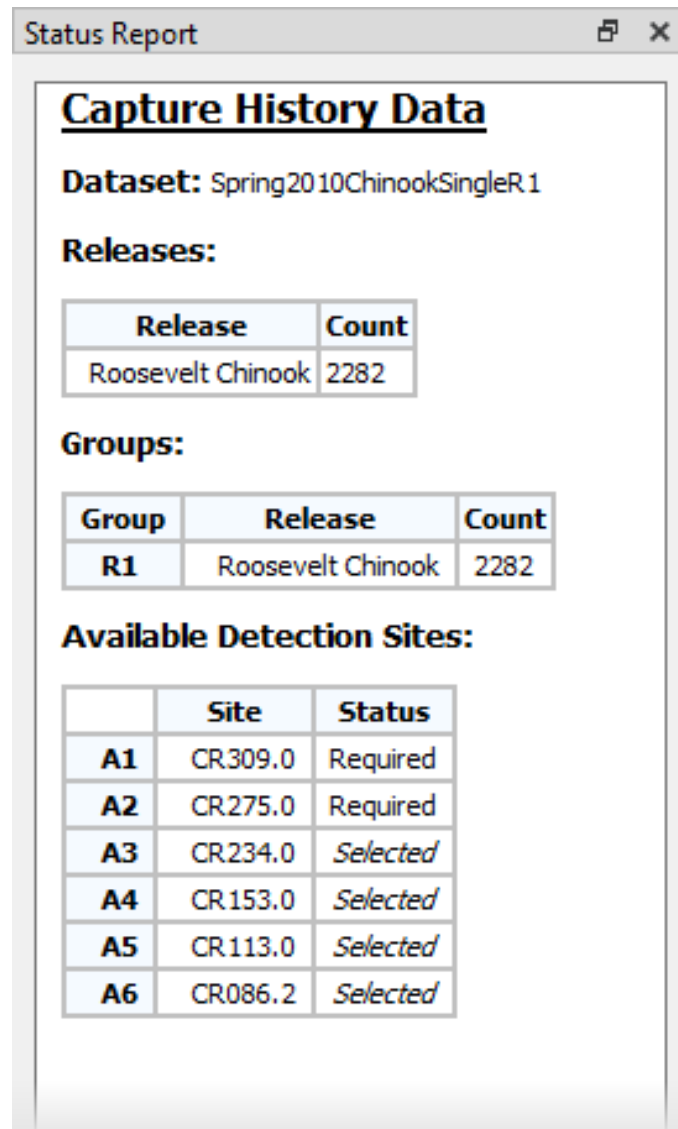


Figure 4.5: Dialog for reviewing single-release study setup.

4.2 Actual Single-release Study Design

Figure 4.6 shows the status report after loading a capture history file with only one release. The status report shows that the single release, in this case named “Roosevelt Chinook,” has 2282 tagged individuals. The release group R_1 is shown to consist of the single release, the only option in this case.



The screenshot shows a window titled "Status Report" with a close button. The content is organized into sections:

- Capture History Data**
 - Dataset:** Spring2010ChinookSingleR1
 - Releases:**

Release	Count
Roosevelt Chinook	2282
 - Groups:**

Group	Release	Count
R1	Roosevelt Chinook	2282
 - Available Detection Sites:**

	Site	Status
A1	CR309.0	Required
A2	CR275.0	Required
A3	CR234.0	<i>Selected</i>
A4	CR153.0	<i>Selected</i>
A5	CR113.0	<i>Selected</i>
A6	CR086.2	<i>Selected</i>

Figure 4.6: Status Report after loading data with only one release for an actual single-release study.

4.2.1 Tag Corrections

Section 3.3.3 describes how to estimate the tag corrections. Figure 4.7 shows the **Tag Correction Report** for an actual single-release study. Each column represents the unconditional probability of a tag surviving to the given site from the time of tag activation, based on the observed travel times to the site.

Tag Correction Report

Detection Site Key:

A1: CR309.0
A2: CR275.0
A3: CR234.0
A4: CR153.0
A5: CR113.0
A6: CR086.2

Release			Detection Sites					
Group	Site	Lot	A1	A2	A3	A4	A5	A6
R1	Roosevelt Chinook	1	0.9875 (0.006533)	0.9865 (0.007067)	0.9854 (0.007636)	0.9836 (0.008674)	0.9827 (0.009052)	0.9822 (0.009304)

Tag Life Dataset: Spring2010TagLifeFINAL

Fit Curve: Vitality
Log-Likelihood: -321.8102
Bootstrap iterations: 1000

Parameters:

r: 0.0296301 (0.00026652)
s: -1.13928e-05 (NA)
k: 0.00173314 (0.00121654)
u: 0.0572978 (0.00677299)

Figure 4.7: Tag Correction Report for an actual single-release study.

4.3 Virtual Single-release Study Design

As mentioned above, a user may define a virtual release group from multiple releases as represented in Figure 4.2. Figure 4.8 shows the status report with all three release groups used to define virtual release group “V1.” Under the **Releases** heading, the number tagged in each release is reported. Under the **Groups** heading, the number in each release that was detected at site “A0,” and thus forms a part of V1, is reported.

Figure 4.9 shows the **Tag Correction Report** for a single-release study with a

virtual release composed of three separate releases. Since the first site now defines a virtual release, the tag correction table must be interpreted differently than in the case of an actual single-release study. The tag corrections in column A0 are the unconditional tag survival probabilities from release to site A0. Under the subsequent columns, “A1” through “A3” in this case, are the **conditional** tag survival probabilities, given that the tag was alive at site A0. Note that the tag corrections under A0 are not used directly in the calculation of the corrected survival estimates; they are used to calculate the subsequent downstream tag corrections and are displayed in the **Tag Correction Report** for reference.

(Warning: All releases included in the virtual release group must be released upstream of the first detection site, or tag-life corrections will be incorrect.)

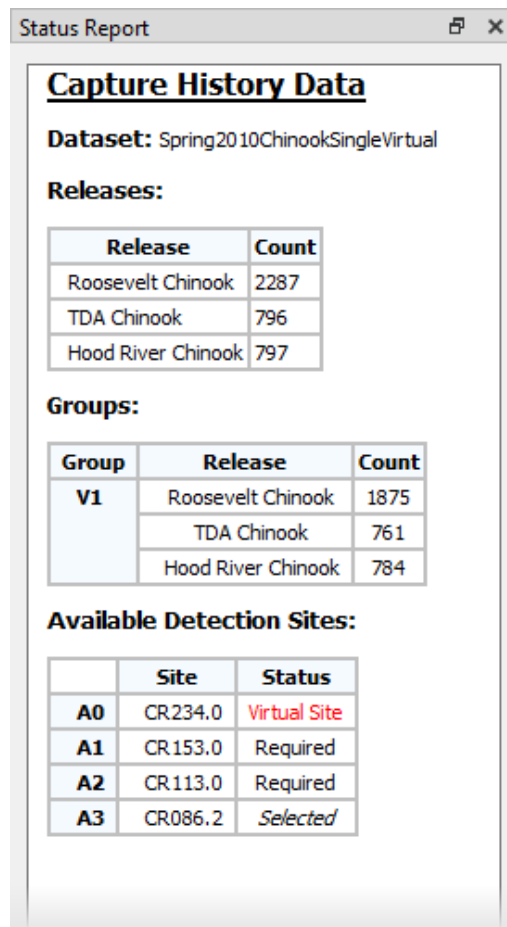


Figure 4.8: Status Report for a virtual single-release study. All three releases are used in forming the virtual release V1.

Tag Correction Report

Detection Site Key:

A0: CR234.0
A1: CR153.0
A2: CR113.0
A3: CR086.2

Release			Detection Sites			
Group	Site	Bin	A0	A1*	A2*	A3*
V1	Roosevelt Chinook	1	0.9853 (0.007661)	0.9981 (0.000993)	0.9973 (0.001451)	0.9967 (0.001760)
	TDA Chinook	1	0.9901 (0.005213)	0.9981 (0.001034)	0.9972 (0.001501)	0.9966 (0.001814)
	Hood River Chinook	1	0.9910 (0.004736)	0.9980 (0.001083)	0.9971 (0.001548)	0.9965 (0.001858)

* Probabilities are conditional on tag being active at A0.

Tag Life Dataset: Spring2010TagLifeFINAL

Fit Curve: Vitality
Log-Likelihood: -321.8102
Bootstrap iterations: 1000

Parameters:

r: 0.0296301 (0.00026652)
s: -1.13928e-05 (NA)
k: 0.00173314 (0.00121654)
u: 0.0572978 (0.00677299)

Figure 4.9: Example of a **Tag Correction Report** for a virtual single-release study.

4.3.1 Closed Form Parameter Report

Figure 4.10 shows the **Closed Form Parameter Report** for a virtual single release. The **Pooled Survival** estimates are the weighted average of the survival estimates from the **Survival Detail** section, weighted by release size.

Closed Form Parameter Report

Pooled Survival:

	CR234.0 to CR153.0		CR153.0 to CR113.0	
	Estimate	s.e.	Estimate	s.e.
V1	0.9412	0.004304	0.9936	0.002135

Survival Detail:

	CR234.0 to CR153.0		CR153.0 to CR113.0	
	Estimate	s.e.	Estimate	s.e.
Roosevelt Chinook	0.9340	0.006051	0.9890	0.004197
TDA Chinook	0.9433	0.008652	1.0010	0.003802
Hood River Chinook	0.9564	0.007722	0.9973	0.004832

Capture Detail:

	CR153.0		CR113.0		CR086.2 Survival*Capture	
	Estimate	s.e.	Estimate	s.e.	Estimate	s.e.
Roosevelt Chinook	0.8089	0.009474	0.9437	0.005699	0.9466	0.005568
TDA Chinook	0.8011	0.014938	0.9350	0.009474	0.9448	0.008825
Hood River Chinook	0.7965	0.014780	0.9267	0.009878	0.9334	0.009483

Configuration:

Dataset	Spring2010ChinookSingleVirtual
---------	--------------------------------

Figure 4.10: Closed Form Parameter Report for a single-release study using a virtual release.

4.3.2 Equate Parameters Across Releases

Figure 4.11 shows the dialog **Equate Parameters Across Releases** for a virtual single release. The user may equate all survival and detection probability parameters across releases (except for the “virtual site”), as well as the final product parameters.

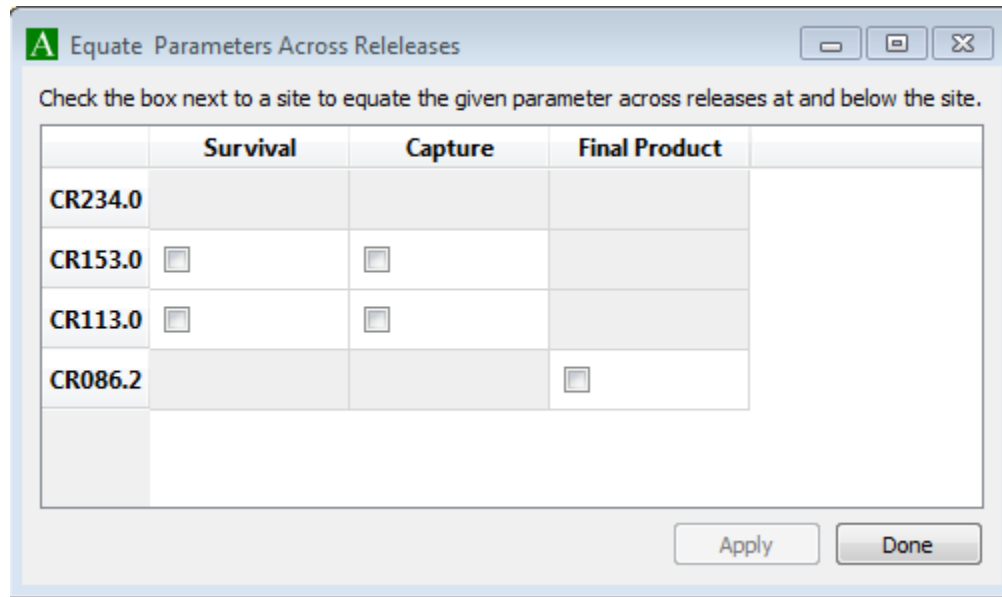


Figure 4.11: Equate Parameters Across Releases with a virtual single release with three releases, default setting; note that “CR234.0” is the virtual site.

4.3.3 Creating a Virtual Release

In order to pool tags from separate releases to create a virtual release, the tagged fish from the disparate release groups should have common survival and detection probabilities. The user can test whether or not different releases have common survival and detection probabilities using an LRT as described here. This test requires first fitting the model using unique parameters for all release groups, refitting the model using common parameters, and then comparing the optimized likelihood function values from the two model fits.

Figure 4.12 shows the **Parameter Report** after performing the **Compute** action with the default settings of no parameters equated across releases (Figure 4.11). We note the log-likelihood value (-59.7625) and the number of parameters (15).

We then equate all parameters across releases as shown in Figure 4.13, perform the **Compute** action again, and look at the **Parameter Report** as shown in Figure 4.14. The new log-likelihood value is -67.9273 with 5 parameters. The LRT

statistic is $2 \times (-59.7625 - (-67.9273)) = 16.3296$. The degrees of freedom are computed as the difference in the number of parameters (10). The P-value for a χ^2 statistic of 16.3296 with 10 degrees of freedom is $1 - 0.91 = 0.09$, indicating that it is valid to combine these three releases into one virtual release group (using an α level of 0.05; the appropriate α level [= maximum acceptable probability of Type I error] depends on the context of the study; smaller α levels are recommended for careful research, whereas preliminary studies may use higher α levels.). If the result had been different or if a larger α level were desired, we could have eliminated one of the releases that seemed to have different survival or detection probabilities and repeated the testing process with two releases in the virtual release group. Once a model configuration has been chosen and the Compute action has been performed, the **Compute Full Variance** action must be taken to obtain the standard errors of the survival estimates, as described in Section 3.4.3.

Parameter Report

Estimates:

Log Likelihood: -59.7625
 Num Parameters: 15
 AIC: 149.525

Pooled Survival:

Pooled survival is calculated only when survival parameters are equated across releases.

Survival Detail for Fitted Model:

	CR234.0 to CR153.0		CR153.0 to CR113.0	
	Estimate	s.e.	Estimate	s.e.
Roosevelt Chinook	0.9340	0.005966	0.9890	0.003260
TDA Chinook	0.9433	0.008586	1.0010	0.002598
Hood River Chinook	0.9564	0.007638	0.9973	0.003886

Capture Detail for Fitted Model:

	CR153.0		CR113.0		CR086.2 Survival*Capture	
	Estimate	s.e.	Estimate	s.e.	Estimate	s.e.
Roosevelt Chinook	0.8089	0.009474	0.9437	0.005699	0.9472	0.005571
TDA Chinook	0.8011	0.014938	0.9350	0.009474	0.9453	0.008830
Hood River Chinook	0.7965	0.014780	0.9267	0.009878	0.9340	0.009488

*Note: all standard errors are based on only the inverse Hessian.
 For full standard errors on the survival estimates, perform the "Estimate Full Variance" action.*



Figure 4.12: Example of a **Parameter Report** for a single-release study, no parameters equated across releases.

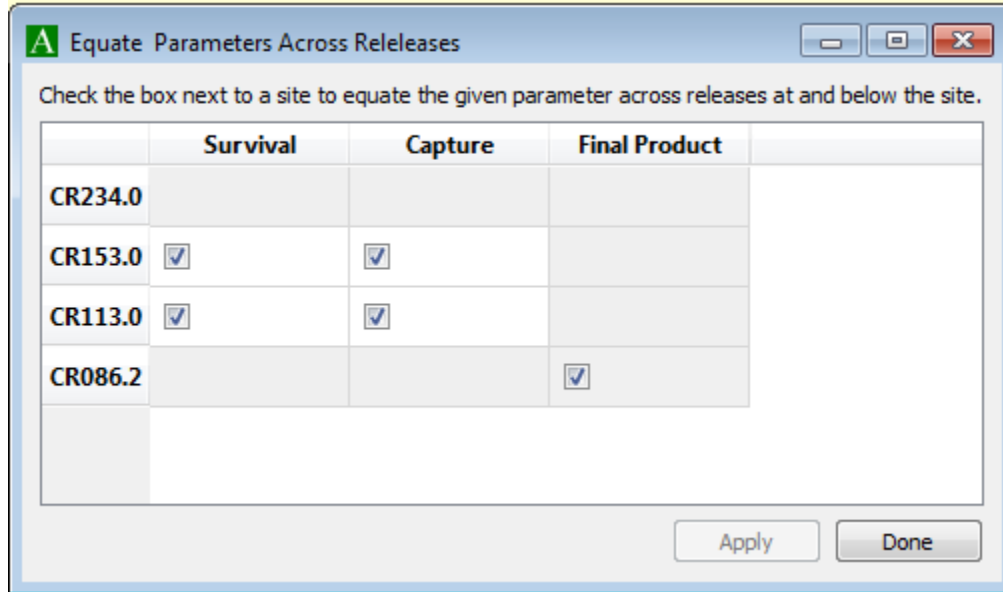


Figure 4.13: Equate Parameters Across Releases for a virtual single-release study with three releases, all parameters equated.

Parameter Report

Estimates:

Log Likelihood: -67.9273
 Num Parameters: 5
 AIC: 145.855

Pooled Survival:

	CR234.0 to CR153.0		CR153.0 to CR113.0	
	Estimate	s.e.	Estimate	s.e.
V1	0.9412	0.004176	0.9935	0.002079

Survival Detail for Fitted Model:

	CR234.0 to CR153.0		CR153.0 to CR113.0	
	Estimate	s.e.	Estimate	s.e.
Roosevelt Chinook	0.9412	0.004176	0.9935	0.002079
TDA Chinook	0.9412	0.004176	0.9935	0.002079
Hood River Chinook	0.9412	0.004176	0.9935	0.002079

Capture Detail for Fitted Model:

	CR153.0		CR113.0		CR086.2 Survival*Capture	
	Estimate	s.e.	Estimate	s.e.	Estimate	s.e.
Roosevelt Chinook	0.8043	0.007038	0.9378	0.004403	0.9437	0.004236
TDA Chinook	0.8043	0.007038	0.9378	0.004403	0.9437	0.004236
Hood River Chinook	0.8043	0.007038	0.9378	0.004403	0.9437	0.004236

*Note: all standard errors are based on **only** the inverse Hessian.
 For full standard errors on the survival estimates, perform the "Estimate Full Variance" action.*

Configuration:

Configuration area (content is obscured in the image)

Figure 4.14: Example of a Parameter Report for a single-release study, all parameters equated across releases.

Chapter 5 — Paired-release Study

Design

This chapter presents details unique to analyzing data from the paired-release study design. Analysis elements that are common to all study designs are described in Chapter 3.

A paired-release study consists of two release groups: an upstream release group labeled “R1,” and a downstream release group labeled “R2.” The parameter of interest, S_{Paired} , is the ratio of the survival probabilities in the first reach common to the two release groups. Details are given in Appendix B.2.2

5.1 Define Release Groups

The capture history data file for a paired-release study must contain two releases. By default, the first one is considered the upstream release group (R1), and the second one is the downstream release group (R2). Figure 5.1 shows the Define Release Groups dialog for a paired-release study with the default configuration; the only other option is to switch the roles of the two releases. Figure 5.2 shows the status report for the default configuration with the release named “TDA Chinook” mapped to the R1 release group and “Hood River Chinook” mapped to the R2 release group. A minimum of two detection sites are required downstream of the initial release.

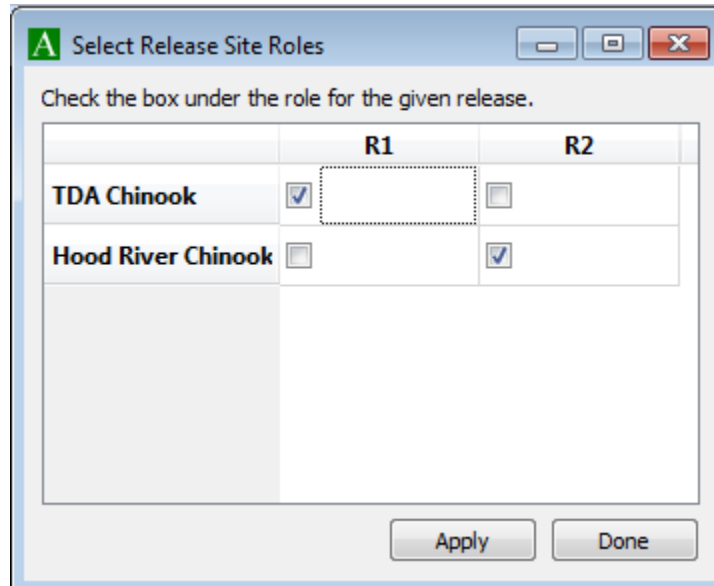


Figure 5.1: Define Release Groups (Select Release Site Roles dialog) for a paired-release study.

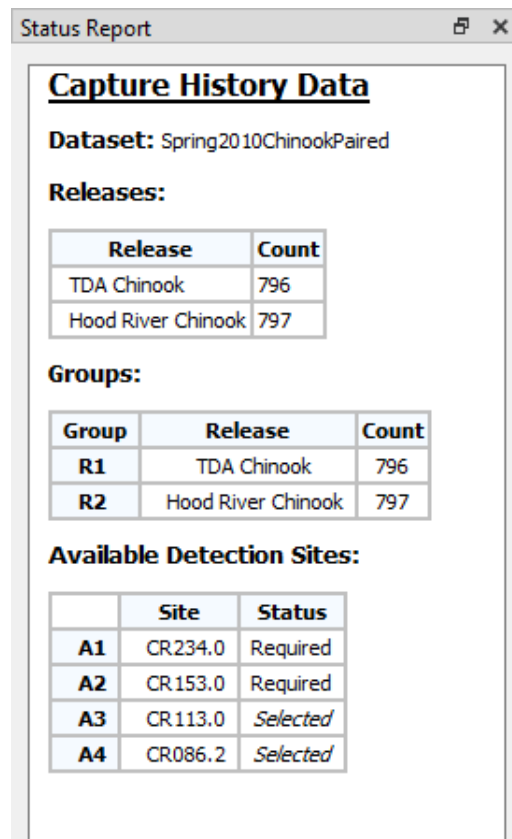


Figure 5.2: Example of a Status Report for a paired-release study.

5.2 Tag Corrections

Figure 5.3 shows the **Tag Correction Report** for a paired-release study. All tag corrections are the unconditional probability of a tag surviving from activation to the given detection site.

Tag Correction Report

Detection Site Key:

A1: CR234.0
A2: CR153.0
A3: CR113.0
A4: CR086.2

Release			Detection Sites			
Group	Site	Lot	A1	A2	A3	A4
R1	TDA Chinook	1	0.9901 (0.005806)	0.9881 (0.006967)	0.9874 (0.007390)	0.9867 (0.007739)
R2	Hood River Chinook	1	0.9910 (0.005276)	0.9891 (0.006421)	0.9881 (0.006939)	0.9876 (0.007241)

Tag Life Dataset: Spring2010TagLifeFINAL

Fit Curve: Vitality
Log-Likelihood: -321.8102
Bootstrap iterations: 1000

Parameters:

r: 0.0296301 (0.00026652)
s: -1.13928e-05 (NA)
k: 0.00173314 (0.00121654)
u: 0.0572978 (0.00677299)

Figure 5.3: Example of a **Tag Correction Report** for a paired-release study.

5.3 View Mixing

In a paired-release study, the paired survival estimate is the ratio of the survival estimates for the two release groups. Therefore, it is important to design the study so that they encounter the same conditions downstream and arrive at downstream detection sites at as close to the same times as possible. The timing of the R2 release group should be scheduled to achieve this goal. The **View Mixing** action on the navigation panel brings up the **Mixing** dialog as shown in Figure 5.4 to investigate how

well that goal was met. The graph shows the distribution of travel times for both release groups. In the box in the lower left corner, the user enters the delay (in hours) between the release of the R1 group and the release of the R2 group. In Figure 5.4, there is a delay of 12 hours between the release of R1 and R2. The **Mixing** dialog can also be used to plan future studies by trying alternative delay (offset) values to align the distributions and determine the best delay time to use in releasing the downstream release group. Note that after adjusting the release time offset using the up and down arrows in the **Mixing** dialog, the user must click outside the arrows in order for the release time offset to be implemented.

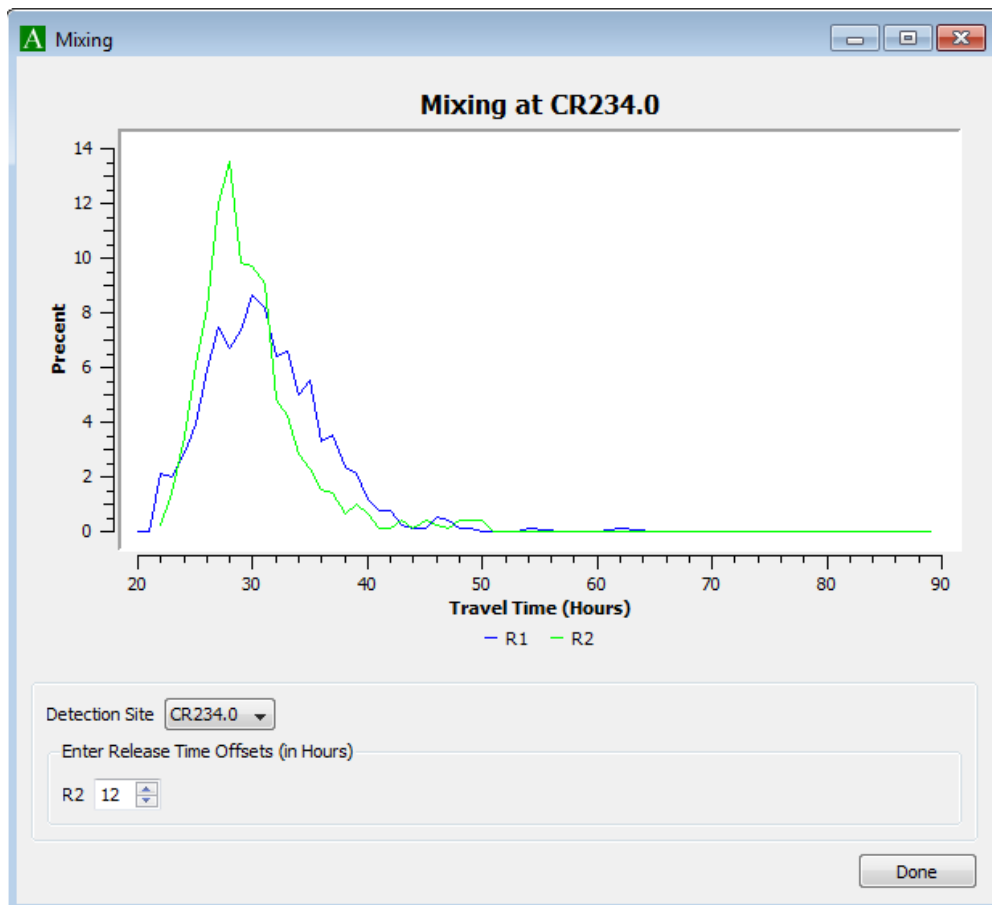


Figure 5.4: Mixing dialog for a paired-release study.

5.4 Closed Form Parameter Report

Figure 5.5 shows the **Closed Form Parameter Report** for a paired-release

study with all parameters freely estimated (i.e., no common or constrained parameters in the likelihood). In addition to reporting the corrected survival estimates, it also displays the paired survival estimate at the top, along with its standard error. Note that the results in this report are not adjusted for tag corrections.

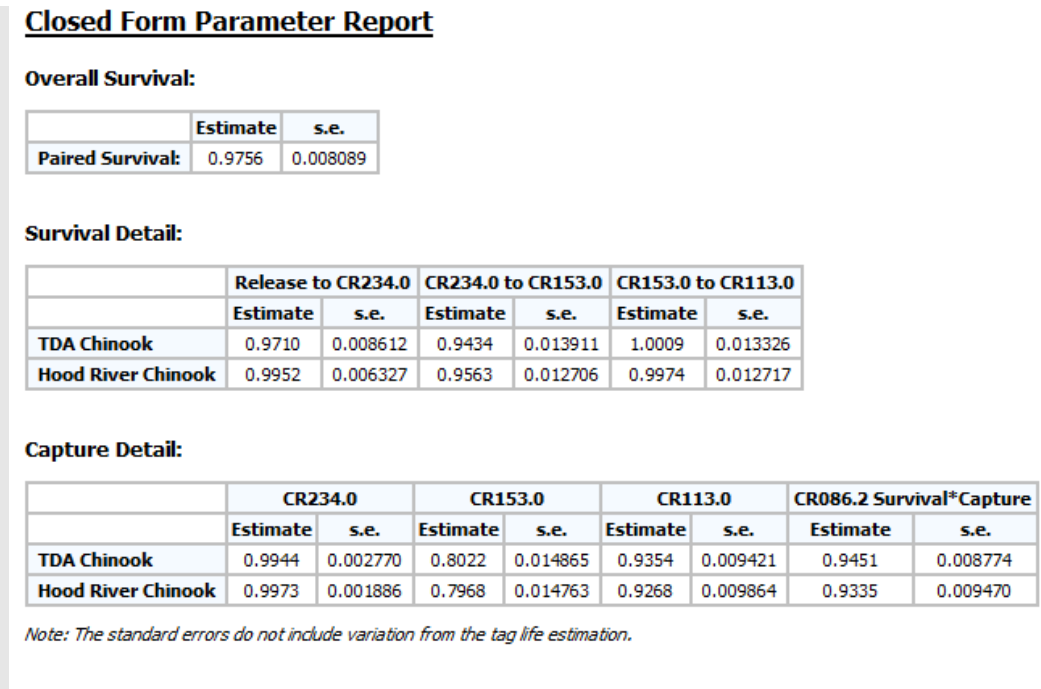


Figure 5.5: Example of a **Closed Form Parameter Report** for a paired-release study.

Chapter 6 — Virtual/Paired-release Study Design

This chapter presents details unique to analyzing data from the virtual/paired-release study design. Analysis elements that are common to all study designs are described in Chapter 3.

A virtual/paired-release study design is used to estimate the survival of smolts through a dam (S_{Dam}). Details are given in Appendix B.2.3.

6.1 Define Release Groups

The capture history data for a virtual/paired-release study consists of three release groups. The first is a virtual release, denoted “V1,” composed of all individuals of the given release detected at the detection site (virtual release site, or virtual site) at the face of the dam. The other two release groups are “R2” and “R3,” which together form the downstream paired release as shown in Figure B.2. By default, the first release in the capture history data file is used to create the virtual release V1 and the second and third releases are assigned to release groups R2 and R3, respectively. Figure 6.1 shows **Define Release Groups** for a virtual/paired-release study, allowing the user to change the default assignment of releases to release groups. Figure 6.2 shows the status report for a virtual/paired-release study. A minimum of three detections sites downstream of the virtual site are required for a virtual/paired-release study design.

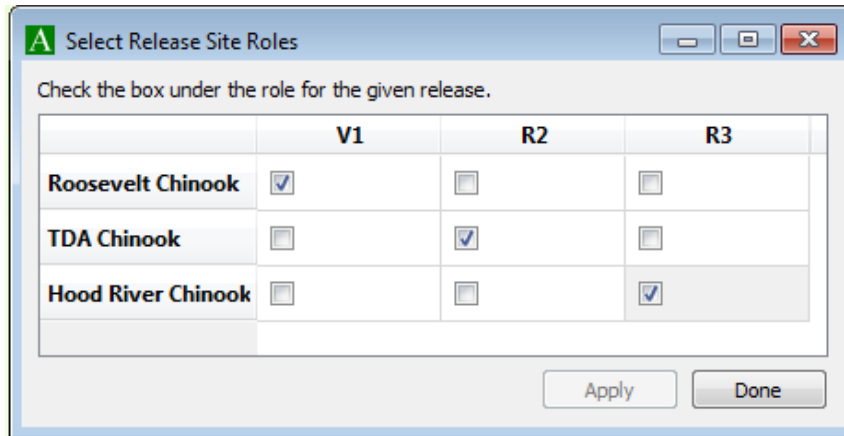


Figure 6.1: Define Release Groups (Select Release Site Roles dialog) for a virtual/paired-release study.

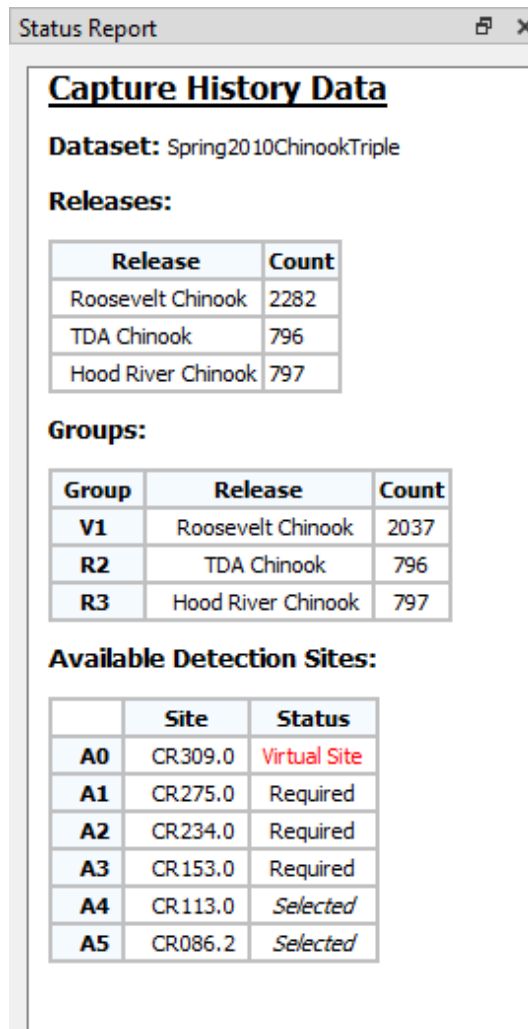


Figure 6.2: Example of a Status Report for a virtual/paired-release study.

6.2 Tag Corrections

Figure 6.3 shows a **Tag Correction Report** for a virtual/paired-release study. The tag correction for the column labeled “A0” is the unconditional probability of a tag being active at site A0 (the virtual site). For the virtual release V1, the tag corrections for the remaining columns, beginning with A1, are the probabilities of a tag being active at the site, conditioned on it being alive at site A0. For the R2 and R3 releases, the tag-life probabilities are unconditional.

Tag Correction Report

Detection Site Key:

A0: CR309.0
A1: CR275.0
A2: CR234.0
A3: CR153.0
A4: CR113.0
A5: CR086.2

Release			Detection Sites					
Group	Site	Bin	A0	A1*	A2*	A3*	A4*	A5*
V1	Roosevelt Chinook	1	0.9875 (0.005576)	0.9990 (0.000472)	0.9978 (0.001004)	0.9960 (0.001958)	0.9951 (0.002254)	0.9945 (0.002515)
R2	TDA Chinook	1	--	--	0.9901 (0.004451)	0.9881 (0.005684)	0.9874 (0.005788)	0.9867 (0.006045)
R3	Hood River Chinook	1	--	--	0.9910 (0.004039)	0.9891 (0.005245)	0.9881 (0.005448)	0.9876 (0.005675)

** For V1 only, probabilities are conditional on tag being active at A0.
 For R2 and R3, the tag-life probabilities are unconditional.*

Tag Life Dataset: Spring2010TagLifeFINAL

Fit Curve: Vitality
Log-Likelihood: -321.8102
Bootstrap iterations: 1000

Parameters:

r: 0.0296301 (0.00026652)
s: -1.13928e-05 (NA)
k: 0.00173314 (0.00121654)
u: 0.0572978 (0.00677299)

Figure 6.3: Example of a **Tag Correction Report** for a virtual/paired-release study.

6.3 View Mixing

With a virtual/paired-release study, as with a paired-release study, it is important that the timing of the releases be such that the fish from all release groups arrive at the downstream sites at about the same time. The **Mixing** dialog

shown in Figure 6.4 allows the user to view how well that requirement has been met and also what release timings should be used for future studies. For the virtual/paired-release study design, the user must specify the delay (offset) for both of the downstream releases R2 and R3 compared to the time when the fish in the V1 group were released at the actual release location upstream of the virtual site.

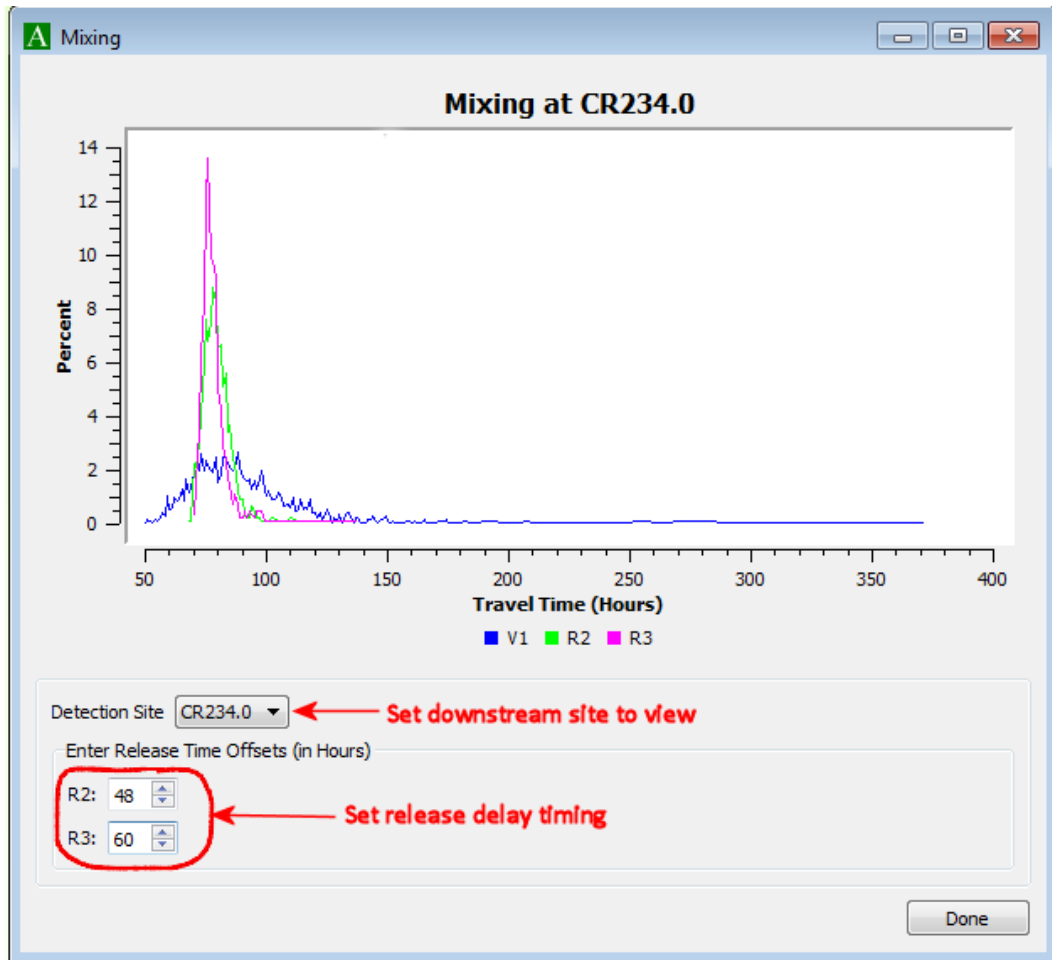


Figure 6.4: Mixing dialog for a virtual/paired-release study.

6.4 Closed Form Parameter Report

Figure 6.5 shows the **Closed Form Parameter Report** for a virtual/paired-release study. At the top of the report, the dam survival probability (Equation B.33) is reported, along with its standard error.

Closed Form Parameter Report

Overall Survival:

	Estimate	s.e.
Dam Survival:	0.9641	0.009644

Survival Summary:

	Estimate	s.e.
V1	0.9406	0.005297
R2	0.9710	0.008252
R3	0.9952	0.005896

Survival Detail:

	CR309.0 to CR275.0		CR275.0 to CR234.0		Release to CR234.0		CR234.0 to CR153.0		CR153.0 to CR113.0	
	Estimate	s.e.	Estimate	s.e.	Estimate	s.e.	Estimate	s.e.	Estimate	s.e.
Roosevelt Chinook	0.9406	0.005303	0.9836	0.003375	---	---	0.9536	0.005909	0.9895	0.005229
TDA Chinook	---	---	---	---	0.9710	0.008252	0.9434	0.012868	1.0009	0.011741
Hood River Chinook	---	---	---	---	0.9952	0.005896	0.9563	0.011721	0.9974	0.011293

Capture Detail:

	CR275.0		CR234.0		CR153.0		CR113.0		CR086.2 Survival*Capture	
	Estimate	s.e.	Estimate	s.e.	Estimate	s.e.	Estimate	s.e.	Estimate	s.e.
Roosevelt Chinook	0.9995	0.000532	0.9950	0.001676	0.8089	0.009505	0.9440	0.005704	0.9469	0.005570
TDA Chinook	---	---	0.9944	0.002770	0.8022	0.014865	0.9354	0.009421	0.9451	0.008774
Hood River Chinook	---	---	0.9973	0.001886	0.7968	0.014763	0.9268	0.009864	0.9335	0.009470

Configuration:

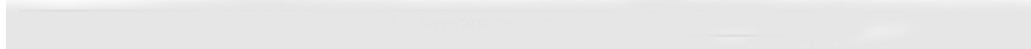


Figure 6.5: Example of a **Closed Form Parameter Report** for a virtual/paired-release study. The survival estimates highlighted in red are used to calculate the dam survival.

6.5 Parameter Report

Figure 6.6 shows the top portion of a **Parameter Report** for a virtual/paired-release study after running **Compute**. As with the **Closed Form Parameter Report**, the dam survival (Equation B.33) is reported at the top of the report. The **Parameter Report** shown in Figure 6.6 reports standard error estimates that include only the variability from the release-recapture model (i.e., the Hessian). Once the final configuration has been determined, the user must perform **Computer Full Variance** as explained in Section 3.4.3 to perform the bootstrapping to obtain the full standard errors for the survival estimates.

Parameter Report

Estimates:

Log Likelihood: 175.9955
 Num Parameters: 23
 AIC: -305.991

Dam Survival:

	Estimate	s.e.
Dam Survival:	0.9641	0.009644

Survival Summary:

	Estimate	s.e.
V1	0.9406	0.005283
R2	0.9710	0.006930
R3	0.9952	0.004171

Survival Detail for Fitted Model:

	CR309.0 to CR275.0		CR275.0 to CR234.0		Release to CR234.0		CR234.0 to CR153.0		CR153.0 to CR113.0	
	Estimate	s.e.	Estimate	s.e.	Estimate	s.e.	Estimate	s.e.	Estimate	s.e.
Roosevelt Chinook	0.9406	0.005283	0.9836	0.003026	---	---	0.9536	0.005210	0.9895	0.003205
TDA Chinook	---	---	---	---	0.9710	0.006930	0.9434	0.008586	1.0009	0.002578
Hood River Chinook	---	---	---	---	0.9952	0.004171	0.9563	0.007647	0.9974	0.003880

Capture Detail for Fitted Model:

	CR275.0		CR234.0		CR153.0		CR113.0		CR086.2 Survival*Capture	
	Estimate	s.e.	Estimate	s.e.	Estimate	s.e.	Estimate	s.e.	Estimate	s.e.
Roosevelt Chinook	0.9995	0.000532	0.9950	0.001676	0.8089	0.009505	0.9440	0.005704	0.9475	0.005574
TDA Chinook	---	---	0.9944	0.002770	0.8022	0.014865	0.9354	0.009421	0.9457	0.008779
Hood River Chinook	---	---	0.9973	0.001886	0.7968	0.014763	0.9268	0.009864	0.9340	0.009475

Note: all standard errors are based on **only** the inverse Hessian.
 For full standard errors on the survival estimates, perform the "Estimate Full Variance" action.

Figure 6.6: Example of a **Parameter Report** for a virtual/paired-release study. The survival estimates highlighted in **red** are used to calculate the dam survival.

Chapter 7 — Full Virtual Release with Dead-fish Correction Study Design

This chapter presents details unique to analyzing data from the virtual release/dead-fish correction study design. Analysis elements that are common to all study designs are described in Chapter 3.

A study uses a virtual release of live smolts in conjunction with a release of dead smolts in the dam tailrace to estimate the survival of smolts through the dam. Detections from the dead release are used to adjust dam survival estimates for the possibility of detection of dead fish at receiver arrays downstream of the dam. Details are given in Appendix B.2.4, and the methodology is given in Harnish et al. (2020). An alternative reduced version of the ViRDCt model is described in Chapter 8.

7.1 Define Release Groups

The data for the full ViRDCt study design consist of one virtual release group created at the dam face array and one release group of dead smolts in the dam tailrace. The virtual release is denoted V_1 , and the dead release D1. By default, the first release in the capture history data file is designated as V1, and the second as D1. Any subsequent releases will not be used. Thus, if there are multiple upstream releases that make up V1, they must be configured with **Define Release Groups** on the **Navigation Panel**, as shown in Figure 7.1.

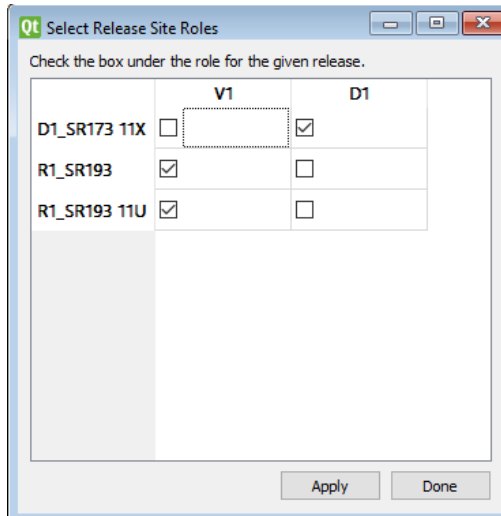


Figure 7.1: Define Release Groups (Select Release Site Roles dialog) for a full ViRDcT study.

The full ViRDcT model requires exactly three detection sites: the site that determines the virtual release (virtual site) and two downstream detection sites consisting of a tailrace detection site and a tailwater detection site (Figure B.3). Figure 7.2 shows the **Status Report** for a full ViRDcT study.

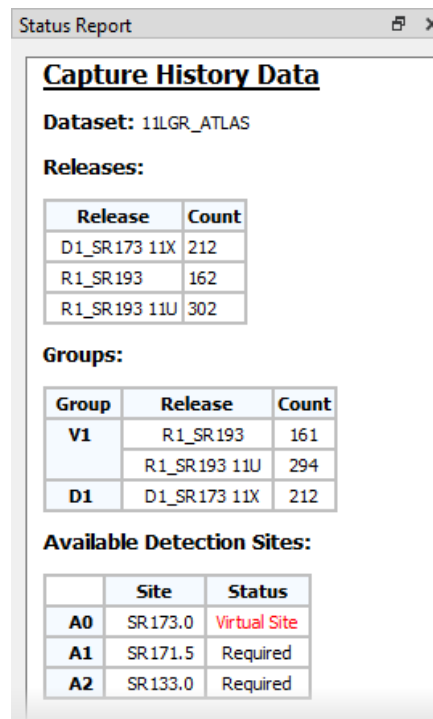


Figure 7.2: Example of a Status Report for a full ViRDcT study.

7.2 View ViRDCt Mixing

For the ViRDCt study design, the mixing plot shows the virtual release dates of the live-released fish (V1 group) in comparison to the release dates of the dead-released fish (D1 group). The release dates can either be displayed on the raw scale or on the cumulative scale. The default settings for the **ViRDCt Mixing** dialog restrict the live-released fish to those that were not detected downstream of the virtual release site, i.e., those that were presumed to have died during dam passage. These are the fish that the dead-released group is intended to represent. Alternatively, the plot can be generated using the entire V1 group, including those that were detected downstream of the dam.

Figure 7.3 shows the **ViRDCt Mixing** plot for the full ViRDCt study using the default settings. Only four of the V1 tags were not detected downstream of the dam (i.e., presumed dead), and they all had virtual release dates in the first half of the release period of the D1 group. Thus, it might be worthwhile exploring the sensitivity of the model results to use of the entire D1 group compared to only the first half of that group.

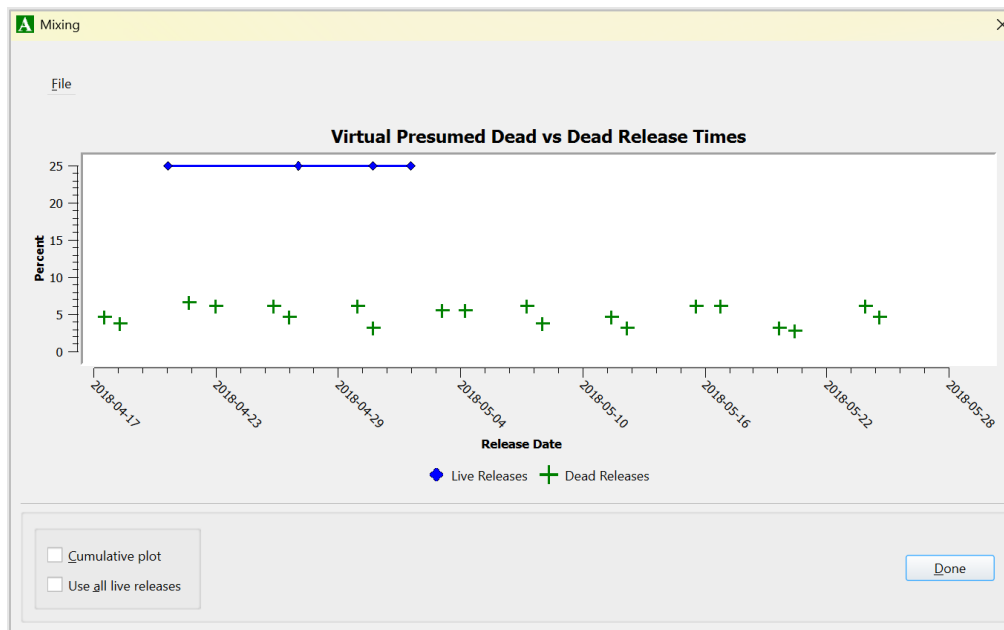


Figure 7.3: ViRDCt Mixing dialog for a full ViRDCt study using the default settings.

Figure 7.4 shows the **ViRDcT Mixing** plot for the same data set but now using the full set of live-released fish (V1) and on the cumulative scale. The dead-released fish were released slightly earlier than the arrival of the live-released fish at the dam, but the difference is small and is consistent throughout the study.

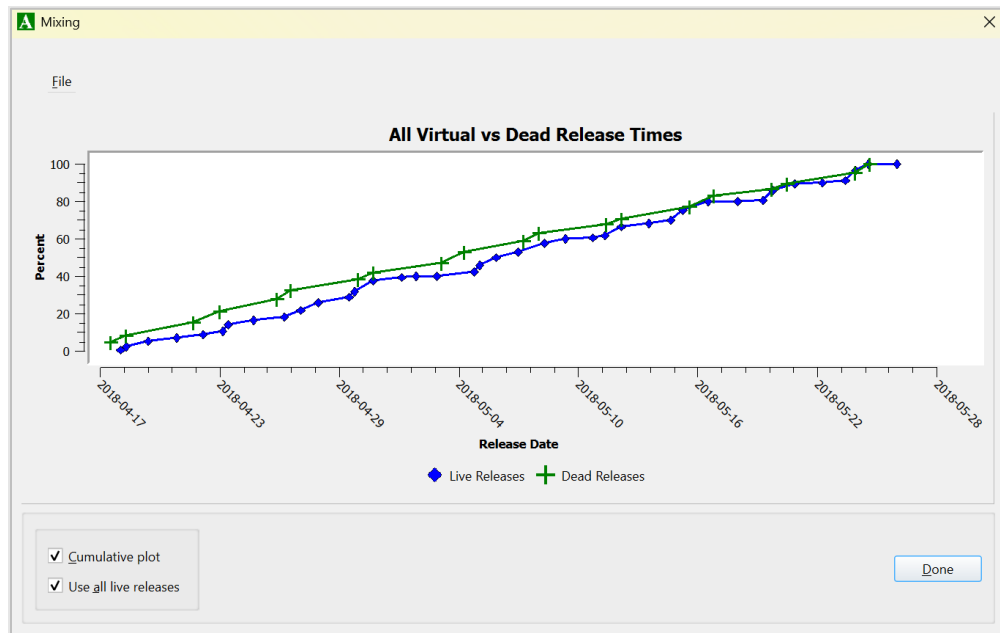


Figure 7.4: ViRDcT Mixing dialog for a full ViRDcT study using all tags from the live release group and showing the cumulative release distributions.

7.3 Tag Corrections

Figure 7.5 shows a **Tag Correction Report** for a full ViRDcT study. Note the value circled in red for the D1 release at site “A2” (the tailwater array). It is sometimes the case for a ViRDcT study that there are too few detections of the dead release at the tailwater array to estimate the tag-life correction variance. These cases are indicated by the message below the table corresponding to the dagger (†), which states that “NAs indicate insufficient data to estimate tag life correction variance.”

Tag Correction Report

Detection Site Key:

A0: SR173.0
A1: SR171.5
A2: SR133.0

Release			Detection Sites		
Group	Site	Lot	A0	A1*	A2*
V1	R1_SR193	1	0.9940 (0.0020)	0.9996 (0.0001)	0.9976 (0.0008)
	R1_SR193 11U	1	0.9955 (0.0015)	0.9997 (0.0001)	0.9985 (0.0005)
D1	D1_SR173 11X	1	--	0.9972 (0.0009)	0.9955 (NA)†

* Probabilities are conditional on tag being active at A0.

† NAs indicate insufficient data to estimate tag life correction variance.

Tag Life Dataset: tag_life_data

Fit Curve: Vitality
Log-Likelihood: -707.2149
Bootstrap iterations: 1000

Parameters:

r: 0.0160278 (0.000229702)
s: -0.0141421 (0.0066349)
k: 0.00116999 (0.000568755)
u: 0.0580244 (0.0980338)

Figure 7.5: Example of a **Tag Correction Report** for a full ViRDcT study where not all tag correction variances are estimable.

7.4 Parameter Report

Figure 7.6 shows the **Modeled Parameter Report** with estimates of dam survival, release-specific survival, and detection probabilities. The implication of not being able to estimate all tag-life correction variances is that upon computing the parameter estimates, the **Modeled Parameter Report** will reflect variances based only on the inverse Hessian. This is equivalent to assuming that the (unestimable) tag correction variances are 0.0, and results in an underestimate of the true variance for the survival and detection probability estimates. Also, the **Compute Full Variance** function will be

unavailable. A warning message is included in the **Modeled Parameter Report** in this case (Figure 7.6).

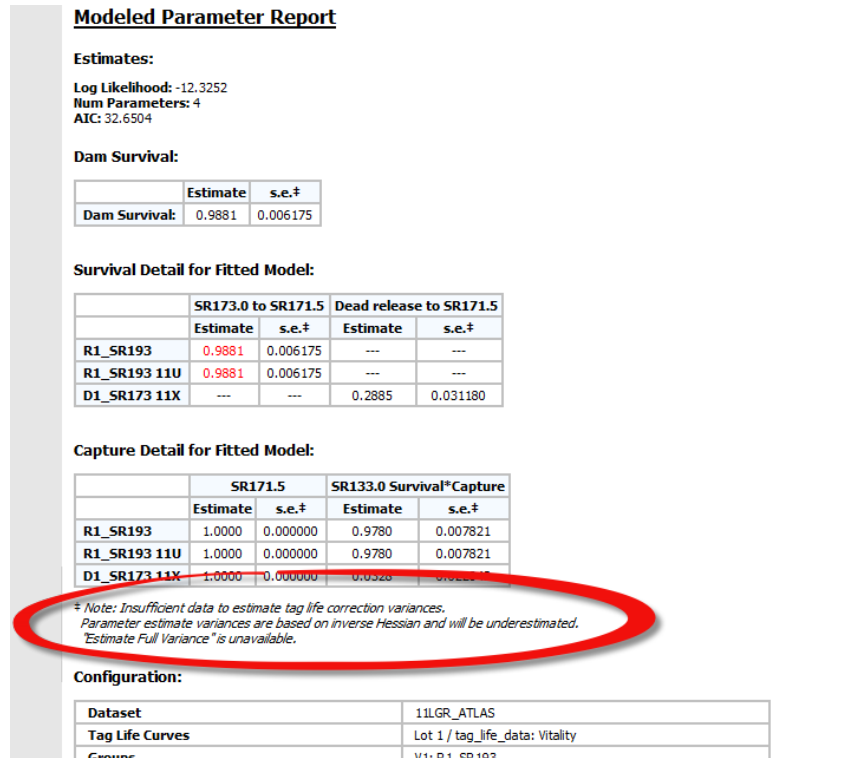


Figure 7.6: Modeled Parameter Report for a full ViRDCT study where not all tag correction variances are estimable. Survival estimates in red are used in the calculation of dam survival.

The **Closed Form Parameter Report** is unavailable for a full ViRDCT study, regardless of whether all tag correction variances are estimable.

7.5 Equate Parameters Across Releases

For the full ViRDCT study design, the only parameters that may be equated across the V1 and D1 releases are the detection probabilities in the tailrace, as shown in Figure 7.7.

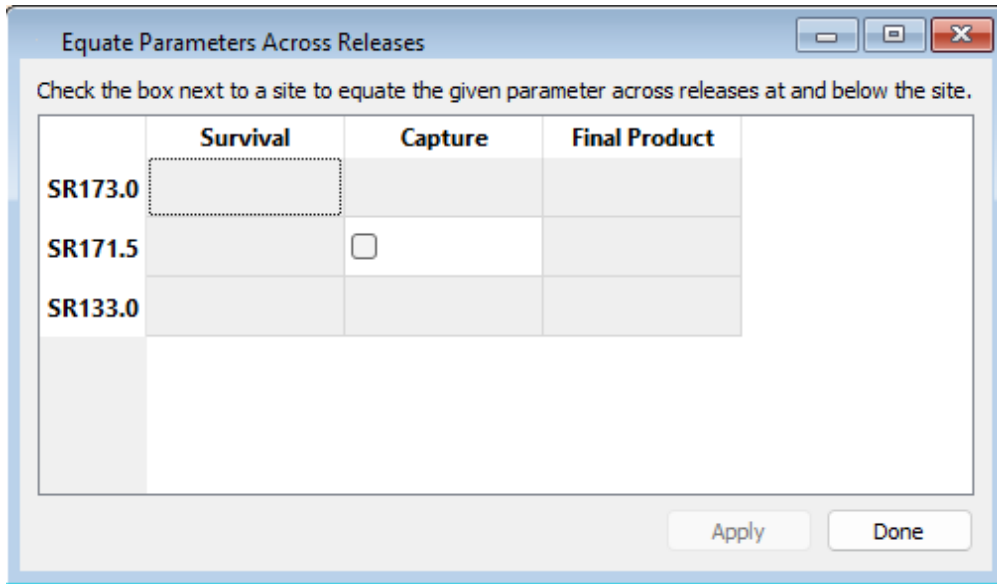


Figure 7.7: Equate Parameter Across Releases dialog for a full ViRDcT study.

7.6 Constrain Parameters

The survival parameters for the full ViRDcT study design may be constrained by the logit function (Figure 7.8), and the capture parameters (including the combined survival and capture probability in the last reach) may be fixed to 1.0 (Figure 7.9).

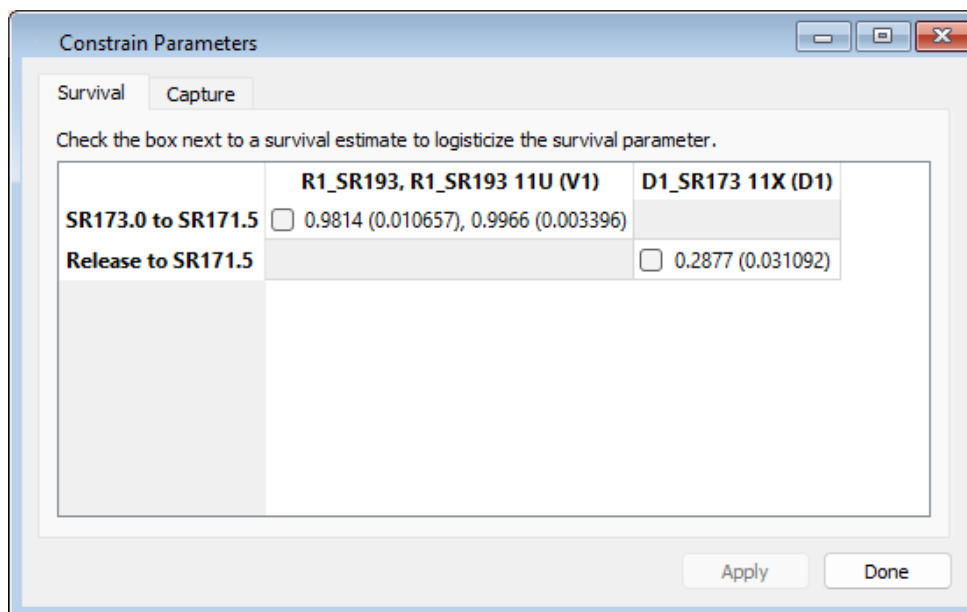


Figure 7.8: Constrain Parameters dialog on the Survival tab for a full ViRDcT study.

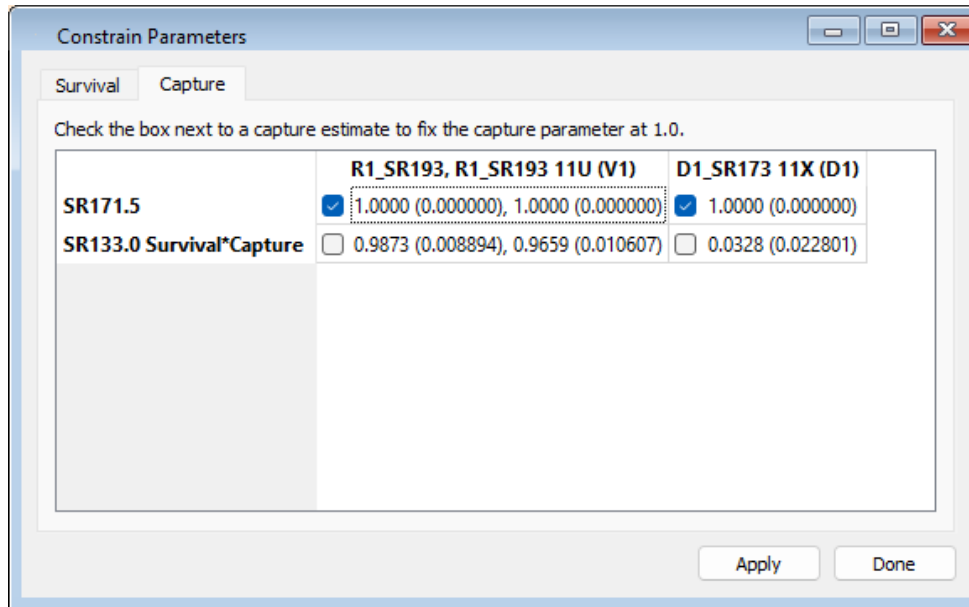


Figure 7.9: Constrain Parameters dialog on the **Capture** tab for a full ViRDcT study.

Chapter 8 – Reduced Virtual Release with Dead-fish Correction Study Design

Like the full ViRDCt model described in Chapter 7, the reduced ViRDCt model is used to analyze data from the virtual release/dead-fish correction study design. The difference is that the reduced ViRDCt model does not use tailwater detections from the dead fish release; it only uses dead-release detections in the tailrace.

The reduced ViRDCt model can be used instead of the full ViRDCt model when there are no dead fish detections in the tailwater, or if the dead-release detections are too sparse for estimation with the full ViRDCt model; if there are detections in the tailwater, they will be ignored by the reduced ViRDCt model. Switching from the full ViRDCt study design to the reduced ViRDCt study design requires the user to reload the data.

8.1 Define Release Groups

The release groups are defined in the same way as described in Section 7.1 for the full model. The reduced ViRDCt model requires exactly three detection sites for the live releases, and one detection site for the dead-fish release (tailrace site); if there are two detection sites for the dead-fish release, detections at the second site will be ignored.

8.2 Tag Corrections

Figure 8.1 shows a **Tag Correction Report** for a reduced ViRDCt study. In contrast to the full ViRDCt example in Figure 7.5, there is only one downstream detection site for the dead-fish release.

Tag Correction Report

Detection Site Key:

A0: SR173.0

A1: SR171.5

A2: SR133.0

Release			Detection Sites		
Group	Site	Bin	A0	A1*	A2*
V1	R1_SR193	1	0.9940 (0.002030)	0.9996 (0.000125)	0.9976 (0.000796)
D1	D1_SR173 11X	1	--	0.9972 (0.000959)	--

* Probabilities are conditional on tag being active at A0.

Tag Life Dataset: tag_life_data

Fit Curve: Vitality

Truncations: None

Log-Likelihood: -707.2149

Bootstrap iterations: 1000

Parameters:

r: 0.0160278 (0.000229702)

s: -0.0141421 (0.0066349)

k: 0.00116999 (0.000568755)

u: 0.0580244 (0.0980338)

Figure 8.1: Tag Correction Report for a reduced ViRDcT study.

8.3 Closed Form Parameter Report

Unlike the full ViRDcT model, closed form estimates exist for the reduced ViRDcT model. Figure 8.2 shows an example of a **Closed Form Parameter Report**. This report is available only if there is only one bin and only one upstream release in the virtual release.

Closed Form Parameter Report

Overall Survival:

	Estimate	s.e.
Dam Survival:	0.9743	0.015028

Survival Detail:

SR173.0 to SR171.5		
	Estimate	s.e.
R1_SR193	0.9743	0.015028

Capture Detail:

	SR171.5		SR171.5 Survival*Capture		SR133.0 Survival*Capture	
	Estimate	s.e.	Estimate	s.e.	Estimate	s.e.
R1_SR193	1.0000	0.000000	---	---	0.9968	0.010112
D1_SR173 11X			0.2885	0.031180	---	---

Note: The standard errors do not include variation from the tag life estimation.

Configuration:

Dataset	11LGR_ATLAS - single
Tag Life Curves	Bin 1 / tag_life_data; Vitality
Groups	V1: R1_SR193 D1: D1_SR173 11X
Active Detection Sites	A0: SR173.0 A1: SR171.5 A2: SR133.0
Optimizer	Fletcher, maxIterations=200, stepSize=1e-06, precision=1e-06

Figure 8.2: Closed Form Parameter Report for a reduced ViRDCt study.

8.4 Parameter Report

Figure 8.3 shows the **Modeled Parameter Report** for the reduced ViRDCt model. In this example, the detection probability has been fixed to 1.0 at the tailrace in order for the parameters to be estimable (see Section 8.6).

Modeled Parameter Report

Estimates:

Log Likelihood: -5.5933
 Num Parameters: 3
 AIC: 17.1865

Dam Survival:

	Estimate	s.e.†
Dam Survival:	0.9743	0.015033

Survival Detail for Fitted Model:

	SR173.0 to SR171.5	
	Estimate	s.e.†
R1_SR193	0.9743	0.015033

Capture Detail for Fitted Model:

	SR171.5		SR171.5 Survival*Capture		SR133.0 Survival*Capture	
	Estimate	s.e.*	Estimate	s.e.*	Estimate	s.e.*
R1_SR193	1.0000	0.000000	---	---	0.9968	0.010112
D1_SR173 11X			0.2885	0.031180	---	---

Notes:

* Standard error is based on only the inverse Hessian.
 † Standard error is based on bootstrapping.

Configuration:

Dataset	11LGR_ATLAS - single
Tag Life Curves	Bin 1 / tag_life_data; Vitality
Groups	V1: R1_SR193
	D1: D1_SR173 11X
Active Detection Sites	A0: SR173.0

Figure 8.3: Modeled Parameter Report for a reduced ViRDCt study. Survival estimates in red are used in the calculation of the dam survival.

8.5 Parameter Report Equate Parameters Across Releases

For the reduced ViRDcT study design, no parameters can be equated.

8.6 Constrain Parameters

The one survival parameter for the reduced ViRDcT study design that may be constrained by the logit function is the dam survival (Figure 8.4).

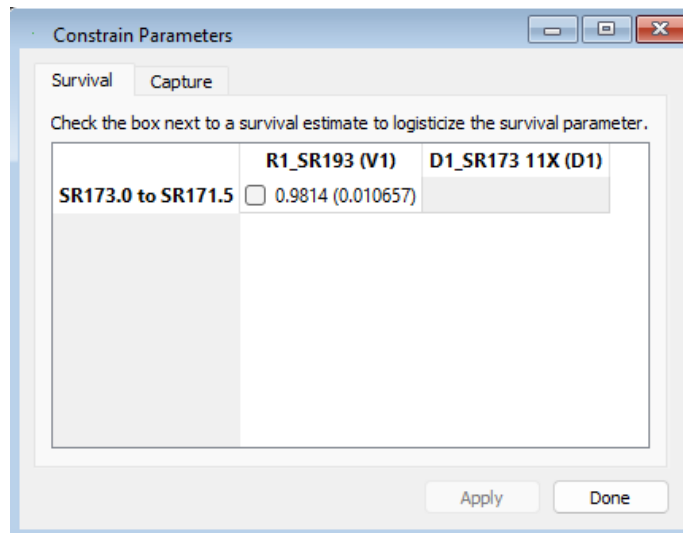


Figure 8.4: Constrain Parameters dialog on the **Survival** tab for a reduced ViRDcT study.

The capture parameters (including the combined survival and capture probabilities in the last reach for each release group) may be fixed to 1.0 as shown in Figure 8.5.

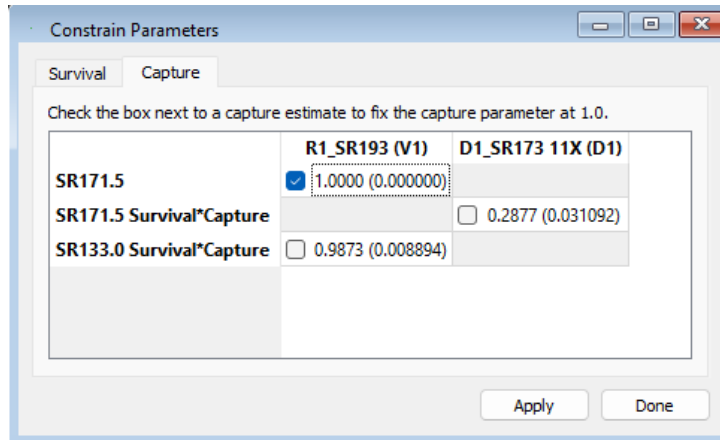


Figure 8.5: Constrain Parameters dialog on the **Capture** tab for a reduced ViRDCT study.

Appendix A — Input Data Files

A.1 Capture History Data File

The capture history data file is a comma separated value (.csv) text file. This data file can be created by using [the TagPro utility available on the Columbia Basin Research website](#). A portion of an example of a capture history data file is shown in Figure A.1. The columns are as follows, in the required order:

1. name of the release
2. bin number
3. tag ID
4. tag activation date and time
5. tag release date and time
6. site name
7. “1” if the tag was detected at the site, “2” if tag is to be censored at that site, or “0” otherwise
8. the detection date and time if detected, blank otherwise

Tag activation and release date and times must be in the form “yyyy-mm-dd hh:mm:ss.” The file must be sorted by, in order of precedence, the release name, bin number, tag ID, and finally by site name (from upstream to downstream). Because fish are assumed to be moving in only one direction, only one detection per site per tag is allowed, and only downstream movement is allowed. Detection times should be the first detection at the sites for each tag in order to minimize the amount of correction estimated for tag failure. The first line of the capture history data file may be column labels if desired; if present, it will be ignored by Program ATLAS.

Because the capture history data file is in CSV format, it can be easily read and edited via a spreadsheet program (**Warning: MS Excel saves date-time fields**

in the wrong format by default). This allows a user to create, for example, multiple bins per release based on the delay between release time and activation time (see Section 3.3.2 for an explanation of bins).

```
TDA Chinook,1,G72018489,2010-04-26 13:19:00,2010-04-30 20:04:00,CR113.0,1,2010-05-05 11:19:28
TDA Chinook,1,G72018489,2010-04-26 13:19:00,2010-04-30 20:04:00,CR086.2,1,2010-05-05 22:49:05
TDA Chinook,1,G72019CD6,2010-04-26 10:35:00,2010-04-30 20:04:00,CR234.0,1,2010-05-02 08:42:47
TDA Chinook,1,G72019CD6,2010-04-26 10:35:00,2010-04-30 20:04:00,CR153.0,1,2010-05-03 13:33:56
TDA Chinook,1,G72019CD6,2010-04-26 10:35:00,2010-04-30 20:04:00,CR113.0,0,
TDA Chinook,1,G72019CD6,2010-04-26 10:35:00,2010-04-30 20:04:00,CR086.2,1,2010-05-04 12:30:21
TDA Chinook,1,G7201B3B4,2010-04-26 10:55:00,2010-04-30 20:06:00,CR234.0,1,2010-05-02 08:30:42
TDA Chinook,1,G7201B3B4,2010-04-26 10:55:00,2010-04-30 20:06:00,CR153.0,1,2010-05-03 12:18:21
TDA Chinook,1,G7201B3B4,2010-04-26 10:55:00,2010-04-30 20:06:00,CR113.0,1,2010-05-03 22:04:24
TDA Chinook,1,G7201B3B4,2010-04-26 10:55:00,2010-04-30 20:06:00,CR086.2,1,2010-05-04 05:12:55
TDA Chinook,1,G7201E5B2,2010-04-26 09:49:00,2010-04-30 20:04:00,CR234.0,1,2010-05-03 08:33:44
TDA Chinook,1,G7201E5B2,2010-04-26 09:49:00,2010-04-30 20:04:00,CR153.0,1,2010-05-05 00:54:22
TDA Chinook,1,G7201E5B2,2010-04-26 09:49:00,2010-04-30 20:04:00,CR113.0,1,2010-05-05 13:20:42
TDA Chinook,1,G7201E5B2,2010-04-26 09:49:00,2010-04-30 20:04:00,CR086.2,1,2010-05-05 22:35:55
TDA Chinook,1,G7201E5B2,2010-04-26 09:49:00,2010-04-30 20:04:00,CR234.0,1,2010-05-02 08:48:28
TDA Chinook,1,G7201E5B2,2010-04-26 09:49:00,2010-04-30 20:04:00,CR153.0,1,2010-05-03 13:33:56
```

Figure A.1: Portion of a capture history data file.

A.2 Attribute Group File

The attribute group file defines one or more attributes and assigns tag codes to attribute values. It is a .csv text file. An example, loaded into a spreadsheet program, is shown in Figure A.2. The first column is always the tag codes. The first row names the tag code column (it can be anything) and also labels each attribute. In Figure A.2, two attributes are defined: “tagger” and “tag lot.” If a combination of columns is desired (e.g., tagger × tag lot), a separate column must be added, appropriately coded.

	A	B	C	D
1	tag_code	tagger	tag lot	
2	G727288C9	Dopey	5	
3	G72630B8F	Happy	2	
4	G724FAC2F	Doc	2	
5	G72333407	Doc	5	
6	G727616FC	Doc	4	
7	G726FE3E9	Happy	2	
8	G7234C07C	Dopey	1	
9	G720A377A	Happy	1	
10	G72518E80	Doc	4	
11	G7233D5B0	Happy	5	
12	G720D47EC	Dopey	1	
13	G72733BDD	Happy	1	
14	G726DE538	Dopey	5	

Figure A.2: Top portion of an attribute group file.

A.3 Tag-life Data File

The tag-life data file contains the results of the independent tag-life test conducted to estimate tag-life corrections. It is a text file with each row containing the observed failure time, in days, for each tag. There must be one line for each tag. For example, if three tags failed at 25.5 days, then the number 25.5 must occur three times in the file. The first line may be an optional label which will be ignored by Program ATLAS. A portion of an example of a tag-life data file is shown in Figure A.3.

```

tag_life_days
32.29
30.87
34.48
32.27
34.16
34.16
35.98
33.44
32.66
32.71
34.63
33.92
32.80
35.07
34.74
32.76
34.19
26.59

```

Figure A.3: Portion of the tag-life data file.

Appendix B — Statistical Methods used in ATLAS

B.1 Tag-life Analyses

Tag-life analysis is performed using tag-life data, in which a group of tags in a test group are monitored for failure. At each failure, the time and number of remaining tags are recorded. The objective of tag-life analysis is to estimate a statistical model of the time of failure, or “tag life,” of tags represented by the test group.

B.1.1 Parametric Failure-time Distributions

One of the simplest models for failure-time data is the exponential distribution. The exponential probability density function (PDF) can be written as

$$f(t) = \begin{cases} \frac{1}{\lambda} e^{-\frac{1}{\lambda}t} & t \geq 0, \\ 0 & t < 0 \end{cases}, \quad (\text{B.1})$$

with survivorship function

$$S(t) = e^{-\frac{1}{\lambda}t}, \quad (\text{B.2})$$

cumulative distribution function (CDF)

$$F(t) = 1 - e^{-\frac{1}{\lambda}t}, \quad (\text{B.3})$$

and hazard function (Lee, 1992, p. 132)

$$h(t) = \frac{1}{\lambda}, t \geq 0. \quad (\text{B.4})$$

The exponentially declining survivorship function for the exponential

distribution (Equation B.2) is too severe for typical tag-failure times and not commonly used to model tag life. However, it is the basis for more commonly used parametric distributions such as the two-parameter and three-parameter Weibull, so it is included here.

B.1.1.1 Two-parameter Weibull

An extension of the exponential distribution, the two-parameter Weibull distribution (Lawless 1982, pp. 15–17; Lee 1992, pp. 136–137) has both a scale parameter (λ) and a shape parameter (β). The PDF for the two-parameter Weibull is

$$f(t) = \frac{\beta}{\lambda} \left(\frac{t}{\lambda}\right)^{\beta-1} e^{-\left(\frac{t}{\lambda}\right)^\beta}, \quad (\text{B.5})$$

with survivorship function

$$S(t) = e^{-\left(\frac{t}{\lambda}\right)^\beta}, \quad (\text{B.6})$$

CDF

$$F(t) = 1 - e^{-\left(\frac{t}{\lambda}\right)^\beta}, \quad (\text{B.7})$$

and hazard function

$$h(t) = \frac{\beta}{\lambda} \left(\frac{t}{\lambda}\right)^{\beta-1}. \quad (\text{B.8})$$

When $\beta = 1$, the two-parameter Weibull (Equation B.5) reduces to the exponential distribution (Equation B.1).

B.1.1.2 Three-parameter Weibull

An extension of the two-parameter Weibull distribution is the three-parameter Weibull distribution (Elandt-Johnson and Johnson, 1980, p. 62) with scale (λ), shape (β), and shift (γ) parameters. The PDF of the three-parameter Weibull distribution is

$$f(t) = \frac{\beta}{\lambda} \left(\frac{t-\gamma}{\lambda} \right)^{\beta-1} e^{-\left(\frac{t-\gamma}{\lambda}\right)^\beta}, \quad (\text{B. 9})$$

with survivorship function

$$S(t) = e^{-\left(\frac{t-\gamma}{\lambda}\right)^\beta}, \quad (\text{B. 10})$$

CDF

$$F(t) = 1 - e^{-\left(\frac{t-\gamma}{\lambda}\right)^\beta}, \quad (\text{B. 11})$$

and hazard function

$$h(t) = \frac{\beta}{\lambda} \left(\frac{t-\gamma}{\lambda} \right)^{\beta-1}. \quad (\text{B. 12})$$

The three-parameter Weibull reduces to the two-parameter Weibull when $\gamma = 0$; it reduces to the exponential distribution when $\beta = 1$ and $\gamma = 0$. Likelihood ratio tests can be used to help select between the two- and three-parameter Weibull distributions (i.e., $H_0: \gamma = 0$ vs. $H_a: \gamma \neq 0$), as can the Akaike Information Criterion.

B.1.1.3 Vitality Model

The vitality model of Li and Anderson (2009) has been found useful in modeling tag failure-time data in cases where the shoulder of the curve has more slope than expected by the Weibull distribution. The steeper slope to the shoulder is the result of one or several tags failing much sooner than the rest. The vitality model is not nested within the Weibull family of distributions and, as such, cannot be directly compared.

The survival function for the vitality model can be written as

$$S(t) = \left[\Phi \left(\frac{1-rt}{\sqrt{u^2 + s^2 t}} \right) - e^{\left(\frac{2u^2 r^2 + 2r}{s^4 + s^2} \right)} \cdot \Phi \left(-\frac{1+rt + \frac{2u^2 r}{s^2}}{\sqrt{u^2 + s^2 t}} \right) \right] e^{-kt} \quad (\text{B. 13})$$

where

ϕ = cumulative normal distribution,

r = average wear rate of components,

s = standard deviation in wear rate,

k = rate of accidental failure, and

u = standard deviation in quality of original components.

The random failure component, in addition to the rate of wear, gives the vitality model additional latitude to fit tag-life data.

B.1.2 Nonparametric Method

The Kaplan and Meier (1958) method, also known as the product-limit estimator, is a nonparametric approach to estimating a survivorship curve. This method is a discrete-time approach to survival curve estimation. At time zero (t_0), survivorship $S(t_0) = 1$. Each declining step in the survivorship curve corresponds to the time of failure for a tag. The survival process continues until the last tag fails at time t_L , where $S(t_L) = 0$. In any time interval from t to $t + 1$, the conditional survival probability is estimated by

$$\hat{P}(X > t + 1|t) = \hat{S}_t = \frac{l_t - d_t}{l_t}, \quad (B.14)$$

where

l_t = number of tags still active and at risk of failure in the time interval t to $t + 1$,

d_t = number of tags that failed during the time interval t to $t + 1$, and

X = random variable for time of failure.

The binomial estimator (Equation B.14) has the estimated variance

$$\widehat{\text{Var}}(\hat{S}_t) = \frac{\hat{S}_t(1 - \hat{S}_t)}{l_t}. \quad (B.15)$$

The product-limit estimator acquires its name because the estimator of survival from time 0 to t is simply the product

$$\begin{aligned}\hat{S}(t) &= \hat{S}_0 \cdot \hat{S}_1 \cdot \hat{S}_2 \cdots \hat{S}_t \\ &= \prod_{i=0}^{t-1} \left(\frac{l_i - d_i}{l_i} \right).\end{aligned}\tag{B.16}$$

These nonparametric estimators are applicable whether or not right-censoring has occurred. The Kaplan and Meier (1958) method may be used when no parametric model adequately fits the tag-life data.

B.1.3 Right-censored Tag-life Analyses

There are at least two scenarios where a right-censored tag-life analysis may be useful and appropriate. The first scenario occurs when the tag-life study is stopped or truncated before the last tag failure. The second scenario can occur when observed travel times are relatively short compared to observed tag-failure times, and it is more accurate and easier to model tag-failure times to some truncation point beyond the longest travel time. The latter truncation strategy may be useful when traditional failure-time distributions have difficulty fitting both the shoulder and tail end of the failure-time curve. When inferences near the tail end of the failure-time distributions are unnecessary, a truncated analysis may do a better job at fitting the shoulder of the survivorship curve where travel times are relevant.

For the right-censored analysis, let T be the time of truncation. The other terms are defined as follows:

$$f(t_i) = \text{PDF for failure times } (t_i; t = 1, \dots, n),$$

$$F(t_i) = \text{cumulative survival function to time } t_i,$$

$$= \int_0^{t_i} f(t) dt,$$

$$S(t_i) = 1 - F(t_i), \text{ survival function,}$$

n = number of tags used in the tag-life study, and

r = number of tags that failed on or before truncation time T out of n tags starting the study.

The likelihood model for a truncated analysis is as follows:

$$L = \prod_{i=1}^r \left(\frac{f(t_i)}{F(T)} \right) \binom{n}{r} (1 - S(T))^r S(T)^{n-r}. \quad (\text{B. 17})$$

Noting $1 - S(T) = F(T)$,

$$\begin{aligned} L &= \prod_{i=1}^r \left(\frac{f(t_i)}{F(T)} \right) \binom{n}{r} F(T)^r S(T)^{n-r} \\ &\propto \prod_{i=1}^r f(t_i) \cdot S(T)^{n-r}. \end{aligned} \quad (\text{B. 18})$$

This follows the development in Lee (1992, p. 203).

B.2 Tag-life Adjusted Estimates of Survival

With active tags, standard CJS models estimate a “perceived” survival probability, i.e., the joint probability of the fish surviving and the tag operating at a downstream detection site. Using the method in Townsend et al. (2006), tag-life-adjusted estimates of survival are calculated, taking into account independent information from a tag-life study.

Program ATLAS provides the ability to calculate tag-life-adjusted survival estimates for a (1) single release-recapture design, (2) paired release-recapture design, (3) virtual/paired release-recapture design, and (4) full ViRDCT release-recapture design. The latter three designs are based on the fundamental multinomial model of the single release-recapture design which will be presented first.

B.2.1 Single Release-recapture Design

The single release-recapture design will be conceptualized as an initial release of tagged animals followed by K subsequent downstream detection events. The initial release event is defined as event 0. The subsequent detection events are numbered 1 through K . The model parameters are defined as follows:

S_i = probability of surviving to event i , given survival to event $i - 1$ ($i = 1, \dots, K - 1$),

p_i = probability of detection at event i , given survival to event i ($i = 1, \dots, K - 1$),

λ = probability of survival to and detection at event K , given survival to event $K - 1$,

T_i = probability that a tag will be active at event i , and

$T_{i/j}$ = probability that a tag will be active at event i , given that it was active at event $j < i$

$$= \frac{T_i}{T_j}, \text{ where } i = j + 1, \dots, K.$$

Other quantities in the model include the following:

R_0 = initial release size.

R_i = number detected and re-released (i.e., not removed from the release group) at event i .

z_i = number detected and re-released before event i , not detected at event i , but detected after event i ,

$$= \sum_{j=0}^{i-1} (r_j - m_{j+1}).$$

m_i = number detected at event i ($i = 1, \dots, K - 1$).

r_i = number detected (and re-released) at event i and detected at a later event
 $(i = 0, \dots, K - 1)$.

For convenience in re-expressing the likelihood model, the following terms are also defined:

χ_i = probability of an individual not being detected after event i , conditional on surviving with a working tag to event i ($i = 0, \dots, K - 1$),

where

$$\begin{aligned}\chi_i &= 1 - T_{i+1/i} + T_{i+1/i}(1 - S_{i+1} + S_{i+1}(1 - p_{i+1})\chi_{i+1}) \\ &= 1 - T_{i+1/i}S_{i+1} + T_{i+1/i}\chi_{i+1}S_{i+1}(1 - p_{i+1}),\end{aligned}$$

and

$$\chi_{K-1} = 1 - T_{K/K-1} + T_{K/K-1}(1 - \lambda) = 1 - T_{K/K-1}\lambda.$$

Also,

$$\begin{aligned}\tau_i &= T_i\chi_i \\ &= T_i - T_{i+1}S_{i+1} + \tau_{i+1}S_{i+1}(1 - p_{i+1}), \quad (i = 1, \dots, K - 2),\end{aligned}$$

where

$$\tau_0 = \chi_0$$

and where

$$\tau_{K-1} = T_{K-1}\chi_{K-1} = T_{K-1} - \tau_K\lambda.$$

The general form of the likelihood can then be written as

$$L(\vec{S}, \vec{p}, \lambda | \vec{R}, \vec{m}, \vec{r}, \vec{z}, \vec{T}) = \left(\prod_{k=1}^{K-1} S_k^{m_k+z_k} p_k^{m_k} (1 - p_k)^{z_k} \right) (T_K \lambda)^{r_{K-1}+z_{K-1}} \prod_{k=0}^{K-1} \tau_k^{R_k-r_k}. \quad (\text{B. 19})$$

Example: Likelihood with three downstream detection locations

With three downstream detection locations, there are $2^3=8$ possible capture/detection histories. Those histories in standard order, along with the corresponding cell probabilities of occurrence, are as follows:

<u>Capture/detection history</u>	<u>Probability of occurrence</u>
1 1 1	$-T_3 S_1 p_1 S_2 p_2 \lambda$
0 1 1	$T_3 S_1 (1 - p_1) S_2 p_2 \lambda$
1 0 1	$T_3 S_1 p_1 S_2 (1 - p_2) \lambda$
0 0 1	$T_3 S_1 (1 - p_1) S_2 (1 - p_2) \lambda$
1 1 0	$S_1 p_1 S_2 p_2 T_2 \chi_2 = S_1 p_1 S_2 p_2 \tau_2$
0 1 0	$S_1 (1 - p_1) S_2 p_2 \tau_2$
1 0 0	$S_1 p_1 \tau_1$
0 0 0	χ_0

The likelihood model in Equation B.19 temporarily treats the probabilities of tag life (T_i) as known constants. For a particular study outcome, the T_i are empirically estimated based on the observed capture data and individual travel times to event i ($i = 1, \dots, K$). For all individuals detected at event i , the estimated probability of tag life is calculated as

$$\hat{T}_i = \frac{\sum_{j=1}^{m_i} P(x_j \geq d_{ij})}{m_i}$$

$$= \frac{\sum_{j=1}^{m_i} S(d_{ij})}{m_i}$$

where

$S(d_{ij})$ = probability a tag is active at least as long as time d_{ij} , where $S()$ is based on the fitted tag-life survivorship function, and

d_{ij} = time between tag activation and detection at event i for the j th individual

detection at event i ($i = 1, \dots, K; j = 1, \dots, m_i$).

The inverse Hessian matrix provides an estimate of the variance-covariance matrix for the maximum likelihood estimators, given the particular set of tag-life probabilities (i.e., $\hat{T}_i; i = 1, \dots, K$) used in the model. However, those variance estimates do not take into account the uncertainties in the estimates \hat{T}_i ($i = 1, \dots, K$). The variance of the survival estimates can be calculated using the total variance formula

$$\text{Var}(\hat{S}) = \text{Var}_{\vec{T}_i} \left[E \left(\hat{S} \middle| \vec{T}_i \right) \right] + E_{\vec{T}_i} \left[\text{Var} \left(\hat{S} \middle| \vec{T}_i \right) \right]. \quad (\text{B. 20})$$

The above variance can be estimated in stages using the expression

$$\widehat{\text{Var}}(\hat{S}) = s_{\hat{S}|\vec{T}_i}^2 + \widehat{\text{Var}} \left(\hat{S} \middle| \vec{T}_i \right). \quad (\text{B. 21})$$

The second term in Equation B.21 is obtained from the inverse Hessian matrix conditional on the observed tag-life probabilities (\vec{T}_i). The first variance component in Equation B.21 can be calculated using bootstrap resampling techniques (Efron and Tibshirani 1993). Alternative estimates of \vec{T}_i are computed by bootstrapping both the observed tag-life data and the travel-time data. For each estimated vector \vec{T}_i , survival estimates are recalculated using the likelihood model in Equation B.19. The empirical variance among those alternative survival estimates is used in estimating the first term in Equation B.21 by the quantity

$$s_{\hat{S}|\vec{T}_i}^2 = \frac{\sum_{b=1}^B (\hat{S}_b - \hat{\hat{S}})^2}{B - 1}, \quad (\text{B. 22})$$

where

$$\hat{\hat{S}} = \frac{\sum_{b=1}^B \hat{S}_b}{B}.$$

We recommend B be of the order 1000 or greater.

An alternative to directly estimating the survival parameters from the likelihood

model is to analyze the detection histories using an ordinary CJS model. This approach will result in a “perceived” survival value ($\hat{\phi}_i$), which is the joint probability of both the fish and tag being “alive” at a detection site. The reach survival estimate for the fish alone (\hat{S}_i) is then obtained from the ratio estimator

$$\hat{S}_i = \frac{\hat{\phi}_i}{\left(\frac{\hat{T}_i}{\hat{T}_{i-1}}\right)} = \hat{\phi}_i \left(\frac{\hat{T}_{i-1}}{\hat{T}_i}\right), \quad (\text{B. 23})$$

where $\hat{T}_0 = 1.0$. Using the exact variance estimator for a product (Goodman 1960)

$$\widehat{\text{Var}}(\hat{S}_i) = \hat{\phi}_i^2 \widehat{\text{Var}}\left(\frac{\hat{T}_{i-1}}{\hat{T}_i}\right) + \left(\frac{\hat{T}_{i-1}}{\hat{T}_i}\right)^2 \widehat{\text{Var}}(\hat{\phi}_i) - \widehat{\text{Var}}\left(\frac{\hat{T}_{i-1}}{\hat{T}_i}\right) \widehat{\text{Var}}(\hat{\phi}_i), \quad (\text{B. 24})$$

where, using the delta method (Seber 1982, pp. 7–9),

$$\widehat{\text{Var}}(\hat{S}_i) = \hat{\phi}_i^2 \widehat{\text{Var}}\left(\frac{\hat{T}_{i-1}}{\hat{T}_i}\right) + \left(\frac{\hat{T}_{i-1}}{\hat{T}_i}\right)^2 \widehat{\text{Var}}(\hat{\phi}_i) - \widehat{\text{Var}}\left(\frac{\hat{T}_{i-1}}{\hat{T}_i}\right) \widehat{\text{Var}}(\hat{\phi}_i), \quad (\text{B. 25})$$

The variance of \hat{T}_i is estimated by the bootstrap technique using both the observed travel times (\vec{d}_{ij}) and tag-life data. The variance of \hat{T}_i is calculated as

$$\widehat{\text{Var}}(\hat{T}_i) = (1 - \hat{p}_i) \left(s_{\hat{T}_i}^2 - s_{\hat{T}_i|\vec{d}}^2 \right) + s_{\hat{T}_i|\vec{d}}^2, \quad (\text{B. 26})$$

where

$s_{\hat{T}_i}^2$ = empirical bootstrap variance for \hat{T}_i when sampling with replacement from both the tag-life and travel-time data, and

$s_{\hat{T}_i|\vec{d}}^2$ = empirical bootstrap variance for \hat{T}_i when sampling with replacement from the tag-life data holding the travel times constant for what was observed.

The quantity $\left(s_{\hat{T}_i}^2 - s_{\hat{T}_i|\vec{d}}^2 \right)$ estimates the variance component associated solely with the variation in travel times. The factor $(1 - \hat{p}_i)$ serves as a finite population correction for this variance component. For example, if $p_i = 1$, then the distribution

of travel times is known without error and should not contribute to the uncertainty of \hat{T}_i .

When estimating two or more tag-life probabilities, their covariance is assumed to be zero if they are from different tag-life datasets; if from the same tag-life dataset, their covariance is estimated by the quantity

$$\widehat{\text{Covar}}(\hat{T}_i, \hat{T}_j) = (1 - \hat{p}_i)(1 - \hat{p}_j)[\widehat{\text{cov}}(\hat{T}_i, \hat{T}_j) - \widehat{\text{cov}}(\hat{T}_i, \hat{T}_j|\vec{d})] + \widehat{\text{cov}}(\hat{T}_i, \hat{T}_j|\vec{d}), \quad (\text{B. 27})$$

where

<u>Variable</u>	<u>Definition</u>
$\widehat{\text{cov}}(\hat{T}_i, \hat{T}_j)$	= empirical bootstrap covariance between \hat{T}_i and \hat{T}_j bootstrapping over the tag-life and travel-time data, and
$\widehat{\text{cov}}(\hat{T}_i, \hat{T}_j \vec{d})$	= empirical bootstrap covariance between \hat{T}_i and \hat{T}_j bootstrapping over only the tag-life data, holding the travel times constant for what was observed,

where once again the \hat{p}_i and \hat{p}_j are estimated detection probabilities at sites i and j , respectively. The quantity $(1 - \hat{p}_i)(1 - \hat{p}_j)$ is the finite correction term when computing the variance.

B.2.2 Paired Release-recapture Design

In Program ATLAS, the paired release-recapture design is modeled as a product of two independent likelihoods of the form in Equation B.19. The joint likelihood model is parameterized as depicted in Figure B.1. The model estimates separate values for each release. Survival between the release points is then estimated by the quotient

$$\hat{S}_{Paired} = \frac{\hat{S}_{11}}{\hat{S}_{21}}, \quad (\text{B. 28})$$

with an associated variance estimate (Goodman, 1960)

$$\widehat{\text{Var}}(\hat{S}_{Paired}) = \hat{S}_{Paired}^2 \left[\frac{\widehat{\text{Var}}(\hat{S}_{11})}{\hat{S}_{11}^2} + \frac{\widehat{\text{Var}}(\hat{S}_{21})}{\hat{S}_{21}^2} - \frac{\widehat{\text{Var}}(\hat{S}_{11})\widehat{\text{Var}}(\hat{S}_{21})}{\hat{S}_{11}^2\hat{S}_{21}^2} \right]. \quad (\text{B. 29})$$

Below the mixing zone of the two release groups in a paired release, likelihood ratio tests can be used to assess homogeneity of downstream capture and survival processes. Modeling of the lower reach survival and detection processes may be used to improve estimation precision. Should model parameters between the two releases be linked (i.e., equated), subsequent estimates of \hat{S}_{11} and \hat{S}_{21} will no longer be independent. In this case, the variance of survival (Equation B.28) will be estimated using the delta method (Seber 1982, pp. 7–9), where

$$\widehat{\text{Var}}(\hat{S}_{Paired}) \approx \hat{S}_{Paired}^2 \left[\frac{\widehat{\text{Var}}(\hat{S}_{11})}{\hat{S}_{11}^2} + \frac{\widehat{\text{Var}}(\hat{S}_{21})}{\hat{S}_{21}^2} - \frac{2\widehat{\text{Covar}}(\hat{S}_{11}, \hat{S}_{21})}{\hat{S}_{11}\hat{S}_{21}} \right]. \quad (\text{B. 30})$$

Alternatively, a closed-form estimator of S can be calculated as

$$\hat{S}_{Paired} = \frac{\begin{pmatrix} \hat{\phi}_{11} \\ \hat{T}_{11} \end{pmatrix}}{\begin{pmatrix} \hat{\phi}_{21} \\ \hat{T}_{21} \end{pmatrix}} = \begin{pmatrix} \hat{\phi}_{11} \\ \hat{\phi}_{21} \end{pmatrix} \begin{pmatrix} \hat{T}_{21} \\ \hat{T}_{11} \end{pmatrix}, \quad (\text{B. 31})$$

where $\hat{\phi}_{ij}$ is the “perceived” survival estimate from a traditional CJS model ignoring tag-life probabilities, and \hat{T}_{ij} is the estimated probability of tag life. In this case, the variance of \hat{S} is estimated by applying the Goodman (1960) approach, i.e.,

$$\widehat{\text{Var}} \left[\begin{pmatrix} \hat{\phi}_{11} \\ \hat{\phi}_{21} \end{pmatrix} \begin{pmatrix} \hat{T}_{21} \\ \hat{T}_{11} \end{pmatrix} \right] = \begin{pmatrix} \hat{\phi}_{11} \\ \hat{\phi}_{21} \end{pmatrix}^2 \widehat{\text{Var}} \begin{pmatrix} \hat{T}_{21} \\ \hat{T}_{11} \end{pmatrix} + \begin{pmatrix} \hat{T}_{21} \\ \hat{T}_{11} \end{pmatrix}^2 \widehat{\text{Var}} \begin{pmatrix} \hat{\phi}_{11} \\ \hat{\phi}_{21} \end{pmatrix} - \widehat{\text{Var}} \begin{pmatrix} \hat{\phi}_{11} \\ \hat{\phi}_{21} \end{pmatrix} \widehat{\text{Var}} \begin{pmatrix} \hat{T}_{21} \\ \hat{T}_{11} \end{pmatrix}. \quad (\text{B. 32})$$

The variance of $\hat{\phi}_{11}/\hat{\phi}_{21}$ is computed analogously to Equation B.29, and the variance of $\hat{T}_{21}/\hat{T}_{11}$ analogously to Equation B.25.

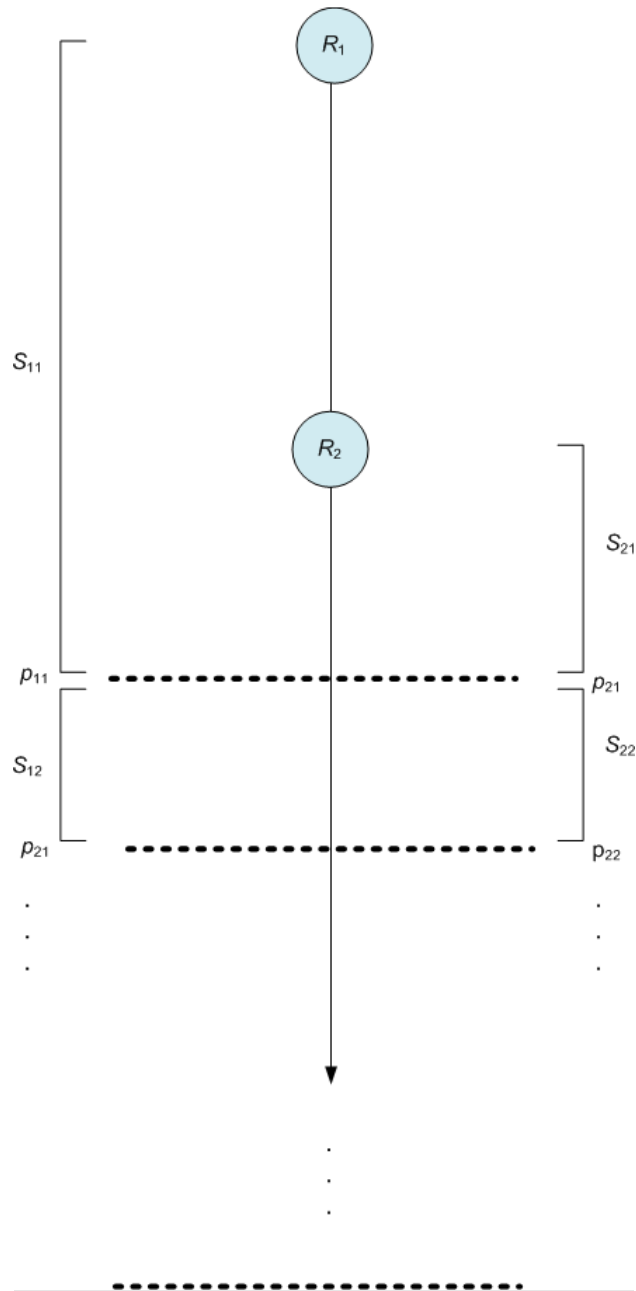


Figure B.1: Schematic of a paired release-recapture design.

B.2.3 Virtual/Paired Release-recapture Design

This release-recapture design is used to estimate the probability of dam passage survival consistent with the 2008 FCRPS Biological Opinion definition of survival from the dam face to the tailrace (Figure B.2). In the simplest of cases, the joint likelihood model consists of three independent multinomial likelihoods of the

form of Equation B.19. In this case, dam passage survival is estimated by the function

$$\hat{S}_{Dam} = \frac{\hat{S}_1}{\left(\frac{\hat{S}_2}{\hat{S}_3}\right)} = \frac{\hat{S}_1 \hat{S}_3}{\hat{S}_2}, \quad (\text{B.33})$$

where the \hat{S}_i variables are the tag-life-corrected estimates of reach survival.

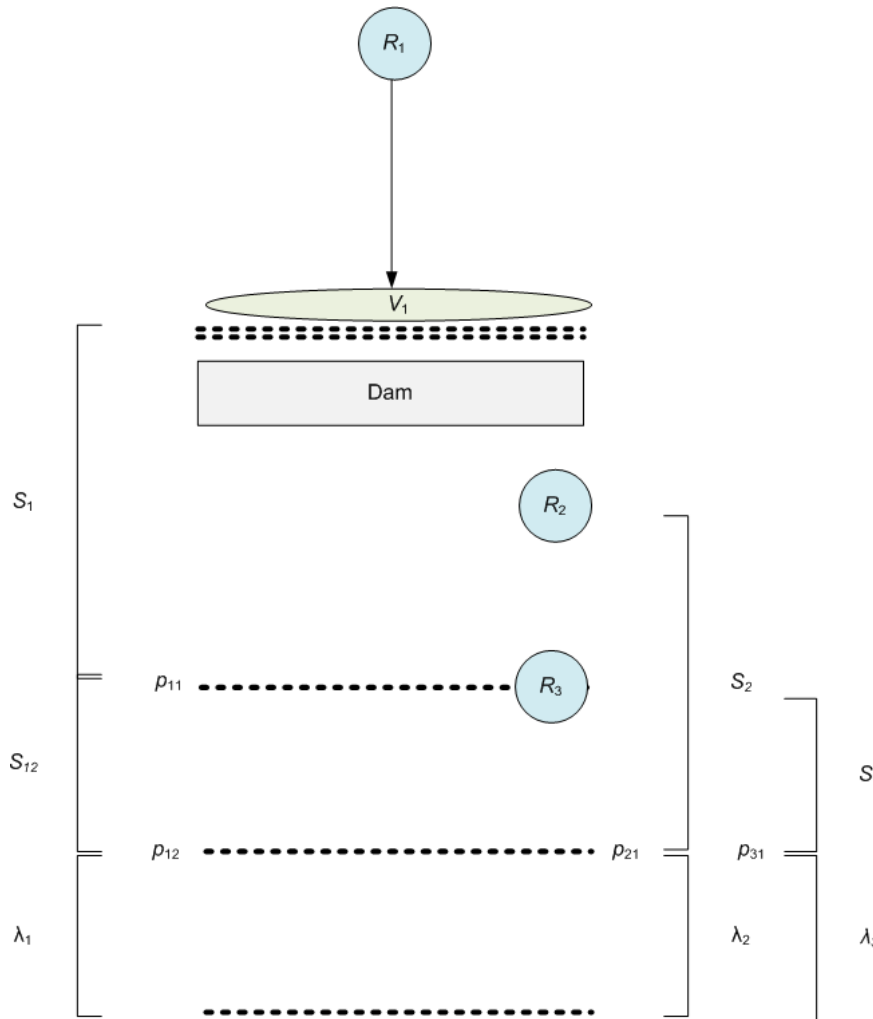


Figure B.2: Schematic of the minimum design configuration to estimate dam passage survival based on a virtual release (i.e., V_1), a paired release (R_2 and R_3), and three downriver hydrophone arrays (shown as dotted lines). At the dam face, a 3D hydrophone array is used to construct the virtual release of fish known to have arrived at the dam.

B.2.3.1 Variance Calculations Under Independence

The variance of \hat{S}_{Dam} can be estimated using a combination of Goodman's (1960) formula for a product of independent estimates and the delta method (Seber 1982, pp. 7–9), where

$$\begin{aligned} \text{Var}(\hat{S}_{Dam}) &= \left(\frac{1}{S_2^2} + \frac{\text{Var}(\hat{S}_2)}{S_2^4} \right) \times \\ &\quad [S_1^2 \text{Var}(\hat{S}_3) + S_3^2 \text{Var}(\hat{S}_1) + \text{Var}(\hat{S}_1) \text{Var}(\hat{S}_3)] + \frac{(S_1 S_3)^2}{S_2^4} \text{Var}(\hat{S}_2) \end{aligned} \quad (\text{B. 34})$$

and estimated by the quantity

$$\begin{aligned} \widehat{\text{Var}}(\hat{S}_{Dam}) &= \left(\frac{1}{\hat{S}_2^2} + \frac{\widehat{\text{Var}}(\hat{S}_2)}{\hat{S}_2^4} \right) \times \\ &\quad [\hat{S}_1^2 \widehat{\text{Var}}(\hat{S}_3) + \hat{S}_3^2 \widehat{\text{Var}}(\hat{S}_1) - \widehat{\text{Var}}(\hat{S}_1) \widehat{\text{Var}}(\hat{S}_3)] + \frac{(\hat{S}_1 \hat{S}_3)^2}{\hat{S}_2^4} \widehat{\text{Var}}(\hat{S}_2). \end{aligned} \quad (\text{B. 35})$$

B.2.3.2 Variance Calculations Under Homogeneity

In the case where the joint likelihood for the three release groups is respecified to allow for downstream homogeneity in survival and/or capture probabilities, the estimates \hat{S}_1 , \hat{S}_2 , and \hat{S}_3 will no longer be independent. In this case, the delta method (Seber 1982) is used to approximate the variance where

$$\begin{aligned} \widehat{\text{Var}}(\hat{S}_{Dam}) &= \left(\frac{\hat{S}_1 \hat{S}_3}{\hat{S}_2} \right)^2 \times \\ &\quad \left[\frac{\widehat{\text{Var}}(\hat{S}_1)}{\hat{S}_1^2} + \frac{\widehat{\text{Var}}(\hat{S}_2)}{\hat{S}_2^2} + \frac{\widehat{\text{Var}}(\hat{S}_3)}{\hat{S}_3^2} + \frac{2\widehat{\text{Covar}}(\hat{S}_1 \hat{S}_3)}{\hat{S}_1 \hat{S}_3} - \frac{2\widehat{\text{Covar}}(\hat{S}_1 \hat{S}_2)}{\hat{S}_1 \hat{S}_2} - \frac{2\widehat{\text{Covar}}(\hat{S}_2 \hat{S}_3)}{\hat{S}_2 \hat{S}_3} \right] \end{aligned} \quad (\text{B. 36})$$

B.2.3.3 Variance Calculations when Dam Survival is Calculated Using Closed-form Estimator

When \hat{S}_{Dam} is estimated in closed form, using the direct results of the CJS model and separate estimates of tag-life probability, then

$$\hat{S}_{Dam} = \frac{\left(\frac{\hat{\phi}_1}{\hat{T}_1}\right)\left(\frac{\hat{\phi}_3}{\hat{T}_3}\right)}{\left(\frac{\hat{\phi}_2}{\hat{T}_2}\right)} = \left(\frac{\hat{\phi}_1\hat{\phi}_3}{\hat{\phi}_2}\right)\left(\frac{\hat{T}_2}{\hat{T}_1\hat{T}_3}\right). \quad (\text{B. 37})$$

In this situation, the variance of \hat{S}_{Dam} is based on separate variance calculations of the factors $(\hat{\phi}_1\hat{\phi}_3/\hat{\phi}_2)$ and $(\hat{T}_1\hat{T}_3/\hat{T}_2)$ analogously to Equations B.35 and B.36, respectively, and then applying Goodman (1960) for the variance of a product.

B.2.3.4 Virtual Release Group as a Composite

The virtual release group is composed of fish known to have arrived alive at an acoustic array. This group may be composed of individuals from multiple release groups upstream. As such, they may have had different times in the river since release and require different tag-life corrections.

Assuming all fish in a virtual release have the same downstream survival and detection processes, their subsequent capture histories may be modeled by a joint likelihood. Fish from the different release sources would have separate likelihoods similar to Equation B.19, but with shared survival and capture/detection parameters. Each fish source would have a different set of tag-life corrections corresponding to their different mean travel times to the detection locations. This joint likelihood is of the form

$$\prod_{i=1}^G L_i(\vec{S}, \vec{p}, \lambda | \vec{R}, \vec{m}, \vec{r}, \vec{z}, \vec{T}), \quad (\text{B. 38})$$

where G is the number of separate release groups contributing to the virtual release group.

In the subsequent estimation of dam passage survival, Equation B.38 is one component of the joint likelihood consisting of releases R_1 , R_2 , and R_3 (Figure B.2). A closed-form estimator of \hat{S}_1 used in the virtual/paired-release design is of the form

$$\hat{S}_1 = \frac{\sum_{i=1}^G \frac{\hat{S}_{1i} R_{1i}}{\hat{T}_{1i}}}{\sum_{i=1}^G R_{1i}} = \sum_{i=1}^G \frac{\hat{S}_{1i} W_i}{\hat{T}_{1i}}, \quad (\text{B.39})$$

where

\hat{S}_{1i} = estimate of survival in the first reach (Figure B.2) for virtual release of fish from the i th source ($i = 1, \dots, G$),

R_{1i} = number of fish in the virtual release from the i th source ($i = 1, \dots, G$),

T_{1i} = tag-life probability for fish from the i th source ($i = 1, \dots, G$) to the first downriver detection site,

$R_1 = \sum_{i=1}^G R_{1i}$, and

$W_i = R_{1i}/R_1$.

The variance of \hat{S}_1 (Equation B.39) is based on the delta method (Seber 1982), treating the R_{1i} variables as known constants.

B.2.3.5 Stratification for Different Tag Activation Periods

Within a release group (i.e., R_1 , R_2 , or R_3), fish from the same release source may have different lag times (delays) between tag activation and fish release. Typically, these lag times range in the order of 24 to 48 hours and are standardized for all fish. When this is not the situation, a release group may need to be stratified into different lag-time subpopulations to account for different distributions in time between tag activation and arrival downstream at a detection array.

Assuming the fish in the different strata share common downstream survival and detection processes but different tag-life corrections, a release group can be

modeled by a joint likelihood similar to Equation B.38. In this manner, different distributions for the times between tag activation and arrival can be taken into account without undue loss of precision.

B.2.4 Full Virtual Release/Dead-fish Correction Study Design

The full ViRDcT study design is used to estimate the probability of dam passage survival using a virtual release at the dam face, a dead smolt release in the dam tailrace, and two downstream detection sites: one at the tailrace and one at the tailwater (Figure B.3).

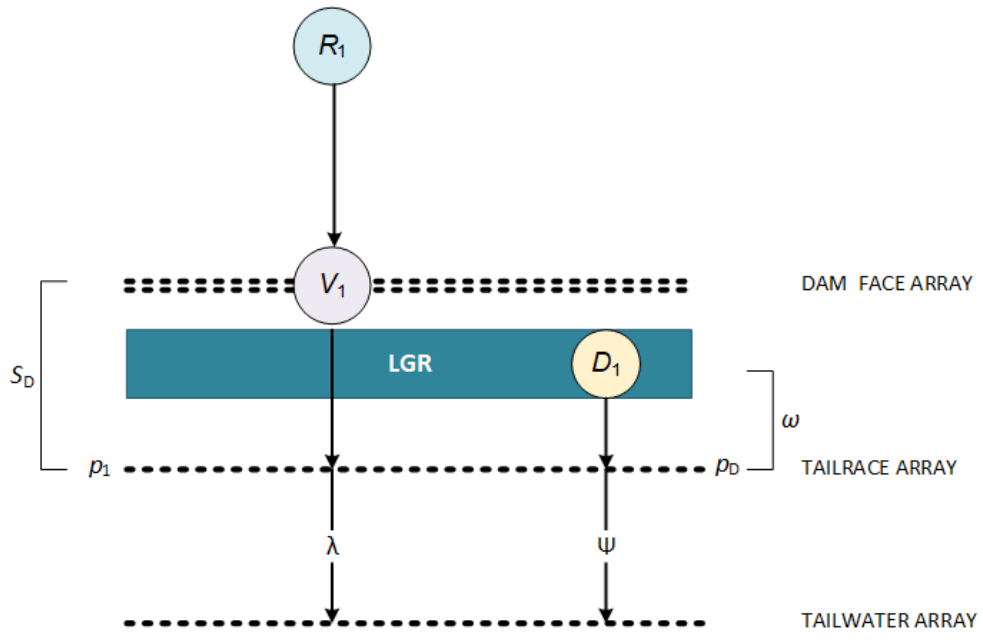


Figure B.3: Schematic of a Full Virtual Release/Dead-fish Correction (ViRDcT) release-recapture design to estimate dam passage survival.

Data

<u>Variable</u>	<u>Definition</u>
V_1	= number of fish in the live virtual release at the dam face,
D_1	= number of fish in the dead release at the dam,
n_{11}	= number of V_1 release fish detected at both tailrace and tailwater arrays,
n_{10}	= number of V_1 release fish detected at tailrace array but not tailwater array,
n_{01}	= number of V_1 release fish not detected at tailrace but detected at tailwater array,
n_{00}	= number of V_1 release fish not detected at either tailrace or tailwater array,
d_{11}	= number of D_1 release fish detected at both tailrace and tailwater arrays,
d_{10}	= number of D_1 release fish detected at tailrace array but not tailwater array,
d_{01}	= number of D_1 release fish not detected at tailrace but detected at tailwater array, and
d_{00}	= number of D_1 release fish not detected at either tailrace or tailwater array.

Parameters

<u>Variable</u>	<u>Definition</u>
S_D	= probability of dam survival to tailrace array conditional on arriving at the dam face,
ω	= probability of drifting to tailrace array conditional on being dead at dam exit,

- p_1 = probability of detection on tailrace array conditional on being alive and arriving at that array,
- p_D = probability of detection on tailrace array conditional on arriving at that array dead,
- λ = joint probability of a live fish arriving at the tailwater array and being detected there, conditional on having arrived at the tailwater array,
- Ψ = joint probability of a dead released fish (D1) arriving at the tailwater array and being detected at that array conditional on having arrived at the tailrace array,
- T_{1V} = probability of tag survival from dam to tailrace array for fish from the (live) virtual release,
- T_{2V} = probability of tag survival from dam to tailwater array for fish from the (live) virtual release,
- T_{1D} = probability of tag survival from dam to tailrace array for fish from the dead fish release, and
- T_{2D} = probability of tag survival from dam to tailwater array for fish from the dead fish release.

The full ViRDCT model uses unique probabilities of tag survival to the detection sites for fish from the live (virtual) release and fish from the dead release. This approach allows for different rates of travel or drift based on release group. All fish from the live release have the same probability of tag survival regardless of fish survival status. The likelihood function is of the form:

$$L = \binom{V_1}{\bar{n}} (S_D p_1 \lambda T_{2V} + (1 - S_D) \omega p_D \Psi T_{2V})^{n_{11}} \cdot (S_D (1 - p_1) \lambda T_{2V} + (1 - S_D) \omega (1 - p_D) \Psi T_{2V})^{n_{01}}$$

$$\begin{aligned}
& \cdot (S_D p_1 (T_{1V} - T_{2V} \lambda) + (1 - S_D) \omega p_D (T_{1V} - T_{2V} \Psi))^{n_{10}} \\
& \cdot [S_D ((1 - T_{1V}) + (1 - p_1) (T_{1V} - T_{2V} \lambda)) \\
& \quad + (1 - S_D) ((1 - \omega T_{1V}) + \omega (1 - p_D) (T_{1V} - T_{2V} \Psi))]^{n_{00}} \\
& \cdot \binom{D}{d} (\omega p_D \Psi T_{2D})^{d_{11}} (\omega (1 - p_D) \Psi T_{2D})^{d_{01}} \\
& \cdot (\omega p_D (T_{1D} - T_{2D} \Psi))^{d_{10}} ((1 - \omega T_{1D}) + \omega (1 - p_D) (T_{1D} - T_{2D} \Psi))^{d_{00}}. \tag{B.40}
\end{aligned}$$

There is no closed form estimator of dam passage survival (S_D) for the full ViRDCt model. Variances are estimated using the total variance formula from Equations (B.20) – (B.22), using the inverted Hessian matrix to estimate the second term in Equation (B.21).

B.2.5 Reduced Virtual Release/Dead-fish Correction Study Design

The reduced ViRDCt study design is used to estimate the probability of dam passage survival using a virtual release at the dam face and a dead smolt release in the dam tailrace. The virtual release requires exactly two downstream detection sites, and the dead smolt release requires one downstream detection site (Figure B.4).

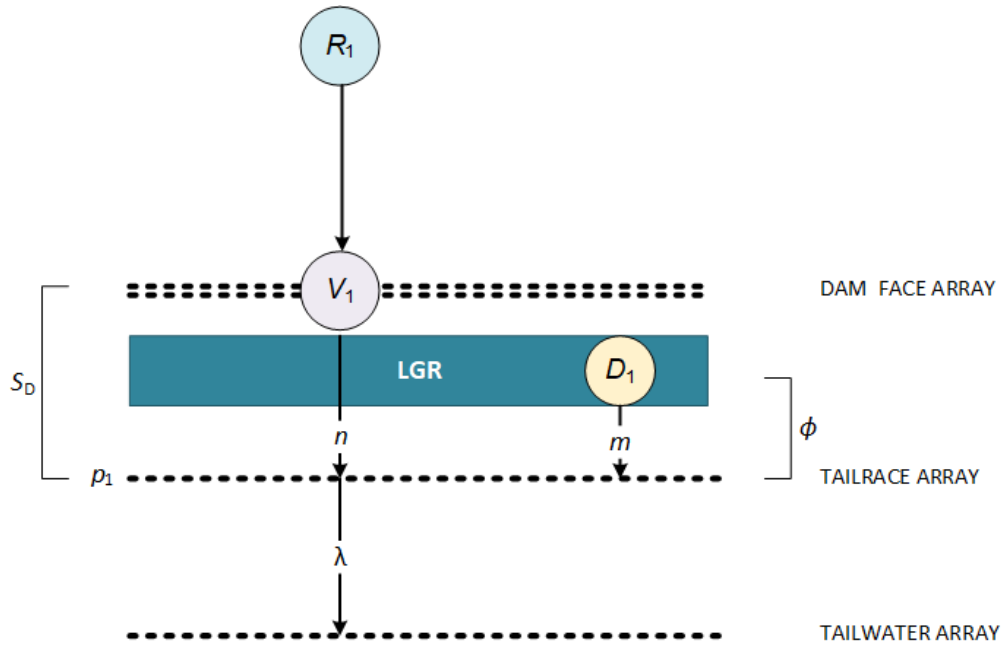


Figure B.4: Schematic of a reduced Virtual Release/Dead-fish Correction (ViRDcT) release-recapture design to estimate dam passage survival.

Data

<u>Variable</u>	<u>Definition</u>
V_1	= number of fish in the live virtual release at the dam face,
zD_1	= number of fish in the dead release at the dam,
n_{11}	= number of V_1 release fish detected at both tailrace and tailwater arrays,
n_{10}	= number of V_1 release fish detected at tailrace array but not tailwater array,
n_{01}	= number of V_1 release fish not detected at tailrace but detected at tailwater array,
n_{00}	= number of V_1 release fish not detected at either tailrace or tailwater array,
n	= number of V_1 release fish detected at tailrace array,
m	= number of D_1 release fish detected at tailrace array.

Parameters

<u>Variable</u>	<u>Definition</u>
S_D	= probability of dam survival to tailrace array conditional on arriving at the dam face,
p_1	= probability of detection on tailrace array conditional on being alive and arriving at that array,
ϕ	= joint probability of arriving at the tailrace and being detected at that array conditional on being dead at dam exit,
λ	= joint probability of a live fish arriving at the tailwater array and being detected there, conditional on having arrived at the tailwater array,
T_{1V}	= probability of tag survival from dam to tailrace array for fish from the (live) virtual release,
T_{2V}	= probability of tag survival from dam to tailwater array for fish from the (live) virtual release,
T_{1D}	= probability of tag survival from dam to tailrace array for fish from the dead fish release.

The reduced ViRDCt model uses different probabilities of tag survival to detection sites for fish from the live (virtual) release and fish from the dead release. All fish from the live release are modeled with the same probability of tag survival regardless of fish survival status.

$$\begin{aligned}
 L = & \binom{V_1}{\vec{n}} (S_D p_1 \lambda T_{2V})^{n_{11}} (S_D (1 - p_1) \lambda T_{2V})^{n_{01}} \\
 & \cdot (S_D p_1 (T_{1V} - T_{2V} \lambda) + (1 - S_D) \phi T_{1V})^{n_{10}} \\
 & \cdot [S_D ((1 - T_{1V}) + (1 - p_1) (T_{1V} - T_{2V} \lambda)) \\
 & \quad + (1 - S_D) (1 - \phi T_{1V})]^{n_{00}} \\
 & \cdot \binom{D}{m} (\phi T_{1D})^m (1 - \phi T_{1D})^{D-m}
 \end{aligned} \tag{B. 41}$$

Closed Form Estimators

$$\hat{S}_D = \frac{\frac{n_{11} + n_{10}}{V_1} - \left(\frac{m}{D}\right) \left(\frac{\tilde{T}_{1V}}{\tilde{T}_{1D}}\right)}{\left(\frac{n_{11}}{n_{11} + n_{01}} - \frac{m}{D\tilde{T}_{1D}}\right) \cdot \tilde{T}_{1V}}$$

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

$$\hat{\lambda} = \left[\frac{\left(\frac{n_{11}}{V_1}\right) \left(\frac{\tilde{T}_{1V}}{\tilde{T}_{2V}}\right)}{\frac{n_{11} + n_{10}}{V_1} - \left(\frac{m}{D}\right) \left(\frac{\tilde{T}_{1V}}{\tilde{T}_{1D}}\right)} \right] \left[1 - \left(\frac{n_{11} + n_{01}}{n_{11}}\right) \left(\frac{m}{D\tilde{T}_{1D}}\right) \right]$$

$$\hat{\phi} = \frac{m}{D\tilde{T}_{1D}}$$

where \tilde{T}_{1V} , \tilde{T}_{2V} , and \tilde{T}_{1D} are the estimates of tag survival probabilities T_{1V} , T_{2V} , and T_{1D} , respectively.

Variance estimators of the closed form estimators can be computed as follows:

$$\widehat{Var}(\hat{p}_1) = \frac{\hat{p}_1(1 - \hat{p}_1)}{V_1 \hat{S}_D \hat{\lambda} \tilde{T}_{2V}}$$

$$\widehat{Var}(\hat{\phi}) = \frac{\hat{\phi}(1 - \hat{\phi}\tilde{T}_{1D})}{D\tilde{T}_{1D}}$$

$$\begin{aligned} \widehat{Var}(\hat{S}_D) = & (A_{11})^2 V_{11} + (A_{10})^2 V_{10} + (A_{01})^2 V_{01} + (A_m)^2 V_m + 2A_{11}A_{10}C_1 + 2A_{11}A_{01}C_2 \\ & + 2A_{10}A_{01}C_3 \end{aligned}$$

and

$$\begin{aligned} \widehat{Var}(\hat{\lambda}) = & (B_{11})^2 V_{11} + (B_{10})^2 V_{10} + (B_{01})^2 V_{01} + (B_m)^2 V_m + 2B_{11}B_{10}C_1 + 2B_{11}B_{01}C_2 \\ & + 2B_{10}B_{01}C_3 \end{aligned}$$

where

$$A_{11} = \frac{\hat{\lambda}\tilde{T}_{2V} - (1 - \hat{p}_1)\tilde{T}_{1V}}{V_1(\hat{p}_1 - \hat{\Phi})\hat{\lambda}\tilde{T}_{1V}\tilde{T}_{2V}}$$

$$A_{10} = \frac{1}{V_1(\hat{p}_1 - \hat{\Phi})\tilde{T}_{1V}}$$

$$A_{01} = \frac{\hat{p}_1}{V_1(\hat{p}_1 - \hat{\Phi})\hat{\lambda}\tilde{T}_{2V}}$$

$$A_m = \frac{-(1 - \hat{S}_D)}{D(\hat{p}_1 - \hat{\Phi})\tilde{T}_{1D}}$$

$$B_{11} = \frac{(1 - \hat{\Phi})\tilde{T}_{1V} - \hat{\lambda}\tilde{T}_{2V}}{V_1\hat{S}_D(\hat{p}_1 - \hat{\Phi})\tilde{T}_{1V}\tilde{T}_{2V}}$$

$$B_{10} = \frac{-\hat{\lambda}}{V_1\hat{S}_D(\hat{p}_1 - \hat{\Phi})\tilde{T}_{1V}}$$

$$B_{01} = \frac{-\hat{\Phi}}{V_1\hat{S}_D(\hat{p}_1 - \hat{\Phi})\tilde{T}_{2V}}$$

$$B_m = \frac{(1 - \hat{S}_D)\hat{\lambda}}{\hat{S}_D(\hat{p}_1 - \hat{\Phi}) \cdot D\tilde{T}_{1D}}$$

and

$$V_{11} = V_1\hat{S}_D\hat{p}_1\hat{\lambda}\tilde{T}_{2V}(1 - \hat{S}_D\hat{p}_1\hat{\lambda}\tilde{T}_{2V})$$

$$V_{10} = V_1[\hat{S}_D\hat{p}_1(\tilde{T}_{1V} - \hat{\lambda}\tilde{T}_{2V}) + (1 - \hat{S}_D)\hat{\Phi}\tilde{T}_{1V}]\{1 - [\hat{S}_D\hat{p}_1(\tilde{T}_{1V} - \hat{\lambda}\tilde{T}_{2V}) + (1 - \hat{S}_D)\hat{\Phi}\tilde{T}_{1V}]\}$$

$$V_{01} = V_1\hat{S}_D(1 - \hat{p}_1)\hat{\lambda}\tilde{T}_{2V}[1 - \hat{S}_D(1 - \hat{p}_1)\hat{\lambda}\tilde{T}_{2V}]$$

$$V_m = D\hat{\Phi}\tilde{T}_{1D}(1 - \hat{\Phi}\tilde{T}_{1D})$$

$$C_1 = -V_1[\hat{S}_D\hat{p}_1\hat{\lambda}\tilde{T}_{2V}][\hat{S}_D\hat{p}_1(\tilde{T}_{1V} - \hat{\lambda}\tilde{T}_{2V}) + (1 - \hat{S}_D)\hat{\Phi}\tilde{T}_{1V}]$$

$$C_2 = -V_1[\hat{S}_D\hat{p}_1\hat{\lambda}\tilde{T}_{2V}][\hat{S}_D(1 - \hat{p}_1)\hat{\lambda}\tilde{T}_{2V}]$$

$$C_3 = -V_1[\hat{S}_D(1 - \hat{p}_1)\hat{\lambda}\tilde{T}_{2V}][\hat{S}_D\hat{p}_1(\tilde{T}_{1V} - \hat{\lambda}\tilde{T}_{2V}) + (1 - \hat{S}_D)\hat{\Phi}\tilde{T}_{1V}]$$

Glossary

actual single-release study A single-release study in which a single release composes the release group.

attribute group file An optional input file that defines one or more attributes and assigns attribute values to each tag code. It allows analysis of a subset of the data based on attribute values.

bin Designates the tag bin; sometimes referred to as “lot.” Tags that come from different manufacturing lots may require different tag-life curves to model tag failure. Tags may also be grouped into different bins if tag handling issues necessitates calculating separate tag-life corrections for some subset of tags within a release.

navigation panel The panel that, by default, occupies the left side of the main ATLAS dialog, showing the list of available actions. An action is initiated by double-clicking on it.

release A group of tagged individuals released at the same location, grouped under a common name in the capture history data file.

release group One or more releases grouped together that fill a certain role in a given study design.

status report The status report that by default is on the right side of the Program ATLAS main window. It indicates the names of the data files currently loaded, the number in each release, the groups configuration, and the sites configuration. It also shows which tag-life curve is selected, if any.

survival probability The probability that a fish transited successfully from one release or detection site to the next detection site, whether or not it was detected.

tag correction The probability that a tag will be alive for a given release at a given

detection site.

TagPro TagPro utility, available at [Columbia Basin Research Tools page: TagPro](#).

virtual release A release group defined by all tagged individuals, possibly from multiple upstream releases, detected at a given site (the virtual site). These individuals form a release group for all subsequent downstream detections.

virtual single-release study A single-release study in which one or more releases is used to create a single virtual release.

virtual site A detection site used to define a virtual release.

Acronyms

CDF cumulative distribution function.

CJS Cormack-Jolly-Seber (Cormack 1964, Jolly 1965, Seber 1965).

LRT Likelihood Ratio Test.

MLE Maximum Likelihood Estimate.

PDF probability density function.

ViRDcT virtual release with dead fish correction.

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