Program ATLAS 1:  
Active Tag Life Adjusted Survival

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Contents

1 Introduction 1

2 Using ATLAS 3
  2.1 Data ................................................. 5
  2.2 Diagnostics and Setup ................................... 5
    2.2.1 Defining Release Groups .......................... 5
    2.2.2 Select Tag-Life Curve ............................. 6
    2.2.3 Truncating Tag-Life Data ......................... 9
    2.2.4 Estimate the Tag Corrections ..................... 10
    2.2.5 View Mixing ..................................... 12
    2.2.6 Select Downstream Sites .......................... 13
    2.2.7 Capture History Report ........................... 13
    2.2.8 CJS Report ..................................... 14
  2.3 Analysis .............................................. 17
    2.3.1 Closed Form Estimates ............................... 17
    2.3.2 Modeled Survival Estimates ....................... 17
    2.3.3 Estimate Full Variance ............................ 24

3 Single-Release Study Design 29
  3.1 Data ................................................. 29
  3.2 Simple Single-Release Study Design .................. 30
    3.2.1 Tag Corrections ................................... 30
3.3 Virtual Single-Release Study Design ........................................ 34
   3.3.1 Closed Form Parameter Report ...................................... 36
   3.3.2 Equate Parameters Across Releases .............................. 36
   3.3.3 Creating a Virtual Release ........................................ 36

4 Paired-Release Study Design ................................................. 41
   4.1 Define Release Groups .................................................. 41
   4.2 Tag Corrections .......................................................... 41
   4.3 View Mixing ............................................................. 42
   4.4 Closed Form Parameter Report ...................................... 42

5 Virtual/Paired-Release Study Design ...................................... 47
   5.1 Define Release Groups .................................................. 47
   5.2 Tag Corrections .......................................................... 47
   5.3 View Mixing ............................................................. 48
   5.4 Closed Form Parameter Report ...................................... 48
   5.5 Parameter Report ....................................................... 48

A Input Data Files ........................................................................ 53
   A.1 Capture History Data File .............................................. 53
   A.2 Tag-Life Data File ........................................................ 54

B Statistical Methods used in ATLAS .......................................... 57
   B.1 Tag-Life Analyses .......................................................... 57
      B.1.1 Parametric Failure-Time Distributions ....................... 57
      B.1.2 Nonparametric Method .......................................... 59
      B.1.3 Right-Censored Tag-Life Analyses ............................ 60
   B.2 Tag-Life Adjusted Estimates of Survival .......................... 61
      B.2.1 Single Release-Recapture Design ............................. 62
      B.2.2 Paired Release-Recapture Design ............................. 66
      B.2.3 Virtual/Paired Release-Recapture Design ................. 68
List of Figures

2.1 Initial dialog for study design selection ........................................... 3
2.2 Program ATLAS at initial startup in single-release mode ................. 4
2.3 Tag-Life Curve selection dialog ...................................................... 7
2.4 Tag-Life Curve with arrival time distributions at a selected site ........... 8
2.5 Tag-Life Curve with arrival time distributions for a selected release group 9
2.6 Tag-Life Curve with simulated data with outliers .............................. 10
2.7 Tag-Life Curve after extreme failure times have been excluded from the truncated analysis ......................................................... 11
2.8 Example of a Tag Correction Table for a virtual/paired-release study 12
2.9 Example of a Tag Correction Table for a virtual/paired-release study with multiple bins ........................................................... 13
2.10 Site Selection Dialog for a single-release study with four downstream sites .............................................................................. 14
2.11 Capture History Report ................................................................. 15
2.12 Cormack-Jolly-Seber Report for a single-release study .................... 16
2.13 Example of a Closed-Form Parameter Report for a single-release study 18
2.14 Equate parameter dialog for a paired-release study ........................... 19
2.15 Parameter Report with default configuration of no parameters equated across releases for a paired-release study .............................. 20
2.16 Parameter Report with all possible parameters equated across releases for a paired-release study .................................................... 21
2.17 Output window showing covariance estimation error after “Compute” action ................................................................................. 22
LIST OF FIGURES

2.18 Parameter Report after failure to estimate the covariance matrix . . . 23
2.19 Constrain Parameters with the Detection tab selected . . . . . . . . 24
2.20 Output window after constraining parameters . . . . . . . . . . . . 25
2.21 Parameter Report after successfully estimating the parameters and the
 covariance matrix. Compare to Figure 2.18 . . . . . . . . . . . . . . . 26
2.22 Dialog asking for the number of bootstrap iterations in estimating the
 full variance . . . . . . . . . . . . . . . . . . . . . . . . . . . . . . . . 26
2.23 Parameter Report after “Estimate Full Variance” action . . . . . . . 27
3.1 Simple single-release study with \( K \) detection sites . . . . . . . . . 29
3.2 Virtual single-release study with \( K \) detection sites . . . . . . . . . . 30
3.3 Status Report after loading data with only one release for a single-
 release study . . . . . . . . . . . . . . . . . . . . . . . . . . . . . . . . 31
3.4 Status Report after loading data with three releases for a single-
 release study. Only the “Roosevelt Chinook” release is selected to form \( R_1 \) . . 32
3.5 Define Release Groups dialog with three releases for a single-release
 study. Only release “TDA Chinook” is selected. . . . . . . . . . . . . 33
3.6 Tag Correction Table for a simple single-release study . . . . . . . . 33
3.7 Define a virtual release group for a single-release study. All three
 groups are selected to from the virtual release group. . . . . . . . . . 34
3.8 Status Report for a virtual single-release study. All three releases are
 used in forming the virtual release \( V_1 \). . . . . . . . . . . . . . . . . . . 35
3.9 Example of a Tag Correction Table for a virtual single-release study . 36
3.10 Closed Form Parameter Report for a single-release study using a virtual
 release . . . . . . . . . . . . . . . . . . . . . . . . . . . . . . . . . . . 37
3.11 Equate Parameters Across Releases with a virtual single-release with
 three releases, default setting . . . . . . . . . . . . . . . . . . . . . . . . 37
3.12 Example of a Parameter Report for a single-release study, no parame-
 ters equated across releases . . . . . . . . . . . . . . . . . . . . . . . . . 38
3.13 Equate Parameters Across Releases for a virtual single-release study
 with three releases, all parameters equated . . . . . . . . . . . . . . . 39
3.14 Example of a Parameter Report for a single-release study, all
 parameters equated across releases . . . . . . . . . . . . . . . . . . . . 40
LIST OF FIGURES

4.1 Define Release Groups dialog for a paired-release study .......................... 42
4.2 Example of a Status Report for a paired-release study ............................ 43
4.3 Example of a Tag Correction Table for a paired-release study ................. 44
4.4 View Mixing dialog for a paired-release study ........................................ 44
4.5 Example of a Closed Form Parameter Report for a paired-release study .... 45

5.1 Define Release Groups dialog for a virtual/paired-release study ................ 48
5.2 Example of a Status Report for a virtual/paired-release study .................. 49
5.3 Example of a Tag Correction Table for a virtual/paired-release study ......... 50
5.4 View Mixing dialog for a virtual/paired-release study ............................ 51
5.5 Example of a Closed Form Parameter Report for a virtual/paired-release study .......................... 52
5.6 Example of a Parameter Report for a virtual/paired-release study ............. 52

A.1 Portion of a capture history data file .................................................. 54
A.2 Portion of the tag-life data file ......................................................... 55

B.1 Schematic of a paired release-recapture design ...................................... 67
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. .................. 69
Chapter 1

Introduction

Program ATLAS was developed to analyze the survival of migrating smolts in the Columbia River Basin using acoustic- and radio-tagging data. Active tagging technologies allows 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 a bias-corrected survival estimate.

Program ATLAS has three mode of operations, corresponding to three study designs:

1. Single-Release,
2. Paired-Release,
3. Virtual/Paired-Release.

Chapter 2 describes how to use Program ATLAS as it pertains to all study designs. See Chapter 3 for Single Release, Chapter 4 for Paired Release, and Chapter 5 for Virtual Paired Release studies.

This manual describes Program ATLAS version 1.1. The latest version of the software, along with a PDF copy of this manual, is available at www.cbr.washington.edu/paramest/atlas.
Chapter 2

Using ATLAS

When running Program ATLAS for the first time, an initial splash screen appears followed by the initial dialog for study design selection as show in Figure 2.1. If the user un-checks the check box in the lower right corner of the dialog, this dialog will not be displayed on subsequent runs.

![ATLAS dialog](image)

Figure 2.1: Initial dialog for study design selection

Once the user selects the desired study design, and presses the “Continue” button, the main window appears. Figure 2.2 shows Program ATLAS upon initial startup in Single-Release mode.

The four areas of the main window (for all study designs) are as follows.

The **navigation panel** at 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.
CHAPTER 2. USING ATLAS

The status report panel at the right side gives the current program state. At initial startup it simply shows that there are no capture history data loaded and no tag-life data loaded.

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.

The navigation panel, status report panel, and the output window can be hidden by clicking the close icon on the right of their respective title bars, or via the View menu. They can also be un-hidden 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.

The navigation panel has three main headings: (1) Data, (2) Diagnostics and Setup, and (3) Analysis. The Data section is described in Section 2.1 and involves loading the required data files into Program ATLAS. The Diagnostics and Setup (Section 2.2) allows the user to define which sites and which releases will be used in...
the analysis, and which probability model will be used to model the tag-life failure curve before proceeding with the analysis (Section 2.3). The results of the analysis may be used to inform the user to use a different setup. Thus, the user may move between the “Diagnostics and Setup” and the “Analysis” in an iterative process before arriving at the optimal setup with its corresponding results.

2.1 Data

At initial startup, before any data have been loaded into Program ATLAS, two commands are available on the Navigation Panel under the “Data” heading: (1) Load Capture History Data, and (2) Load Tag-Life Data. These correspond to the two types of data needed for full survival analysis in ATLAS.

The capture history data file contains the detection history for each individual in each release of the study. Typically this file is created by the TagPro utility, available at [www.cbr.washington.edu/telem](http://www.cbr.washington.edu/telem). Details of this file are given in Appendix A.1. 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. Note that once the capture history data are loaded, the “Capture History Report” and the “CJS Report” become available under the “Report” heading on the navigation panel since neither of these reports depend on the tag-life data.

In order to obtain independent estimates of the tag 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 in the tag-life data file as described in Appendix A.2. To load the tag-life data, double-click on “Load Tag-Life Data” and select the appropriate tag-life data file.

2.2 Diagnostics and Setup

2.2.1 Defining Release Groups

Program ATLAS distinguishes between a release and a release group. A release is defined within the capture history data file and consists of tagged individuals grouped together under a release name, presumably all released from the same site at about the same time. A release group, on the other hand, is made up of one or more releases, and defines a particular role specific to a given study design. The “Define Release Groups” action on the navigation panel allows the user to map releases to release groups, in other words, define what role each release plays within
a selected study design. The specifics of the Define Release Groups dialog are described in Sections 3.2 and 3.3 for single-release studies, Section 4.1 for paired-release studies, and Section 5.1 for virtual/paired-release studies.

### 2.2.2 Select Tag-Life Curve

In order to estimate the tag corrections, a probability distribution must be selected to model the tag-life failure. Program ATLAS provides four distributions to choose from:

1. The Nonparametric estimator, also known as the Kaplan-Meier estimator (Kaplan and Meier 1958),
2. The two-parameter Weibull distribution,
3. The three-parameter Weibull distribution,
4. The vitality survival function (Li and Anderson 2009, see also http://www.cbr.washington.edu/vitality).

When the user selects the “Select Tag-Life Curve” action, the Tag-Life Curve dialog opens as is shown in Figure 2.3. The points on the plot represent the data from the tag-life data file (Appendix A.2); the X-axis is time in days, and the Y-axis is the proportion of tags still functioning at a given time. The drop-down box at the bottom allows the user to select one of the above distributions. Once selected, ATLAS immediately estimates the parameters for the tag-life curve and plots the resulting curve in red, allowing the user to select the failure curve that best fits the tag-life data. Figure 2.3 shows the vitality survival function fitted to the tag-life data.

Along the top of the the Tag-Life dialog are four tabs. The first one, “Tag-Life Data vs Curve,” is the default when the “Select Tag-Life Curve” action is initiated since selecting the tag-life distribution is always the first step (Figure 2.3). Once the appropriate distribution has been selected, the user may select either the “Curve vs Data by Detection” tab or the “Curve vs Data by Release” tab. Both of these tabs allow the user to view the arrival timing of individuals as a function of the selected tag-life curve.
2.2. DIAGNOSTICS AND SETUP

Figure 2.3: Tag-Life Curve selection dialog
2.2.2.1 Curve vs Data by Detection

Figure 2.4 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. 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 releases from the analysis.

2.2.2.2 Curve vs Data by Release

Figure 2.5 shows the Tag-Life dialog with the “Curve vs Data by Release” tab selected. With this tab, the user selects the release of interest, and the plot
2.2. DIAGNOSTICS AND SETUP

Figure 2.5: Tag-Life Curve with arrival time distributions for a selected release group shows the arrival distribution for that release at all downstream detection sites. If a selected release arrives too far down the tag-life curve, the user may need to consider either not using the release, or not using the particular site (along with all sites further downstream).

2.2.3 Truncating Tag-Life Data

In a well-designed study, the tag detections will occur very early with respect to the tag-life curve, on the flat area of the curve, rather than towards the tail of the curve (see Figures 2.4 and 2.5). It may be the case that in the tag-life study, there might be a few outlier tags that last much longer than the rest. Figure 2.6 shows simulated tag-life data with two outliers. Although no fish are detected at this tail end of the curve, the outliers may exert undue influence on the parameter...
estimation for the tag-life curve. As shown in the circled area of Figure 2.6, the user has the option of removing the outliers from being considered in estimating the tag-life curve parameters. Figure 2.7 shows the same simulated data with the last two tags removed. Notice how much better the estimated curve fits the data.

### 2.2.4 Estimate the Tag Corrections

After selecting the tag-life curve, the Apply button is pressed on any one of the Tag-Life dialog tabs in order to estimate the tag corrections along with their corresponding variances. Once the Apply button is pressed, it will take several minutes to calculate the tag corrections due to the bootstrapping that must be performed in order to calculate the variances. The details of the bootstrapping are given in Appendix B.2.1.

After the probabilities of a tag being active at the downstream detection sites have been calculated, the user may select the “Tag Correction Table” tab to
Figure 2.7: Tag-Life Curve after extreme failure times have been excluded from the truncated analysis
CHAPTER 2. USING ATLAS

2.2.5 View Mixing

The “View Mixing” action is applicable only to Paired-Release and Virtual/Paired-Release study designs. Section 4.3 discusses the View Mixing function for a Paired-Release study design, and 5.3 for a Virtual/Paired-Release study design.
2.2. DIAGNOSTICS AND SETUP

2.2.6 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 2.10. Note that the first two sites are listed as “Required.” This is because a minimum of two downstream sites is required for a single-release study; the number of required downstream sites is a function of the study design. In the data for Figure 2.10, there are two optional sites downstream for a total of four sites. By default, the check boxes for the optional sites are selected, meaning they will be included in the analysis. If a user de-selects 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 checked for any changes to take effect.

2.2.7 Capture History Report

The capture history report is the first of two reports under the “Diagnostics and Setup” section of the navigation panel. Double-clicking on it produces a capture history report, such as shown in Figure 2.11. A capture history is a symbolic representation of the detection history of an individual fish: “1” indicates detection at a site, “0” indicates no detection, and “2” indicates detection and...
removal (e.g., PIT-tag records may indicate removal from the river at or above the site). The capture history reads 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 2.11, 123 fish in the “TDA Chinook” release have a capture history of “1 0 1 1”, meaning that they were detected at the first site, not detected at the next downstream site, and detected again at the final two downstream sites.

If there are six or less 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.

2.2.8 CJS Report

Figure 2.12 shows a Cormack-Jolly-Seber (Cormack 1964, Jolly 1965, Seber 1965) (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-life failure and thus are the combined probability of fish survival and tag survival.
### Capture History Report

**TDA Chinook**

<table>
<thead>
<tr>
<th>Pattern</th>
<th>Count</th>
</tr>
</thead>
<tbody>
<tr>
<td>1 1 1 1</td>
<td>510</td>
</tr>
<tr>
<td>0 1 1 1</td>
<td>4</td>
</tr>
<tr>
<td>1 0 1 1</td>
<td>123</td>
</tr>
<tr>
<td>0 0 1 1</td>
<td>0</td>
</tr>
<tr>
<td>1 1 0 1</td>
<td>35</td>
</tr>
<tr>
<td>0 1 0 1</td>
<td>0</td>
</tr>
<tr>
<td>1 0 0 1</td>
<td>9</td>
</tr>
<tr>
<td>0 0 0 1</td>
<td>0</td>
</tr>
<tr>
<td>1 1 2 0</td>
<td>0</td>
</tr>
<tr>
<td>0 1 2 0</td>
<td>0</td>
</tr>
<tr>
<td>1 0 2 0</td>
<td>0</td>
</tr>
<tr>
<td>0 0 2 0</td>
<td>0</td>
</tr>
<tr>
<td>1 1 1 0</td>
<td>27</td>
</tr>
</tbody>
</table>

Figure 2.11: Capture History Report
### Cormack-Jolly-Seber Report

#### Survival Estimates:

<table>
<thead>
<tr>
<th></th>
<th>Release to CR234.0</th>
<th>CR234.0 to CR153.0</th>
<th>CR153.0 to CR113.0</th>
</tr>
</thead>
<tbody>
<tr>
<td></td>
<td>Estimate</td>
<td>s.e.</td>
<td>Estimate</td>
</tr>
<tr>
<td>TDA Chinook</td>
<td>0.9614</td>
<td>0.005861</td>
<td>0.9415</td>
</tr>
</tbody>
</table>

#### Capture Estimates:

<table>
<thead>
<tr>
<th></th>
<th>CR234.0</th>
<th>CR153.0</th>
<th>CR113.0</th>
<th>CR086.2 Survival*Capture</th>
</tr>
</thead>
<tbody>
<tr>
<td></td>
<td>Estimate</td>
<td>s.e.</td>
<td>Estimate</td>
<td>s.e.</td>
</tr>
<tr>
<td>TDA Chinook</td>
<td>0.9974</td>
<td>0.002770</td>
<td>0.8022</td>
<td>0.014665</td>
</tr>
</tbody>
</table>

#### Configuration:

<table>
<thead>
<tr>
<th>Dataset</th>
<th>Spring2010ChinookPaired.csv</th>
</tr>
</thead>
<tbody>
<tr>
<td>Tag life data</td>
<td>Sprng2010TagLife.csv</td>
</tr>
<tr>
<td>Tag life curve</td>
<td>Vialty</td>
</tr>
<tr>
<td>Groups</td>
<td>R1: TDA Chinook</td>
</tr>
<tr>
<td>Active Detection Sites</td>
<td>D0: CR234.0</td>
</tr>
<tr>
<td></td>
<td>D1: CR153.0</td>
</tr>
<tr>
<td></td>
<td>D2: CR113.0</td>
</tr>
<tr>
<td></td>
<td>D3: CR086.2</td>
</tr>
<tr>
<td>Optimizer</td>
<td>Powell</td>
</tr>
</tbody>
</table>

Figure 2.12: Cormack-Jolly-Seber Report for a single-release study
2.3. Analysis

Program ATLAS provides two methods for estimating survival parameters corrected for tag life: (1) Closed-form estimates, available under Closed Form Parameter Report, and (2) modeled estimates under the “Modeled Survival Estimates” of the navigation panel.

2.3.1 Closed Form Estimates

Figure 2.13 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 2.2.8), 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 (all estimates and standard errors under the “Capture Detail” section of the report are the same as those on the CJS report).

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 and the extent of dam passage survival, respectively (Sections 4.4 and 5.4). See Appendix B.2.1 for details on calculating the estimates and the corresponding standard errors.

Note that the Closed Form Parameter Report is not available if any one of the releases have more than one bin associated with it.

2.3.2 Modeled Survival Estimates

Program ATLAS uses numerical optimization to calculate the Maximum Likelihood Estimates (MLEs) of the model parameters. Whatever the study design (single-release, paired-release, or virtual/paired-release), Program ATLAS models each release (including virtual release groups) with a single-release likelihood as described in Appendix B.2.1. Once the tag corrections have been computed (Section 2.2.4), the user may simply double-click on the “Compute” action on the navigation panel. The output of the optimizer are displayed in the output window and an “Estimation Complete” message will appear, and the “Parameter 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.
Any one 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 2.3.2.2 to estimate the parameters.

### 2.3.2.1 Set Common Parameters across releases

The closed-form estimates (Section 2.3.1) 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 “Set Common Parameters Across Releases” action 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 2.14 shows the Equate Parameters 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. Selecting a site for survival or detection causes all downstream sites to be selected.
as well; conversely, de-selecting a site causes all upstream sites to be de-selected as well. The parameters that can be equated vary for each study design; hence, the Equate Parameters Dialog will look slightly different.

In Figure 2.14, 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 2.15 shows the Parameter Report from a paired-release study with no parameters equated across releases. Figure 2.16 shows the parameter report with all possible 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 \(2(–39.7240 – (–41.8122)) = 4.18\). The degrees of freedom is the difference in the number of parameters (14 – 8 = 6). The P-value for a \(\chi^2 = 4.18\) with 6 degrees of freedom is 0.35, indicating that the parameters are equal for the two releases. Using a 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).
Figure 2.15: Parameter Report with default configuration of no parameters equated across releases for a paired-release study
Figure 2.16: Parameter Report with all possible parameters equated across releases for a paired-release study.
2.3.2.2 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 Parameter” 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 are treated as constants set to 1.0 rather than parameters to be estimated, and survival parameters are constrained using the logit function

$$S = \frac{\exp(S_0)}{1 - \exp(S_0)}$$ (2.1)

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 2.17 shows the output window after double-clicking the “Compute” action on the navigation panel with data from a paired-release study design. Note that Program ATLAS was able to estimate the point estimates, but not the covariance matrix (the “no convergence in 30 svdcmp iterations” message is a diagnostic message from the estimation algorithm). Figure 2.18 shows the resulting Parameter Report; there are point estimates for the parameters, but the standard error estimates are not available (indicated by “NA”). Notice the aberrant point estimate for the detection probability at the first site for the first release.
2.3. ANALYSIS

Figure 2.18: Parameter Report after failure to estimate the covariance matrix
Figure 2.19: Constrain Parameters with the Detection tab selected

Figure 2.19 shows the Constrain Parameters dialog for the same data with the Capture tab selected. The rows represent detection sites, and the columns represent releases. The CJS estimates are displayed for each release and site. The first release has a detection probability of 1.0 for the first detection site, so the corresponding box has been checked to constrain the detection probability for that release site to 1.0. Again, the “Apply” button must be pushed for the specified constraints to take effect.

Figure 2.20 shows the output window after constraint is applied and the “Compute” action is selected again. This time Program ATLAS was able to estimate the covariance matrix. Figure 2.21 shows the resulting Parameter Report. The previously ill-behaved detection probability is fixed at 1.0, and there are now estimates for the standard errors of the remaining parameters.

2.3.3 Estimate Full Variance

Once the “Compute” action has been performed and the MLEs calculated, the Parameter Report is available as shown in Figure 2.20. However, near the
2.3. ANALYSIS

Figure 2.20: Output window after constraining parameters

bottom of the Parameter Report will be the phrase, “Note: all standard errors are based on the inverse Hessian.” The Hessian is the matrix of second derivatives, and under maximum likelihood theory, the inverse of the Hessian is the covariance matrix from which the standard errors are derived. This covariance matrix is based on the likelihood model. The likelihood model necessarily assumes that tag corrections are constant, and does not incorporate the actual standard errors of the tag corrections as reported in the Tag Correction Report.

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 “Estimate Full Variance” action will bring up the dialog shown in Figure 2.22 asking the user for the number of bootstrap iterations. A higher the number of iterations will improve the estimate of variance, but will also take longer to compute. The default, as shown in Figure 2.22, is 1,000.

Once the “Estimate Full Variance” action has completed, the Parameter Report will be updated as shown in Figure 2.23 to reflect the full standard errors for all survival parameters in the first reach (the standard errors for the other survival probabilities, and the detection and product probabilities remain unchanged).
### Parameter Report

**Estimates:**

- Log Likelihood: 9.6739
- Num Parameters: 5

**Paired Survival:**

<table>
<thead>
<tr>
<th></th>
<th>Estimate</th>
<th>s.e.</th>
</tr>
</thead>
<tbody>
<tr>
<td>Dam Survival</td>
<td>0.9552</td>
<td>0.012188</td>
</tr>
</tbody>
</table>

**Survival Detail:**

<table>
<thead>
<tr>
<th></th>
<th>Release to CBAR</th>
<th></th>
<th></th>
</tr>
</thead>
<tbody>
<tr>
<td></td>
<td>Estimate</td>
<td>s.e.</td>
<td>Estimate</td>
</tr>
<tr>
<td>Rocky Reach Tailrace Steelhead (day)</td>
<td>0.9551</td>
<td>0.010403</td>
<td></td>
</tr>
<tr>
<td>Rock Island Tailrace Steelhead (day)</td>
<td>0.9895</td>
<td>0.006322</td>
<td></td>
</tr>
</tbody>
</table>

**Capture Detail:**

|                                | CBAR     | SUND Survival*Capture |                  |
|                                | Estimate | s.e.     | Estimate | s.e.     |
| Rocky Reach Tailrace Steelhead (day) | 1.0000   | 0.000000 | 0.9870   | 0.005574 |
| Rock Island Tailrace Steelhead (day)       | 0.9979   | 0.002090 | 0.9774   | 0.007011 |

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

Figure 2.21: Parameter Report after successfully estimating the parameters and the covariance matrix. Compare to Figure 2.18

Figure 2.22: Dialog asking for the number of bootstrap iterations in estimating the full variance
### Parameter Report

**Estimates:**

<table>
<thead>
<tr>
<th>Log Likelihood</th>
<th>-9.6789</th>
</tr>
</thead>
<tbody>
<tr>
<td>Num Parameters</td>
<td>5</td>
</tr>
</tbody>
</table>

**Paired Survival:**

<table>
<thead>
<tr>
<th></th>
<th>Estimate</th>
<th>s.e.†</th>
</tr>
</thead>
<tbody>
<tr>
<td>Paired Survival</td>
<td>0.9642</td>
<td>0.012195</td>
</tr>
</tbody>
</table>

**Survival Detail:**

<table>
<thead>
<tr>
<th></th>
<th>Release to CBAR</th>
</tr>
</thead>
<tbody>
<tr>
<td></td>
<td>Estimate</td>
</tr>
<tr>
<td>Rocky Reach Tailrace Steelhead (day)</td>
<td>0.9501</td>
</tr>
<tr>
<td>Rock Island Tailrace Steelhead (day)</td>
<td>0.9853</td>
</tr>
</tbody>
</table>

**Capture Detail:**

<table>
<thead>
<tr>
<th></th>
<th>CBAR</th>
<th>SLND Survival*Capture</th>
</tr>
</thead>
<tbody>
<tr>
<td></td>
<td>Estimate</td>
<td>s.c.°</td>
</tr>
<tr>
<td>Rocky Reach Tailrace Steelhead (day)</td>
<td>1.0000</td>
<td>0.000000</td>
</tr>
<tr>
<td>Rock Island Tailrace Steelhead (day)</td>
<td>0.9979</td>
<td>0.000290</td>
</tr>
</tbody>
</table>

**Notes:**

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

Figure 2.23: Parameter Report after “Estimate Full Variance” action
Chapter 3

Single-Release Study Design

A single-release study consists of a single release group with multiple downstream detections. It may be either as simple single-release study with the release group consisting of a single release as illustrated in Figure 3.1, or a virtual single-release study with a virtual release group comprised of multiple upstream releases illustrated in Figure 3.2.

3.1 Data

The capture history data file for a single-release study may contain one or more releases, but they must all contain the same number of detection sites. If there is only one release, a simple single-release study (Figure 3.1) is the only option available. If the capture history data file contains multiple releases, the user may select any one of them to be the $R_1$ release group for a simple single-release study, or select multiple releases to define the $V_1$ virtual release group for a virtual single-release study.

![Figure 3.1: Simple single-release study with $K$ detection sites](image)

\[ R_1 \rightarrow Site 1 \rightarrow Site 2 \rightarrow \cdots \rightarrow Site K \rightarrow \lambda = \phi_K P_K \]

\[ P_1 \rightarrow \phi_1 \rightarrow P_2 \rightarrow \phi_2 \rightarrow \cdots \rightarrow \phi_{K-1} \rightarrow P_{K-1} \]

Site 1 2 K-1 K

$R_1$ release group

$V_1$ virtual release group

$P_i$ detection sites

$\phi_i$ transition probabilities

$\lambda$ total immigration

$\phi_K P_K$ total immigration at site $K$
3.2 Simple Single-Release Study Design

Figure 3.3 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 “Define Release Groups” option is not available when the capture history data file contains only one release.

Figure 3.4 shows the status report after loading a capture history file with three releases. By default, release group \( R_1 \) is defined to be the first release in the capture history data file. The release that is used for \( R_1 \) may be changed by the user by selecting “Define Release Groups” on the navigation panel. Figure 3.5 shows the dialog for “Define Release Groups” for capture history data with three releases. Leaving the “Define virtual releases” un-checked, the user selects which of the releases will be used as release group \( R_1 \), making sure to press the “Apply” button to put into effect any changes made.

3.2.1 Tag Corrections

Section 2.2.4 describes how to estimate the tag correction. Figure 3.6 shows the Tag Correction table for a simple single release study. Each column is the unconditional probability of a tag surviving to the given site from release, given the travel times to each site.
3.2. SIMPLE SINGLE-RELEASE STUDY DESIGN

Figure 3.3: Status Report after loading data with only one release for a single-release study
Figure 3.4: Status Report after loading data with three releases for a single-release study. Only the “Roosevelt Chinook” release is selected to form $R_1$. 
3.2. SIMPLE SINGLE-RELEASE STUDY DESIGN

Figure 3.5: Define Release Groups dialog with three releases for a single-release study. Only release “TDA Chinook” is selected.

Figure 3.6: Tag Correction Table for a simple single-release study.
CHAPTER 3. SINGLE-RELEASE STUDY DESIGN

3.3 Virtual Single-Release Study Design

As was mentioned above, a user may define a virtual release group from multiple releases as shown in Figure 3.2. Figure 3.7 shows the “Define Virtual Releases” with all three releases used to define the virtual release group \( V_1 \). The user checks the “Define Virtual Releases” check box, allowing two or more releases to be selected.

Figure 3.8 shows the status report with all three release groups used to define virtual release group \( V_1 \). 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 D0, and thus a part of \( V_1 \), is reported.

Figure 3.9 shows the tag corrections for a single-release study with a virtual release comprised of three separate releases. Since the first site now defines a virtual site, the tag corrections table must be interpreted differently than in the case of a simple single release. The tag corrections in column D0 are the unconditional tag survival probabilities from release to site D0. Under the subsequent columns, D1 through D3 in this case, are the conditional tag survival probabilities, given that the tags were alive at site D0. Note that the tag corrections under “D0” 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 Table for reference.
3.3. VIRTUAL SINGLE-RELEASE STUDY DESIGN

Figure 3.8: Status Report for a virtual single-release study. All three releases are used in forming the virtual release $V_1$.  

<table>
<thead>
<tr>
<th>Capture History Data</th>
</tr>
</thead>
<tbody>
<tr>
<td><strong>Dataset:</strong> Spring2010ChinookSingle/virtual.csv</td>
</tr>
</tbody>
</table>

**Releases:**
- Roosevelt Chinook: 2237
- TDA Chinook: 796
- Hood River Chinook: 797

**Groups:**
- $V_1$: Roosevelt Chinook 1875
- TDA Chinook 761
- Hood River Chinook 784

**Available Detection Sites:**
- **D0:** CR234.0 \(\text{Virtual Site}\)
- **D1:** CR153.0 \(\text{Required}\)
- **D2:** CR113.0 \(\text{Required}\)
- **D3:** CR086.2 \(\text{Selected}\)

**Tag Life Data**
None loaded
3.3.1 Closed Form Parameter Report

Figure 3.10 shows the Closed Form Parameter Report for a virtual single release. Even though the goal is to have common survival and capture probabilities across releases as illustrated in Figure 3.2, Program ATLAS provides unique parameter estimates for each release. This allows the user to test if the separate releases do in fact share common survival and detection probabilities and, thus, to decide which releases should be used to create the virtual release group $V_1$.

3.3.2 Equate Parameters Across Releases

Figure 3.11 shows the dialog for equating parameters across releases for a virtual single release. The user may equate all survival and detection probability parameters across releases, as well as the final product parameters.

3.3.3 Creating a Virtual Release

Figure 3.12 shows the parameter report after performing the “Compute” action with the default settings of no parameters equated across releases (Figure 3.11). Note that all the standard errors have “NA”. This may be due to the fact that one survival probability is greater than 1.0. We could use the “Constrain
3.3. VIRTUAL SINGLE-RELEASE STUDY DESIGN

Figure 3.10: Closed Form Parameter Report for a single-release study using a virtual release

<table>
<thead>
<tr>
<th>Survival Detail</th>
<th>CR234.0 to CR153.0</th>
<th>CR153.0 to CR113.0</th>
</tr>
</thead>
<tbody>
<tr>
<td>Roosevelt Chinook</td>
<td>0.9340</td>
<td>0.006026</td>
</tr>
<tr>
<td>TDA Chinook</td>
<td>0.9433</td>
<td>0.008632</td>
</tr>
<tr>
<td>Hood River Chinook</td>
<td>0.9564</td>
<td>0.007595</td>
</tr>
</tbody>
</table>

<table>
<thead>
<tr>
<th>Capture Detail</th>
<th>CR153.0</th>
<th>CR113.0</th>
<th>CR086.2 Survival*Capture</th>
</tr>
</thead>
<tbody>
<tr>
<td>Roosevelt Chinook</td>
<td>0.0009</td>
<td>0.009474</td>
<td>0.9437</td>
</tr>
<tr>
<td>TDA Chinook</td>
<td>0.8011</td>
<td>0.014938</td>
<td>0.9350</td>
</tr>
<tr>
<td>Hood River Chinook</td>
<td>0.7965</td>
<td>0.014780</td>
<td>0.9267</td>
</tr>
</tbody>
</table>

Figure 3.11: Equate Parameters Across Releases with a virtual single-release with three releases, default setting
Parameters” action to constrain that survival probability, but the problem may go away after the survival probabilities are equated across releases.

We can perform a LRT to see if it is valid to equate the parameters across releases, so we note the log-likelihood value (-59.7625) and the number of parameters (21). We then equate all parameters across releases as shown in Figure 3.13. We then perform the “Compute” action again, and look at the Parameter Report as shown in Figure 3.14. 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 is the difference in the number of parameters (16). The P-value for a \( \chi^2 \) statistics of 16.3296 with 16 degrees of freedom is 0.57, indicating that it is valid to combine these three releases into one virtual release group. If the result had been different, we could have eliminated one of the releases that seemed to have

Figure 3.12: Example of a Parameter Report for a single-release study, no parameters equated across releases

Note: all standard errors are based on the inverse Hessian.
3.3. VIRTUAL SINGLE-RELEASE STUDY DESIGN

Figure 3.13: Equate Parameters Across Releases for a virtual single-release study with three releases, all parameters equated

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 “Estimate Full Variance” action must be taken to obtain the standard errors of the survival estimates, as described in Section 2.3.3
### Parameter Report

**Estimates:**
- Log Likelihood: -67.9273
- Num Parameters: 5

**Survival Detail:**

<table>
<thead>
<tr>
<th></th>
<th>CR234.0 to CR153.0</th>
<th></th>
<th>CR153.0 to CR113.0</th>
<th></th>
</tr>
</thead>
<tbody>
<tr>
<td>Roosevelt Chinook</td>
<td>0.9412</td>
<td>0.004176</td>
<td>0.9935</td>
<td>0.002079</td>
</tr>
<tr>
<td>TDA Chinook</td>
<td>0.9412</td>
<td>0.004176</td>
<td>0.9935</td>
<td>0.002079</td>
</tr>
<tr>
<td>Hood River Chinook</td>
<td>0.9412</td>
<td>0.004176</td>
<td>0.9935</td>
<td>0.002079</td>
</tr>
</tbody>
</table>

**Capture Detail:**

<table>
<thead>
<tr>
<th></th>
<th>CR153.0</th>
<th></th>
<th>CR113.0</th>
<th></th>
<th>CR086.2 Survival×Capture</th>
<th></th>
</tr>
</thead>
<tbody>
<tr>
<td>Roosevelt Chinook</td>
<td>0.8043</td>
<td>0.007038</td>
<td>0.9578</td>
<td>0.004403</td>
<td>0.9437</td>
<td>0.004236</td>
</tr>
<tr>
<td>TDA Chinook</td>
<td>0.8043</td>
<td>0.007038</td>
<td>0.9578</td>
<td>0.004403</td>
<td>0.9437</td>
<td>0.004236</td>
</tr>
<tr>
<td>Hood River Chinook</td>
<td>0.8043</td>
<td>0.007038</td>
<td>0.9578</td>
<td>0.004403</td>
<td>0.9437</td>
<td>0.004236</td>
</tr>
</tbody>
</table>

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

Figure 3.14: Example of a Parameter Report for a single-release study, all parameters equated across releases.
Chapter 4

Paired-Release Study Design

A paired-release study consists of two release groups: an upstream release group labeled $R_1$, and a downstream release group labeled $R_2$. The parameter of interest, $S_{\text{Paired}}$, is the ratio of the survival probabilities in the first reach for the two release groups. Details are given in Appendix B.2.2.

4.1 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 ($R_1$), and the second one is the downstream release group ($R_2$). Figure 4.1 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 4.2 shows the status report for the default configuration with the release named “TDA Chinook” mapped to the $R_1$ release group and “Hood River Chinook” mapped to the $R_2$ release group. A minimum of two downstream detection sites are required downstream of the initial release.

4.2 Tag Corrections

Figure 4.3 shows the Tag Correction table for a paired-release study. All tag corrections are the unconditional probability of a tag surviving from activation to the given detection site.
4.3 View Mixing

With 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 $R_2$ release group is scheduled to achieve this goal. The “View Mixing” action on the navigation panel brings up the Mixing dialog as shown in Figure 4.4 to see how well the goal was met. The graph shows the distribution of travel times for both of the release groups. In Figure 4.4, there is a delay of 12 hours between the release of $R_1$ and $R_2$. In the box in the lower left corner, the user can enter the number of hours the $R_2$ release group was released after the $R_1$ release group. The View Mixing dialog can also be used to plan future studies, to find out the best delay time in releasing the downstream release group.

4.4 Closed Form Parameter Report

Figure 4.5 shows the Closed Form Parameter Report for a Paired Release Study. In addition to reporting the corrected survival estimates, it also displays the paired survival estimate at the top, along with its standard error. As was explained in Section 2.3.3, the standard errors are from the inverse Hessian; “Estimate Full Variance” must be done in order to obtain the full standard errors of the survival estimates.
Figure 4.2: Example of a Status Report for a paired-release study
 CHAPTER 4. PAIRED-RELEASE STUDY DESIGN

Tag Correction Table

Tag Life Function: Vitality

Detection Site Key:

D1: CR234.0
D2: CR153.0
D3: CR113.0
D4: CR085.2

<table>
<thead>
<tr>
<th>Release</th>
<th>Site</th>
<th>Bin</th>
<th>D1:</th>
<th>D2:</th>
<th>D3:</th>
<th>D4:</th>
</tr>
</thead>
<tbody>
<tr>
<td>R1</td>
<td>TDA Chinook</td>
<td>1</td>
<td>0.9901 (0.004711)</td>
<td>0.9881 (0.005677)</td>
<td>0.9874 (0.006024)</td>
<td>0.9867 (0.006313)</td>
</tr>
<tr>
<td>R2</td>
<td>Hood River Chinook</td>
<td>1</td>
<td>0.9910 (0.004276)</td>
<td>0.9891 (0.005225)</td>
<td>0.9881 (0.005650)</td>
<td>0.9876 (0.005901)</td>
</tr>
</tbody>
</table>

Tag Life Function Log-Likelihood: -221.8102

Figure 4.3: Example of a Tag Correction Table for a paired-release study

Figure 4.4: View Mixing dialog for a paired-release study
4.4. CLOSED FORM PARAMETER REPORT

Figure 4.5: Example of a Closed Form Parameter Report for a paired-release study
Chapter 5

Virtual/Paired-Release Study Design

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

5.1 Define Release Groups

The capture history data for a virtual/paired-release study consists of three release groups. The first is a virtual release group, denoted $V_1$, comprised of all individuals of the given release detected at the virtual site at the face of the dam. The other two release groups are $R_2$ and $R_3$, and comprise 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 group $V_1$, the second and third releases are assigned to release groups $R_2$ and $R_3$, respectively. Figure 5.1 shows the Define Release Groups dialog for a virtual/paired-release study, allowing the user to change the default assignment of releases to release groups. Figure 5.2 shows the status report for a virtual/paired-release study. A minimum of three detections sites downstream from the virtual site is required with a virtual/paired-release study design.

5.2 Tag Corrections

Figure 5.3 shows the top portion of a Tag Correction Table for a virtual/paired-release study. The tag corrections for the column labeled “D0” are the unconditional probability of a tag being active at site “D0” (the virtual site).
The tag corrections for the remaining columns, beginning with “D1”, are the probabilities of a tag being alive at the site, conditioned on it being alive at site “D0”.

5.3 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 “View Mixing” dialog, shown in Figure 5.4, allows the user to view how well that requirement has been met, and also what release timings should be used for future studies.

5.4 Closed Form Parameter Report

Figure 5.5 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), along with its standard error, is reported.

5.5 Parameter Report

Figure 5.6 shows the top portion of a Parameter Report for a virtual/paired-release study after “Compute.” As with the Closed Form Parameter
Figure 5.2: Example of a Status Report for a virtual/paired-release study
Figure 5.3: Example of a Tag Correction Table for a virtual/paired-release study

Report, the dam survival is reported at the top of the report. Once the final configuration has been determined, the user must perform “Estimate Full Variance,” as explained in Section 2.3.3, to perform the bootstrapping to obtain the standard errors for the survival estimates.
Figure 5.4: View Mixing dialog for a virtual/paired-release study
CHAPTER 5. VIRTUAL/PAIRED-RELEASE STUDY DESIGN

Figure 5.5: Example of a Closed Form Parameter Report for a virtual/paired-release study

<table>
<thead>
<tr>
<th>Closed Form Parameter Report</th>
</tr>
</thead>
<tbody>
<tr>
<td>Overall Survival:</td>
</tr>
<tr>
<td>Dam Survival:</td>
</tr>
<tr>
<td>Estimate</td>
</tr>
<tr>
<td>0.9641</td>
</tr>
</tbody>
</table>

<table>
<thead>
<tr>
<th>Survival Detail:</th>
</tr>
</thead>
<tbody>
<tr>
<td>CR209.0 to CR275.0</td>
</tr>
<tr>
<td>CR275.0 to CR234.0</td>
</tr>
<tr>
<td>Release to CR234.0</td>
</tr>
<tr>
<td>CR234.0 to CR153.0</td>
</tr>
<tr>
<td>CR153.0 to CR113.0</td>
</tr>
<tr>
<td>Estimate</td>
</tr>
<tr>
<td>Estimate</td>
</tr>
<tr>
<td>0.9408</td>
</tr>
<tr>
<td>0.9647</td>
</tr>
<tr>
<td>0.9632</td>
</tr>
<tr>
<td>0.9537</td>
</tr>
<tr>
<td>0.9638</td>
</tr>
<tr>
<td>TDA Chinook:</td>
</tr>
<tr>
<td>Estimate</td>
</tr>
<tr>
<td>0.0009</td>
</tr>
<tr>
<td>0.0094</td>
</tr>
<tr>
<td>0.0185</td>
</tr>
<tr>
<td>0.0281</td>
</tr>
<tr>
<td>1.9129</td>
</tr>
<tr>
<td>Hood River Chinook:</td>
</tr>
<tr>
<td>Estimate</td>
</tr>
<tr>
<td>0.0009</td>
</tr>
<tr>
<td>0.0094</td>
</tr>
<tr>
<td>0.0185</td>
</tr>
<tr>
<td>0.0281</td>
</tr>
<tr>
<td>1.9129</td>
</tr>
</tbody>
</table>

<table>
<thead>
<tr>
<th>Capture Detail:</th>
</tr>
</thead>
<tbody>
<tr>
<td>CR275.0</td>
</tr>
<tr>
<td>CR234.0</td>
</tr>
<tr>
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Figure 5.6: Example of a Parameter Report for a virtual/paired-release study

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<td>CR275.0 to CR234.0</td>
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<tr>
<td>Release to CR234.0</td>
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<tr>
<td>CR234.0 to CR153.0</td>
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<td>CR153.0 to CR113.0</td>
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Appendix A

Input Data Files

A.1 Capture History Data File

The capture history data file is a comma separated value (CSV) text file. Typically, this is created by the TagPro utility available at www.cbr.washington.edu/utility. A portion of an example of a capture history data file is shown in Figure A.1. The columns, in the required order, are as follows:

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, “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). The first line of the capture history data file may be column labels if desired; if present, it will be ignored by Program ATLAS.
APPENDIX A. INPUT DATA FILES

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

Since the capture history data file is in CSV format, it can be readily read and edited via a spreadsheet program. This allows a user to create, for example, multiple bins per release based on the time between release time and activation time (see Section 2.2.4 for an explanation of bins).

A.2 Tag-Life Data File

The tag-life data file contains the results of the independent tag-life test conducted to estimate tag-file 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; so if three tags failed after, say, 25.5 days, than 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 if Figure A.2.


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</table>

Figure A.2: Portion of the tag-life data file
Appendix B

Statistical Methods used in ATLAS

B.1 Tag-Life Analyses

B.1.1 Parametric Failure-Time Distributions

The exponential distribution is among the simplest models for failure-time data. The exponential pdf can be written as

\[
f(t) = \begin{cases} 
\frac{1}{\lambda} e^{-\frac{1}{\lambda} t} & t \geq 0 \\
0 & t < 0
\end{cases}
\]  \hspace{1cm} (B.1)

with survivorship function

\[S(t) = e^{-\frac{1}{\lambda} t},\]  \hspace{1cm} (B.2)

cumulative distribution function (CDF)

\[F(t) = 1 - e^{-\frac{1}{\lambda} t},\]  \hspace{1cm} (B.3)

and hazard function (\textcite{Lee1992}, p. 132)

\[h(t) = \frac{1}{\lambda}, t \geq 0.\]  \hspace{1cm} (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.
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 ($\lambda$) and a shape parameter ($\beta$). The probability density function (PDF) for the two-parameter Weibull is

\[ f(t) = \frac{\beta}{\lambda} \left( \frac{t}{\lambda} \right)^{\beta-1} e^{-\left( \frac{t}{\lambda} \right)^\beta}, \]  

(B.5)

with survivorship function

\[ S(t) = e^{-\left( \frac{t}{\lambda} \right)^\beta}, \]  

(B.6)

CDF

\[ F(t) = 1 - e^{-\left( \frac{t}{\lambda} \right)^\beta} \]  

(B.7)

and hazard function

\[ h(t) = \frac{\beta}{\lambda} \left( \frac{t}{\lambda} \right)^{\beta-1}. \]  

(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 ($\lambda$), shape ($\beta$), and shift ($\gamma$) parameters. The PDF of the three-parameter Weibull distribution is

\[ f(t) = \frac{\beta}{\lambda} \left( \frac{t - \gamma}{\lambda} \right)^{\beta-1} e^{-\left( \frac{t - \gamma}{\lambda} \right)^\beta}, \]  

(B.9)

with survivorship function

\[ S(t) = e^{-\left( \frac{t - \gamma}{\lambda} \right)^\beta}. \]  

(B.10)

CDF

\[ F(t) = 1 - e^{-\left( \frac{t - \gamma}{\lambda} \right)^\beta}, \]  

(B.11)

and hazard function

\[ h(t) = \frac{\beta}{\lambda} \left( \frac{t - \gamma}{\lambda} \right)^{\beta-1}. \]  

(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 (AIC).
B.1. TAG-LIFE ANALYSES

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 few 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 PDF for the vitality model can be rewritten as

\[ f(t) = 1 - \left[ \Phi \left( \frac{1 - rt}{\sqrt{u^2 + s^2}} \right) - \exp \left( \frac{2u^2r^2}{s^4} + \frac{2r}{s^2} \right) \Phi \left( \frac{2u^2r + rt + 1}{\sqrt{u^2 + s^2}} \right) \right] \exp(-kt) \]  

(B.13)

where

\[ \Phi = \text{cumulative normal distribution}, \]
\[ r = \text{average wear rate of components}, \]
\[ s = \text{standard deviation in wear rate}, \]
\[ k = \text{rate of accidental failure}, \]
\[ u = \text{standard deviation in quality of original components}. \]

The PDF for the vitality model can be rewritten as

\[ f(t) = 1 - \left[ \Phi \left( \frac{1 - rt}{\sqrt{u^2 + s^2}} \right) - \exp \left( \frac{2u^2r^2}{s^4} + \frac{2r}{s^2} \right) \Phi \left( \frac{2u^2r + rt + 1}{\sqrt{u^2 + s^2}} \right) \right] \exp(-kt) \]  

(B.13)

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. It monitors the group of tags in a test group, and at each failure, the time and number of tags remaining are recorded. This method is therefore 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 \( t_L \), \( S(t_L) = 0 \).

In any time interval from \( t \) to \( t + 1 \), the conditional survival probability is estimated by

\[ \hat{P}(X > t + 1 | t) = \hat{S}_t = \frac{l_t - d_t}{l_t}, \]  

(B.14)

where
APPENDIX B. STATISTICAL METHODS USED IN ATLAS

\[ l_t = \text{number of tags still active and at risk of failure in the time interval } t \text{ to } t + 1, \]
\[ d_t = \text{number of tags that failed during the time interval } t \text{ to } t + 1, \]
\[ X = \text{random variable for time of failure.} \]

The binomial estimator (Equation B.14) has the estimated variance
\[
\hat{\text{Var}}(\hat{S}_t) = \frac{\hat{S}_t(1 - \hat{S}_t)}{l_t}. \tag{B.15}
\]

The product-limit estimator acquires its name because the estimator of survival from time 0 to \( t \) is simply the product
\[
\hat{S}(t) = \hat{S}_0 \cdot \hat{S}_1 \cdot \hat{S}_2 \cdots \hat{S}_t = \prod_{i=0}^{t-1} \left( \frac{l_i - d_i}{l_i} \right). \tag{B.16}
\]

These nonparametric estimators are applicable whether right-censoring has occurred or not. 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/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 last truncation strategy may be useful when traditional failure-time distributions may 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:
B.2. TAG-LIFE ADJUSTED ESTIMATES OF SURVIVAL

\[ f(t_i) = \text{PDF} \text{ for failure times } (t_i; t = 1, \ldots, n), \]
\[ F(t_i) = \text{cumulative survival function to true } t_i, \]
\[ = \int_0^{t_i} f(t) dt, \]
\[ S(t_i) = 1 - F(t_i), \text{ survival function}, \]
\[ n = \text{number of tags used in the tag-life study}, \]
\[ r = \text{number of tags that failed on or before truncation time } T \text{ out of } n \text{ tags} \]
\[ \text{starting the study.} \]

The likelihood model for a truncated analysis is as follows:

\[ L = \prod_{i=1}^{r} \left( \frac{f(t_i)}{F(T)} \right) \left( \begin{array}{c} n \cr r \end{array} \right) (1 - S(T))^r S(T)^{n-r} \tag{B.17} \]

Noting \( 1 - S(T) = F(T) \)

\[ L = \prod_{i=1}^{r} \left( \frac{f(t_i)}{F(T)} \right) \left( \begin{array}{c} n \cr r \end{array} \right) F(T)^r S(T)^{n-r} \]
\[ \propto \prod_{i=1}^{r} f(t_i) \cdot S(T)^{n-r}. \tag{B.18} \]

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, and (3) virtual/paired release-recapture design. The latter two 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:

$$S_i = \text{probability of surviving to event } i, \text{ given survival to event } i - 1 \ (i = 1, \ldots, K - 1).$$

$$p_i = \text{probability of detection at event } i \text{ given survival to event } i \ (i = 1, \ldots, K - 1).$$

$$\lambda = \text{probability of survival to and detection at event } K, \text{ given survival to event } K - 1.$$

$$T_i = \text{probability that a tag will be active at event } i, \text{ given } T_0 = 1.$$

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

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

Other quantities in the model include the following:

$$R_0 = \text{initial release size}.$$ 

$$R_i = \text{number detected and re-released at event } i.$$ 

$$z_i = \text{number detected and re-released before event } i, \text{ not detected at event } i, \text{ but detected after event } i.$$

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

$$m_i = \text{number detected at event } i \ (i = 1, \ldots, K - 1).$$

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

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

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

where

$$\chi_i = 1 - T_{i+1/i} + T_{i+1/i}(1 - S_{i+1} + S_{i+1}(1 - p_{i+1})\chi_{i+1})$$

$$= 1 - T_{i+1/i}S_{i+1} + T_{i+1/i}\chi_{i+1}S_{i+1}(1 - p_{i+1})$$
and

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

Also,

\[ \tau_i = T_i \chi_i \]
\[ = T_i - T_{i+1} S_{i+1} + \tau_{i+1} S_{i+1}(1 - p_{i+1}) \quad (i = 1, \ldots, K - 2) \]

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

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

(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:

- 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 \(S_1 p_1 S_2 T_2 \chi_2 = S_1 p_1 S_2 p_2 \tau_2\)
- 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 \(\chi_0\)

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 \(i = 1, \ldots, K\). 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

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

\[
d_{ij} = \text{time between tag activation and detection at event } i \text{ for the } j\text{th individual detected at event } i(i = 1, \ldots, K; j = 1, \ldots, m_i).
\]

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., \(\hat{T}_i; i = 1, \ldots, K\)) used in the model. However, those variance estimates do not take into account the uncertainties in the estimates \(\hat{T}_i(i = 1, \ldots, K)\). The variance of the survival estimates can be calculated using the total variance formula

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

The above variance can be estimated in stages using the expression

\[
\text{Var}(\hat{S}) = s^2_{\hat{S}|\hat{T}_i} + \text{Var}(\hat{S}|\hat{T}_i).
\] (B.21)

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

\[
s^2_{\hat{S}|\tilde{T}_i} = \frac{\sum_{b=1}^{B} \left( \hat{S}_b - \hat{S} \right)^2}{B - 1},
\] (B.22)
where

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

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 (\( \hat{S}_i \)) is then obtained from the ratio estimator

\[ \hat{S}_i = \frac{\hat{\phi}_i}{\left(\frac{T_{i-1}}{T_i}\right)} = \hat{\phi}_i \left(\frac{T_{i-1}}{T_i}\right) \]  

(B.23)

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

\[ \bar{\text{Var}}(\hat{S}_i) = \hat{\phi}_i^2 \text{Var} \left( \frac{T_{i-1}}{T_i} \right) + \left( \frac{T_{i-1}}{T_i} \right)^2 \text{Var}(\hat{\phi}_i) - \text{Var} \left( \frac{T_{i-1}}{T_i} \right) \text{Var}(\hat{\phi}_i) \]  

(B.24)

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

\[ \bar{\text{Var}} \left( \frac{T_{i-1}}{T_i} \right) \approx \left( \frac{T_{i-1}}{T_i} \right) \left[ \text{Var}(\hat{T}_i) \frac{\hat{T}_i^2}{T_i^2} + \text{Var}(\hat{T}_{i-1}) \frac{\hat{T}_{i-1}^2}{T_{i-1}^2} - 2 \frac{\text{Cov}(\hat{T}_i, \hat{T}_{i-1})}{T_{i-1}T_i} \right]. \]  

(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

\[ \bar{\text{Var}}(\hat{T}_i) = (1 - \hat{p}_i) \left( s^2_{\hat{T}_i} - s^2_{\hat{T}_i|\vec{d}} \right) + s^2_{\hat{T}_i|\vec{d}}, \]  

(B.26)

where

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

\[ s^2_{\hat{T}_i|\vec{d}} = \text{empirical bootstrap variance for } \hat{T}_i \text{ when sampling with replacement from the tag-life data holding the travel times constant for what was observed.} \]
The quantity \( s_{T_i}^2 - s_{T_i|d}^2 \) is estimating 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 \( T_i \).

When estimating two or more tag-life probabilities, their covariance is estimated by the quantity

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

where

\[
\widehat{\text{cov}}(\hat{T}_i, \hat{T}_j) = \text{empirical bootstrap covariance between } \hat{T}_i \text{ and } \hat{T}_j \text{ bootstrapping over both the tag-life and travel-time data},
\]

\[
\widehat{\text{cov}}(\hat{T}_i, \hat{T}_j|\vec{d}) = \text{empirical bootstrap covariance between } \hat{T}_i \text{ and } \hat{T}_j \text{ bootstrapping over only the tag-life data, holding the travel times constant for what was observed},
\]

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 to 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

\[
\hat{S}_{\text{Paired}} = \frac{\hat{S}_{11}}{\hat{S}_{21}} \tag{B.28}
\]

with an associated variance estimate \( \text{Goodman, 1960} \)

\[
\hat{\text{Var}}(\hat{S}_{\text{Paired}}) \approx \frac{\hat{S}_{\text{Paired}}}{\hat{S}_{11}^2} \text{Var}(\hat{S}_{11}) + \frac{\hat{S}_{\text{Paired}}}{\hat{S}_{21}^2} \text{Var}(\hat{S}_{21}) - \frac{\hat{S}_{\text{Paired}}^2}{\hat{S}_{11}^2 \hat{S}_{21}^2} \text{Var}(\hat{S}_{11}) \text{Var}(\hat{S}_{21}) \tag{B.29}
\]

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
Figure B.1: Schematic of a paired release-recapture design
releases be linked (i.e., equated), subsequent estimates of \( \hat{S}_{11} \) and \( \hat{S}_{21} \) will be no longer independent. In this case, the variance of survival (Equation B.28) will be estimated using the delta method (Seber, 1982, pp. 7-9), where

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

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

\[
\hat{S}_{\text{Paired}} = \left( \frac{\hat{\phi}_{11}}{\hat{\phi}_{21}} \right) \left( \frac{\hat{T}_{21}}{\hat{T}_{11}} \right), \quad (B.31)
\]

where \( \hat{\phi}_{ij} \)'s are the “perceived” survival estimates from a traditional CJS model ignoring tag-life probabilities and \( \hat{T}_{ij} \)'s, the estimated probabilities of tag life. In this case, the variance of \( \hat{S} \) is estimated by applying the Goodman (1960) approach, i.e.,

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

The variance of \( \hat{\phi}_{11}/\hat{\phi}_{21} \) is computed analogous to Equation B.29 and the variance of \( \hat{T}_{21}/\hat{T}_{11} \) analogous to Equation B.25.

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 BiOp 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 which case, dam passage survival is estimated by the function

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

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

$$\text{Var}(\hat{S}_{\text{Dam}}) = \left( \frac{1}{S_2^2} + \frac{\text{Var}(\hat{S}_2)}{S_2^4} \right) \left[ S_2^2 \text{Var}(\hat{S}_3) + S_3^2 \text{Var}(\hat{S}_1) + \text{Var}(\hat{S}_1)\text{Var}(\hat{S}_3) \right]$$

$$+ \left( \frac{S_1 S_3}{S_2^2} \right)^2 \text{Var}(\hat{S}_2)$$

(B.34)

and estimated by the quantity

$$\text{Var}(\hat{S}_{\text{Dam}}) = \left( \frac{1}{S_2^2} - \frac{\text{Var}(\hat{S}_2)}{S_2^4} \right) \left[ S_1^2 \text{Var}(\hat{S}_3) + S_3^2 \text{Var}(\hat{S}_1) - \text{Var}(\hat{S}_1)\text{Var}(\hat{S}_3) \right]$$

$$+ \left( \frac{S_1 S_3}{S_2^2} \right)^2 \text{Var}(\hat{S}_2).$$

(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

$$\text{Var}(\hat{S}_{\text{Dam}}) = \left( \frac{\hat{S}_1 \hat{S}_3}{\hat{S}_2} \right)^2 \left[ \frac{\text{Var}(\hat{S}_1)}{S_1^2} + \frac{\text{Var}(\hat{S}_2)}{S_2^2} + \frac{\text{Var}(\hat{S}_3)}{S_3^2} \right]$$

$$+ \frac{2\text{Covar}(\hat{S}_1 \hat{S}_3)}{S_1 S_3} - \frac{2\text{Covar}(\hat{S}_1 \hat{S}_2)}{S_1 S_2} - \frac{2\text{Covar}(\hat{S}_2 \hat{S}_3)}{S_2 S_3}.$$  

(B.36)

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

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

$$\hat{S}_{\text{Dam}} = \left( \frac{\hat{\phi}_1}{T_1} \right) \left( \frac{\hat{\phi}_3}{T_3} \right) = \left( \hat{\phi}_1 \hat{\phi}_3 \right) \left( \frac{T_2}{T_1 T_3} \right).$$

(B.37)
In this situation, the variance of $\hat{S}_{\text{Dam}}$ is based on separate variance calculations $\hat{\phi}_1 \hat{\phi}_3/\hat{\phi}_2$ and $\hat{T}_1 \hat{T}_3/\hat{T}_2$ analogous 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 to an acoustic array. These fish may be composed of individuals from multiple release groups upstream. As such, they may have had different times inriver 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

$$
\prod_{i=1}^{G} L(\bar{S}, \bar{r}, \lambda | \bar{R}, \bar{m}, \bar{r}, \bar{z}, \bar{T}),
$$

(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

$$
\hat{S}_1 = \frac{\sum_{i=1}^{G} \frac{\hat{S}_{1i} R_{1i}}{T_{1i}}}{\sum_{i=1}^{G} R_{1i} \frac{\hat{S}_{1i}}{T_{1i}}},
$$

(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 ($i = 1, \ldots, G$),
- $R_{1i}$ = number of fish in the virtual release from the $i$th source ($i = 1, \ldots, G$),
- $T_i$ = tag-life probability for fish from the $i$th source ($i = 1, \ldots, G$),
- $R_1 = \sum_{i=1}^{G} R_{1i}$,
- $W_i = \frac{R_{1i}}{R_1}$.
The variance of $\hat{S}_1$ (Equation B.39) is based on the delta method (Seber 1982), assuming the $R_{1i}$’s are 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 tag times between tag activation and fish release. Typically, these 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.
Glossary

**bin** A subcategory within a [release](#) allowing a unique tag-life correction to be estimated for each bin within a release. This may be necessary when some tags within a release have been active longer than others prior to release. Thus, fish within a release may share common survival and detection probabilities but different [tag corrections](#) [12, 17, 54].

**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. [3, 5, 13, 17, 22, 30, 42].

**release** A group of tagged individuals released at the same location, grouped under a common name in the capture history data file. [5, 8, 9, 12, 14, 17, 19, 22, 24, 29, 30, 34, 36, 38, 41, 47, 53, 73].

**release group** One or more releases grouped together that fill a certain role in a given study design. [5, 18, 29, 30, 34, 41, 42, 47, 48, 73].

**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. [30, 34, 41].

**tag correction** The probability that a tag will be alive for a given release at a given detection site. [5, 6, 10, 12, 17, 25, 30, 34, 41, 47, 48, 73].

**virtual release group** A release group defined by all detections at a virtual site. [36, 47, 73].

**virtual release group** A release group defined by all tagged individuals, possibly from multiple releases, detected at a given site (the virtual site). These individuals then make up a release group for all subsequent downstream detections. [17].

**virtual site** A detection site used to define a virtual release group. [47, 73].
Acronyms

**AIC**  Akaike Information Criterion. [58]

**CDF**  cumulative distribution function. [57, 58]


**LRT**  Likelihood Ratio Test. [19, 38]

**MLE**  Maximum Likelihood Estimate. [17, 24]

**PDF**  probability density function. [58, 59, 61]
Literature Cited


