cbrATLAS

Program Atlas (http://www.cbr.washington.edu/analysis/apps/atlas) is a desktop application that provides the ability to analyze mark-recapture data from active-tag technology, and to adjust the observed survival estimates for potential tag-failure that may be misidentified as a mortality of the marked animal. The cbrATLAS R package was created to allow this analysis to be conducted in R. In addition, cbrATLAS incorporates an update of the original program to include the R package **failCompare**, increasing the number of model fitting options of tag-life data to predict tag survival of the active tags used in the study. The failCompare package also provides goodness-of-fit tests and rankings of the various models to assist in selection of the most appropriate model of tag-life, along with plotting the expected tag-life curve against observed tag failures.

cbrATLAS is currently capable of analyzing detection histories from the Single Release study design (with and without censoring events) that may or may not require correction for active-tag failure. Future iterations are planned to incorporate Paired Release, Virtual-Paired Release (ViPRe), and the Virtual Release Dead Fish Correction (ViRDCt) study designs.

Downloading and installing the **cbrATLAS** package

To download the package, navigate to the Columbia Basin Research website and click on the hyperlink for the latest version at: http://www.cbr.washington.edu/analysis/apps/atlas. You will not need to unzip the compressed folder after you have saved it to your computer.
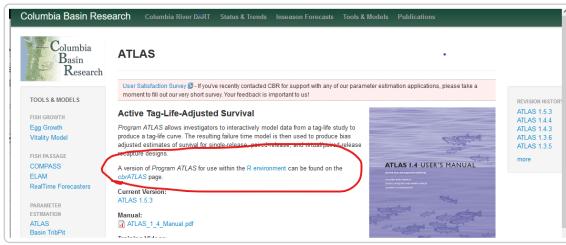
ATLAS webpage with link to current cbrATLAS version

We assume that the user has previously installed program R and is familiar with basic operations (e.g., importing data, basic plotting). Program R can be downloaded freely at: https://cran.r-project.org. There are many freely accessible instruction books and online resources that explain the use of R. The user might also want to consider installing RStudio (https://www.rstudio.com), a free program that serves as a wrapper for the basic R graphic user interface with a built-in text editor.

To install from the base R graphical interface, select the option *install package(s) from local files…* from the **Packages** dropdown menu, and then navigate to the location of the compressed folder. Alternatively, to install cbrATLAS from within RStudio, select the **Packages** tab and click the *Install* button. From there, choose the ***Package Archive File (.zip; tar.gz)*** and then navigate to the location of the compressed folder, select it, and click *Install*.

Once the package is installed, it must be loaded into the working environment before it can be used. This installation needs to be performed only once, but the package must be loaded during every R session using the library() command:

```r
library(cbrATLAS)
```

Load in the Single Release ATLAS Practice File. This can be a dataframe or the file name of a csv file.

```
data(single.rel)

AdjSurv.fn(taghist.file=single.rel) # cjs unadjusted for taglife
#> $taghist
#> [1] "single.rel"
#>
#> $unadjusted.cjs
#> $unadjusted.cjs$cjs.param
#>    Estimate         s.e.
#> S1 0.9699491 0.0034374195
#> S2 0.9587843 0.0040560618
#> S3 0.8912260 0.0064617259
#> p1 0.9909639 0.0019628004
#> p2 1.0000000 0.0003107385
#> p3 0.9974849 0.0011224813
#> l  0.9598258 0.0043201987
#>
#> $unadjusted.cjs$d
#> d1 d2 d3
#>  0  0  0
```

The output from this run is a list object with the name of the detection history file and the unadjusted Cormack-Jolly-Seber survival estimates and standard errors.

To apply a taglife correction, add results from a tag-life study. This can be a data.frame object or the file name of a csv file. If a particular model is not pre-selected to fit the taglife data, failCompare will try a suite of models, print a ranking based on model fit, and automatically use the best fitting model to apply the corrections due to estimated tag-life.

```
data(taglife.data) # Taglife ATLAS Practice File

tmp=AdjSurv.fn(taglife.file=taglife.data,taghist.file=single.rel,plot.taglife=F) # cjs adjusted
        for taglife
#> Candidate models ranked by goodness of fit measure:
#>
#>        model     SSE_KM   n npars denom     GOF
#> 1   gengamma 0.03521232 100     3    96  0.0004
#> 2     llogis 0.06538324 100     2    97  0.0007
#> 3   weibull3 0.08057453 100     3    96  0.0008
#> 4  lognormal 0.12362540 100     2    97  0.0013
#> 5      gamma 0.13573240 100     2    97  0.0014
#> 6    weibull 0.51697193 100     2    97  0.0053
#> 7   gompertz 0.61043491 100     2    97  0.0063

tmp[-c(1:2)] # additional analysis performed
#> $tagfile
#> [1] "taglife.data"
#>
#> $taglife.model
#> gengamma failure model object
```

```
#>
#> Parameter estimates:
#>          est          se
#> 1  3.13274617 0.006644931
#> 2  0.04175106 0.003273907
#> 3 -0.49640971 0.241116929
#>
#> $mean.tag.pLive
#> $mean.tag.pLive$L
#>     Site.1    Site.2    Site.3    Site.4
#> 1.0000000 1.0000000 0.9999977 0.9999931
#>
#> $mean.tag.pLive$L.se
#>       Site.1       Site.2       Site.3       Site.4
#> 2.428403e-16 3.925147e-18 1.102550e-07 1.361938e-06
#>
#>
#> $adjusted.cjs
#> $adjusted.cjs$cjs.param
#>     Estimate          s.e.
#> S1 0.9699491 0.0034374195
#> S2 0.9587843 0.0040560618
#> S3 0.8912281 0.0064617406
#> p1 0.9909639 0.0019628007
#> p2 1.0000000 0.0003107385
#> p3 0.9974849 0.0011224813
#> l  0.9598323 0.0043202188
```

In addition to the unadjusted Cormack-Jolly-Seber estimates, the additional output includes the model fit results printed to the screen, the selected model for tag survival, the average probability and associated standard error that a tag was active upon arrival at each detection site in the study, and the adjusted CJS estimates based on those probabilities.

If a particular tag-life model is desired, an fc_obj object must be created first using the failCompare package. This object is then provided to AdjSurv.fn and applied to the given detection history.

```
TL_weib2=failCompare::fc_fit(time=taglife.data$tag_life_days,model="weibull")
#'\dontrun{
#'AdjSurv.fn(taglife.file=taglife.data,taghist.file=single.rel,taglife.model=TL_weib2,plot.taglife=F)
#'}
```

The mark-recapture method for the unadjusted Cormack-Jolly-Seber model is based on Skalski, J. R., S. G. Smith, R. N. Iwamoto, J. G. Williams, and A. Hoffmann. 1998. Use of passive integrated transponder tags to estimate survival of migrating juvenile salmonids in the Snake and Columbia Rivers. Canadian Journal of Fisheries and Aquatic Sciences 55:1484-1493.

The adjustment to those estimates is based on Townsend, R. L., J. R. Skalski, P. Dillingham, and T. W. Steig. 2006. Correcting bias in survival estimation resulting from tag failure in acoustic and radiotelemetry studies. Journal of Agricultural, Biological, and Environmental Statistics 11:183-196.