# ShinyWhale

Bayesian multi-state mark-recapture-recovery model

## Overview

This app is designed to provide simplified tool for estimating abundance and demographic information using a Bayesian multi-state mark-recapture-recovery framework. This app was originally designed for North Atlantic right whales, with the aim to provide managers, NGOs, government organisations and conservationists a tool to assess the changes in the population trends, without the need to understand the complete workings of Bayesian mark-recapture techniques, or strong programming skills. The app was designed to be used with data provided by the North Atlantic Right Whale Consortium, and uses their data structure to conduct the model. The columns required for this app are as below, with one row for each unique sighting. Ensure that the column headings match:

| SightingEGNo | SightingYear | SightingMonth | SightingDay | Behaviors |
| --- | --- | --- | --- | --- |
| Unique identifier for each individual | year(YYYY) | month (MM) | day of the year | list of behaviors for each sighting in CAPITALS, separated by commas. Also contains information on the fate of individuals, if they were found DEAD |

**Before you start you must download** [**JAGS (Just Another Gibbs Sampler)**](https://sourceforge.net/projects/mcmc-jags/files/JAGS/4.x/)**.**

#### Setup

ShinyWhale relies on the following packages:

* data prep: unix, dplyr, reshape2, MASS, stringr
* Shiny: shiny, shinybusy
* Model: R2jags
* Outputs: MCMCvis, ggplot2

## Data

The user supplied data needs to be converted into an observation matrix that can be used in the Open-population Jolly-Seber framework.

#### Capture histories

Observations of individuals (i) in a given year (t) are compressed into a single value:

1. seen alive
2. recovered dead, or
3. neither seen nor recovered

The culmination of observations for each individual during the sampling periods for the study forms the capture history. Each year of the capture history represents a year for the study population, which we set as the first month of the reproductive period, which can be set by the user in the *Capture Histories* tab of the app. The capture history is then combined with an additional period at the beginning of the study period where all individuals are assigned a **3** (neither seen nor recovered) which results in the observation matrix.

#### Data augmentation

The data set can also be adjusted to include data augmentation. This is the inclusion of additional individuals into the observation matrix, who are in state 3 (neither seen nor recovered). This is to account for individuals who could exist in the population over the study period, though have never been sighted. Individuals added in data augmentation are not all going to enter the population, but can provide more realistic estimates for abundance if it is believed that not every individual has been sighted. More information on data augmentation can be found here: (Royle, Dorazio, and Link 2007; Royle 2008; Royle and Dorazio 2010).

## Model

The model used in ShinyWhale is a Bayesian multi-event Jolly-Seber framework (Thomson, Cooch, and Conroy 2009; Schaub and Royle 2013) fit with a mark-recapture-recovery model (Barker 1999; Liljestrand, Wilberg, and Schueller 2019). In the model, we considered five true biological states:

1. not yet entered the population (NE)
2. alive within the study area (AI)
3. alive outside the study area (AO)
4. recovered dead (RD) and
5. dead (D)

The focal temporal parameters that are estimated in this model are:

* true survival (*s*)
* recapture (*p*)
* site fidelity (*F*)
* dead recovery (*r*) and
* abundance (*N*)

The state of all individuals *i* in the first occasion (*zi,1*) was set so that they were considered to not have entered the population (*NE*):

The state of individual *i* from the second occasion (*zi,2*) until they enter the population is:

where is the probability that an individual who has not already entered the population, enters. While the subsequent states are dependent on that state of the previous time period, thus the state model is denoted as:

where zi,t denotes the state of individual *i* at time *t*, and denotes state membership over time, where *s* is the number of true states.

The observation model is denoted as:

where yi,t denotes the observation of individual *i* at time *t*, and  denotes the observational process, linking the true states zi,t to the observed states yi,t, where *o* is the number of observed states.

The number of individuals entering the population at time *t* (Bt) can be calculated as:

while the total population size at time *t* is:

Therefore, the full conditional probability of the model can be expressed as:

## References

Barker, Richard J. 1999. “Joint Analysis of Markrecapture, Resighting and Ring-Recovery Data with Age-Dependence and Marking-Effect.” *Bird Study* 46 (sup1): S82–91. <https://doi.org/10.1080/00063659909477235>.

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