# NARWPop

Estimate abundance and demographic parameters for North Atlantic right whales.

### Overview

This app is designed to provide simplified tool for estimating abundance and demographic information for North Atlantic right whales. With the use of this app, we aim to provide managers, NGOs, government organisations and conservationists a tool to assess the changes in the NARW population, without the need to understand the complete workings of Bayesian mark-recapture techniques, or strong programming skills. This app is designed to use 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, please ensure that the column headings match:

| SightingEGNo | SightingYear | SightingMonth | SightingDay | Behaviors |
| --- | --- | --- | --- | --- |
| Unique identifier for each individual whale | year(YYYY) | month (MM) | day of the year | list of behaviors for each sighting in capitals, separated by commas |

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

##Setup NARWPop 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 whale during the sampling periods for the study forms the capture history. 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:

### Model

The model used in NARWPop is a Bayesian multi-event Jolly-Seber framework (Thomson, Cooch, and Conroy 2009; Schaub and Royle 2013) fit with a mark-recapture-recovery model [Liljestrand, Wilberg, and Schueller (2019)]{Lebreton, 2001 #162}. 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:

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:

Liljestrand, Emily M., Michael J. Wilberg, and Amy M. Schueller. 2019. “Multi-State Dead Recovery Mark-Recovery Model Performance for Estimating Movement and Mortality Rates.” *Fisheries Research* 210 (February): 214–23. <https://doi.org/10.1016/j.fishres.2018.10.014>.

Schaub, Michael, and J. Andrew Royle. 2013. “Estimating True Instead of Apparent Survival Using Spatial Cormack-Jolly-Seber Models.” Edited by Richard Barker. *Methods in Ecology and Evolution* 5 (12): 1316–26. <https://doi.org/10.1111/2041-210x.12134>.

Thomson, David L, Evan G. Cooch, and Michael J. Conroy, eds. 2009. *Modeling Demographic Processes in Marked Populations*. Springer US. <https://doi.org/10.1007/978-0-387-78151-8>.