

Introduction to Program MARK

Objectives: The main program now used for mark-recapture analyses is Program MARK. This program is powerful because it offers a wide range of potential statistical models that can be used to analyse mark-recapture data. It offers some potential for bootstrapping and does the calculations for a number of complex analyses that would be difficult to implement otherwise. The goal of this exercise is to familiarize you with the procedures for installing MARK on your computer and to have a look at some of the capabilities of this software.

Installing Program MARK

Pull up your favorite web browser and go to the following site: www.phidot.org

Click on the link at the bottom to `Software`.

This page offers capsule summaries of many of the software programs out there for mark-recapture analyses. The links give you locations to download the software. Find Program Mark and click on `Local Mark Page`.

On this menu, first look at `Discussion` and `Documentation` to view the listserver dedicated to topics re: Mark and to find the user manual for this program. Then click on `Download Mark` to download the installation file for the software. Put it in 'my downloads' or 'window\temp' and then run the executable file to install the software.

Running Program MARK

Click on `File | New` to view the range of possible models that can be fit. 'Recaptures only' at the top is the one we will likely use the most in the class. Input formats of the capture histories vary among these different models.

Recaptures only use LLLLL where each year has one entry for a live recapture or resighting.

Both (Burnham) combines live resightings and dead recoveries and uses LDLDLDLDL where each year has two entries for live recapture or dead recovery.

Look at the right-hand side to see the information in the input file that must be recorded. This includes 'number of occasions' (e.g., no. of years of data), 'attribute groups' (e.g., no. of sexes or sites or any other group variable), 'individual covariates' (if you wanted to model survival vs. a continuous variable like body size) and 'strata' (for multistate models where you would code the capture histories with state information like 0, B for breeding or N for nonbreeding instead of ust 0 and 1).

Table of Model Results

Exit out of this and click on `File | Open` and go to the `mark\examples` directory. Open `dipper.dbf`. This gives the analysis for the European Dipper that appears in the Lebreton et al. monograph in the reader. Mark gives a Results table with 17 models. The table contains values for some of the metrics used to describe mark-recapture models.

On the left is the model name. $\Phi_{(.)}$ = local survival and p = the resighting rate. The notation in the brackets is some abbreviation for the effect on ϕ or p . g = group which here is sex (females and males), t = time which here is annual variation, '.' or dot = constant (hence 'www.phidot.org'). 'Flood' = modeling effect of floods as an annual covariate. Symbols between the effects indicate the model

structure: $g*t$ = factorial (effects of g t and interaction), $g+t$ = additive (just g and t , no interaction), g = just group effect of sex, t = just effect of time, $.$ = no effect of g or t .

On the right side of the table are the metrics describing the fit of the model, the deviance and the number of parameters. These are combined to calculate the AIC-value. Mark uses a more complex formula than just $AIC = DEV + 2np$ but it is basically the same idea. AIC is a relative measure and cannot be compared among completely separate analyses. Instead, within a set of candidate models, the difference from the 'best-fit model' is used. The model with the lowest AIC value is the best model. The delta-AICc value is the difference in AIC value between that model and the other models that were tested.

Specific model output

Move the cursor so that $\Phi_i(g*t)$, $p(g*t)$ at the bottom of the list is highlighted. This is effectively the CJS model with time-dependence in both rates and the sexes treated separately. This is the starting model and as it is on the bottom of the list, it is a bad model not supported by the data.

In the upper left hand corner of the screen is a garbage can. Don't click on that! Click on the button immediately to the right. This gives you all of the output statistics for this one model. Scroll down and you will see the triangular Parameter Index Matrices (or PIMS) .

Go to the very bottom and view the real function parameters. These are the annual estimates of ϕ and p for males and females. Go back to the PIMS to sort out which are which.

Note that there are 24 parameters listed under the real function parameters but only 22 in the number of parameters in the window listing all of the models. This reflects that there are two beta-terms in this model, can you figure out which ones they are?

Go back and 'retrieve current model'. Click on PIM at the top of the bar, and then 'Open Parameter Index Matrix'. 'Select All' and then 'OK'. Here are all of the PIMs for this model. You could modify these to run a different model of your choice. Close these.

Click on some of the other buttons on the bar above the table of results and spend some time trying to sort what these other features are.