

Mark-recapture data for tigers

Lab guide

This “lab guide” accompanies the web page on the WCS Malaysia Program site at http://www.wcsmalaysia.org/analysis/Mark-recap_tigers.htm.

You will need to read the web page for explanation of the reasons behind the steps and the interpretation of the results. The lettered blocks (A, B, C, etc) are referred to in the web page.

A. Setting up the project and entering data in MARK

Start MARK and select ‘File > New’ from the pull-down menus. In the “Enter Specifications for MARK Analysis” window, under “Select Data Type”, click on “Closed Captures”. A new “Model Selection...” window appears.

Highlight Closed captures and click on OK. In the ‘Enter Specifications...’ window, type a title for the set of data (eg ‘Kanha tigers’). Then click on ‘Click to select file’, browse to ‘Kanha_tiger.inp’ and click ‘Open’.

Change ‘Encounter occasions’ to 10, and leave ‘Attribute groups’ as 1. Click OK.

B. Running a first analysis in MARK

When you’ve entered all the specifications, a PIM (Parameter Index Matrix) window opens. There are three of these; open all three: select ‘PIM > Open Parameter Index Matrix’. In the box that appears click ‘Select All’ then ‘OK’. Drag the three windows so that you can see the main items in all three.

The M0 model:

Change all the values in the Capture Probabilities PIM to “1”. You could type them in one by one, but a quicker way is to use ‘Initial > Constant’ from the drop-down menus.


Change the values for Recapture Probability to “1” also, with ‘Initial > Make c=p’.

Change the value for Population Size to “2”. (Not essential: if you leave it as “20”, MARK will change it for you.)

Select ‘Run > Current Model’ from the drop-down menus.

In the ‘Setup Numerical Estimation Run’ window, give the model the name “M0”, leave all the other default values as they are and click ‘OK to Run’.

Click ‘Yes’ when MARK asks if it should use an identity design matrix, and ‘Yes’ again when it asks if it should add the output to the database.

The Results Browser appears, but with only one model to “browse”. Display the detailed output in Notepad by clicking on the second button  on the toolbar or using Output > Specific Model Output > Numerical Output > Output in Editor.

C. Comparing models

Mb : Increase the value in the Recapture Probability window to “2”, and in the Population Size window to “3”. Run the analysis as before, naming the model ‘Mb’.

Mt : Click in the Capture Probability window and select ‘Initial > Time’ from the pull-down menu, then ‘Initial > Make c=p’. Change the parameter index for Population Size to 11 (or any number above 10). Run the model as before, naming it ‘Mt’.

D. Modeling heterogeneity

Mh : We initially selected the plain vanilla option ‘Closed Captures’ as our data type. Now we need to change the data type by going to ‘PIM > Change Data Type’ and selecting ‘Closed Captures with Heterogeneity’. Leave the Number of Mixtures as “2”.

Open all three PIMs to see what parameters are being estimated, but leave the default values.

Run the model with the default values, naming it “Mh”.

E. The default model, Mbt

Change the data type again by going to ‘PIM > Change Data Type’ and selecting ‘Closed Population Estimation’.

Open all three PIMs. The default values should have reappeared, with parameters #1 - #10 for Capture Probability, #11 - #19 for Recapture Probability, and #20 for Population Size.

Run the model with these default values, naming it “Mbt”.

F. Comparison with CAPTURE

Model selection in CAPTURE:

Select ‘Tests > Program CAPTURE’ from the pull-down menus. In the ‘Program CAPTURE Models’ box, check ‘Appropriate’ to ask CAPTURE to look for the most appropriate model. Click on OK.

Individual heterogeneity:

Select ‘Test > Program CAPTURE’ from the pull-down menus again, but this time check ‘Jackknife – M(h)’. Click on OK.

G. Getting finished

MARK automatically saves all the results of analyses when you run them in files with the .dbf and .fpt extensions. You do not need to save results manually. (If you copy these files to a new location, be sure to copy *both* of them.)

To exit MARK, select ‘File > Exit’ or press Alt-F4 or click on the  button at the top right of the window.

To re-open the project, use ‘File > Open’ and select the appropriate .dbf file. If you do this when a project is already open, MARK will automatically close it. You cannot have two projects open at the same time.