

Lab 3: Fitting Models with Parameter Index Matrices in Program MARK

Objectives: The purpose of this exercise is to introduce you to using Parameter Index Matrices for fitting models to mark-recapture data in Program MARK. A useful approach to learning any new statistical technique is to work through a published example. In this case, we will use the survival analysis for Snowy Plovers published by Paton 1994 that is included in your course reader. A nice feature of this paper is that the capture histories can be found in Table 1. Our results may differ because Program MARK reports AICc whereas Paton used AIC values.

Downloading snowy.inp

I have typed the capture histories for adult Snowy Plovers into a file named snowy.inp that can be retrieved from the course website: www.ksu.edu/bsanderc/biol823. Go to this site, right-click on the file and save it to your hard drive (in the example directory of Program MARK is a good place). Pull it up in Wordpad or a text editor and it should look the following:

```
1000 9 18;  
1001 2 1;  
1010 1 8;  
1011 0 4;  
1100 6 12;  
1101 3 2;  
1110 6 2;  
1111 4 4;  
0100 37 48;  
0101 4 7;  
0110 15 11;  
0111 12 8;  
0010 31 44;  
0011 32 30;
```

The first column is the capture histories, the second the totals of adult males and the third the totals of adults females. Each line has a semicolon at the end.

Importing the file into Program MARK

Startup Program MARK and click on File | New to create a new Mark database. Click to select file and find snowy.inp wherever you saved it on your hard drive. Click View File and the file should open in a Notepad view window. Close that and go back to the opening menu.

The first steps are to tell MARK what kind of file this is. Click the button for 'Recaptures only'. Add a title for the analyses: 'Snowy Plovers are my friends'. How many encounter occasions? Go back and view the file if you can't remember. Attribute groups is 2 for each sex. Click on Group labels to describe these. The format is left to right across the input file so the first group is males, the second is females. When you have done all this, click OK to proceed and MARK will advise you it has created a database file to hold your analyses for snowy.inp.

Running models in Program MARK

Now we are ready to start running models in Program MARK. Click on PIM | Open PIM. Select all and then click OK. If Mark gives you a bizarre error message and crashes, start the program again and try opening the PIMs one at a time. Once all of the PIMs are open, click Window | Tile to view all windows at the same time. Each window corresponds to a combination of ϕ and p for males and females. What would the subscripts look like for the current model?

$\phi(\quad), p(\quad)$

Click Run | Current Model to implement this model. This will give you a menu where you can specify some choices in model building. In the lower left corner is the link function. For today, we will use the default sin link for all. Give this model a title, preferably whatever you have entered for subscripts above. Click OK to run.

MARK will then ask you 'Use identity design as none was specified?' Respond yes to this rather personal question and proceed. The next thing that will happen is that window with a black background will pop up. You will see this window when MARK is iteratively stuffing values in the log-likelihood equation for your selected model - it is trying to get the best possible values for the parameter estimates that minimize the deviance value for the equation (i.e, -2 times the log-likelihood). If the model is small and simple it will converge fast and another window will pop up asking you whether you want to append the model results to the Results window. Click OK to proceed. You have just run your first model in MARK. The delta-AICc value is zero because this is the best-fit model for all of the models you have tested so far - that is, just the one.

Let's explore this model a bit. Click on the symbol to the right of the garbage can on the bar above the Results Window : 'View output from highlighted model'. Look at the model structure at the top of the file. How many inestimable beta-terms are in this particular model? Inspect the estimates of the real parameters at the bottom. Does it look like the sexes differ in ϕ or p ?

Now you are ready to run another model. Pull up the PIMs so that you can see all four at once. Let's run a model with time-dependence but no effect of sex in recapture rates: $\phi(\text{sex}*t)$, $p(t)$. What should the PIMs for this model look like? When you are sure you have the answer, go in and edit the PIMs and then click Run | Current model. Give this model a different name, again use the sin link, say ok to the identity question and ok to append to the output window. Is this model a better or worse fit than the starting model? Recall that models with $\text{delta-AICc} \leq 2$ can be considered equally parsimonious.

Let's try something different. Highlight the starting model and click Retrieve | Current Model. click Window | Tile to view all PIMs at once. Let's run a model with sex-dependence but no effect of time in recapture rates: $\phi(\text{sex}*t)$, $p(\text{sex})$. What should the PIMS look like for this? Go to the window for male recapture and put the cursor in the box for parameter 7. Click Initial | Constant. Go to the window for female recapture and put the cursor in the box for parameter 10. Again, click Initial | Constant. Then click Renumber | No overlap. Does this look like what you want? If so, click Run | Current model and go through the same steps as above.

Go through the same steps to calculate the metrics for model $\phi(\text{sex}^*t), p(c)$. We have just calculated all of the possible permutations for p for one possible model of ϕ . Transfer the AICc values from the Results window to fill out the first line of the table below. Don't fill in the ΔAICc values for the moment. Continue to modify the PIMs and calculate the additional models needed to complete the table below.

	Model for p			
Model for ϕ	sex^*t	t	sex	c
sex^*t	ΔAICc AICc	ΔAICc AICc	ΔAICc AICc	ΔAICc AICc
t	ΔAICc AICc	ΔAICc AICc	ΔAICc AICc	ΔAICc AICc
sex	ΔAICc AICc	ΔAICc AICc	ΔAICc AICc	ΔAICc AICc
c	ΔAICc AICc	ΔAICc AICc	ΔAICc AICc	ΔAICc AICc

Your selection of the best fit model from the set of candidate models above would likely be based on the delta-AICc values. However, Program MARK will also do the calculations for the Likelihood Ratio Tests. Once you have a few models in the results window, Click on the blue button that looks like a calculator. This will generate a table with LRT for all pairs of models in the results window. Some of the pairs of models are not nested and the test is then meaningless - the ones with zero degrees of freedom most obviously. You would have to go through the table and take the subset of tests for only pairs of models that are nested:

Of the models we have tested so far...

$\phi(\text{sex}^*t), p(\text{sex}^*t)$	vs.	$\phi(\text{sex}^*t), p(\text{sex})$	is nested
$\phi(\text{sex}^*t), p(\text{sex}^*t)$	vs.	$\phi(\text{sex}^*t), p(t)$	is nested
$\phi(\text{sex}^*t), p(\text{sex}^*t)$	vs.	$\phi(\text{sex}^*t), p(c)$	is nested
$\phi(\text{sex}^*t), p(\text{sex})$	vs.	$\phi(\text{sex}^*t), p(t)$	is <i>not</i> nested