Lab 6: Parameter Estimation in Program Mark

Objectives: The purpose of this exercise is to introduce you to some of the advanced methods for parameter estimation in Program Mark. These tools allow you to obtain the best possible estimates of selected rates for annual and overall rates. In this example, we will continue to use the survival analysis for Snowy Plovers published by Paton 1994.

Model Averaging

Model averaging is used to obtain annual estimates of the mean and SE of ϕ and p. This procedure is most appropriate when it turns out that a group of candidate models are equally parsimonious (ΔAICc $\leq$ 2) and have similar Akaike weights (e.g., $w_i \approx 0.3$ for three models).

The models in the Results window likely differ among different groups from previous weeks. Complete the following steps to ensure that everyone has the same set of models for this procedure. Select any of the current models and click on the Garbage Can icon to delete. Repeat until all models are discarded. Then click on Run | Predefined Models, then click on Select Models. Check the box for Design Matrix Coding to get the additive models. For phi, click on (g*t) and for *p*, click Select All. The number of models to run should be 5. Click OK to run these five.

The three top models have a mixture of group and time-dependence in *p*. Two older approaches to parameter estimation would be to present: 1) the parameter estimates from Phi(g*t), p(g+t) only, or 2) the parameter estimates from the top three models. With model averaging, we can do a little better.

Click on Output | Model Averaging | Real. This will generate a chart that resembles the PIM charts. Note that every parameter has it's own unique number. Because we are basically using time structured models without age-dependence, picking a cell out of each column will give you the same basic results as if you selected cells from the diagonals. Go through and put check marks in the boxes of the first row for each PIM for the apparent survival rates for males (parameters: 1 to 3). Click OK to run this procedure.

This will generate a table for each of the selected parameters that looks like the following:

```
                               Snowy Plovers

             Apparent Survival Parameter (Phi) males Parameter 1
Model                                     Weight    Estimate       Standard Error
----------------------------------------  -------   --------------  --------------
{Phi(g*t) p(g+t) Design Matrix}           0.44434   0.8713238       0.1154332
{Phi(g*t) p(g) Design Matrix}             0.23558   0.8357763       0.1036145
{Phi(g*t) p(g*t) Design Matrix}           0.19091   0.8042525       0.1073404
{Phi(g*t) p(.) Design Matrix}             0.07123   0.8992386       0.1106450
{Phi(g*t) p(t) Design Matrix}             0.05794   0.9522875       0.1276891
----------------------------------------  -------   --------------  --------------
Weighted Average                                    0.8568249       0.1114731
Unconditional SE                                                    0.1170989
95% CI for Wgt. Ave. Est. (logit trans.) is 0.4795792 to 0.9749145
Percent of Variation Attributable to Model Variation is 9.38%
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Apparent Survival Parameter (Phi) males Parameter 2

Model	Weight	Estimate	Standard Error
{Phi(g*t) p(g+t) Design Matrix}	0.44434	0.5739794	0.0660587
{Phi(g*t) p(g) Design Matrix}	0.23558	0.5937459	0.0668082
{Phi(g*t) p(g*t) Design Matrix}	0.19091	0.6126806	0.0754839
{Phi(g*t) p(.) Design Matrix}	0.07123	0.6305773	0.0724162
{Phi(g*t) p(t) Design Matrix}	0.05794	0.5966712	0.0731534
Weighted Average		0.5913706	0.0688985
Unconditional SE			0.0711905

95% CI for Wgt. Ave. Est. (logit trans.) is 0.4482406 to 0.7205215
Percent of Variation Attributable to Model Variation is 6.34%

Apparent Survival Parameter (Phi) males Parameter 3

Model	Weight	Estimate	Standard Error
{Phi(g*t) p(g+t) Design Matrix}	0.44434	0.7643022	12.1925430
{Phi(g*t) p(g) Design Matrix}	0.23558	0.6876767	0.0866063
{Phi(g*t) p(g*t) Design Matrix}	0.19091	0.8271573	0.0000000
Invalid parameter estimate with zero SE?			
{Phi(g*t) p(.) Design Matrix}	0.07123	0.7872230	0.0961432
{Phi(g*t) p(t) Design Matrix}	0.05794	0.7123247	62.8781920
Weighted Average		0.7568712	9.0883624
Unconditional SE			9.1078278

95% CI for Wgt. Ave. Est. (logit trans.) is 0.0000000 to 1.0000000
Percent of Variation Attributable to Model Variation is 0.43%

Each table presents a model-averaged estimate for one parameter. Each row in the tables is one model in the set of candidate models, the Akaike weight of the model, followed by the estimate of the parameter generated by this particular model. At the bottom of the table is the weighted average and two estimates of the SE. The unconditional SE is larger because it includes the variance due to both the sampling error and model uncertainty. This is the SE you would want to report. In parameters 1 and 2, model uncertainty added an additional 9.4% and 6.3% to the variance. Parameter 3 is the apparent survival rate over the last interval of the study period. In models with time-dependence in both Phi and p, parameter 3 is part of an inestimable beta-term that is the product of phi and p for the last interval. In the table, you can see that the SE of parameter 3 are zero or > 12 for the three models with time-dependence in both parameters. This is an indication that model-averaging cannot give a reliable estimate of phi for this transition because the top models have time-dependence in both Phi and p.

The statistical underpinnings of model-averaging may seem dense but the procedures are relatively easy to implement and interpret with the assistance of Program Mark.

Variance Components

Sometimes an overall estimates of the mean and SE of ϕ and p is desired, possibly to parameterize a matrix population model. The variance components procedure can be used to obtain the best overall mean and a variance that includes only process variance and not sampling variance. Like the goodness-of-fit procedures, the variance components procedure is applied to the starting global model that is unconstrained and has time-dependence in all parameters.

Start by highlighting the global starting model Phi(g*t), *p*(g*t) for Snowy Plovers. A useful first step is to inspect the model output to remind yourself of what the model structure. You can view this by clicking the button to the right of the garbage can. Jot the PIMs down on a scrap of paper (Phi male: 1-3, Phi female 4-6, p male 7-9, p female 10-12). Like model averaging, you will want to discard the beta-terms among these parameters.

Now click Output | Specific model output | Variance components | Real parameter estimates.

Deselect Graphical output by taking the check mark out of the box.

Select parameters 1, 2, 4, and 5 by holding down the Ctrl button and clicking on these parameters. Look at the PIM structure of this model that you jotted down, does this make sense to you? What would you do if you wanted an overall estimate for *p*?

Click okay to run this procedure. The output should look something like the following:

```
Snowy Plovers

    Beta-hat SE(Beta-hat)
 ------------------------
    0.731293     0.113958

      S-hat     SE(S-hat)     S-tilde  SE(S-tilde) RMSE(S-tilde)
 -------------------------------------------------------------
    0.804253    0.107340    0.795456    0.098155     0.098548
    0.612681    0.075484    0.619995    0.071841     0.072213
    1.000000    0.000000    1.000000    0.000000     0.000000
    0.489043    0.068232    0.500134    0.065901     0.066827

 Naive estimate of sigma^2 = 0.0443744 with 95% CI (0.0103639 to 0.6903172)

 Estimate of sigma^2 = 0.0473807 with 95% CI (0.0136365 to 0.6931614)

 Estimate of sigma = 0.2176712 with 95% CI (0.1167754 to 0.8325631)

 Trace of G matrix = 3.8395798
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Beta-hat is the overall mean for the set of parameter estimates that you selected. SE(Beta-hat) is the standard error of this value and includes the effects of both process and sampling variance.

The next table is the four annual means in the set of parameter estimates that you selected to average across. The S-hat value in the first row should be the first parameter that you selected and so forth. I am unable to state in layman's terms what the differences among the other columns are but they are intermediate calculations used to obtain sigma-values.

sigma^2 is an estimate of the variance of the overall mean across years, and includes the effects of process variance only, the sampling variance has been removed. Similarly, sigma is an estimate of the standard deviation of the overall mean across years, and includes the effects of only process variance.

What percentage of the variance is due to process versus sampling variance? To do this calculation, you will need to put values in the same currency. SE(Beta-hat) is a standard error, whereas sigma is a standard deviation. Recall that: SE = SD / sqrt (*N*)

Convert sigma to a standard error by dividing it by the square root of the sample size (i.e., the number of S-hat observations in the table above). Hence, 0.218 divided by square root of 4 equals 0.109. Thus, the best overall estimate of apparent survival is 0.731 with a SE of 0.114 if total variance is used, or a SE of 0.109 if only process variance is used. The latter estimate is smaller and will lead to tighter confidence intervals for any parameter estimated for a matrix population model. In total, 100*(1-(0.109/0.114) = 4.4% of the standard error at the top of the output was due to sampling variance. Repeat these same steps to obtain an overall estimate of the mean and variance of the resighting rate *p*.