

Exercise 13: Direct Estimation of Lambda

This exercise closely follows the content of the 6th lecture and is mostly intended to show how to run program MARK to compute estimates of lambda 'known-fate' data.. We have prepared exercises for use in either MARK or RMark.



Data input

Input data consists of individual capture-histories.

The example we'll use for this model contains 2 groups of animals: Males and Females. So, each capture-history will have 2 frequencies following the encounter-history. Since the data are not summarized, one of the frequencies will be zero and one will be one. The following is a sample MARK input file (nwc_lamb.inp):

```
/*1177-06702 M A*/0000000000000111111110111 1 0;  
/*1177-06708 F A*/0000000000011111111111100 0 1;  
/*1177-06724 M A*/0000000000011111111111100 1 0;  
/*1177-06728 M A*/0000000000001111111110000 1 0;  
/*1177-06730 F S1*/0000000000001000000000000 0 1;  
/*1177-06731 F S1*/0000000000001110000000000 0 1;  
/*1177-06732 M S2*/0000000000000111111111111 1 0;  
/*1177-06737 M A*/0000000000001110000000000 1 0;  
/*1177-06740 F S1*/0000000000001000000000000 0 1;
```

Note: Comments can appear in the input file, surrounded by “/*” and “*/”.

For R users

- 1) Open the file “ex13_direct_est_lambda.r” in your preferred text editor for R. **You will need to modify the working directory.** Execute the lines which clear the workspace, set the working directory and load the RMark library.

```
rm(list=ls()); setwd('h:/x/workshops/uf2016/exercises/ex13_direct_est_lambda')
library(RMark)
```

- 2) The first step in using RMark is to convert the input file into an RMark input “data-frame”. This conversion is done with the “convert.inp” function. The only required argument is the input filename (nwc_lamb.inp), but since we have 2 groups in our input file, we also need to specify the group names to the convert.inp function. This is done with the group.df argument. The converted data-frame is saved with the name, “owlinp”. Execute that line, then type the new variable name into the R window.

```
owlinp = convert.inp('nwc_lamb.inp',group.df=data.frame(sex=c('M','F')))
```

- 3) The 2nd step is to create a processed-data variable which contains other variables needed to setup and run the MARK models. The RMark function to do this is “process.data” and requires the converted input from the previous step, the type of MARK models which will be run, and the group variable name (if applicable). Execute this line, then type ‘owlpr’ to see the contents of this variable.

```
owlpr = process.data(owlinp,model='Pradrec',groups="sex")
```

- 4) The 3rd step is to create design-matrix data variables, needed by MARK to build models. The RMARK function is “make.design.data” and the processed-data variable created in the previous step is needed as an argument to the function. Execute this line and type ‘owldd’ to view the contents of this variable. This is a list-type variable and it contains a data-frame variable (S) for the estimated parameter for the model-type (Known) we specified. The columns of S are the variables we can use in building MARK models.

```
owldd = make.design.data(owlpr)
```

Modeling strategy is to develop models corresponding to our hypotheses of how survival, fecundity and/or capture probabilities are affected by sex and time.

- 5) Now we’re ready to build and run our MARK models. Instead of specifying each model and running it, we will create a model structure for each parameter which corresponds to our

belief of what makes the parameter vary. For example, we believe that survival (Phi) might be constant or might be time-specific. So, we create two variables which contain a formula for a possible model:

```
Phi.dot=list(formula=~1)
Phi.t=list(formula=~time)
```

Next, we create two more new variables containing formulae for our belief about capture probabilities:

```
p.dot=list(formula=~1)
p.t=list(formula=~time)
p.s=list(formula=~sex)
```

And two variables containing formulae for our belief about how fecundity might vary:

```
f.dot=list(formula=~1)
f.t=list(formula=~time)
```

- 6) With these formula variables, we can create a list of all possible combinations of those parameters and formula using the “create.model.list” function.

```
mod.list=create.model.list("Pradrec")
```

- 7) Now, we can run all models in this list using the “mark.wrapper” function. This function runs each model in the model list and saves the output of each model as a list variable.

```
mod.out=mark.wrapper(mod.list,data=owlpr,ddl=owldd)
```

- 8) The “mark.wrapper” function automatically creates a results AIC table, as well as storing the results of each model. We can obtain the model table from the output variable, “mod.out” by selecting the sub-variable, “model.table” from the list variable, “mod.out”:

```
tbl=mod.out$model.table
```

and print the table (without 1st 3 columns) with:

```
cat('\nTable of model results:\n')
```

```
print(tbl[,-1:-3,]) # print table (without redundant columns 1 to 3)
```

Questions:

1. Why do you suppose that scientists shifted from the use of matrix models to direct estimation of λ_t ?
2. Which model would you choose to best describe these data? Why?
3. Models included time-specific variation for survival and recruitment. Based on general principles of evolutionary ecology, which of these parameters would you think most likely to exhibit year-to-year variation? Does the evidence provided by model selection agree with this prediction?
4. In the model with all parameters time-specific, are there any parameter estimates that you would view as unusable? If so, which estimates would you not use? Why?
5. So how are owls on this study area doing? Compute the proportional change in population size between years 4 and 23. By what fraction has the population grown or declined?