

Exercise 13: Contributions to Lambda

This exercise closely follows the content of the 6th lecture and is mostly intended to show how to run program MARK to compute seniority and capture probabilities from 'capture-recapture' data. We have prepared exercises for use in RMark.



Data input

Background

Data for this example came from the trapping of meadow voles, *Microtus pennsylvanicus*, at Patuxent Wildlife Research Center, Laurel, MD (Nichols *et al.*, 1984). Data were collected on a 10 x 10 grid of trapping stations spaced at 7.6m intervals in old field habitat. A single modified Fitch live trap (Rose, 1973) was placed at each station. Hay and dried grass were placed in the traps and whole corn was used as bait. Sampling occurred for five consecutive days each month, from June 1981 through December 1981. During each 5-day trapping session, traps were opened in the evening of the first day, checked the following morning, locked open during the day, and reset in the evening, with the sequence repeated each day until 5 days had elapsed. A racoon, *Procyon lotor* (later captured), visited the traps on the final two nights of the second trapping session, essentially leaving only 3 days of trapping for this session. At each capture, animals were examined for a tag, sexed, weighed, and examined for external reproductive characteristics. Tagged animals were ear tagged with numbered fingerling tags, and tag numbers of marked animals were recorded at each capture.

We used 'adult' (>22g) animals and collapsed the 5 days of sampling each month into a single assessment of presence or absence, leaving 6 monthly sampling occasions.

```
# Data input
```

```
# Input data consists of summarized frequencies of capture-histories.
```

```
#
```

```
# The example we'll use for this model contains 2 groups of animals: Males and
```

```
# females, initially captured as adults. So, each capture-history will
# have 2 frequencies following the capture-history. The input file has already
# been created and is named: 'mp1age.inp'.
```

```
#
100000 7 8 /* F M */;
100000 -1 -3;
110000 10 21;
110000 -4 -2;
111000 7 5;
111100 2 3;
111100 0 -1;
# : : :
```

```
# Explanation: The 1st line indicates that 7 female and 8 male individuals were captured only
in
# time period 1 and were released. The 2nd line indicates that 1 female and 3 male
# individuals were captured onl in time period 1 and not released ("- " indicates
# not released).
```

```
# Here are the steps to run MARK on this input file:
```

```
rm(list=ls()) # clear workspace
library(RMark) # add RMark functions to our R workspace
```

```
# convert MARK input file to RMARK data frame, while defining the 2 groups
```

```
mpinp =
convert.inp('mp1age.inp',group.df=data.frame(sex=c('F','M')),use.comments=F)
```

```
# process data frame, specifying model type
# (Pradrec=Pradel model, recruitment parameterization)
```

```
mppr = process.data(mpinp, model='Pradel', groups=c("sex"))
```

```
# make design matrix data variables from processed data frame
```

```
mpdd = make.design.data(mppr)
```

```
# Modeling strategy is to develop a pre-defined set of models. Each model represents a
# plausible hypothesis about seniority or capture probabilities of the animals.
```

```
Gamma.dot=list(formula=~1)
Gamma.s=list(formula=~sex)
Gamma.t=list(formula=~time)
Gamma.sXt=list(formula=~sex*time)
Gamma.sPt=list(formula=~sex+time)
p.dot=list(formula=~1)
p.s=list(formula=~sex)
p.t=list(formula=~time)
p.sXt=list(formula=~sex*time)
p.sPt=list(formula=~sex+time)
```

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

```
# create AIC table of model results for model comparison
```

```

mod.out=mark.wrapper(mod.list,data=mppr,ddl=mpdd)
tbl=mod.out$model.table

# print table (without redundant columns 1 & 2)
print(tbl[,-1:-2,])

# print/plot seniority estimates from top model...

i=as.numeric(rownames(tbl))[1] # get top model number from table
cat('\nEstimates from top model:',as.character(tbl$model[1]),'\n')
print(mod.out[[i]]$results$real) # print estimates from top model

plot(1:5,mod.out[[i]]$results$real$estimate[1:5],type='b',ylim=c(0,1),
     main=as.character(tbl$model[1]),xlab='time',ylab='seniority')

```

Questions:

- (1) Define in words the probability estimated by the seniority parameter, gamma.
- (2) In this example, do the gammas suggest that survival (of previous members of the population) or recruitment (of new members) make the larger contribution to population growth?
- (3) This vole example is from Maryland and uses monthly intervals between trapping sessions. If you had to guess, during what season of the year do you think the last 2 months occurred?
- (4) The various methods that we have discussed for making inferences about lambda and contributions to lambda are all interrelated. Say we used Pradel's full temporal symmetry model for inference about lambda, but used the $\phi(i)$, $f(i)$ parameterization (survival and per capita recruitment). How could you use these parameters to estimate the same relative contributions provided by the gammas?