

Lab 08 – Goodness-of-fit & Time Symmetry

Reverse-time models of recruitment and population growth rate

Open the MARK example file Pradel_copy.inp. It includes data for 1 group observed on 13 occasions. This is the data set used by Pradel (1996). Develop hypotheses and models necessary to determine whether changes in resighting effort resulted in differences in resighting probabilities during the study and whether population growth rate increased during the study as animals became acclimated to the study area or whether they varied at random while holding survival constant.

Estimate \hat{c} using the bootstrap method with 100 iterations based on the most general model and adjust the model selection results. Use File/Simulations/View Simulations to open the results of the simulation and click the calculator button to view the summary statistics.

Paste these results table from MARK in the lab_08 spreadsheet on the page labeled "RT models." Beside each model provide a description of the hypothesis it represents. At the bottom of the worksheet interpret the model selection results. Be sure to consider model deviance, QAICc, model weights, and parameter estimates to support your interpretation.

Robust Design

Download the input file [robust5.inp](#). These are simulated data for a mark-resight study using Robust Design. In this study there were 5 primary sampling periods and 4 secondary sampling periods for a total of 20 occasions and 423 captures. The data consist of 1 group. In this species, animals have home ranges that are relatively large in comparison to the size and scope of the trapping grid. Thus, it is possible that temporary emigration is a factor.

Start a new results file for Robust5 in MARK. The models in exercise 1 examine hypotheses regarding recapture probabilities in the closed periods as well as variation in survival probabilities assuming that population size changes across the primary periods.

1. Cast, run and compare the models described in the table below:

Model Name (notation)	Closed periods	Open periods	Temporary Emigration
$S. g''=g.'=0 p.. N_t$	M_0	$\phi.p.$	None
$S. g''=g.'=0 p.. c.. N_t$	M_b	$\phi.p.$	None
$S. g''=g.'=0 p.t=c.t N_t$	M_t	$\phi.p.$	None
$S_t g''=g.'=0 p_t. N_t$	M_0	$\phi_t p_t$	None
$S_t g''=g.'=0 p_t. c_t. N_t$	M_b	$\phi_t p_t$	None
$S_t g''=g.'=0 p_{tt} c_{tt} N_t$	M_t	$\phi_t p_t$	None
$S. g''=g.' p.. N_t$	M_0	$\phi.p.$	Random
$S. g''=g.' p.. c.. N_t$	M_b	$\phi.p.$	Random
$S. g''=g.' p.t=c.t N_t$	M_t	$\phi.p.$	Random
$S_t g''=g.' p_t. N_t$	M_0	$\phi_t p_t$	Random
$S_t g''=g.' p_t. c_t. N_t$	M_b	$\phi_t p_t$	Random
$S_t g''=g.' p_{tt} c_{tt} N_t$	M_t	$\phi_t p_t$	Random
$S. g'' g.' p.. N_t$	M_0	$\phi.p.$	Markovian
$S. g'' g.' p.. c.. N_t$	M_b	$\phi.p.$	Markovian
$S. g'' g.' p.t c.t N_t$	M_t	$\phi.p.$	Markovian
$S_t g'' g.' p_t. N_t$	M_0	$\phi_t p_t$	Markovian

$S_t, g_t, g', p_t, c_t, N_t$	M_b	$\phi_t p_t$	Markovian
$S_t, g_t, g', p_{tt}, c_{tt}, N_t$	M_t	$\phi_t p_t$	Markovian

Paste these results in the lab_10 spreadsheet on the page labeled "RD models."

2. Provide a biological hypothesis that could be associated with each model in the columns to the right of the results table.
3. In the text box, discuss the result of model selection.
4. Use the formula from the lecture notes to calculate the population birth rates from the real parameter estimates for each year for the 3 best models on the second worksheet, labeled "RD births."