

Ανοικτά Ακαδημαϊκά Μαθήματα



ΑΝΑΛΥΣΗ ΣΥΛΛΗΨΕΩΝ - ΕΠΑΝΑΣΥΛΛΗΨΕΩΝ



Άδειες Χρήσης

Το παρόν υλικό διατίθεται με τους όρους της άδειας χρήσης Creative Commons Αναφορά, Μη Εμπορική Χρήση Παρόμοια Διανομή 4.0 [1] ή μεταγενέστερη, Διεθνής Έκδοση. Για εκπαιδευτικό υλικό, όπως εικόνες, διαγράμματα, κείμενα, που υπόκειται σε άλλου τύπου άδειας χρήσης, η άδεια χρήσης αναφέρεται ρητώς.





The swift *Apus apus* is an abundant and noisy colonial breeder in Asian and European cities. It nests from March to June, nearly exclusively in buildings. The data set we use contains capture histories of swifts nesting in wall cavities in the Museum of Natural History of Nîmes, southern France. Birds of three different colonies have been captured on the nest each year since 1982 by G. Gory. The data used are analyzed in Lebreton *et al.* (1992). More complete data (3 colonies, years 1982-1993) are analyzed as an example of handling problems of parameters identifiability by Viallefont *et al.* (1998). It is this more complete data set which serves as a basis to the present exercise. Because colony 2 is less exposed to the cool northerly wind typical of the French Mediterranean area, the local survival probability and the attendance at nest are supposed to be higher than in the other colony (colony 1).

DATA

We use capture-recapture data from 1982-1990. The data base includes 128 individuals ringed birds and is provided as a file named AA.INP.

11100000	10;
11100000	10;
11001000	10;
11000000	10;

The swift data in file AA.inp

Each line corresponds to an individual recapture history, followed by two columns separated by spaces and ending with a ";". These two columns indicate the numbers of individuals in each colony. There are 128 lines, corresponding to different

individuals. This file is ready for analysis with MARK. The number of occasions of captures is 8 (these include markings and recaptures), the number of groups is 2.

ANALYSIS

In MARK, work with Data type = Recaptures only

- Fit the various models from {phi colony*t, p colony*t}, down to {phi, p} passing through { phi colony + t, p colony + t}. Run in MARK "Pre-defined models" and Select models "Design Matrix coding".

- Select the preferred model based on **AIC**. Comment on the differences between colonies in survival and capture probabilities, in relation with the hypothesized differences between colonies.

- Estimate the survival probabilities using model averaging.

- Plot the recapture probabilities for both colonies on the same plot.