

GENCAPH1 - Generate Capture Histories

No User-Manual has been written for GENCAPH1 (yet). Here is a short description:

This program generates capture-histories of a virtual population of animals with given survival and capture probabilities. Output from this program includes all observable capture-histories, along with the number of animals which exhibited each history. This output may be used as input to other programs (like MARK, CAPTURE, JOLLY) to compute estimates of survival, capture probabilities, or population size.

Uses of this program include:

- Calculate bias in estimated parameters for incorrectly specified models,
- Calculate confidence-interval coverage,
- Compute model goodness-of-fit

Here's how it works:

The expected numbers of animals exhibiting each capture history are computed using a recursive algorithm coded in C. The algorithm follows a population of animals, exposing them to capture and survival until death or the end of the study, while saving a vector of codes (0=not captured, 1=captured) indicating capture history. The process is repeated for each cohort of injected animals in capture occasions after the first.

There are two modes of operation of the program - Deterministic and Stochastic. Under Deterministic mode, the number of animals is retained throughout the process as a fractional number and is multiplied by the parameters to get the final number of animals with each capture-history. This results in two things: capture-history frequencies are not integers, and parameter estimates will match input parameters exactly (almost). In Stochastic mode, the number of animals is achieved via a simulation function (binomial) on the parameters. In this mode, the number of animals with each capture-history will be integers, and the data (and resulting estimates) will be different for each program run.

Terminology and Notation for Input Data

- $N(i)$ = Number of new animals introduced into the population just before time i
 - $\phi(i)$ = survival rate from time i to $i+1$,
 - $\theta(i)$ = tag-retention rate from age or time i to $i+1$
 - $p(i)$ = capture probability for *unmarked* animals in time i
 - $c(i)$ = capture probability for *marked* animals in time i
 - $f(i)$ = number of new individuals in time i per old individual in time $i-1$
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