References: Estimating Population Parameters: Closed and Open populations

Population Biology:


two introductory biological texts, cover much more biology than what we look at.


General introduction to the biology and statistics of monitoring.


If you do monitoring, this is the book to have. Covers from the basics to the detailed.

Statistical Theory (introductions for biologists):


Still my favorite non-technical summary of different philosophical approaches. Chapter 7 is a simple introduction to maximum likelihood


Chapter 2 is an introductory discussion of statistical concepts, including ml estimation.


Chapter 2 is a review of ml estimation (one of the assigned readings). Chapter 6 is an introduction to mark-recapture.

Texts / Monographs:


Edited volume. source of many of this year’s readings. Includes detailed presentation of using program MARK to fit models.
Buckland, S.T. and Morgan, B.J.T. 2016. 50-year anniversary of papers by Cormack, Jolly and Seber. Special issue of Statistical Science 31(2)

Collection of papers celebrating the 50’th anniversary of the Cormack, Jolly and Seber open population model papers. Includes conversations with Cormack and Seber.


Concise intermediate-level treatment of classical and modern approaches. Summarizes a huge amount of literature.


Classic reference on estimation for Mt, Mh, Mb models and their generalizations. Includes complete examples; mathematical details are in the appendices.


Comprehensive overview of Jolly-Seber and related techniques for open populations, including robust design. Includes short summary of methods for closed populations.


Textbook covering spatially explicit CR from simple to advanced (landscape connectivity, resource selection) and “super-advanced” (spatial mark-resight, telemetry)


Pulls together the early literature for both closed and open populations.


Combining population models with mark-recapture (etc.) data.


Compendium of lots of different approaches for “quantitative wildlife management”, ranging from mark-recapture to linear programming and decision making. Huge book, but treatment of individual topics is very lean “just-the-facts” style.

Closed population models:


Derives the approximately unbiased version of the hypergeometric model estimator and its variance.

Analyzes 1535 data sets from 33 spp of mammals using the standard models to look for general patterns across species (e.g. find heterogeneity in capture probabilities in larger data sets for any species).


The second, more accessible, of two papers on how to use individual covariates to model heterogeneity. Probably the best solution to heterogeneity if you can choose the right covariates.


ci’s based on distribution of $\frac{1}{\hat{N}}$ under binomial and hypergeometric models. Easy to compute.


Central paper in a sequence by Pledger on mixtures to model between individual heterogeneity in capture probability

Open population models:


Uses simulation and case studies to assess the bias in survival arising from heterogeneity in capture probabilities. Finds a small negative bias that “may greatly impact management decisions”.


Review and summary of Bayesian approaches to estimation for open populations.


Develops a model that on quick inspection seems very similar to Pledger’s (2011) open population heterogeneity model.


The two original papers on the Jolly-Seber model


A full likelihood analysis of data from a robust design

Applies Pledger’s mixture model for heterogeneity to open populations. Considers heterogeneity in capture probability and heterogeneity in survival. Also considers the bias introduced by conditioning on first capture (the Cormack trick) when survival probability is not constant.


The robust design is a way of combining open and closed population models to get the best of both. This is the most accessible early paper. Estimation is a combination of ml and ad-hoc.

White, G.C., Kendall, W.L., and Barker, R.J. 2006. Multistate survival models and the extensions in program MARK. J. Wildlife Management 70:1521-1529

Multistate models add another dimension to an individual. The state could be breeder/nonbreeder, or spatial area, or something else. This is a nice review of multistate models.

Model Selection and Model Averaging:


Introductory paper on Reversible Jump MCMC, probably the most appropriate way to switch between multiple models.


Source of the non-Bayesian model averaging presented in lecture. Can be used with AIC-derived weights, BIC-derived weights, or true Bayesian posterior model probabilities.


Section 4.2.6 presents the AIC approach to model averaging. Section 2.2 and 2.4 discuss AIC and refinements. There is now a second edition, but I don’t have a copy of it.


Lengthy comparison of AIC and BIC approaches. Partly theory, partly philosophy, partly practical. B&A argue that AIC and BIC are no more than different choices of prior probability of models.


Compares AIC, BIC and a more recent criterion, ICL, to choose the number of components in a mixture. AIC works slightly better than BIC. When it errs, it tends to choose more components than needed. ICL is biased.

Multistate models are mark-recapture models where individuals can change “state”, i.e. what region of the country they are in. Capture and survival parameters can vary among regions. This paper develops a simple model-selection procedure that does not require fitting a model, because it is based on a score test conducted at the null hypothesis.


Spatial Capture-recapture:


If traps are in known locations, you can estimate density (#/area), not just population size.


A review of various CR models that incorporate spatial information


Two data sources “expensive” spatial CR data and “cheap” occupancy data informing a spatial population dynamics model.

Specialized Computer Programs:

Program Mark: see its web page: http://www.phidot.org/software/mark/
and Gary White’s page: http://warnercnr.colostate.edu/~gwhite/mark/mark.htm

R-capture: An R library implementing log-linear models, a different probability model for capture-recapture data. Historically these models are associated with Cormack. A description is at:

E-SURGE: French software for “multiEvent SURvival Generalized Estimation”
http://www.cefe.cnrs.fr/biostatistiques-et-biologie-des-populations/logiciels
Appendix G in Williams et al. is a tabulation of software and download sites.

**Other approaches:**


Five observers surveyed for patches of a rare plant in a burned and an unburned prairie. Detection probabilities varied by observer, whether patch was flowering, and patch size. 3-4 observers found 90-99% of plants; 1 or 2 observers had high error rates.


Two papers describing the very first approach to heterogeneity, the jackknife estimator for the Mh model. Current sense is that more recent methods are better.


Using multiple lists to estimate sizes of human populations (e.g., infected with a particular disease).


One entry into a current research topic: how to account for tag loss.


Develop a multi-state mark recapture model with individual random effects to account for heterogeneity in sighting rate or site preference. Requires special software, admb-re, an extension of AD Model Builder to approximate the integrated likelihood.


Develops a Bayesian approach to combine information from many sampling periods, each with a small number of recaptures. Haven’t checked all the details, but I believe the ‘sequential Bayes algorithm’ is similar to what is now known as the Gibbs sampler.

The “apparent survival” issue is that permanent emigration cannot be separated from death. Develops a hierarchical Bayesian multistate model to account for predicted rates of permanent emigration.


Evaluates sampling designs (e.g. size of sampling area, number of sampling occasions) by simulating fish using an individual-based population model.


Compares three methods for estimating density (not just $N$): Mean maximum distance moved, Spatially explicit capture-recapture, and Telemetry. Telemetry is best SECR may be preferable to Telemetry at low capture probabilities. MMDM is biased.


Traditional multistate models require no uncertainty in the state at each observation. Hidden Markov Models account for uncertainty in the state. Develops a flexible framework to account for state uncertainty.


Combines traditional point sampling for birds with mark-recapture. Choice of assumptions about independence matters.


Considers data from from several related species in the same area. models survival for each species as a sum of a random effect for year (synchronous component) and a species-specific asynchronous component.


Uses linear models to relate covariates (e.g. time or experimental treatments) to model parameters (e.g. survival probability or capture probability).


Develops a simple method to incorporate random effects to model unexplained environmental variation.

Various papers by Chao describe the coverage approach. This one is a relatively accessible treatment of all closed models; a 1992 paper by Chao gives more details on a subset of models.


Mark-resight data are where individuals are captured to be marked, but the marks are sufficiently visible that individuals just need to be resighted to be identified. This sort of data requires more complicated models.


Evaluation of non-invasive methods.


Theory and an example of Pradel’s temporal symmetry model to estimate recruitment and population growth rate directly from capture-recapture data.


Estimates density using a combination of mark-resight data and telemetry data, which informs parameters related to movement and individual location.

**Novel tagging methods: Genetic marks, camera traps, and mark-resight**


Camera trapping is non-invasive and low effect, but capture probabilities are often low and heterogeneous. Simulation evaluation of heterogeneity in capture probability, using Burnham’s jackknife estimator.


One of the key assumptions in mark-recapture is that marks are identified without error. This is a serious concern for genetic marks because genotyping errors do occur. The consequence (almost always) is that two records of the same individual appear to be from different individuals. This is a Bayesian latent variable model that accounts for misidentification.

Introduction to another current research area - using genetic markers (e.g. RFLP’s from dung) to identify individuals.


Using both photo-identification and DNA markers. New issue considered here is that the two surveys are done separately, so some individuals are in both, some are in only one, and others are completely missed. This method estimates the overlap between the two lists by computing a constant that serves as an adjustment factor.


Argues that Madon et al.’s approach is bad. Need something more complicated than a constant adjustment factor. Need to model the observation process.


Mark-resight methods handle individuals once to mark them, but then don’t require capturing them again, only resighting them. Traditional models assume the number of marked individuals is known precisely, which is a problem if survival not perfect. This is a Bayesian approach deal with that uncertainty.


The ideas in Madon et al. 2011 applied to double camera traps. The issue is that any particular animal may be photoed by the left, the right, or both cameras.


Closely related individuals are likely to have similar genotypes, so are more likely to be mis-identified as the same individual. This paper suggests strategies to reduce the frequency of mismatches without requiring lots of extra lab effort.