Stat 534: formulae referenced in lecture, week 8:
Open population models and extensions

Age-based models

- 1st yr survival often different from "adult" survival
- can separate age and time effects if mark and age individuals in multiple years
- can use age-based models to evaluate senescence at older ages
  - birds and many mammals: often banded as nestlings / new borns, before they leave the nest / den.
- Biggest conceptual issue: age $\neq$ year of life.
  Age 0 individuals = 1st year of life
- likelihood is just a bookkeeping exercise
- Notation used in McCrea and Morgan:

$p_j(a)$	"probability that an individual alive and in it's a^{th} year of life at time t_j is captured at that time"
$\phi_j(a)$	"apparent probability that an individual in its a^{th} year of life at occasion t_j survives until time t_{j+1}

- CJS-like likelihood depends on # releases for each age and time and # age-specific recaptures at each time
- McCrea and Morgan, p. 74, gives the expression for the log likelihood - not illuminating
- RMark code is at Mike Conroy's (U Georgia) site:
  `https://sites.google.com/site/cmrsoftware/`
  `lecture-lab-schedule/5--covariates-age-and-cohort-structure`
  `/known-age-releases-each-occasion`

Pradel reverse time estimators

- see hand-written notes
- Notation

  - γ_{i+1}: "seniority" parameter
  - fraction of population at time $i+1$ also alive at time i

- # Births between i and $i+1 = N_{i+1}(1-\gamma_{i+1})$
- Pradel gives a direct estimate of birth rate
  - Included in the likelihood
  - Not a derived parameter
- CJS estimates survival of marked individuals
- Pradel estimates birth rate for individuals that are or will be marked

Pradel temporal symmetry model: estimate pop growth rate

- Combine CJS (forward time) and Pradel (reverse time)
- ⇒ direct estimate population growth rate

$$\frac{N_{i+1}}{N_i} = \lambda_i = \frac{\phi_i}{\gamma_i}$$

- Explanation/derivation in hand-written notes

Mark-recovery data:

- Individuals recaptured when dead
- Very common for harvested species
- Don't have to worry about trailing 0's in the capture history
- Other big difference: know when death occurs
- Notation:
  - ϕ: apparent survival, 1 - (death + emigration)
  - S: true survival: death only
- Capture probability becomes reporting probability

- Assess with reward bands, commonly worth \$100. Assume $p_i = 1.0$ for a bird with a reward band
- Two parameterizations, Brownie and Seber, see handwritten notes
- Brownie f = Seber $r(1-s)$

POPAN = "superpopulation" models

- Explicit model for births
- Two founding papers: Crosby-Manly (1985) and Schwartz-Arneson (1996)
- N is now the size of the superpopulation
  - All individuals ever born into the population during the study period
  - Not the # alive individuals at time i
- # unmarked at time $i = B_i +$ (# born earlier, not seen until i)
- One set of parameters is "Pent" = Probability that an individual in the superpopulation enters the population at time i
  - Connected to births: $B_i = NP$[enter live population at time i]
  - Sum Pent = 1, because everyone enters the live population at some time
  - Requires a multinomial probability
- "Stop over" models, Pledger 2009
  - birth = arrive at a migratory rest area
  - death = depart - may depend on time since birth = "age"
  - N = # using the migratory area

Robust Design

- Motivation (Pollock 1981, 82)
  - Models make assumptions, almost never met exactly.

  - How robust are estimates to violations of assumptions?
  - estimates of survival probabilities are more robust than abundance estimates

- Two sampling levels
  - Primary, e.g. years, population open
  - Secondary, e.g. days or weeks, population closed $\Rightarrow N_i$
- survival:
  - open pop model on collapsed abundance (seen if seen in any 2nd period)
  - Can be done with CJS
  - Or full likelihood model (Kendall 1995)
- recruitment:
  - Combine abundance (closed) and survival (open)

Temporary emigration

- Animals leave area, but then return
- "on vacation" confounded with "not seen"
- Robust design provides two estimates of capture probability
  - From the closed pop model over the 2nd sampling intervals
  - From the open pop model over the primary sampling intervals
- Kendall's approach: two emigration parameters
  - $\gamma_j^{'}$ = P[unavailable | not available at $j-1$]
    "stayed away"
  - $\gamma_j^{''}$ = P[unavailable | available at $j-1$]
    "was here but went away"
- Conditional on first capture (like CJS)

- So $\mathrm{P}[101] = S_1 \left[\gamma_2^{''}(1-\gamma_3^{'} + (1-\gamma_2^{''}(1-p_2)(1-\gamma_3^{''})\right] S_2 p_3$

- And $\mathrm{P}[110] = S_1 p_2 (1-\gamma_2^{''}) \left[S_2(1-\gamma_2^{''})(1-p_3) + S_2(\gamma_3^{''} + (1-S_2)\right]$

Multi-state / Multi-site models

- Examples:
  - 3 sites: individuals can move between them, know where caught each time
  - 2 states: breeding / not breeding, obs each capture time
  - 4 size groups: small, juvenile, breeding adult, large adult
- Big difficulty: only know site/state when captured, not when not detected
  - Age groups: if observe at 2nd and 4th year of life, know in 3rd in between
  - Size groups: if observe at juvenile in year 2 and breeding in year 4, don't know state in year 3
- Notation:
  - ϕ_i^r: apparent survival,
    animal in state r at year i, to year i+1
  - p_i^r: recapture probability,
    animal in state r at year i
  - $\Psi_i^{r,s}$: P[surviving animal from r at i to s at $i+1$]
    - diagonal elements = P[stays in same state]
    - Transitions between states assumed to be first order Markov process
    - State at $i+1$ depends only on state at i, not earlier history

    - Can extend to 2nd order Markov - many more transition parameters

- P[A0B]: Don't know time 2 state (A or B?)

  $$\text{P[A0B]} = \phi_1^A p_3^B \left[\Psi_1^{AA}(1-p_2^A)\phi_2^A\Psi_2^{AB} + \Psi_1^{AB}(1-p_2^B)\phi_2^B\Psi_2^{BB}\right]$$

- Efficient way to calculate these probabilities

- Reminder about CJS m-array with 4 occasions

# released	next captured			never
R_1	m_{12}	m_{13}	m_{14}	$R_1 - (m_{12} + m_{13} + m_{14})$
R_2		m_{23}	m_{24}	$R_2 - (m_{23} + m_{24})$
R_3			m_{34}	$R_3 - m_{34}$

- Each entry is a scalar

- Multi-site/stage: Each entry is a matrix, classified by state at i and $i+1$, e.g.:

$$M_{ij} = \left[\begin{array}{cc} M_{ij}^{AA} & M_{ij}^{AB} \\ M_{ij}^{AB} & M_{ij}^{BB} \end{array}\right]$$

- Parameters also organized as matrices. For 3 sites:

$$\begin{aligned}
\Phi_i &= \left[\begin{array}{ccc} \phi_i^1 & 0 & 0 \\ 0 & \phi_i^2 & 0 \\ 0 & 0 & \phi_i^3 \end{array}\right] \\
\Psi_i &= \left[\begin{array}{ccc} \Psi_i^{11} & \Psi_i^{12} & \Psi_i^{13} \\ \Psi_i^{21} & \Psi_i^{22} & \Psi_i^{23} \\ \Psi_i^{31} & \Psi_i^{32} & \Psi_i^{33} \end{array}\right] \\
P_i &= \left[\begin{array}{ccc} p_i^1 & 0 & 0 \\ 0 & p_i^2 & 0 \\ 0 & 0 & p_i^3 \end{array}\right]
\end{aligned}$$

- Use matrix multiplication to account for all paths from i to j

$$M_{ij} = \prod_{k=i}^{j-2} \left[\Phi_k \Psi_k (I - P_{k+1})\right] \Phi_{j-1}\Psi_{j-1}P_j$$