POPAN and Model Selection

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We already did a POPAN model! (In a Bayesian way)
Recall:

- 3 latent states
- two proceses ("recruitment", death)
- full-capture modelling

Transition Matrix

from $t-1$ to t

$$\Phi_t = \begin{matrix} & \text{Unborn} & \text{Alive} & \text{Dead} \\ \text{Unborn} \\ \text{Alive} \\ \text{Dead} \end{matrix} \begin{pmatrix} 1-\psi_t & 0 & 0 \\ \psi_t & \phi_{t-1} & 0 \\ 0 & 1-\phi_{t-1} & 1 \end{pmatrix}$$

where:

- ϕ_t is the apparent survival at t
- ψ_t are *related* to the POPAN pent

Emission Matrix

capture at t
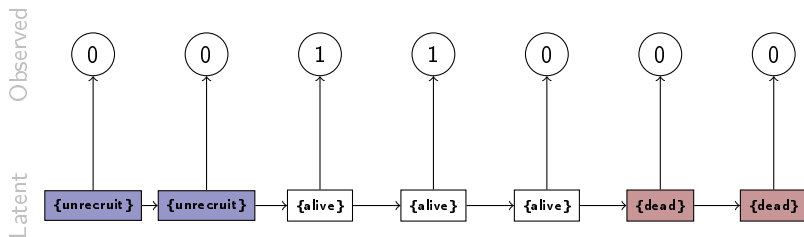
$$\Psi_t = \begin{matrix} & \text{Unborn} & \text{Alive} & \text{Dead} \\ \text{Capture} \\ \text{No Capture} \end{matrix} \begin{pmatrix} 0 & p_t & 0 \\ 1 & 1-p_t & 1 \end{pmatrix}$$

- p_t is the capture-probability at t

We already did a POPAN model! (In a Bayesian way)

▶ example capture history ($\mathbf{y} = \{0011000\}$) and plausible latent state sequence (Z)

Some notes on the real POPAN. . .

POPAN

- ▶ `pent`: probabilty of entry at each capture period
- ▶ `super population`: estimated total number of animals who recruited into the study area during the study, over all captures periods. Includes animals who you *may have never seen*. Mostly important to estimate N_t
- ▶ `births`: more like "apparent births" (anologous to apparent survival). Derived.

POPAN-like Bayesian HMM

- ▶ `pent`: no pent, must be derived from `psi`
- ▶ `psi` are not technically a recruitment parameter, but a "removal entry parameter": the movement from the "unborn" (or unrecruited) state to "alive".
- ▶ can similar derive `Births`, `Superpopulation`, and `N_t`

- recall to estimate the entry probabilities pent:

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```
cumprob[1] <- psi[1]
for(t in 2:T){  cumprob[t] <- psi[t]*prod(1-psi[1:(t-1)]) }
cumprob.norm <- sum(cumprob[1:T])
for(t in 1:T){ pent[t] <- cumprob[t]/cumprob.norm } #t
```

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- note: `pent[1]` equals `psi[1]`

and both are entirely MEANINGLESS!
(Program MARK won't even report `pent[1]`
Confounded with `p[1]`

Confounded Parameters in full-time-varying parameterization

- `phi[T-1]` and `p[T]` : final survival and final capture
- `psi[1]` and `p[1]` : initial entry and initial capture
- `psi[T]` and `phi[T-1]` : final entry and final survival

(one reason why the robust design is so important)

```
for(i in 1:M){ # loop through individuals
  # check if i was a new recruit at t=1
  recruit_i[i,1] <- equals(z[i,1],2)
  for(t in 1:T){
      # check if individual i was a new recruit at t
      recruit_i[i,t] <- equals(z[i,t-1],1)*equals(z[i,t],2)
    } # t
} # M
for(t in 1:T){
    recruits[t] <- sum(recruit_i[1:M,t])
}
```

in our Bayesian HMM Popan-like model. . .

```
cumprob[1] <- psi[1]
for(t in 2:T){
    cumprob[t] <- psi[t]*prod(1-psi[1:(t-1)])
}
cumprob.norm <- sum(cumprob[1:T])
Superpop <- M*cumprob.norm
```

(idea: sum(cumprob[1:T]) is the total probability that one of the Mth individuals will enter the study area (i.e., leave the 'un-recruited' or 'unborn' state.)

Pradel recruitment models are related to POPAN, and our Bayesian HMM Popan-like model. Another important parameter to estimate could be the:

- "realized" population rate-of-growth λ_t

$$\lambda_t = \frac{N_{t+1}}{N_t} = \frac{N_t \phi_t + \text{recruits}_t}{N_t}$$

In the Bayesian POPAN, the λ_t are not a process parameters: but derivatives

- To estimate the population $\bar{\lambda}$, consider a hierarchical model:

$$\lambda_t \sim \mathcal{N}(\bar{\lambda}, \sigma_\lambda)$$

Recall: the difference between first-capture (e.g., CJS) and full-capture modelling (POPAN).

$$\mathbf{y}_i = \underbrace{0000\overbrace{101011000}^{\text{first-capture}}}_{\text{full-capture}}$$

leading zeros : what are they?

- ▸ the animal was missed?
- ▸ the animal was not-yet-born? or not yet recruited? or not yet immigrated?
- ▸ existed in a temporary emigration state?

Recall: the difference between first-capture (e.g., CJS) and full-capture modelling (POPAN).

$$\mathbf{y}_i = \underbrace{0000\ \overbrace{101011}^{\text{first-capture}}000}_{\text{full-capture}}$$

To model recruitment we will use the idea of pseudo-individuals and PXDA parameter-expansion and data-augmentation. [1][Royle and Dorazio, 2012]}. These are animals with an all-zero capture-history: y_{aug}=0000000000 Implimentation

▶ we add $n^{(\text{aug})}$ *pseudo-individuals* to our data set. $M = n^{(\text{obs})} + n^{(\text{aug})}$

▶ we add a "unrecruited" latent state

▶ we add a "removal entry" process ϕ that models the movement z=unrecruited $\rightarrow$ alive
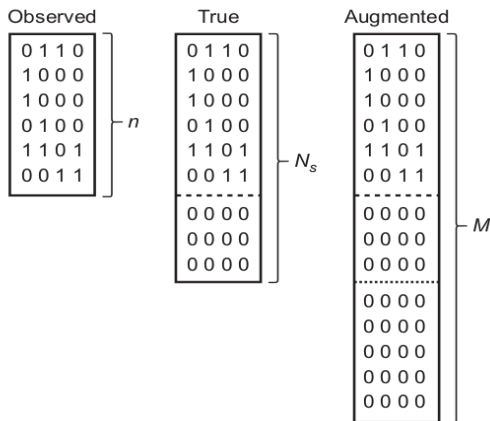
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[1]{

Figure: Kery and Schaub, 2001

$n \equiv$ observed animals
$N_s \equiv$ the "true" super-population (to estimate)
$M \equiv$ n+n$^{(Aug)}$

What are "pseudo-individuals?"

- ▶ recruited but missed (un-captured)
- ▶ recruited but died/left before capture
- ▶ some never recruited (stay in state {*unrecruited*})

Pseudo individuals are important beyond POPAN:

- ▶ full-capture PCRD [Rankin et al., 2016]
- ▶ spatial capture-recapture [Royle et al., 2011]
- ▶ occupancy models [Kéry and Schaub, 2011]
- ▶ and more. . .

Technical advice:

- set $n^{\text{aug}} \approx n$
- check that it is enough (or too much): Monitor the *cumulative entry probability*

$$\psi_1 + \psi_2(1 - \psi_1) + \cdots + \psi_T \cdot \prod_{\tau=1}^{T-1}(1 - \psi_\tau)$$

... ensure its posterior distribution stays $\ll 1$.

$$\psi_1 + \psi_2(1 - \psi_1) + \cdots + \psi_T \cdot \prod_{\tau=1}^{T-1}(1 - \psi_\tau)$$

or in JAGS. . .

```
cumprob[1] <- psi[1]
for(t in 2:T){  cumprob[t] <- psi[t]*prod(1-psi[1:(t-1)]) }
cumprob.norm <- sum(cumprob[1:T])
```

. . . make sure its $95\% CI$ doesn't get close to 1.

- ▶ if yes, then increase n^{aug}
- ▶ if `cumprob.norm` $\ll 0.8$, you could consider decreasing n^{aug} (to save computation time)

Time to open up JAGS!

▶ Demonstration: Analyze a POPAN model for Hunt et al. [2017].

Pay-attention to *data-augmentation* and `cumprob`

▶ Next: Exercise: Model Selection on the POPAN

Tim N. Hunt, Lars Bejder, Simon J. Allen, Robert W. Rankin, Daniella Hanf, and Guido J. Parra. Demographic characteristics of Australian humpback dolphins reveal important habitat toward the south-western limit of their range. *Endangered Species Research*, 32:71–88, 2017. doi: $10.3354/\mathrm{esr}00784$.

Marc Kéry and Michael Schaub. *Bayesian Population Analysis Using WinBUGS: A Hierarchical Perspective*. Academic Press, Oxford, UK, October 2011. ISBN 978-0-12-387021-6. URL `http://www.sciencedirect.com/science/book/9780123870209`.

Robert W. Rankin, Krista E. Nicholson, Simon J. Allen, Michael Krützen, Lars Bejder, and Kenneth H. Pollock. A full-capture Hierarchical Bayesian model of Pollock's Closed Robust Design and application to dolphins. *Frontiers in Marine Science*, 3(25), 2016. doi: $10.3389/\mathrm{fmars}.2016.00025$.

J Andrew Royle and Robert M Dorazio. Parameter-expanded data augmentation for Bayesian analysis of capture–recapture models. *Journal of Ornithology*, 152(2):521–537, 2012. doi: $10.1007/\mathrm{s}10336\text{-}010\text{-}0619\text{-}4$.

J.A. Royle, M. Kéry, and J. Guélat. Spatial capture-recapture models for search-encounter data. *Methods in Ecology and Evolution*, 2(6):602–611, 2011.