Cormack-Jolly-Seber

Rob W Rankin

Post-doc (Georgetown University),PhD (Murdoch University)

October 27, 2017

First-Capture

- conditions on first-capture
- no modelling of recruitment
- open population

Parameters

- p_t (capture probability) and ϕ_t (apparent survival)
- N_t via Horvitz-Thompson-type estimator

$$\hat{N}_t \approx \underbrace{\sum_{i=1}^{n} \frac{\mathbb{I}[y_{i,t} = 1]}{\hat{p}_{i,t}}}_{\text{individual heterogeneity}} = \underbrace{\frac{n_t^{(observed)}}{\hat{p}_t}}_{\text{homogeneous } p_t} \tag{1}$$

Data:

1. $\{t_i^0\}_{i=1}^{n} \equiv$ the primary-period of each individuals' first-capture.
2. $\mathbf{Y}^{(t_i^0 < T)}$ ragged matrix of 0-1 outcomes *for individuals whose first-capture is less than T*

Cormack-Jolly-Seber

some notes

- non-separable: ϕ_{T-1} & p_T (in a $\phi(\cdot)p(\cdot)$ model. Need to either constrain one (or use hierarchical model)

often set $\phi_{T-1} = \phi_{T-2}$ and/or $p_T = p_{T-1}$

- no p_1 (first captures are not modelled)

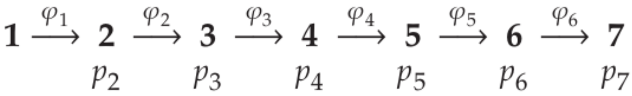


Figure: CJS process fom Program MARK: A Gentle Introduction

- can include individual heterogeneity with external covariates

$$\text{logit}(p_{i,t}) = \underbrace{\beta_0}_{\textit{intercept}} + \underbrace{x_i\beta_x}_{\textit{covariate}}$$

CJS as an HMM

simplest HMM
only 2 latent states:

1. {alive} and
2. {dead}

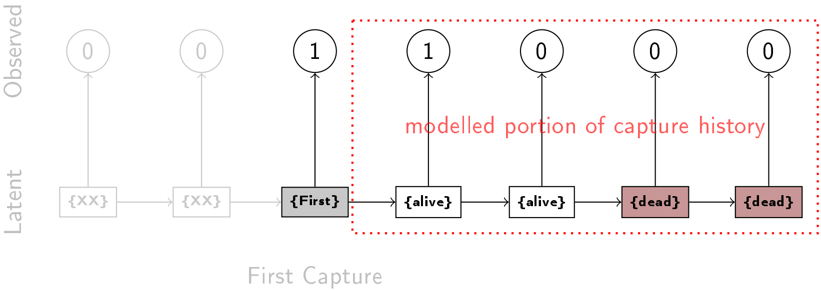
Transition Matrix

$$\mathbf{\Phi}_t = \begin{array}{c c} & \begin{array}{cc} \textbf{Alive} & \textbf{Dead} \end{array} \\ \begin{array}{c} \textbf{Alive} \\ \textbf{Dead} \end{array} & \begin{pmatrix} \phi_{t-1} & 0 \\ 1-\phi_{t-1} & 1 \end{pmatrix} \end{array}$$

Emission Matrix

$$\mathbf{\Psi}_t = \begin{array}{c c} & \begin{array}{cc} \textbf{Alive} & \textbf{Dead} \end{array} \\ \begin{array}{c} \textbf{Capture} \\ \textbf{No Capture} \end{array} & \begin{pmatrix} p_t & 0 \\ 1-p_t & 1 \end{pmatrix} \end{array}$$

Latent States and the CJS



As an HMM, the CJS is very simple

```
# HMM TRANSITION MATRIX
# FROM alive to...
tr[1,1] <- phi   # alive
tr[2,1] <- 1-phi # dead
# FROM dead to ...
tr[1,2] <- 0 # alive (illegal)
tr[2,2] <- 1 # dead to dead

# HMM EMISSION MATRIX
# state 1: alive
em[1,1]<-1-p # miss
em[2,1]<- p  # capture
# state 2: dead
em[1,2]<- 1  # miss
em[2,2]<- 0  # capture
```

The CJS conditional likelihood in JAGS...
(notice it starts at t= first capture+1 period)

```
for(i in 1:N){
  # loop though capture periods after first capture
  for(t in (first[i]+1):T){
     y[i,t] ~ dcat(em[,z[i,t]])
  } # t
} # i
```

beware the for loop

```
for(t in (first[i]+1):T){
```

The CJS latent state process in JAGS. . .
(notice it starts at t= first capture period)

```
for(i in 1:N){
  # HMM LATENT STATE PROCESS: at t=1
  z[i,first[i]+1] ~ dcat(tr[,1]) # initialize state 1 (alive)
  # loop though capture periods after first capture
  for(t in (first[i]+1):(T-1)){
     z[i,t+1] ~ dcat(tr[,z[i,t]]) # z_t+1 | z_t
  } # t
} # i"
```

Horvitz-Thompson Estimator in JAGS

```
for(t in 2:T){ # loop through time
    for(i in 1:n){ # loop through individuals
      N_i[i,t-1] <- equals(y[i,t],2)/p[t-1]
    } # i
    # H-T estimate of abundance at time t
    N[t-1] <- sum(N_i[,t-1]) # sum over all individuals
} # t
```

(notice weird offset of t and t-1)

First Capture vs Full Capture

Full Capture

- N in likelihood (for mle)
- $\hat{N}$ often more reliable
- estimates recruitment
- uses full capture history leading zeros
- no individual covariates (sometimes)

First Capture

- N not in likelihood
- $\hat{N}$ biased at low p
- no recruitment
- models only $t >$ first capture
- easier to model individual covariates

In JAGS

- Notice the `for loop` and its structure `first[i]+1:T`
- N estimation: no longer about counting `equals(z[i,t], alive)`
- N estimation: Horvitz-type, now we sum `equals(y[i,t],capture)/p`

Because the CJS is so easy, it is time to complicate things with . . . .

SEX and

EFFORT

JAGS CJS DEMONSTRATION: Sex

In the following demonstrataion (using data from Nicholson et al [1]), there will be two ways to parameterize $\phi(\text{sex})p(\text{sex})$.

Beta Priors

$$\pi(p_f) = Beta(p; a_f, b_f)$$
$$\pi(p_m) = Beta(p; a_m, b_m)$$
$$\pi(p_u) = Beta(p; a_u, b_u)$$

- *independent* priors and parameters per sex

Logit-Normal Priors

$$\pi(\mu_p) = \mathcal{N}(x; \mu_0, \tau_0)$$
$$\pi(\beta_m) = \mathcal{N}(\beta; \mu_m, \tau_m)$$
$$\pi(\beta_u) = \mathcal{N}(\beta; \mu_u, \tau_u)$$

$$\left.\begin{aligned} p_f &= \frac{1}{1+e^{-\mu_p}} \\ p_m &= \frac{1}{1+e^{-(\mu_p+\beta_m)}} \\ p_u &= \frac{1}{1+e^{-(\mu_p+\beta_u)}} \end{aligned}\right\} \textbf{inverse-logit}$$

- sex effect

[1] Nicholson et al 2012. Abundance, survival and temporary emigration of bottlenose dolphins (Tursiops sp.) off Useless Loop in the western gulf of Shark Bay, Western Australia. Mar. Freshwater Res. 63

JAGS CJS DEMONSTRATION: Beta Priors

Beta Priors

$$\pi(p_f) = Beta(p; a_f, b_f)$$

Advantages

- Simple
- Independent parameters for F,M,U
- Clear connection between p and priors

Disadvantages

- Bad for: multiple covariates (time, effort, individual covariates)
- Need <u>lots</u> of separate priors for complex effects: $p_{f,t=1}$, $p_{f,t=2}$, $p_{f,t=3}$, $p_{f,t=4}$, $p_{f,t=5}$, . . .

logit-Normal Priors

$$\pi(\mu_p) = \mathcal{N}(x; \mu_0, \tau_0) \;\; p_f = \frac{1}{1+e^{-\mu_p}}$$

Advantages

- Some like the Normal
- complex linear-models with multiple effects

$$p_x = \frac{1}{1 + e^{-(\beta_0+\beta_1 \cdot X_1+\beta_2 \cdot X_2+\cdots+\beta_j \cdot X_j)}}$$

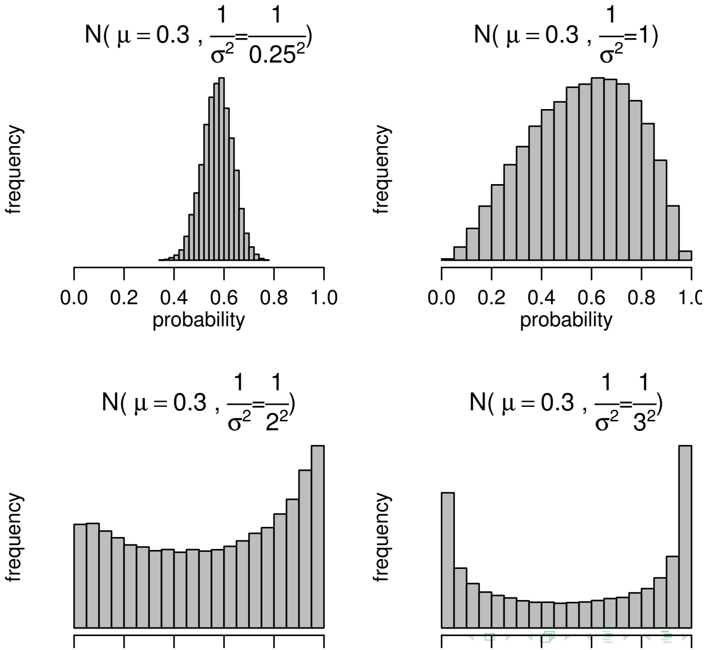
$$\text{logit}(p_x) = \beta_0 + \beta_1 \cdot X_1 + \beta_2 \cdot X_2 + \cdots + \beta_j \cdot X_j$$

- just a type of logistic regresion

Disadvantages

- must master the logit transformation
- boundaries, strange behaviour

Logit-Normal: Recall



... *just a type of logistic regression*
Recall: main effects and interactions
Let's say we have two covariates: sex and effort

- main effects model:

$$\mathrm{logit}(p_i) = \overbrace{\beta_0}^{\text{intercept}} + \underbrace{\beta_{\mathrm{m}} \cdot \mathbb{I}[\mathrm{sex}_i = \mathrm{M}]}_{\text{sex effect}} + \overbrace{\beta_{\mathrm{eff}} \cdot X_{\mathrm{eff}}}^{\text{effort effect}}$$

- interaction model:

$$\mathrm{logit}(p_i) = \beta_0 + \beta_{\mathrm{m}} \cdot \mathbb{I}[\mathrm{sex}_i = \mathrm{M}] + \beta_{\mathrm{eff}} \cdot X_{\mathrm{eff}} + \underbrace{\beta_{m\times\mathrm{eff}} \cdot \mathbb{I}[\mathrm{sex}_i = \mathrm{M}] \cdot X_{\mathrm{eff}}}_{\text{interaction term}}$$

- the logit-Normal (or probit-Normal) is very common for specifying Hierarchical Bayesian models

$$\begin{aligned} \text{logit}(p_{i,t}) &= \beta_0 + \beta_{t=2}\mathbb{I}[t=2] + \cdots + \beta_T \mathbb{I}[t=T] + \epsilon_i \\ \epsilon_i &\sim \mathcal{N}(0, \tau_0) \end{aligned}$$

Time to open up JAGS!

- Demonstration 1 : CJS model $\phi(\text{sex})p(\text{sex})$ with Beta priors
- Demonstration 2 : CJS model $\phi(\text{sex})p(\text{sex}, \text{effort})$ with logit-Normal Priors
- Exercise : Convert one of the models into a fully-time-varying model $\phi(t, \text{sex})p(\text{sex}, t)$

Remeber to watch out for. . .

- different handling of first capture period
- special way to estimate abundance (Horvitz-Thompson-type)
- inclusion of sex: how different in Beta vs Logit-Normal priors