Intro to Hidden Markov Models in JAGS: Practical Exercise 2

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Recap

you have run a HMM model (like a POPAN) for:

- **time-invariant** processes ($\phi(\cdot)$, $p(\cdot)$, $\psi(\cdot)$), and
- a **single** capture history

Next Exercise: Extending the HMM

1. time-varying ψ_t parameters `psi[t]` [1]
2. many capture histories. `y` will be a `matrix` with
3. `ncol=T` (capture periods) and
4. `nrow=M` (number of individuals)

Goals

- inference about `phi` and `p`
- learn how to use `for` loops to generalize the HMM over many individuals and time-varying processes

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[1] POPAN-like models always have time-varying recruitment parameters

- capture histories are a matrix: with a row per individual (like Program MARK)
- use a for loop to generalize the following for multiple individuals

```
z[?,t] ~ dcat(tr[,z[?,t-1]]) # z_t | z_t-1
y[?,t] ~ dcat(em[,z[?,t]]) # conditional capture
```

1. Qu: if y is a matrix, what dimensions does z have?

- `psi[t]`: use a `for` loop.
- don't *literally* do:

$$
\begin{aligned}
\text{psi}[1] &\sim \text{dbeta}(\text{pr.beta}[1,1],\ \text{pr.beta}[1,2]) \\
\text{psi}[2] &\sim \text{dbeta}(\text{pr.beta}[2,1],\ \text{pr.beta}[2,2]) \\
\text{psi}[3] &\sim \text{dbeta}(\text{pr.beta}[3,1],\ \text{pr.beta}[3,2]) \\
&\cdots \\
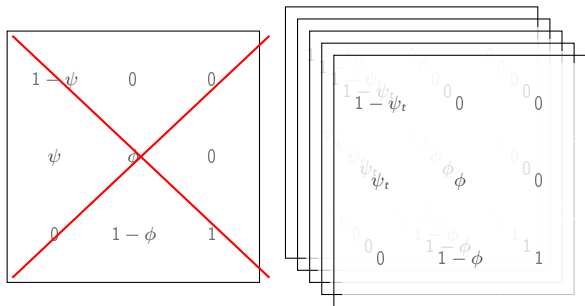\text{psi}[11] &\sim \text{dbeta}(\text{pr.beta}[11,1],\ \text{pr.beta}[11,2])
\end{aligned}
\tag{1}
$$

- instead use a for loop

A time-varying `psi[t]` has an important consequence for the transition matrix (`tr`).

- there is <u>no longer</u> a single transition matrix.
- but a 3D array of values

The matrix is to a PAGE as an array is to a book

HINT:

1 `tr[1,1]<- 1-psi`

TRANSLATION set element of <u>row</u> 1 and <u>column</u> 1 to $1-\psi$
what is the 3D array equivalent?

2 `tr[1,1,t]<- 1-psi[t]`

TRANSLATION set element of <u>row</u> 1 and <u>column</u> 1 and <u>slice</u> t to $1-\psi_t$

arrays in general

$$\text{tr[row, column, slice]}$$

▸ rows are the 1st dimension

▸ columns are the 2nd dimension

▸ slices are the 3rd dimension

. . .

▸ it continues in n-dimensions

time to open up JAGS!

see file: `/BayesCMR_workshop/PART4_introHMM/R_hmm_intro.R`

- go to PART 2

Bonus!

Once you complete Exercise 2 (time-varying ψ and multiple capture histores), let's add POPAN-like estimates of:

- Population abundance N
- Births B (or, `recruits`)[2]
- Entry probabilities (what MARK calls `pent`)

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[2]"Apparent Births" include permanent immigrants in in-situ new individuals

In our Bayesian POPAN, we get a posterior for abundance (or "super abundance") by tallying latent-states, per MCMC

```
# DERIVATIVES: Pop abundance
for(i in 1:M){
    # check whether an individual was actually alive
    for(t in 1:T){
        N_i[i,t] <- equals(z[i,t],2)
    } # t
} # M
# tally total population abundance per t
for(t in 1:T){
    N[t] <- sum(N_i[1:M,t]) # sum over all individuals
}
```

```
N_i[i,t] <- equals(z[i,t],2)
```

- this scores whether each individual i was alive (z equals 2) at t
- N_i is just a bunch of 0'so (not alive) and 1's (yes alive)

$$N_{i,t}^{(j)} \equiv \mathbb{I}[z_{i,t}^{(j)} = 2] \; \forall \; j \; \text{MCMC samples}$$

```
N[t] <- sum(N_i[1:M,t])
```

... this merely adds all the "yes alive" over all individuals

$$N_t^{(j)} = \sum_{i=1}^{M} N_{i,t}^{(j)} = \sum_{i=1}^{M} \mathbb{I}[z_{i,t}^{(j)} = 2]$$

Apparent Births / Recruits: also just an exercise in tallying events[3]

```
for(i in 1:M){
    # check when each individual was born/recruited
    recruit_i[i,1] <- equals(z[i,1],2)
    for(t in 2:T){
        recruit_i[i,t] <- equals(z[i,t-1],1)*equals(z[i,t],2)
    } # t
} # M
for(t in 1:T){
    # tally total recruits per t
    recruits[t] <- sum(recruit_i[1:M,t])
}
```

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[3]This method is contingent on the "Pseudo-Individuals" method of
parameter-expansion/data-augmentation technique explained in Rankin, Nicholson et al 2016

```
recruit_i[i,t] <- equals(z[i,t-1],1)*equals(z[i,t],2)
```
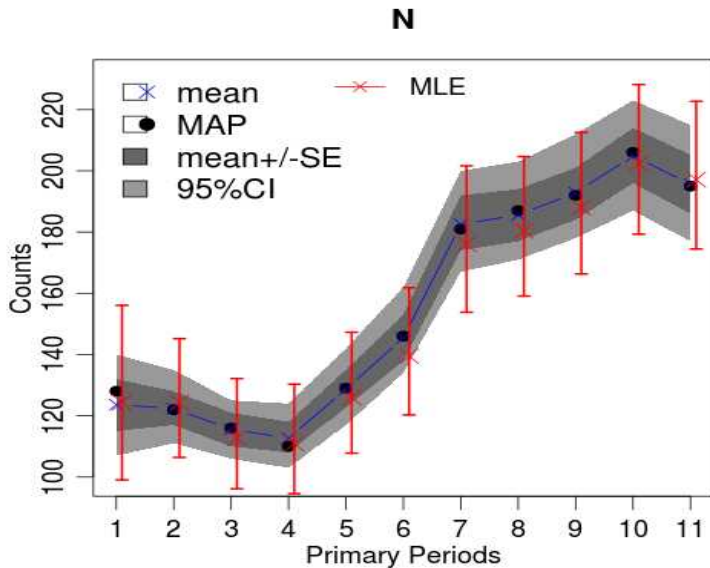
- ▶ this asks: was individual i "unborn" at t-1 and then "alive" at t
- ▶ i.e., `z[i,t-1]` equals 1 and `z[i,t]` equals 2
- ▶ `recruit_i` is just a bunch of 0's (not new-recruit) and 1's (yes new-recruit)
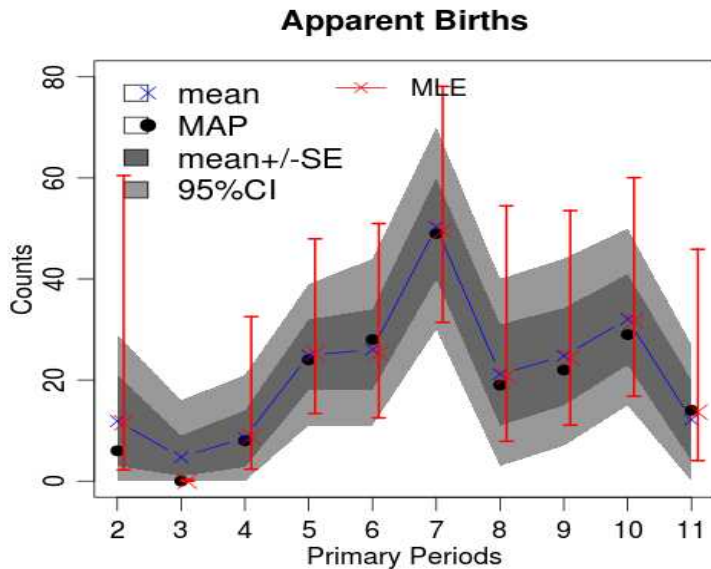
$$\text{recruit}_{i,t}^{(j)} \equiv \mathbb{I}[z_{i,t-1}^{(j)} = 1] \cdot \mathbb{I}[z_{i,t}^{(j)} = 2]$$

```
recruits[t] <- sum(recruit_i[1:M,t])
```
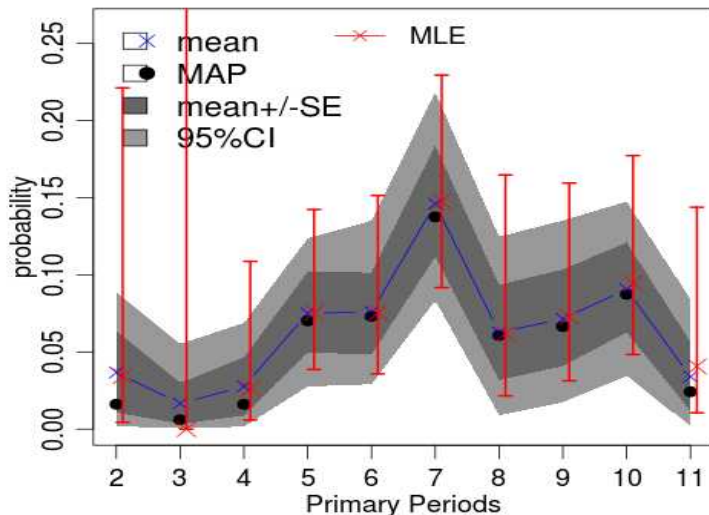
... this merely adds all the "yes recruit" over all individuals

$$\text{recruits}_{t}^{(j)} = \sum_{i=1}^{M} \text{recruit}_{i,t}^{(j)} = \sum_{i=1}^{M} \left(\mathbb{I}[z_{i,t-1}^{(j)} = 1] \cdot \mathbb{I}[z_{i,t}^{(j)} = 2] \right)$$

Apparent Births

Entry Probabilities pent

Similarities and differences depend strongly on:

- sample size (n, T, etc.)

Posterior MAP $\rightarrow$ MLE as $n \rightarrow$ large

- strength of priors
- capture probabilities (lower p implies less information in the data)

Point Estimates

1. MLEs are close to the MAPS
2. Posterior means include information about the full posterior distribution. Can be very different for *skewed* distributions

e.g., see recruits in T=3

- ▶ MAPS easy interpretation: "what was the *most likely value*?"
- ▶ Posterior mean interpretation: depends on philosophy of probabilities

$$\mathbb{E}_{p(x|y)}[x] = \sum_{x=0}^{\infty} x p(x|\mathbf{Y}) dx \qquad (2)$$

The mathematical intepretation is easy; physical interpretation is less clear.

Intervals

VERY DIFFERENT!

- ▶ frequentist procedure: estimate MLE -> estimate intervals | MLE

Breaks-down when MLE is close to a boundary (like `pent[3] = 0`)

- ▶ Bayesian: intervals are estimated using full posterior

Apparent Births at t=3