

Minimal Background on Hidden Markov Models

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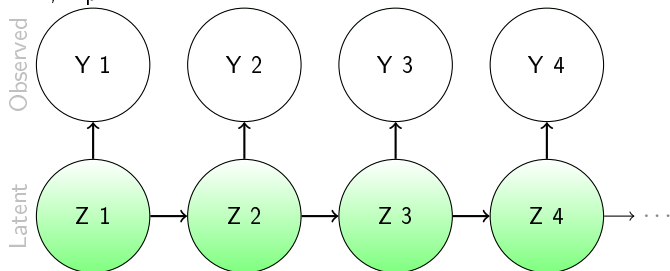
Hidden Markov Models (HMM)

- ▶ provides a unified approach to capture-mark-recapture models
- ▶ **essential** for JAGS CMR models
- ▶ widely used framework outside CMR

H M M

- ▶ Hidden: the process model is *latent*, i.e., unobservable
- ▶ Markov: the dependence between states Z_t at t and Z_{t+1} at $t + 1$ has order 1.

separate the **observed error (Y)** from the **process model**
a.k.a, separate the **observed event** from the **latent state**



Why do HMM?

- decomposes the complex product-multinomial distribution of capture histories into a series of simple distributions.

e.g.,

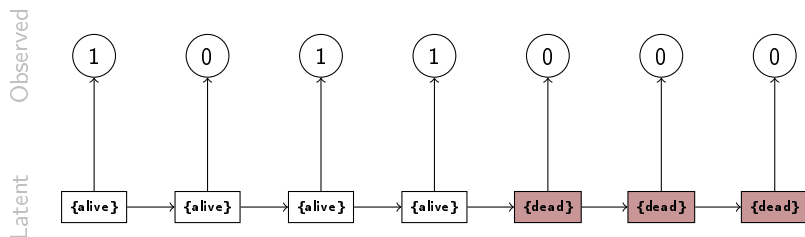
$$p(y_t = \text{capture} | z_t) = \begin{cases} p_t, & \text{if } z_t = \{\text{alive}\}, \\ 0, & \text{if } z_t = \{\text{dead}\} \end{cases} \quad (1)$$

- calculate biological (derived) parameters (N_t , births_t , super-population) as simple summaries of latent states

$$N_t = \sum_{i=1}^M \mathbb{I}[z_t = \{\text{alive}\}] \quad (2)$$
$$B_t = \sum_{i=1}^M (\mathbb{I}[z_t = \{\text{alive}\}] \cdot \mathbb{I}[z_{t-1} = \{\text{unrecruited}\}])$$

Latent States: Example (CJS)

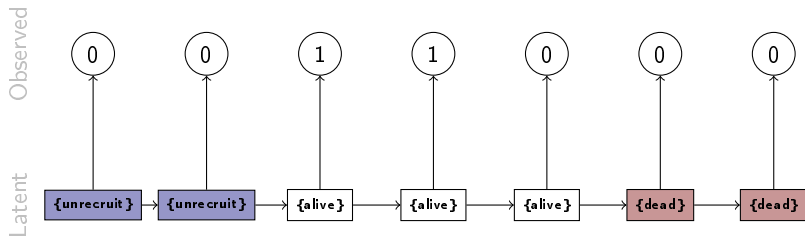
- ▶ example capture history ($y = \{1011000\}$) and plausible latent state sequence (Z)



(This is the **Cormack-Jolly-Seber** model)

Latent States: Example (POPAN)

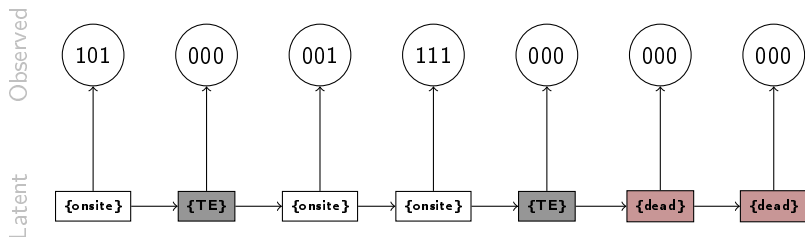
- ▶ example capture history ($y = \{0011000\}$) and plausible latent state sequence (Z)



(This could be the **POPAN** model)

Latent States: Example (PCRD)

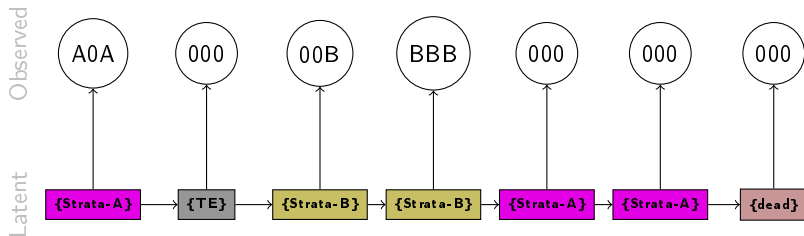
- ▶ example capture history ($y = \{101000001111000000000\}$) and plausible latent state sequence



(This is the **Pollock's Closed Robust Design** model with 3 secondary periods)

Latent States: Example (MSCRD)

- ▶ example capture history ($y = \{A0A00000BBBB0000000000\}$) and latent state sequence



(This is a **Multistate Robust Design Model** with 2 strata (A,B) and Temporary Emigration (TE) and 3 secondary periods per primary period)

Many capture-mark-recapture models can be formulated as a type of HMM, e.g.,

- ▶ Cormack-Jolly-Seber
- ▶ POPAN
- ▶ Pollock's Closed Robust Design
- ▶ Multistate models

Mastering the HMM framework opens-up a lot of possibilities for standard and customized models

Quick Note:

- ▶ Latent states are *stochastic*.
- ▶ They are **random variables**, like ϕ, p, γ, ψ , etc.

Each capture history has a *distribution* of plausible latent states sequences
For example:

$$\mathbf{y} = \{1011000\}$$

could have latent state sequences...

$$\mathbf{z}^* \in \left\{ \begin{array}{l} \{1111111\} \\ \{1111112\} \\ \{1111122\} \\ \{1111222\} \\ \dots \\ \{1112222\} \\ \{2211111\} \end{array} \right. \quad (3)$$

... where $1 \equiv \text{alive}$, $2 \equiv \text{dead}$

- ▶ if we knew the latent states, we could easily estimate survival, births, etc.
- ▶ instead we **marginalize** over the latent states via Gibbs Sampling

i.e., sample \mathbf{Z} , impute their values and to update θ
a.k.a Monte-Carlo integration

Gibbs Sampling HMM

within each j MCMC iteration, we ...

- ▶ 1) Sample parameters conditional on latent states \mathbf{Z} and data \mathbf{Y}

$$\theta^{(j+1)} \sim \pi(\theta | \mathbf{Z}^{(j)}, \mathbf{Y}) \quad (4)$$

- ▶ 2) Sample latent states conditional on parameters θ and data \mathbf{Y}

$$\mathbf{Z}^{(j+1)} \sim \pi(\mathbf{Z} | \theta^{(j+1)}, \mathbf{Y}) \quad (5)$$

- ▶ 3) repeat for all MCMC iterations

for JAGS scripts, we must:

- ▶ specify **Priors** (like before)

```
# priors
p ~ dbeta(a,b)
```

- ▶ specify the **Conditional Data Likelihood** (like before, but conditional on the latent states)

```
# likelihood
y[t] ~ dbern(p * equals(z[t],1))
```

- ▶ AND specify the Markov **latent state process** (new)

```
# latent state process
z[t] ~ dcat(transition.matrix[,z[t-1]])
```

To understand HMM models, you must **master the matrix**

Transition Matrix

- ▶ governs the probabilistic transition: $z_t \rightarrow z_{t+1}$

$$\Phi = \begin{array}{c} \text{Unborn} \\ \text{Alive} \\ \text{Dead} \end{array} \begin{array}{ccc} \text{Unborn} & \text{Alive} & \text{Dead} \\ \left(\begin{array}{ccc} .7 & 0 & 0 \\ .3 & .9 & 0 \\ 0 & .1 & 1 \end{array} \right)$$

- ▶ read: from *columns* (t) to *rows* ($t+1$)
- ▶ columns sum to 1

Emission Matrix

- ▶ governs capture process $p(y_t|z_t)$ (i.e., probability of a capture, **given** each latent state)

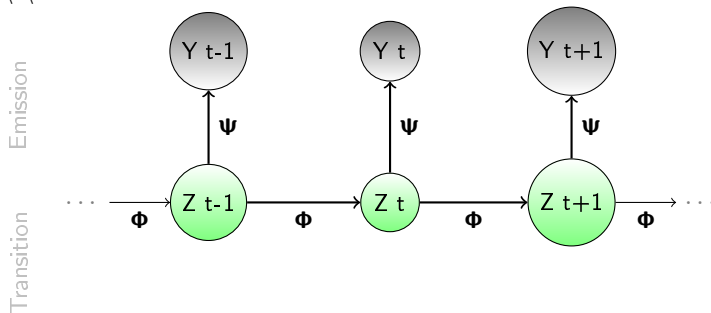
$$\Psi = \begin{array}{c} \text{Capture} \\ \text{No Capture} \end{array} \begin{array}{ccc} \text{Unborn} & \text{Alive} & \text{Dead} \\ \left(\begin{array}{ccc} 0 & .5 & .0 \\ 1 & .5 & 1 \end{array} \right)$$

- ▶ read: from *columns* (z at t) to *row* (y at t)
- ▶ columns sum to 1

HMM is a Bunch of Matrices

$$\Psi = \begin{matrix} & \begin{matrix} \text{Unborn} & \text{Alive} & \text{Dead} \end{matrix} \\ \begin{matrix} \text{Capture} \\ \text{No Capture} \end{matrix} & \begin{pmatrix} 0 & .5 & .0 \\ 1 & .5 & 1 \end{pmatrix} \end{matrix}, \quad \Phi = \begin{matrix} & \begin{matrix} \text{Unborn} & \text{Alive} & \text{Dead} \end{matrix} \\ \begin{matrix} \text{Unborn} \\ \text{Alive} \\ \text{Dead} \end{matrix} & \begin{pmatrix} .7 & 0 & 0 \\ .3 & .9 & 0 \\ 0 & .1 & 1 \end{pmatrix} \end{matrix}$$

//



How to Read Transition and Emission Matrices

- ▶ Read: FROM columns TO rows
- ▶ example: Let's say $z_{t-1} = \{\text{Unborn}\}$ at $t - 1$

What is $p(z_t = \{\text{Alive}\} | z_{t-1} = \{\text{Unborn}\}, \Phi)$?

$$\Phi = \begin{array}{c} \text{Unborn} \\ \text{Alive} \\ \text{Dead} \end{array} \begin{pmatrix} \text{Unborn} & \text{Alive} & \text{Dead} \\ \text{.7} & 0 & 0 \\ \text{.3} & .9 & 0 \\ 0 & .1 & 1 \end{pmatrix}$$

What is $p(y_t = \{\text{Capture}\} | z_t = \{\text{Alive}\}, \Psi)$?

$$\Psi = \begin{array}{c} \text{Capture} \\ \text{No Capt} \end{array} \begin{pmatrix} \text{Unborn} & \text{Alive} & \text{Dead} \\ 0 & \text{.5} & .0 \\ 1 & .5 & 1 \end{pmatrix}$$

The matrices merely codify the **conditional probabilities** of the HMM processes

Understanding Transition and Emission Matrices (2)

- Likewise, let's say $z_t = \{\text{Alive}\}$ at t

$$\Phi = \begin{matrix} & \begin{matrix} \text{Unborn} & \text{Alive} & \text{Dead} \end{matrix} \\ \begin{matrix} \text{Unborn} \\ \text{Alive} \\ \text{Dead} \end{matrix} & \left(\begin{array}{ccc} .7 & 0 & 0 \\ .3 & .9 & 0 \\ 0 & .1 & 1 \end{array} \right) \end{matrix}$$

Translation: IF z_t is in state $\{\text{Alive}\}$ at time t , then there is:

- 0 chance of returning to $\{\text{Unborn}\}$,
- 0.9 chance of staying $\{\text{Alive}\}$,
- 0.1 chance of going to $\{\text{Dead}\}$

$$\Psi = \begin{matrix} & \begin{matrix} \text{Unborn} & \text{Alive} & \text{Dead} \end{matrix} \\ \begin{matrix} \text{Capture} \\ \text{No Capt} \end{matrix} & \left(\begin{array}{ccc} 0 & .5 & .0 \\ 1 & .5 & 1 \end{array} \right) \end{matrix}$$

Translation: IF z_t is in state $\{\text{Alive}\}$ at time t , then there is:

- 50% chance getting a $\{\text{Capture}\}$,
- 50% chance of getting $\{\text{No Capture}\}$

Let's do a worked example!

A demonstration of the data-generating process for a POPAN-like recruitment model

3 latent states:

- ▶ $1 \equiv$ unborn (or pre-immigrant),
- ▶ $2 \equiv$ alive (and marked),
- ▶ $3 \equiv$ dead (or permanent-emigrant)

1 capture history to generate

7 primary periods

time-invariant recruitment¹, survival and capture-probabilities

¹In practise, the recruitment parameters are ALWAYS time-varying

Generative Model for POPAN (2)

Initialize: $z_0 = 1$ at $t = 0$ ($\{\text{unborn}\}$).

No captures in $t=0$

done!



t_0 dummy
state

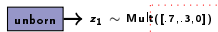
Generative Model for POPAN (3)

Sample: $z_1 | z_0$ at $t=1$.

Use column 1 from $\Phi[., 1]$ (because $z_0 = 1$)

Use the Multinomial distribution (a.k.a categorical)

$$\Phi = \begin{matrix} & \begin{matrix} Unborn & Alive & Dead \end{matrix} \\ \begin{matrix} Unborn \\ Alive \\ Dead \end{matrix} & \begin{pmatrix} .7 & 0 & 0 \\ .3 & .9 & 0 \\ 0 & .1 & 1 \end{pmatrix} \end{matrix}$$


$$\text{unborn} \rightarrow z_1 \sim \text{Mult}([.7, .3, 0])$$

t_0 dummy
state t_1

Generative Model for POPAN (4)

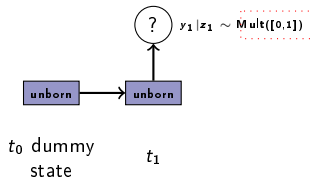
We got $z_1 = 1$! (unborn)!

Next: Sample a capture $y_1 | z_1$

Use column 1 from $\Psi[, 1]$ (because $z_1 = 1$)

Use the Multinomial Distribution

$$\Phi = \begin{matrix} & \begin{matrix} Unborn & Alive & Dead \end{matrix} \\ \begin{matrix} Unborn \\ Alive \\ Dead \end{matrix} & \begin{pmatrix} .7 & 0 & 0 \\ .3 & .9 & 0 \\ 0 & .1 & 1 \end{pmatrix} \end{matrix}$$
$$\Psi = \begin{matrix} & \begin{matrix} Unborn & Alive & Dead \end{matrix} \\ \begin{matrix} Capture \\ No Capt \end{matrix} & \begin{pmatrix} 0 & .5 & .0 \\ 1 & .5 & 1 \end{pmatrix} \end{matrix}$$



Generative Model for POPAN (5)

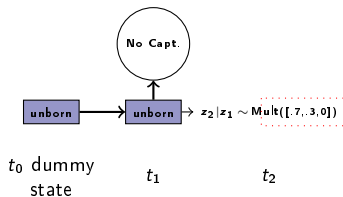
We got $y_1 = 2!$ (No-capture)

Next: sample $z_2|z_1$ at $t=2$.

Use column 1 from $\Phi[., 1]$ (because $z_1 = 1$)

$$\Phi = \begin{matrix} & \begin{matrix} Unborn & Alive & Dead \end{matrix} \\ \begin{matrix} Unborn \\ Alive \\ Dead \end{matrix} & \begin{pmatrix} .7 & 0 & 0 \\ .3 & .9 & 0 \\ 0 & .1 & 1 \end{pmatrix} \end{matrix}$$

$$\Psi = \begin{matrix} & \begin{matrix} Unborn & Alive & Dead \end{matrix} \\ \begin{matrix} Capture \\ No Capt \end{matrix} & \begin{pmatrix} 0 & .5 & .0 \\ 1 & .5 & 1 \end{pmatrix} \end{matrix}$$



Generative Model for POPAN (6)

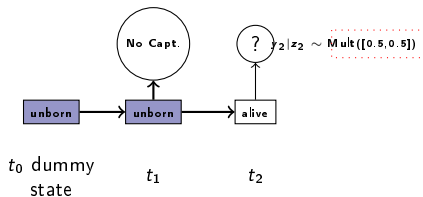
We got $z_2 = 2!$ (alive)

Next: Sample a capture $y_2 | z_2$

Use column 2 from $\Psi[, 2]$ (because $z_1 = 2$)

$$\Phi = \begin{matrix} & \begin{matrix} Unborn & Alive & Dead \end{matrix} \\ \begin{matrix} Unborn \\ Alive \\ Dead \end{matrix} & \begin{pmatrix} .7 & 0 & 0 \\ .3 & .9 & 0 \\ 0 & .1 & 1 \end{pmatrix} \end{matrix}$$

$$\Psi = \begin{matrix} & \begin{matrix} Unborn & Alive & Dead \end{matrix} \\ \begin{matrix} Capture \\ No Capt \end{matrix} & \begin{pmatrix} 0 & .5 & .0 \\ 1 & .5 & 1 \end{pmatrix} \end{matrix}$$



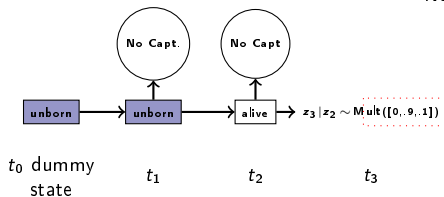
Generative Model for POPAN (7)

We got $y_2 = 2!$ (No-capture)

Next: sample $z_3|z_2$ at $t=3$.

Use column 2 from $\Phi[, 2]$ (because $z_2 = 2$)

$$\Phi = \begin{matrix} & \begin{matrix} \text{Unborn} & \text{Alive} & \text{Dead} \end{matrix} \\ \begin{matrix} \text{Unborn} \\ \text{Alive} \\ \text{Dead} \end{matrix} & \begin{pmatrix} .7 & 0 & 0 \\ .3 & .9 & 0 \\ 0 & .1 & 1 \end{pmatrix} \end{matrix}$$
$$\Psi = \begin{matrix} & \begin{matrix} \text{Unborn} & \text{Alive} & \text{Dead} \end{matrix} \\ \begin{matrix} \text{Capture} \\ \text{No Capt} \end{matrix} & \begin{pmatrix} 0 & .5 & .0 \\ 1 & .5 & 1 \end{pmatrix} \end{matrix}$$

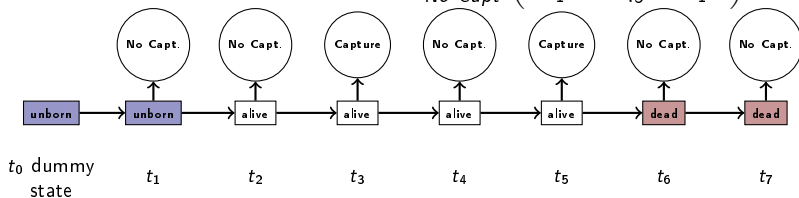


Generative Model for POPAN (n)

REPEAT UNTIL $t=7$

$$\Phi = \begin{matrix} & \begin{matrix} \text{Unborn} & \text{Alive} & \text{Dead} \end{matrix} \\ \begin{matrix} \text{Unborn} \\ \text{Alive} \\ \text{Dead} \end{matrix} & \begin{pmatrix} .7 & 0 & 0 \\ .3 & .9 & 0 \\ 0 & .1 & 1 \end{pmatrix} \end{matrix}$$

$$\Psi = \begin{matrix} & \begin{matrix} \text{Unborn} & \text{Alive} & \text{Dead} \end{matrix} \\ \begin{matrix} \text{Capture} \\ \text{No Capt} \end{matrix} & \begin{pmatrix} 0 & .5 & .0 \\ 1 & .5 & 1 \end{pmatrix} \end{matrix}$$



- Generated capture history: $\{0, 0, 1, 0, 1, 0, 0\}$

Generative Model for POPAN (in R)

conceptually simple generative HMM
in R, it would look like:

```
z<-numeric(7)
y<-numeric(7)
z[1]<-rmultinom(n=1,size=1,prob=PHI[,1]) # first primary
y[1]<-rmultinom(n=1,size=1,prob=PSI[,z[1]]) # first capture
for(t in 2:7){
  z[t]<-rmultinom(n=1,size=1,prob=PHI[,z[t-1]])
  y[t]<-rmultinom(n=1,size=1,prob=PSI[,z[t]])
}
```

conceptually simple generative HMM

- ▶ generate: \mathbf{y}^* given Φ (*transition matrix*) and Ψ (*emission matrix*) (via \mathbf{z})

BUT What about **inference** about Φ and Ψ for a *given* (\mathbf{y})?

- ▶ **Real Answer**: Forwards-Backwards algorithm²
- ▶ **Quick Answer** JAGS will take care of it for us...

so long as we specify:

- ▶ priors
- ▶ conditional data likelihood
- ▶ latent state process

²Commonly referenced tutorial: Rabiner et al.

HMM Matrices: Connection with CMR (CJS)

How to specify the emission and transition matrices for a CMR model?

Each cell in the matrices are parameterized by products of CMR parameters

Example in **Cormack Jolly Seber**:

Transition Matrix

from $t - 1$ to t

$$\Phi_t = \begin{array}{c} \text{Alive} \\ \text{Dead} \end{array} \begin{array}{cc} \text{Alive} & \text{Dead} \\ \left(\begin{array}{cc} \phi_{t-1} & 0 \\ 1 - \phi_{t-1} & 1 \end{array} \right) \end{array}$$

where:

- ▶ ϕ_{t-1} is the apparent survival between $t - 1$ and t

Emission Matrix

capture at t

$$\Psi_t = \begin{array}{c} \text{Capture} \\ \text{No Capture} \end{array} \begin{array}{cc} \text{Alive} & \text{Dead} \\ \left(\begin{array}{cc} p_t & 0 \\ 1 - p_t & 1 \end{array} \right) \end{array}$$

where

- ▶ p_t is the capture-probability at t

HMM Matrices: Connection with CMR (POPAN)

How to specify the emission and transition matrices for a CMR model?

Each cell in the matrices are parameterized by products of CMR parameters

Example in **POPAN**:

Transition Matrix

from $t - 1$ to t

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

where:

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

Emission Matrix

capture at t

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

- ▶ p_t is the capture-probability at t

HMM Matrices: Connection with CMR (PCRD)

Example in the **Pollock's Closed Robust Design** (*conditioning on first capture*):

Transition Matrix

from $t - 1$ to t

$$\Phi_t = \begin{matrix} & \begin{matrix} \text{Onsite} & \text{TE} & \text{Dead} \end{matrix} \\ \begin{matrix} \text{Onsite} \\ \text{TE} \\ \text{Dead} \end{matrix} & \begin{pmatrix} \phi_{t-1}(1-\gamma_t'') & \phi_{t-1}(1-\gamma_t') & 0 \\ \phi_{t-1}\gamma_t'' & \phi_{t-1}\gamma_t' & 0 \\ 1 - \phi_{t-1} & 1 - \phi_{t-1} & 1 \end{pmatrix} \end{matrix}$$

- ▶ ϕ_{t-1} is the apparent survival between primary periods $t - 1$ and t
- ▶ γ_t'' is the probability of becoming a temporary emigrant between $t - 1$ and t
- ▶ γ_t' is the probability of staying as a temporary emigrant between $t - 1$ and t

Emission Matrix

capture at s_t

$$\Psi_{s,t} = \begin{matrix} & \begin{matrix} \text{Onsite} & \text{TE} & \text{Dead} \end{matrix} \\ \begin{matrix} \text{Capture} \\ \text{No Capture} \end{matrix} & \begin{pmatrix} p_{s,t} & 0 & 0 \\ 1 - p_{s,t} & 1 & 1 \end{pmatrix} \end{matrix}$$

- ▶ $p_{s,t}$ is the capture-probability at *secondary period* s_t

HMM Matrices: Connection with CMR (PCRD)

Example in the **Pollock's Closed Robust Design** (*full capture* model):

Transition Matrix

from $t - 1$ to t

$$\Phi_t = \begin{array}{c} \text{Unborn} \\ \text{Onsite} \\ \text{TE} \\ \text{Dead} \end{array} \begin{array}{c} \text{Unborn} \\ \text{Onsite} \\ \text{TE} \\ \text{Dead} \end{array} \begin{pmatrix} 1 - \psi_t & 0 & 0 & 0 \\ \psi_t & \phi_{t-1}(1 - \gamma_t'') & \phi_{t-1}(1 - \gamma_t') & 0 \\ 0 & \phi_{t-1}\gamma_t'' & \phi_{t-1}\gamma_t' & 0 \\ 0 & 1 - \phi_{t-1} & 1 - \phi_{t-1} & 1 \end{pmatrix}$$

- ▶ ϕ_{t-1} is the apparent survival between primary periods $t - 1$ and t
- ▶ γ_t'' is the probability of becoming a temporary emigrant between $t - 1$ and t
- ▶ γ_t' is the probability of staying as a temporary emigrant between $t - 1$ and t
- ▶ ψ_t are "recruitment" parameters between $t - 1$ and t

Emission Matrix

$$\Psi_{s,t} = \begin{array}{c} \text{Capture} \\ \text{No Capture} \end{array} \begin{array}{c} \text{Unborn} \\ \text{Onsite} \\ \text{TE} \\ \text{Dead} \end{array} \begin{pmatrix} 0 & p_{s,t} & 0 & 0 \\ 1 & 1 - p_{s,t} & 1 & 1 \end{pmatrix}$$

Example in the **Multi-State Closed Robust Design** with 3 strata and TE (*first-capture* conditioning):

Transition Matrix

from $t - 1$ to t

$$\Phi_t = \begin{matrix} & \begin{matrix} \text{Strata A} & \text{Strata B} & \text{Strata C} & \text{TE} & \text{Dead} \end{matrix} \\ \begin{matrix} \text{Strata A} \\ \text{Strata B} \\ \text{Strata C} \\ \text{TE} \\ \text{Dead} \end{matrix} & \begin{pmatrix} \phi_{t-1}\gamma_t^{aa} & \phi_{t-1}\gamma_t^{ba} & \phi_{t-1}\gamma_t^{ca} & \phi_{t-1}\gamma_t^{ta} & 0 \\ \phi_{t-1}\gamma_t^{ab} & \phi_{t-1}\gamma_t^{bb} & \phi_{t-1}\gamma_t^{cb} & \phi_{t-1}\gamma_t^{tb} & 0 \\ \phi_{t-1}\gamma_t^{ac} & \phi_{t-1}\gamma_t^{bc} & \phi_{t-1}\gamma_t^{cc} & \phi_{t-1}\gamma_t^{tc} & 0 \\ \phi_{t-1}\gamma_t^{at} & \phi_{t-1}\gamma_t^{bt} & \phi_{t-1}\gamma_t^{ct} & \phi_{t-1}\gamma_t^{tt} & 0 \\ 1 - \phi_{t-1} & 1 - \phi_{t-1} & 1 - \phi_{t-1} & 1 - \phi_{t-1} & 1 \end{pmatrix} \end{matrix}$$

- ϕ_{t-1} is the apparent survival between primary periods $t - 1$ and t
- γ_t^{xy} are the probability of moving from strata X to Y between $t - 1$ and t , and $\gamma_t^{xa} + \gamma_t^{xb} + \gamma_t^{xc} + \gamma_t^{xt} = 1$

Example in the **Multi-State Closed Robust Design** with 3 strata and TE
(*first-capture* conditioning):

MSCRD Emission Matrix

$$\Psi_{s,t} = \begin{array}{c} \text{Capture A} \\ \text{Capture B} \\ \text{Capture C} \\ \text{No Capture} \end{array} \begin{pmatrix} \text{Strata A} & \text{Strata B} & \text{Strata C} & \text{TE} & \text{Dead} \\ p_{s,t}^a & 0 & 0 & 0 & 0 \\ 0 & p_{s,t}^b & 0 & 0 & 0 \\ 0 & 0 & p_{s,t}^c & 0 & 0 \\ 1 - p_{s,t}^a & 1 - p_{s,t}^b & 1 - p_{s,t}^c & 1 & 1 \end{pmatrix}$$

- $p_{s,t}^x$ is the capture probability per secondary period conditional on being in strata X at t

JAGS: How To Make a Matrix?

A POPAN (unrealistic³) Example: making a matrix in JAGS

```
# FROM unborn (col1) to...
tr[1,1] <- 1-psi # unborn to unborn
tr[2,1] <- psi   # unborn to alive
tr[3,1] <- 0     # (illegal)
# FROM alive (col2) to...
tr[1,2] <- 0     # (illegal)
tr[2,2] <- phi   # alive to alive
tr[3,2] <- 1-phi # alive to dead
# FROM dead (col3) to...
tr[1,3] <- 0     # (illegal)
tr[2,3] <- 0     # (illegal)
tr[3,3] <- 1     # dead to dead
```

Note: `matrix[r, c]` :

- ▶ 1st integer is the row,
- ▶ 2nd is the column (like R)

³in practise, the recruitment parameters are always time-varying

Let's do a simple HMM in JAGS

Parameters:

- ▶ ϕ time-constant survival (`phi`)
- ▶ ψ time-constant "recruitment" (`psi`)
- ▶ p time-constant capture probability (`p`)

Goal:

- ▶ *inference* about `phi`, `psi`
- ▶ demonstrate the latent states posterior distribution `z`

Inputs

- ▶ One capture history: `y<-c(0,0,0,0,1,0,1,1,0,0,0)`
- ▶ `T=11` capture periods
- ▶ prior parameters: `pr.phi`, `pr.psi`, `pr.p`

- In JAGS:

```
# specify the priors
p ~ dbeta(pr.p[1], pr.p[2]) # prior on capture history
phi ~ dbeta(pr.phi[1], pr.phi[2]) # prior on survival
psi ~ dbeta(pr.psi[1], pr.psi[2]) # prior on recruitment
```

- On the R side:

```
jags.data<-list(
  pr.p=c(1,1), # flat prior on capture probability
  pr.phi=c(1,1),# flat prior on survival
  pr.psi=c(1,1) # flat prior on recruitment
)
```

- Qu: why beta?⁴

⁴reasonable distribution for probability parameters

```
# specify the conditional data likelihood
for(t in 1:length(y)){ # loop through capture periods
  y[t] ~ dcat(em[,z[t]])
}
```

... where `em` is the emission matrix

1 Qu: Why `dcat` and not `dbern` ? ⁵

2 QU: Why is it called the “conditional” likelihood? ⁶

⁵We could use `dbern`. The Multinoulli distribution (`dcat`) generalizes the Bernoulli for more than 2 outcomes.

⁶Conditional on the value of `z[t]`

```
# specify the latent state process (for t=1)
z[1] ~ dcat(tr[,1])
# specify the latent state process (for t>1)
for(t in 2:length(y)){
  z[t] ~ dcat(tr[,z[t]])
}
```

...where `tr` is the transition matrix

- Qu: why is $t=1$ handled differently from $t > 1$ ⁷

⁷The latent state process is Markovian, depends on values one-step-back. For $t=1$, there is no one-step-back with observation information.

Transition Matrix

```
# Build the Transition Mat
# state 1
tr[1,1]<-1-psi
tr[2,1]<-psi
tr[3,1]<-0
# state 2
tr[1,2]<-0
tr[2,2]<-phi
tr[3,2]<-1-phi
# state 3
tr[1,3]<-0
tr[2,3]<-0
tr[3,3]<-1
```

Emission Matrix

```
# Build the Emission Mat
# state 1: unborn (100% no capture)
em[1,1]<-1
em[2,1]<-0
# state 2: alive
em[1,2]<-1-p
em[2,2]<-p
# state 3: dead (100% no capture)
em[1,3]<-1
em[2,3]<-0
```

where $y=1 \equiv$ no-capture and $y=2 \equiv$ capture

Time to open up JAGS!

open the file `PART4_introHMM/R_hmm_intro.R` and see exercise 1