## Bayesian State Space Models

ESS 575 Models for Ecological Data

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# Roadmap

- Overview
- Model types with examples
  - discrete time
    - single state
    - multiple states
  - continuous time (briefly)
- Forecasting
- Coding tips

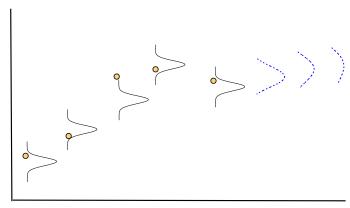
Coding tips

## What are state space models?

$$[y_t|\boldsymbol{\theta}_d, z_t]$$
$$[z_t|\boldsymbol{\theta}_p, z_{t-1}]$$

The idea is simple. We have a stochastic model of an unobserved, true state  $(z_t)$  and a stochastic model that relates our observations  $(y_t)$  to the true state.

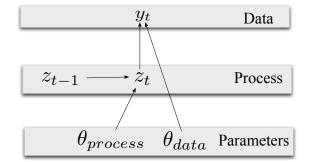
Overview



Time

# A broadly applicable approach to modeling dynamic processes in ecology

$$\begin{split} [\mathbf{z}, \theta_{process}, \theta_{data} | \mathbf{y}] &\propto \\ &\prod_{t=2}^{T} [y_t | \theta_{data}, z_t] [z_t | \theta_{process}, z_{t-1}] [\theta_{process}, \theta_{data}, z_1] \end{split}$$



## Sources of uncertainty in state space models

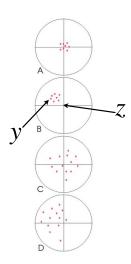
#### Process uncertainty

- Failure to perfectly represent process
- Propagates in time
- Decreases with model improvement
- Estimation allows forecasting

#### Observation uncertainty

- Failure to perfectly observe process
- Does not propagate
- ► Sampling uncertainty decreases with increased sampling effort.
- Measurement uncertainly decreases with improved instrumentation, calibration, etc.

## Components of observation uncertainty



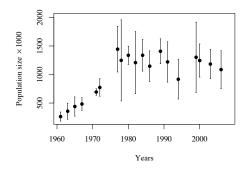
- Measurement  $[y|h(z,\theta_d),\sigma_{measurement}^2]$
- ▶ Sampling  $[y|z, \sigma_{sampling}^2]$

# When can we separate process variance from observation variance?

- ▶ Replication of the observation for the same latent state
- Calibration model with properly estimate prediction variance
- Strongly differing "structure" in process and observation models
- We may not need to separate them—sometimes the observed state and the true state are the same.

Deterministic model = 
$$g(\boldsymbol{\theta}_{process}, z_{t-1}, \mathbf{x}_{t-1})$$
  
 $[\mathbf{z}, \boldsymbol{\theta}_{process}, \boldsymbol{\theta}_{data}, \sigma_p^2, \sigma_d^2 | \mathbf{y}] \propto \prod_{t=2}^T [y_t | \boldsymbol{\theta}_{data}, z_t, \sigma_o^2]$   
 $\times [z_t | g(\boldsymbol{\theta}_{process}, z_{t-1}, \mathbf{x}_{t-1}), \sigma_p^2]$   
 $\times [\boldsymbol{\theta}_{process}, \boldsymbol{\theta}_{data}, \sigma_p^2, \sigma_o^2, z_1]$ 

## Modeling the Serengeti wildebeest population





- ▶ 48 year time series
- Annual means and standard deviations of population size for 19 years
- Spatially replicated census
- Annual data on dry season rainfall



## How does rainfall influence density dependence?

$$g(\boldsymbol{\beta}, z_{t-1}, x_{t-1}) = z_{t-1} e^{(\beta_0 + \beta_1 z_{t-1} + \beta_2 x_{t-1} + \beta_3 z_{t-1} x_{t-1})\Delta t}$$

- $ightharpoonup z_t = ext{true population size}$
- $x_{t-1} = \text{standardized}$ , annual dry season rainfall during time t-1 to t.
- $m{\beta}_0 = r_{max} = ext{intrinsic}$ , per-capita rate of increase at average rainfall
- $m m eta_1 =$  strength of density dependence,  $rac{r}{K}$  at average rainfall.
- $m{\beta}_2 = \text{change in rate of increase per standard deviation change in rainfall}$
- ho  $ho_3 =$  effect of rainfall on strength of density dependence

$$z_t \sim \mathsf{lognormal}\left(\log\left(g\left(oldsymbol{eta}, z_{t-1}, x_{t-1}
ight)
ight), oldsymbol{\sigma}_p^2
ight)$$

- ▶  $\log(g(\pmb{\beta}, z_{t-1}, x_{t-1}))$ , the centrality parameter, the mean of  $z_t$  on the log scale
- lacksquare  $\sigma_p^2$ , the scale parameter, the variance of  $z_t$  on the log scale
- What does the deterministic model predict?
  - $\triangleright$  define centrality parameter =  $\alpha_1$
  - ightharpoonup median $(z_t) = e^{\alpha_t}$
  - $ightharpoonup \alpha_t = \log(\operatorname{median}(z_t))$
  - ▶ median  $(z_t) = g(\beta, z_{t-1}, x_{t-1})$

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# Review of relationships between normal and lognormal

- 1.  $z_t = g\left(\boldsymbol{\beta}, z_{t-1}, x_{t-1}\right) \exp\left(\boldsymbol{\varepsilon}_t\right), \ \boldsymbol{\varepsilon}_t \sim \operatorname{normal}\left(0, \sigma_p^2\right)$
- 2.  $\log(z_t) = \log(g(\boldsymbol{\beta}, z_{t-1}, x_{t-1})) + \varepsilon_t, \ \varepsilon_t \sim \text{normal}(0, \sigma_p^2)$
- 3.  $\log(z_t) \sim \text{normal}\left(\log\left(g\left(\boldsymbol{\beta}, z_{t-1}, x_{t-1}\right)\right), \sigma_p^2\right)$
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## Review of relationships between normal and lognormal

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### It is also possible to moment match the mean

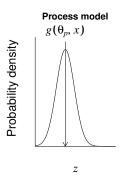
$$\mu_t = g(\boldsymbol{\beta}, z_{t-1}, x_{t-1}) \tag{1}$$

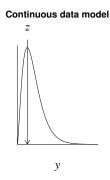
$$\alpha_t = \log(\mu_t) - \frac{1}{2} \log\left(\frac{\mu_t^2 + \sigma^2}{\mu_t^2}\right) \tag{2}$$

$$z_t \sim \mathsf{lognormal}(\alpha_t, \sigma^2)$$
 (3)

You should do it this way if you have derived quantities computed as sums of the  $z_t$ , for example when modeling a total population from subpopulations in different sites.

#### Why a continuous distribution for a "discrete state"?







#### The data

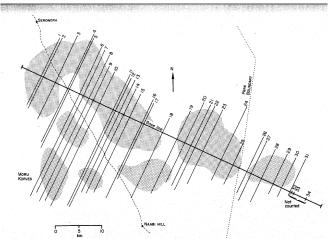


Fig. 2. The orientation of the base-line and of the random transects in the May 1971 sample count. Shading shows approximate positions of the main wildebeest herds.



#### Observation model

$$y_t \sim \mathsf{normal}\left(z_t, y.sd_t\right)$$

- $\triangleright$   $y_t$  is the observed mean number of animals across all transects
- $lacktriangleq y.sd_t$  is the observed standard deviation across transects
- z<sub>t</sub> is the unobserved, true state, the mean of the data distribution

We choose a normal distribution for the likelihood because the  $y_t$  are the annual mean of means of densities of wildebeest on many transects. For now, we ignore the potential for spatial autocorrelation among transects.

Overview

$$\begin{split} \left[\mathbf{z}, \pmb{\beta}, \sigma_p^2 | \mathbf{y}\right] & \propto \underbrace{\prod_{\forall t \in \mathbf{y}.i} \left[y_t \mid z_t, y.sd_t\right]}_{\text{data model}} \\ & \times \underbrace{\prod_{t=2}^{48} \left[z_t | g\left(\pmb{\beta}, z_{t-1}, x_{t-1}\right), \sigma_p^2\right]}_{\text{process model}} \times \underbrace{\left[\beta_0\right] \left[\beta_1\right] \left[\beta_2\right] \left[\beta_3\right] \left[\sigma_p^2\right] \left[z_1\right]}_{\text{parameter models}} \end{split}$$

- ightharpoonup y.i is a vector of years with non-missing census data
- $ightharpoonup y_t \sim \mathsf{normal}(z_t, y.sd_t)$
- $ightharpoonup z_t \sim \mathsf{lognormal}\left(\log\left(g\left(oldsymbol{\beta}, z_{t-1}, x_{t-1}
  ight)\right), oldsymbol{\sigma}_p^2\right)$
- $\beta_0 \sim \text{normal}\left(.234,.136^2\right)$  informative prior
- ▶  $\beta_{i \in 1,2,3} \sim \text{normal}(0,1000)$
- $\sigma_p^2 \sim \text{gamma}(.01,.01)$
- $ightharpoonup z_1 \sim \mathsf{normal}(y_1, y.sd_1)$



#### Autocorrelation?

#### Observation errors:

$$egin{array}{ll} y_t &=& z_t + oldsymbol{arepsilon}_{obs,t} \ &\sim & {\sf normal}\left(0, oldsymbol{\sigma}^2
ight) \end{array}$$

$$\boldsymbol{\varepsilon}_{obs,t} \sim iid$$

# General joint and posterior distribution for multi-state model

$$\begin{split} \pmb{\mu}_t &= \mathbf{A}\mathbf{z}_t, \text{ process parameters are elements of matrix } \mathbf{A} \\ & \left[\mathbf{z}, \pmb{\theta}_{process}, \pmb{\theta}_{data} \middle| \mathbf{Y} \right] \propto \\ & \prod_{t=2}^T \left[\mathbf{y}_t \middle| \pmb{\theta}_{data}, \mathbf{z}_t \right] \left[\mathbf{z}_t \middle| \pmb{\mu}_t \right] \left[\pmb{\theta}_{process}, \pmb{\theta}_{data}, \mathbf{z}_1 \right] \end{split}$$

## Multiple states: Ann Raiho's matrix model<sup>1</sup>



- Problem: Evaluate management alternatives for managing overabundant deer in national parks.
- Data
  - Annual census, corrected for uncounted animals using distance sampling
  - Annual classification counts

<sup>&</sup>lt;sup>1</sup>Raiho, A. M., M. B. Hooten, S. Bates, and N. T. Hobbs. 2015. Forecasting the effects of fertility control on overabundant ungulates: white-tailed deer in the National Capital Region. PLoS ONE 10. 10.1371/journal.pone.0143122 ⟨♂ → ⟨ ≧ → ⟨ ∠ → ⟨ → ⟨ ∆ → ¬ ∧ ¬ ∧ ¬ ) | ¬ ⟩ | ) } } )

#### **States**

state	definition
$n_1$	The number of juvenile deer, aged 6 months on their
	first census
$n_2$	The number of adult female deer, aged 18 months and
	older
$n_3$	The number of adult male deer, aged 18 months and
	older

#### Deterministic Model

m

number of recruits per female surviving to census probability that a juvenile (aged 6 months) survives to 18 months annual survival probabilty of adult females  $\phi_d$  $\phi_b$ annual survival probability of adult males proportion of juveniles surviving to adults that are female

$$\mathbf{A} = \begin{pmatrix} 0 & \phi_d^{\frac{1}{2}} f & 0 \\ m \phi_j & \phi_d & 0 \\ (1-m) \phi_j & 0 & \phi_b \end{pmatrix}$$

# The posterior and joint distribution

$$\underbrace{\begin{bmatrix} \pmb{\phi}, m, f, \mathbf{N}, & \pmb{\sigma}_p, \pmb{\rho} & | \mathbf{y}^{\mathsf{census}}, \mathbf{y}^{\mathsf{census}.\mathsf{sd}}, \mathbf{Y}^{\mathsf{class}} \end{bmatrix}}_{\mathsf{elements of } \mathbf{\Sigma}} \propto \underbrace{\underbrace{\begin{bmatrix} T \\ t=2 \end{bmatrix}}_{\mathsf{process model}} (\log(\mathbf{n}_t) | \log(\mathbf{A}_t \mathbf{n}_{t-1}), \mathbf{\Sigma})}_{\mathsf{process model}} }_{\mathsf{process model}} \times \mathsf{data models} \times \mathsf{priors}$$

## The posterior and joint distribution

Overview

#### The posterior and joint distribution

$$\left[ \boldsymbol{\phi}, m, f, \mathbf{N}, \quad \underbrace{\boldsymbol{\sigma}_p, \boldsymbol{\rho}}_{\text{elements of } \boldsymbol{\Sigma}} | \mathbf{y}^{\text{census}}, \mathbf{y}^{\text{census.sd}}, \mathbf{Y}^{\text{class}} \right] \quad \propto \quad$$

$$\prod_{t=2}^{T}$$
 multivariate normal  $(\log(\mathbf{n}_t)|\log\left(\mathbf{A}_t\mathbf{n}_{t-1}
ight), \mathbf{\Sigma})$ 

process model

$$\times \prod_{t=2}^{T} \underbrace{\mathsf{normal}\left(y_t^{\mathsf{census}} | \sum_{i=1}^{3} n_{i,t}, y_t^{\mathsf{census.sd}}\right)}_{}$$

data model 1

$$\times \text{multinomial}\left(\mathbf{y}^{\text{class}}_t \ \middle| \ \left(\frac{n_{1,t}}{\sum_{i=1}^3 n_{i,t}}, \frac{n_{2,t}}{\sum_{i=1}^3 n_{i,t}}, \frac{n_{1,t}}{\sum_{i=1}^3 n_{i,t}}\right), \sum_{i=1}^3 y^{\text{class}}_{i,t}\right)$$

data model 2

#### Continuous time models

$$\frac{dz_1}{dt} = k_1 z_1 - k_2 z_1 z_2 (4)$$

$$\frac{dz_2}{dt} = -k_3 z_1 + \alpha k_2 z_1 z_2 \tag{5}$$

$$\frac{dz_3}{dt} = \frac{k_4 z_3}{k_5 + z_3} \tag{6}$$

$$\left[\mathbf{z_t}|g\left(\left(\mathbf{k},\mathbf{z}_{t-1},x_t\right),\boldsymbol{\sigma}_p^2\right]\right]$$

Implementing the process model may need a numerical solver to align the states with the data.

#### Continuous time models

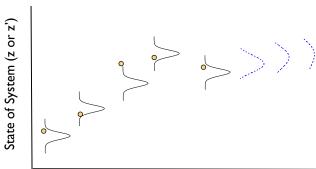
- Must deterministically update states at discrete intervals to match with data
- ▶ To estimate states:
  - Use analytical solutions to ODE system if available.
  - For models without analytical solutions:
    - OpenBUGS and STAN have ODE solvers.
    - Euler's or Runge-Kutta IV can be embedded in JAGS or OpenBUGS for simple models.
    - Best: Write your own MCMC sampler with embedded numerical solver.
    - See: Campbell, E. E., W. J. Parton, J. L. Soong, K. Paustian, N. T. Hobbs, and M. F. Cotrufo. 2016. Using litter chemistry controls on microbial processes to partition litter carbon fluxes with the Litter Decomposition and Leaching (LIDEL) model. Soil Biology & Biochemistry 100:160-174.

## Bayesian forecasting future states z'

$$[z'_{T+1}|\mathbf{y}]$$
 =

predictive process distribution

$$\int_{\theta_1...\theta_P} \int_{z_1...} \int_{z_T} \left[ z'_{T+1} | \mathbf{z}, \boldsymbol{\theta}_{process} \right] \underbrace{\left[ \mathbf{z}, \boldsymbol{\theta}_{process}, \boldsymbol{\theta}_{data} | \mathbf{y} \right]}_{\text{posterior distribution}} dz...dz_t d\theta_1...d\theta_P$$



Time 36/54

# Predictive process distribution

#### The MCMC output:

```
n =  number of iterations T =  final time with data
```

F = number of forecasts beyond data

$$\begin{aligned} \boldsymbol{\mu}_t &= g(\boldsymbol{\theta}_{process}, z_{t-1}, \mathbf{x}_{t-1}) \\ & [\mathbf{z}, \boldsymbol{\theta}_{process}, \boldsymbol{\theta}_{data} | \mathbf{y}] \propto \\ & \prod_{t=2}^T [y_t | \boldsymbol{\theta}_{data}, z_t] \prod_{t=2}^{T+F} [z_t | \boldsymbol{\mu}_t] [\boldsymbol{\theta}_{process}, \boldsymbol{\theta}_{data}, z_1] \end{aligned}$$

# Posterior and joint distribution with missing data

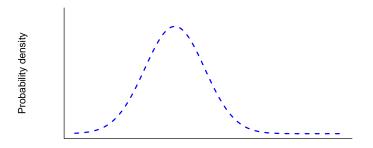
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# Forecasting

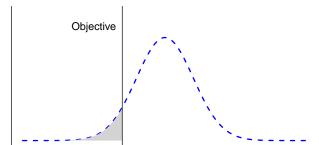
#### The fundamental problem of management:

What actions can we take today that will allow us to meet goals for the future?



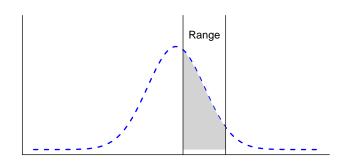


#### Objective: reduce state below a target



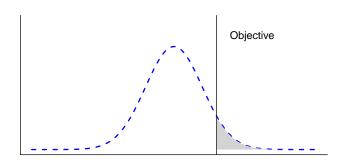
Future state z'

#### Objective: maintain state within acceptable range

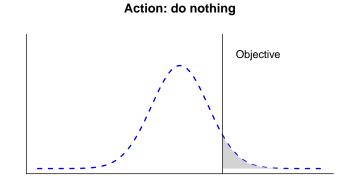


Future state z'

#### Objective: increase state above a target

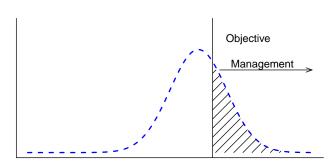


Future state z'



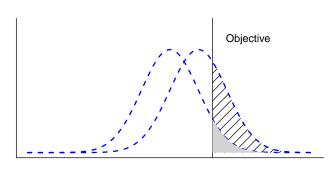
Future state z'

#### **Action: implement managment**



Future state of system, z'

#### Net effect of management



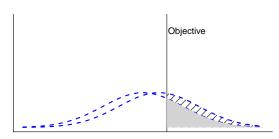
Probability density

Future state z'

Hobbs, N. T., C. Geremia, J. Treanor, R. Wallen, P. J. White, M. B. Hooten, and J. C. Rhyan. 2015. State-space modeling to support management of brucellosis in the Yellowstone bison population. Ecological Monographs 85:3-28.

# Probability density

#### Net effect of management



Future state z'

# JAGS code for posterior and joint distributions

$$\left[\mathbf{z}, \pmb{\beta}, \sigma_p^2 | \mathbf{y}\right] \propto \underbrace{\prod_{\forall t \in \mathcal{Y}.i} \left[ y_t \mid z_t, y.sd_t \right]}_{\text{data model}}$$

Overview

$$\underbrace{\underbrace{\prod_{t=2}^{48} \left[z_{t} | g\left(\pmb{\beta}, z_{t-1}, x_{t-1}\right), \sigma_{p}^{2}\right]}_{\text{process model}} \times \underbrace{\left[\beta_{0}\right] \left[\beta_{1}\right] \left[\beta_{2}\right] \left[\beta_{3}\right] \left[\sigma_{p}^{2}\right] \left[z_{1}\right]}_{\text{parameter models}}$$

```
model{
#Priors
b[1] ~ dnorm(.234,1/.136^2)
for(i in 2:n.coef){
b[j] ~ dnorm(0,.0001)
tau.p ~ dgamma(.01..01)
sigma.p <- 1/sqrt(tau.p)
      ~ dnorm(N.obs[1],tau.obs[1]) #this must be treated as prior so that you have z[t-
##Process model
for(t in 2:(T+F)){
mu[t] \leftarrow log(z[t-1]*exp(b[1] + b[2]*z[t-1] + b[3]*x[t] + b[4]*x[t]*z[t-1]))
z[t] ~ dlnorm(mu[t], tau.p)
#Data model
for(i in 2:n.obs){
N.obs[j] ~ dnorm(z[index[j]],tau.obs[j]) #index to match z[t] with data
}#end of model
                                                            4 日 5 4 周 5 4 3 5 4 3 5 6
```

# Posterior predictive checks for time series data

Test statistic:

Overview

$$\frac{1}{T-1} \sum_{t=2}^{T} |y_t - y_{t-1}| \tag{7}$$

Conventional statistics are also used (mean, CV, discrepancy statistic for the  $y_t$ .

Reilly, C., A. Gelman, and J. Katz, 2001. Poststratification without Population Level Information 731 on the Poststratifying Variable, with Application to Political Polling. Journal of the American 732 Statistical Association 96:1–11.

## Posterior predictive checks and test for autocorrelation

```
#Derived quantities for model evaluation
for(i in 1:n.obs){
     #for auto correlation test
epsilon.obs[i] <- N.obs[i] - z[index[i]]</pre>
 # simulate new data
         N.new[i] ~ dnorm(z[index[i]],tau.obs[i])
sq[i] \leftarrow (N.obs[i] - z[index[i]])^2
sq.new[i] < -(N.new[i] - z[index[i]])^2
fit <- sum(sq[])</pre>
fit.new <- sum(sq.new[])</pre>
pvalue <-step(fit.new-fit)</pre>
```

### Slicer errors

Fix: Make offending priors less vague:

```
#right
tau.p ~ dgamma(.01, .01)
sigma.p <- 1/sqrt(tau.p)
#or
tau.p ~ dunif(0,200) # depends on scale
sigma.p <- 1/sqrt(tau.p)</pre>
#or
sigma.p ~ dunif(0, 10)
tau.p <- 1/sqrt(sigma.p)</pre>
#Instead of:
#wrong
tau.p ~ dgamma(.0001, .0001)
sigma.p <- 1/sqrt(tau.p)</pre>
```

#### An odd error

```
Error in jags.samples(model, vari-
able.names, n.iter, thin, type = "trace", : Failed to s
itor for node .....
```

You have a variable in the variable.names vector of your coda.samples or jags.samples function that is not in your model or you have a vector of derived quantities and you never calculate the first value.