

# Bayesian State Space Models

## Bayesian Modeling for Socio-Environmental Data

N. Thompson Hobbs

August 10, 2016



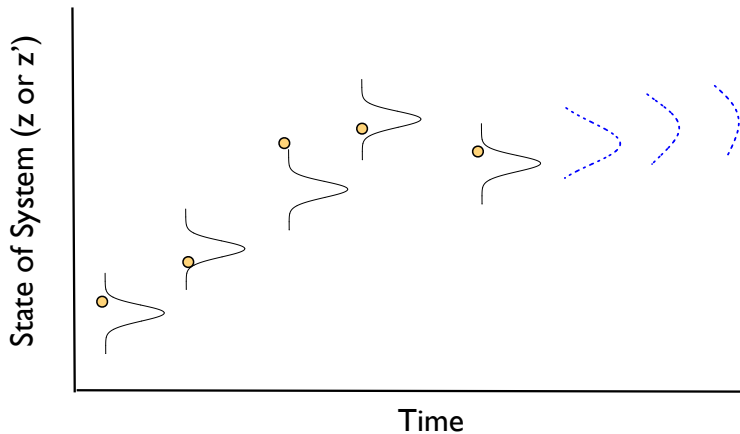
# Roadmap

- ▶ Overview
- ▶ Model types with examples
  - ▶ discrete time
  - ▶ continuous time (briefly)
- ▶ Forecasting
- ▶ Coding tips (later, in lab)

# What are state space models?

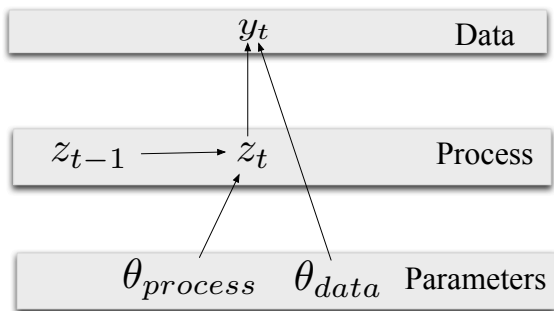
$$\begin{aligned} &[y_t | \boldsymbol{\theta}_d, z_t] \\ &[z_t | \boldsymbol{\theta}_p, z_{t-1}] \end{aligned}$$

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.



# A broadly applicable approach to modeling dynamic processes in ecology

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



# Sources of uncertainty in state space models

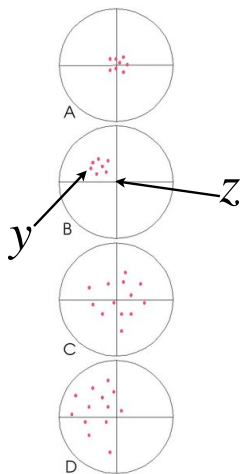
## Process uncertainty

- ▶ 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 uncertainty decreases with improved instrumentation, calibration, etc.

# Components of observation uncertainty



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

# When can we separate process variance from observation variance?

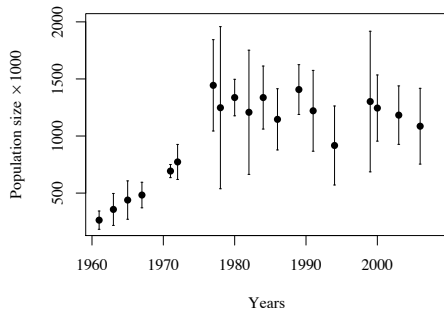
- ▶ Replication of the observation for the same latent state
- ▶ Calibration model with properly estimate prediction variance
- ▶ Strongly differing “structure” in process and observation models
- ▶ We may not need to separate them—sometimes the observed state and the true state are the same.



# General joint and posterior distribution for single state model

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

# 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?

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

- ▶  $z_t$  = true population size
- ▶  $x_{t-1}$  = standardized, annual dry season rainfall during time  $t-1$  to  $t$ .
- ▶  $\beta_0 = r_{max}$  = intrinsic, per-capita rate of increase at average rainfall
- ▶  $\beta_1$  = strength of density dependence,  $\frac{r}{K}$  at average rainfall.
- ▶  $\beta_2$  = change in rate of increase per standard deviation change in rainfall
- ▶  $\beta_3$  = effect of rainfall on strength of density dependence

# Process model

$$z_t \sim \text{lognormal}(\log(g(\boldsymbol{\beta}, z_{t-1}, x_{t-1})), \sigma_p^2)$$

- ▶  $\log(g(\boldsymbol{\beta}, z_{t-1}, x_{t-1}))$ , the centrality parameter, the mean of  $z_t$  on the log scale
- ▶  $\sigma_p^2$ , the scale parameter, the variance of  $z_t$  on the log scale
- ▶ What does the deterministic model predict?
  - ▶ define centrality parameter  $= \alpha$
  - ▶  $\text{median}(z_t) = e^\alpha$
  - ▶  $\alpha = \log(\text{median}(z_t))$
  - ▶  $\text{median}(z_t) = g(\boldsymbol{\beta}, z_{t-1}, x_{t-1})$

# Process model

$$z_t \sim \text{lognormal}(\log(g(\boldsymbol{\beta}, z_{t-1}, x_{t-1})), \sigma_p^2)$$

- ▶  $\log(g(\boldsymbol{\beta}, z_{t-1}, x_{t-1}))$ , the centrality parameter, the mean of  $z_t$  on the log scale
- ▶  $\sigma_p^2$ , the scale parameter, the variance of  $z_t$  on the log scale
- ▶ What does the deterministic model predict?
  - ▶ define centrality parameter =  $\alpha$
  - ▶  $\text{median}(z_t) = e^\alpha$
  - ▶  $\alpha = \log(\text{median}(z_t))$
  - ▶  $\text{median}(z_t) = g(\boldsymbol{\beta}, z_{t-1}, x_{t-1})$

# Process model

$$z_t \sim \text{lognormal}(\log(g(\boldsymbol{\beta}, z_{t-1}, x_{t-1})), \sigma_p^2)$$

- ▶  $\log(g(\boldsymbol{\beta}, z_{t-1}, x_{t-1}))$ , the centrality parameter, the mean of  $z_t$  on the log scale
- ▶  $\sigma_p^2$ , the scale parameter, the variance of  $z_t$  on the log scale
- ▶ What does the deterministic model predict?
  - ▶ define centrality parameter  $= \alpha$
  - ▶  $\text{median}(z_t) = e^\alpha$
  - ▶  $\alpha = \log(\text{median}(z_t))$
  - ▶  $\text{median}(z_t) = g(\boldsymbol{\beta}, z_{t-1}, x_{t-1})$

# Process model

$$z_t \sim \text{lognormal}(\log(g(\boldsymbol{\beta}, z_{t-1}, x_{t-1})), \sigma_p^2)$$

- ▶  $\log(g(\boldsymbol{\beta}, z_{t-1}, x_{t-1}))$ , the centrality parameter, the mean of  $z_t$  on the log scale
- ▶  $\sigma_p^2$ , the scale parameter, the variance of  $z_t$  on the log scale
- ▶ What does the deterministic model predict?
  - ▶ define centrality parameter  $= \alpha$
  - ▶  $\text{median}(z_t) = e^\alpha$
  - ▶  $\alpha = \log(\text{median}(z_t))$
  - ▶  $\text{median}(z_t) = g(\boldsymbol{\beta}, z_{t-1}, x_{t-1})$

# Process model

$$z_t \sim \text{lognormal}(\log(g(\boldsymbol{\beta}, z_{t-1}, x_{t-1})), \sigma_p^2)$$

- ▶  $\log(g(\boldsymbol{\beta}, z_{t-1}, x_{t-1}))$ , the centrality parameter, the mean of  $z_t$  on the log scale
- ▶  $\sigma_p^2$ , the scale parameter, the variance of  $z_t$  on the log scale
- ▶ What does the deterministic model predict?
  - ▶ define centrality parameter  $= \alpha$
  - ▶  $\text{median}(z_t) = e^\alpha$
  - ▶  $\alpha = \log(\text{median}(z_t))$
  - ▶  $\text{median}(z_t) = g(\boldsymbol{\beta}, z_{t-1}, x_{t-1})$



# Review of relationships between normal and lognormal

1.  $z_t = g(\boldsymbol{\beta}, z_{t-1}, x_{t-1}) \exp(\varepsilon_t)$ ,  $\varepsilon_t \sim \text{normal}(0, \sigma_p^2)$
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.  $\log(z_t) \sim \text{normal}(\log(g(\boldsymbol{\beta}, z_{t-1}, x_{t-1})), \sigma_p^2)$
4.  $z_t \sim \text{lognormal}\left(\underbrace{\log(g(\boldsymbol{\beta}, z_{t-1}, x_{t-1}))}_{\text{centrality parameter}}, \underbrace{\sigma_p^2}_{\text{scale parameter}}\right)$

# Review of relationships between normal and lognormal

1.  $z_t = g(\boldsymbol{\beta}, z_{t-1}, x_{t-1}) \exp(\varepsilon_t)$ ,  $\varepsilon_t \sim \text{normal}(0, \sigma_p^2)$
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.  $\log(z_t) \sim \text{normal}(\log(g(\boldsymbol{\beta}, z_{t-1}, x_{t-1})), \sigma_p^2)$
4.  $z_t \sim \text{lognormal}\left(\underbrace{\log(g(\boldsymbol{\beta}, z_{t-1}, x_{t-1}))}_{\text{centrality parameter}}, \underbrace{\sigma_p^2}_{\text{scale parameter}}\right)$

# Review of relationships between normal and lognormal

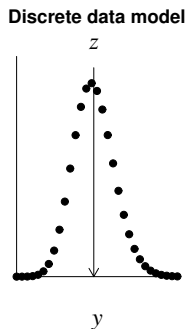
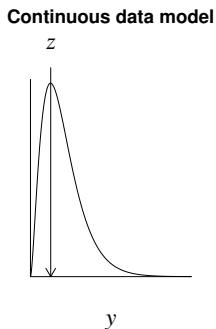
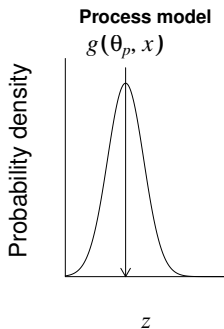
1.  $z_t = g(\boldsymbol{\beta}, z_{t-1}, x_{t-1}) \exp(\varepsilon_t)$ ,  $\varepsilon_t \sim \text{normal}(0, \sigma_p^2)$
2.  $\log(z_t) = \log(g(\boldsymbol{\beta}, z_{t-1}, x_{t-1})) + \varepsilon_t$ ,  $\varepsilon_t \sim \text{normal}(0, \sigma_p^2)$
3.  $\log(z_t) \sim \text{normal}(\log(g(\boldsymbol{\beta}, z_{t-1}, x_{t-1})), \sigma_p^2)$

4.  $z_t \sim \text{lognormal}\left(\underbrace{\log(g(\boldsymbol{\beta}, z_{t-1}, x_{t-1}))}_{\text{centrality parameter}}, \underbrace{\sigma_p^2}_{\text{scale parameter}}\right)$

# Review of relationships between normal and lognormal

1.  $z_t = g(\boldsymbol{\beta}, z_{t-1}, x_{t-1}) \exp(\varepsilon_t)$ ,  $\varepsilon_t \sim \text{normal}(0, \sigma_p^2)$
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.  $\log(z_t) \sim \text{normal}(\log(g(\boldsymbol{\beta}, z_{t-1}, x_{t-1})), \sigma_p^2)$
4.  $z_t \sim \text{lognormal}\left(\underbrace{\log(g(\boldsymbol{\beta}, z_{t-1}, x_{t-1}))}_{\text{centrality parameter}}, \underbrace{\sigma_p^2}_{\text{scale parameter}}\right)$

# Why a continuous distribution for a “discrete state”?



# Observation model

$$y_t \sim \text{normal}(z_t, y.sd_t)$$

- ▶  $y_t$  is the observed mean number of animals across all transects
- ▶  $y.sd_t$  is the observed standard deviation across transects
- ▶  $z_t$  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.

## Posterior and joint distributions

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

- ▶  $\mathbf{y}.i$  is a vector of years with non-missing census data
- ▶  $y_t \sim \text{normal}(z_t, y.sd_t)$
- ▶  $z_t \sim \text{lognormal}(\log(g(\boldsymbol{\beta}, z_{t-1}, x_{t-1})), \sigma_p^2)$
- ▶  $\beta_1 \sim \text{normal}(.234, .136^2)$  informative prior
- ▶  $\beta_{i \in 2,3} \sim \text{normal}(0, 1000)$
- ▶  $\sigma_p^2 \sim \text{gamma}(.01, .01)$
- ▶  $z_1 \sim \text{normal}(y_1, y.sd_1)$

# Autocorrelation?

Observation errors:

$$\begin{aligned}y_t &= z_t + \varepsilon_{obs,t} \\ \varepsilon_{obs,t} &\sim \text{normal}(0, y.sd)\end{aligned}$$

$$\varepsilon_{obs,t} \sim iid$$



# General joint and posterior distribution for multi-state model

$\boldsymbol{\mu}_t = \mathbf{A}\mathbf{z}_t$ , process parameters are elements of matrix  $\mathbf{A}$

$$[\mathbf{z}, \boldsymbol{\theta}_{process}, \boldsymbol{\theta}_{data} | \mathbf{Y}] \propto$$

$$\prod_{t=2}^T [y_t | \boldsymbol{\theta}_{data}, \mathbf{z}_t] [\mathbf{z}_t | \boldsymbol{\mu}_t] [\boldsymbol{\theta}_{process}, \boldsymbol{\theta}_{data}, \mathbf{z}_1]$$

## 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>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

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

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

$$\mathbf{n}_t = \mathbf{A}\mathbf{n}_{t-1}.$$

# The posterior and joint distribution

$$\begin{aligned}
 & \left[ \phi, m, f, \mathbf{N}, \underbrace{\boldsymbol{\sigma}_p, \boldsymbol{\rho}}_{\text{elements of } \boldsymbol{\Sigma}} \mid \mathbf{y}^{\text{census}}, \mathbf{y}^{\text{census.sd}}, \mathbf{Y}^{\text{class}} \right] \propto \\
 & \underbrace{\prod_{t=2}^T \text{multivariate normal}(\log(\mathbf{n}_t) \mid \log(\mathbf{A}_t \mathbf{n}_{t-1}), \boldsymbol{\Sigma})}_{\text{process model}} \\
 & \qquad \times \text{data models} \times \text{priors}
 \end{aligned}$$

# The posterior and joint distribution

$$\begin{aligned}
 & \left[ \phi, m, f, \mathbf{N}, \underbrace{\boldsymbol{\sigma}_p, \boldsymbol{\rho}}_{\text{elements of } \boldsymbol{\Sigma}} \mid \mathbf{y}^{\text{census}}, \mathbf{y}^{\text{census.sd}}, \mathbf{Y}^{\text{class}} \right] \propto \\
 & \underbrace{\prod_{t=2}^T \text{multivariate normal}(\log(\mathbf{n}_t) \mid \log(\mathbf{A}_t \mathbf{n}_{t-1}), \boldsymbol{\Sigma})}_{\text{process model}} \\
 & \underbrace{\prod_{t=2}^T \text{normal} \left( y_t^{\text{census}} \mid \sum_{i=1}^3 n_{i,t}, y_t^{\text{census.sd}} \right)}_{\text{data model 1}}
 \end{aligned}$$

# The posterior and joint distribution

$$\begin{aligned}
 & \left[ \phi, m, f, \mathbf{N}, \underbrace{\boldsymbol{\sigma}_p, \boldsymbol{\rho}}_{\text{elements of } \boldsymbol{\Sigma}} \mid \mathbf{y}^{\text{census}}, \mathbf{y}^{\text{census.sd}}, \mathbf{Y}^{\text{class}} \right] \propto \\
 & \underbrace{\prod_{t=2}^T \text{multivariate normal}(\log(\mathbf{n}_t) \mid \log(\mathbf{A}_t \mathbf{n}_{t-1}), \boldsymbol{\Sigma})}_{\text{process model}} \\
 & \times \underbrace{\prod_{t=2}^T \text{normal} \left( y_t^{\text{census}} \mid \sum_{i=1}^3 n_{i,t}, y_t^{\text{census.sd}} \right)}_{\text{data model 1}} \\
 & \times \underbrace{\text{multinomial} \left( \mathbf{y}_t^{\text{class}} \mid \left( \frac{n_{1,t}}{\sum_{i=1}^3 n_{i,t}}, \frac{n_{2,t}}{\sum_{i=1}^3 n_{i,t}}, \frac{n_{3,t}}{\sum_{i=1}^3 n_{i,t}} \right), \sum_{i=1}^3 y_{i,t}^{\text{class}} \right)}_{\text{data model 2}} \\
 & \times \text{appropriate priors}
 \end{aligned}$$

## Continuous time models

$$\frac{dz_1}{dt} = k_1 z_1 - k_2 z_1 z_2 \quad (1)$$

$$\frac{dz_2}{dt} = -k_3 z_1 + \alpha k_2 z_1 z_2 \quad (2)$$

$$\frac{dz_3}{dt} = \frac{k_4 z_3}{k_5 + z_3} \quad (3)$$

$$[\mathbf{z}_t | g((\mathbf{k}, \mathbf{z}_{t-1}, x_t), \sigma_p^2)]$$

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



## Continuous time models

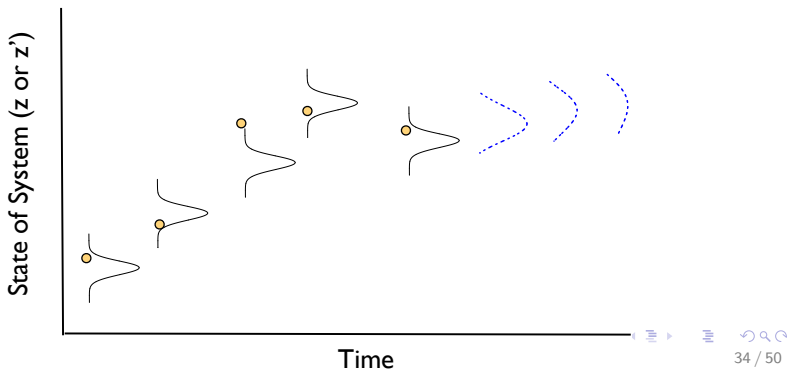
- ▶ Must deterministically update states at discrete intervals to match with data
- ▶ To estimate states:
  - ▶ Use analytical solutions to ODE system if available.
  - ▶ For models without analytical solutions:
    - ▶ OpenBUGS and STAN have ODE solvers.
    - ▶ Euler's or Runge-Kutta IV can be embedded 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. In press. Using litter chemistry controls on microbial processes to partition litter carbon fluxes with the Litter Decomposition and Leaching (LIDEL) model. Soil Biology and Biochemistry.

# Bayesian forecasting future states $z'$

$$\underbrace{[z'_{T+1} | \mathbf{y}]}_{\text{predictive process distribution}} =$$

predictive process distribution

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



# Predictive process distribution

The MCMC output:

$i$	$\theta_1$	$\theta_1$	$\theta_3$								
1	.42	3.3	20.3	$z_{1,1}$	$z_{1,2}$	$\cdots$	$z_{1,T}$	$z'_{1,T+1}$	$z'_{1,T+2}$	$\cdots$	$z'_{1,T+F}$
2	.41	2.3	18.5	$z_{2,1}$	$z_{1,2}$	$\cdots$	$z_{2,T}$	$z'_{2,T+1}$	$z'_{2,T+2}$	$\cdots$	$z'_{2,T+F}$
3	.46	3.1	16.6	$z_{3,1}$	$z_{1,2}$	$\cdots$	$z_{3,T}$	$z'_{3,T+1}$	$z'_{3,T+2}$	$\cdots$	$z'_{3,T+F}$
$\vdots$	$\vdots$	$\vdots$	$\vdots$	$\vdots$	$\vdots$	$\vdots$	$\vdots$	$\vdots$	$\vdots$	$\vdots$	$\vdots$
$n$	.39	3.4	22.1	$z_{n,1}$	$z_{n,2}$	$\cdots$	$z_{n,T}$	$z'_{n,T+1}$	$z'_{n,T+2}$	$\cdots$	$z'_{n,T+F}$

$n$  = number of iterations

$T$  = final time with data

$F$  = number of forecasts beyond data

# Posterior and joint distribution with forecasts

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

# Posterior and joint distribution with missing data

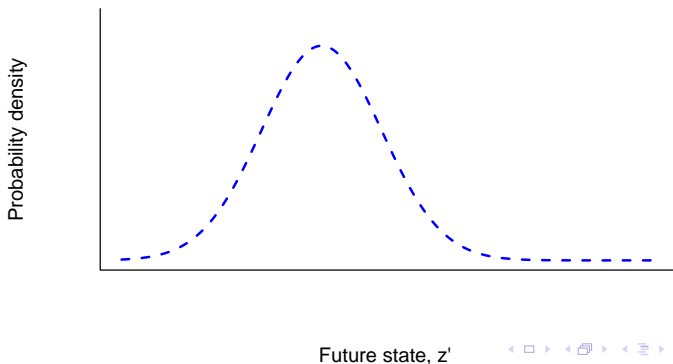
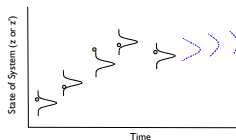
$$\begin{aligned}\mu_t &= g(\boldsymbol{\theta}_{process}, z_{t-1}, \mathbf{x}_{t-1}) \\ [\mathbf{z}, \boldsymbol{\theta}_{process}, \boldsymbol{\theta}_{data} | \mathbf{y}] &\propto \\ \prod_{\forall t \in \mathbf{y}.i}^T [y_t | \boldsymbol{\theta}_{data}, z_t] &\prod_{t=2}^T [z_t | \mu_t] [\boldsymbol{\theta}_{process},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

# Forecasting

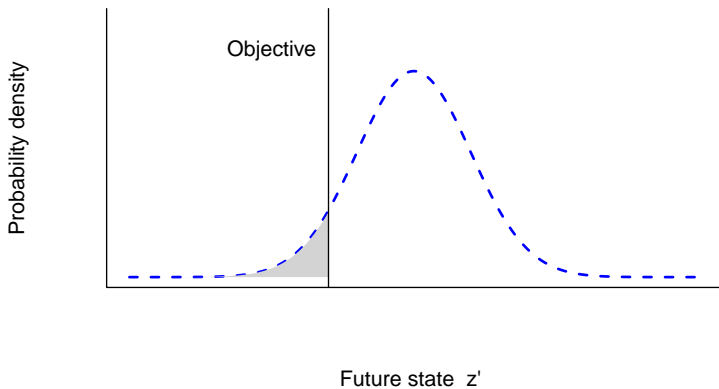
The fundamental problem of management:

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

# Posterior predictive distribution of $z'$

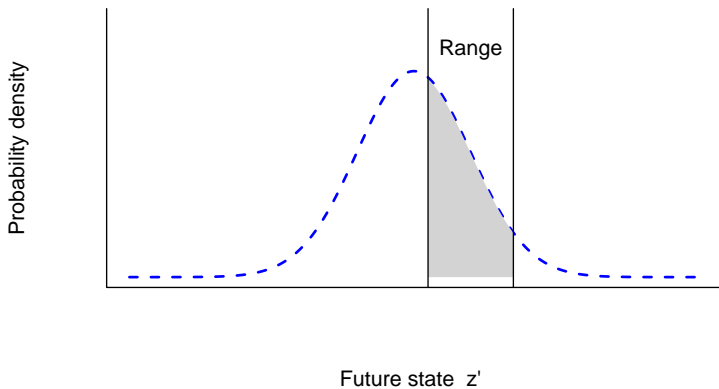


## Objective: reduce state below a target

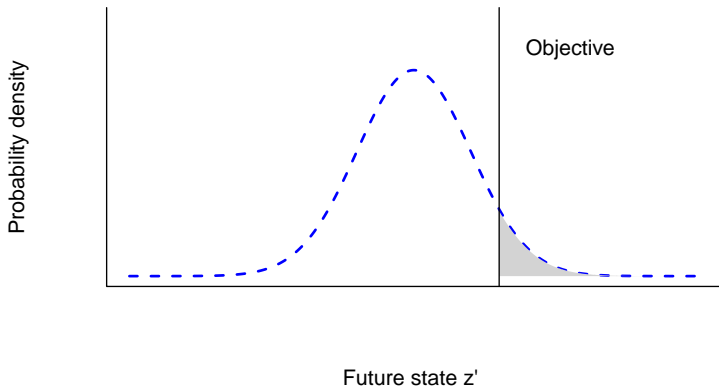




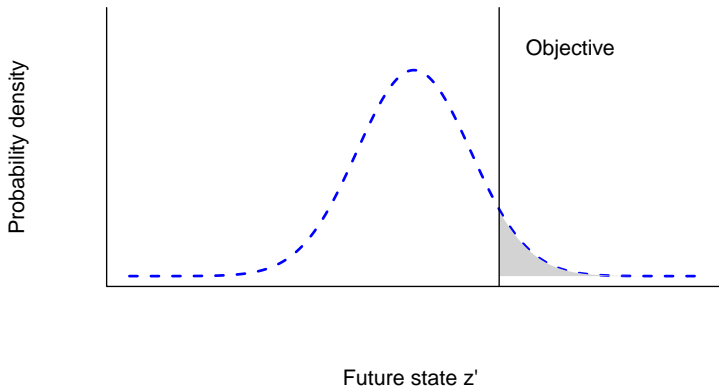
**Objective: maintain state within acceptable range**



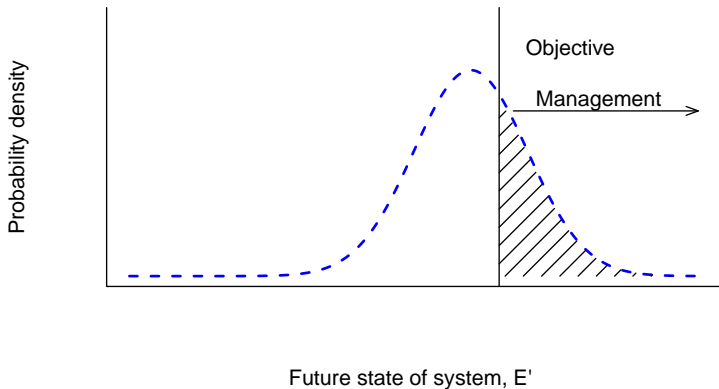
## Objective: increase state above a target



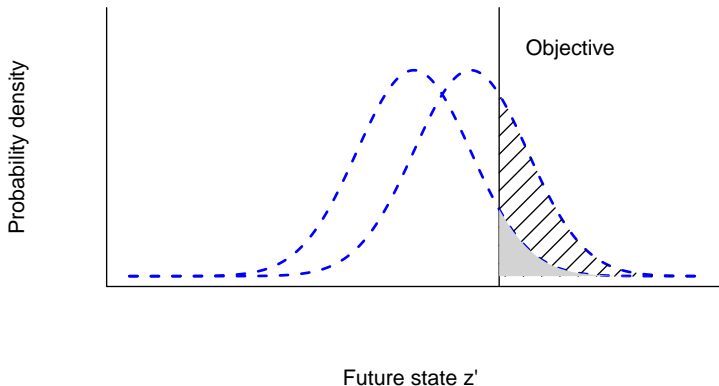
## Action: do nothing



## Action: implement management

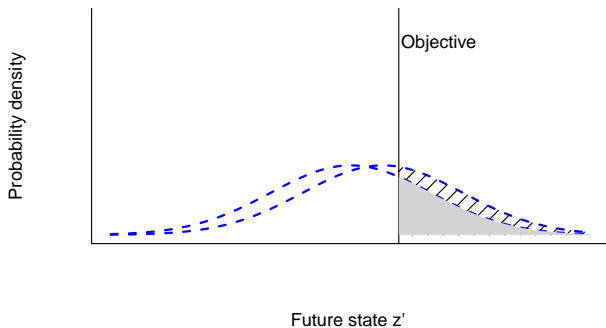


## Net effect of management



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

## Net effect of management



# JAGS code for posterior and joint distributions

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

$$\times \underbrace{\prod_{t=2}^{48} [z_t | g(\boldsymbol{\beta}, z_{t-1}, x_{t-1}), \sigma_p^2]}_{\text{process model}} \times \underbrace{[\beta_0][\beta_1][\beta_2][\beta_3][\sigma_p^2][z_1]}_{\text{parameter models}}$$

```

model{
  #Priors
  b[1] ~ dnorm(.234,1/.136^2)
  for(j in 2:n.coef){
    b[j] ~ dnorm(0,.0001)
  }
  tau.p ~ dgamma(.01,.01)
  sigma.p <- 1/sqrt(tau.p)
  z[1] ~ dnorm(N.obs[1],tau.obs[1]) #this must be treated as prior so that you have z[t-1]
  ##Process model
  for(t in 2:(T+F)){
    mu[t] <- 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(j in 2:n.obs){
    N.obs[j] ~ dnorm(z[index[j]],tau.obs[j]) #index to match z[t] with data
  }
}#end of model

```

# 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]]
  # simulate new data
  N.new[i] ~ dnorm(z[index[i]],tau.obs[i])
  sq[i] <- (N.obs[i] - z[index[i]] )^2
  sq.new[i] <-(N.new[i] - z[index[i]]) ^2
}
fit <- sum(sq[])
fit.new <- sum(sq.new[])
pvalue <-step(fit.new-fit)
```



## 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)
#or
sigma.p ~ dunif(0, 10)
tau.p <- 1/sqrt(sigma.p)
#Instead of:
#wrong
tau.p ~ dgamma(.0001, .0001)
sigma.p <- 1/sqrt(tau.p)
```

## An odd error

```
Error in jags.samples(model, variable.names, n.iter, thin, type = "trace", : Failed to sample iterator 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.**