Bayesian Dynamic 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

Dynamic hierarchical models (aka state space models)
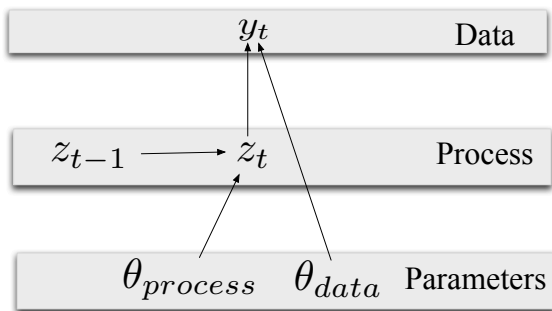
Also called "state space" models

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

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.
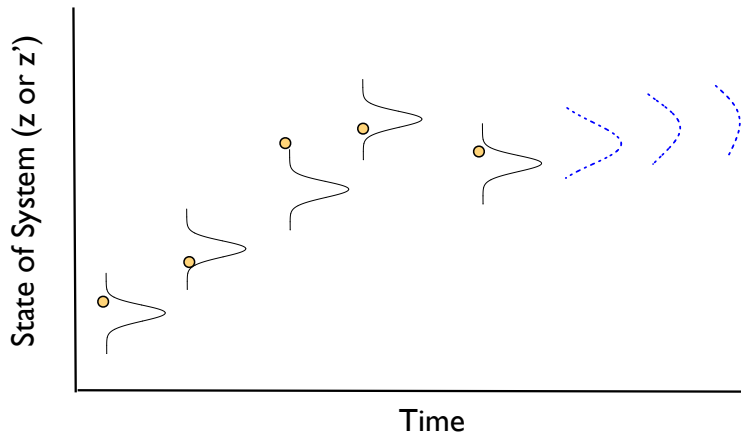
A broadly applicable approach to modeling dynamic processes in ecology

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

y_t	Data

$z_{t-1} \longrightarrow z_t$	Process

$\theta_{process} \quad \theta_{data}$	Parameters

## Sources of uncertainty in state space models

Process uncertainty

- ▶ Failure to perfectly represent process
- ▶ Propagates in time
- ▶ Decreases with model improvement
- ▶ Basis for forecasting

Observation uncertainty

- ▶ Failure to perfectly observe process
- ▶ Does not propagate
- ▶ Sampling uncertainty decreases with increased sampling effort.
- ▶ Observation (calibration) uncertainly decreases with improved instrumentation, calibration, etc.

Components of observation uncertainty
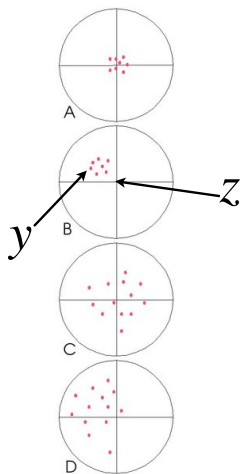
▶ Observation (aka calibration)
$[y|h(z, \boldsymbol{\theta}_d), \sigma_o^2]$

▶ Sampling $[y|z, \sigma_s^2]$

When can we separate process variance from observation variance?

- ▶ Replication of the observation for the latent state with sufficient n
- ▶ 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

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

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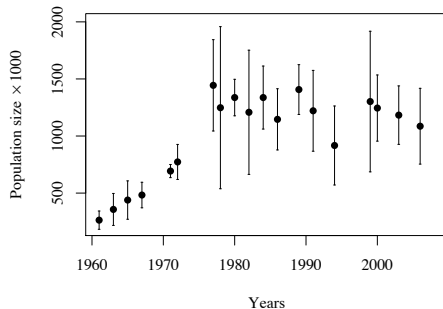
- ▶ 48 year time series
- ▶ Annual means and standard deviations of population size for 19 years
- ▶ Spatially replicated census
- ▶ Annual data on dry season rainfall

How does rainfall influence density dependence?

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

- $z_t =$ 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 predicting medians

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

► $\log\left(g\left(\boldsymbol{\beta}, z_{t-1}, x_{t-1}\right)\right)$, the centrality parameter, the mean of z_t on the log scale

► σ_p^2, the scale parameter, the variance of z_t on the log scale

► What does the deterministic model predict?

  ► define centrality parameter $= \alpha_t$
  ► median$(z_t) = e^{\alpha_t}$
  ► $\alpha_t = \log(\text{median}(z_t))$
  ► median $(z_t) = g\left(\boldsymbol{\beta}, z_{t-1}, x_{t-1}\right)$

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Review of relationships between normal and lognormal

1. $z_t = g\left(\boldsymbol{\beta}, z_{t-1}, x_{t-1}\right)\exp\left(\varepsilon_t\right),\ \varepsilon_t \sim \mathsf{normal}\left(0, \sigma_p^2\right)$

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

3. $\log\left(z_t\right) \sim \mathrm{normal}\left(\log\left(g\left(\boldsymbol{\beta}, z_{t-1}, x_{t-1}\right)\right), \sigma_p^2\right)$

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

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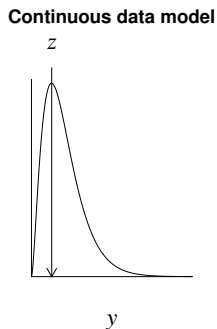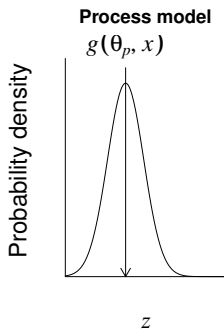
It is also possible to moment match the mean

$$
\begin{aligned}
\mu_t &= g\left(\boldsymbol{\beta}, z_{t-1}, x_{t-1}\right) &(1)\\
\alpha_t &= \log(\mu_t) - \frac{1}{2}\log\left(\frac{\mu_t^2 + \sigma_p^2}{\mu_t^2}\right) &(2)\\
z_t &\sim \text{lognormal}(\alpha_t, \sigma_p^2) &(3)
\end{aligned}
$$

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.

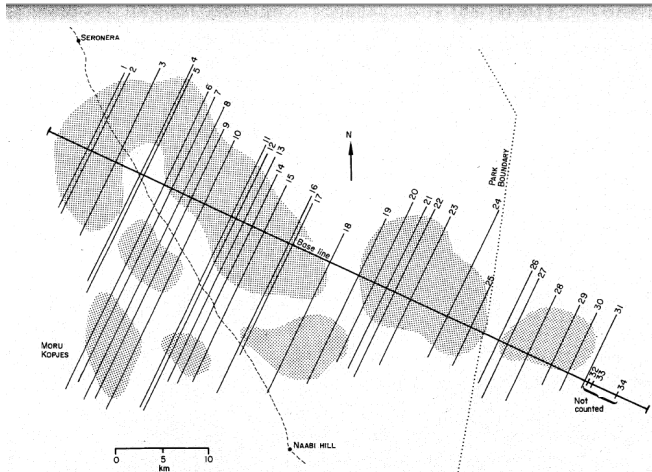## Why a continuous distribution for a "discrete state"?
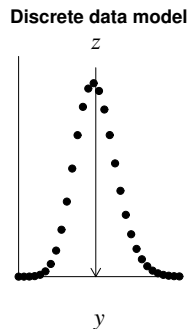
The data

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

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

- 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

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

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

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

General joint and posterior distribution for multi-state model

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

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

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

Multiple states: Ann Raiho's matrix model[1]

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

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[1]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

ϕ_j probability that a juvenile (aged 6 months) survives to 18 months

ϕ_d annual survival probabilty of adult females

ϕ_b annual survival probability of adult males

m proportion of juveniles surviving to adults that are female

$$
\begin{aligned}
\mathbf{A} &= \begin{pmatrix}
0 & \phi_d^{\frac{1}{2}} f & 0 \\
m\phi_j & \phi_d & 0 \\
(1-m)\,\phi_j & 0 & \phi_b
\end{pmatrix} \\
\mathbf{n}_t &= \mathbf{A}\mathbf{n}_{t-1}.
\end{aligned}
$$

The posterior and joint distribution

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

$$
\underbrace{\prod_{t=2}^{T} \text{multivariate normal} \left(\log(\mathbf{n}_t) \big| \log\left(\mathbf{A}_t \mathbf{n}_{t-1} \right), \boldsymbol{\Sigma} \right)}_{\text{process model}}
$$

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

$$
\times \underbrace{\text{multinomial} \left(\mathbf{y}_t^{\text{classification}} \Bigg| \left(\sum_{i=1}^{3} y_{i,t}, \frac{n_{1,t}}{\sum_{i=1}^{3} n_{i,t}}, \frac{n_{2,t}}{\sum_{i=1}^{3} n_{i,t}}, \frac{n_{3,t}}{\sum_{i=1}^{3} n_{i,t}} \right)' \right)}_{\text{data model 2}}
$$

$$
\times \text{ priors}
$$

Systems of differential equations

$$
\begin{aligned}
\frac{dz_1}{dt} &= k_1 z_1 - k_2 z_1 z_2 \\
\frac{dz_2}{dt} &= -k_3 z_1 + \alpha k_2 z_1 z_2 \\
\frac{dz_3}{dt} &= \frac{k_4 z_3}{k_5 + z_3}
\end{aligned}
$$

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

Implementing the process model usually needs 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:

    ▶ STAN has superb ODE solver. [2]
    ▶ R's Nimble package [3] allows you to embed functions in JAGS. A sturdy ODE solver (Runge–Kutta IV) can be written in 6-8 lines of code.
    ▶ Write your own MCMC sampler with embedded numerical solver (e.g. `lsoda()` in R). [4]

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[2] https://mc-stan.org/events/stancon2017-notebooks/
stancon2017-margossian-gillespie-ode.html

[3] https://r-nimble.org/

[4] 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.
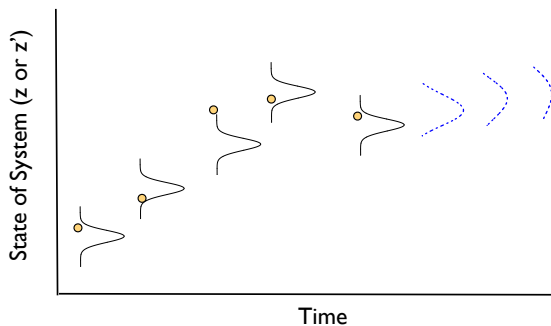
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Bayesian forecasting future states z'

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

$$\int_{\boldsymbol{\theta}_1\ldots\boldsymbol{\theta}_P}\int_{z_1\ldots}\int_{z_T}\left[z'_{T+1}|\mathbf{z},\boldsymbol{\theta}_{process},\mathbf{y}\right]\underbrace{\left[\mathbf{z},\boldsymbol{\theta}_{process},\boldsymbol{\theta}_{data}|\mathbf{y}\right]}_{\text{posterior distribution}}dz\ldots dz_t\,d\boldsymbol{\theta}_1\ldots d\boldsymbol{\theta}_P$$

Predictive process distribution

The MCMC output:

i	θ_1	θ_1	θ_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	$z_{2,1}$	$z_{2,2}$	$\cdots$	$z_{2,T}$	$z'_{2,T+1}$	$z'_{,2T+2}$	$\cdots$	$z'_{2,T+F}$
3	.46	3.1	16.6	$z_{3,1}$	$z_{3,2}$	$\cdots$	$z_{3,T}$	$z'_{3,T+1}$	$z'_{3,T+2}$	$\cdots$	$z'_{3T+,F}$
$\vdots$	$\vdots$	$\vdots$	$\vdots$	$\vdots$	$\vdots$	$\vdots$	$\vdots$	$\vdots$	$\vdots$	$\vdots$	$\vdots$
n	.39	3.4	22.1	$z_{n,1}$	$z_{n,2}$	$\cdots$	$z_{n,T}$	$z'_{n,T+1}$	$z'_{n,T+2}$	$\cdots$	$z'_{n,T+F}$

$$
\begin{aligned}
n &= \text{number of iterations} \\
T &= \text{final time with data} \\
F &= \text{number of forecasts beyond data}
\end{aligned}
$$

Posterior and joint distribution with forecasts

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

Posterior and joint distribution with missing data

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

Can put NA's in data for all missing values or use the indexing trick shown below.

Forecasting

The fundamental problem of management:

What actions can we take today that will allow us to meet goals for the future?
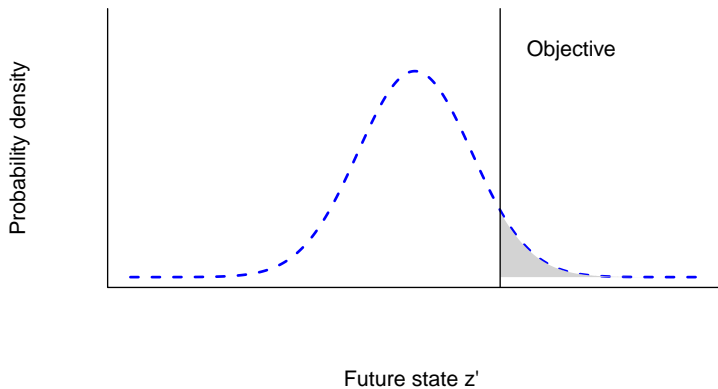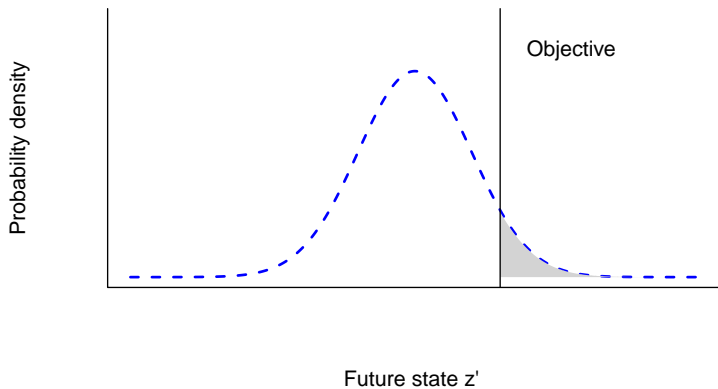
Predictive process distribution of z'

Probability density

Future state, z'
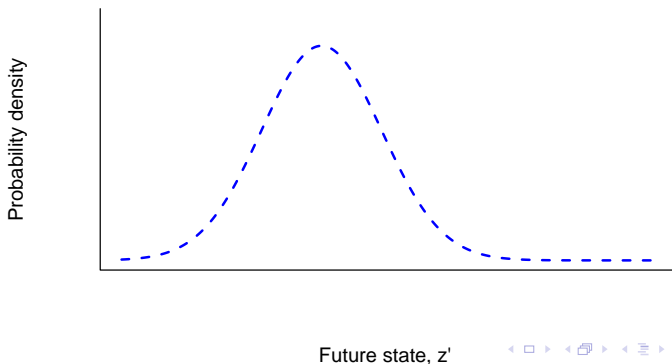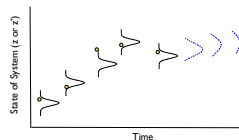
Objective: reduce state below a target
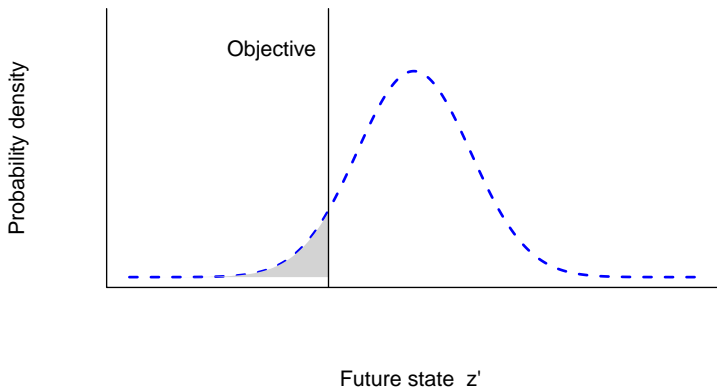
Objective: maintain state within acceptable range

Future state z'
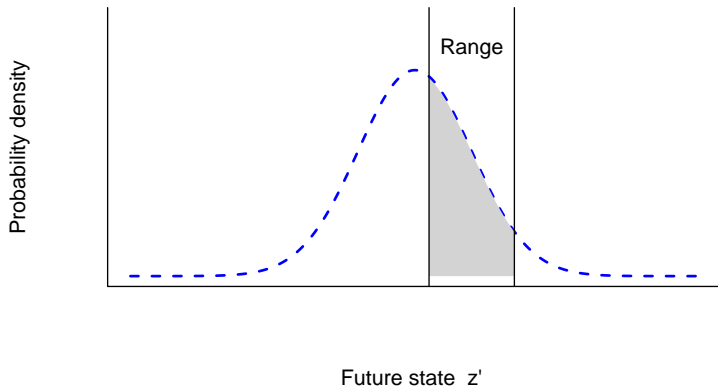
Objective: increase state above a target

Action: do nothing

Probability density

Objective

Future state z'

Action: implement managment

Probability density

Objective

Management

Future state of system, z'
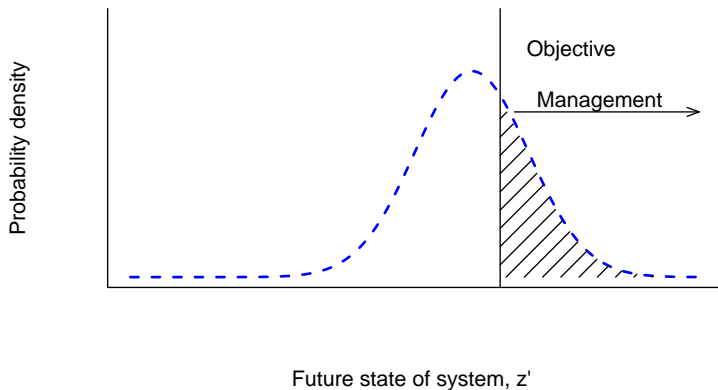
Net effect of management

Net effect of management

Future state z'
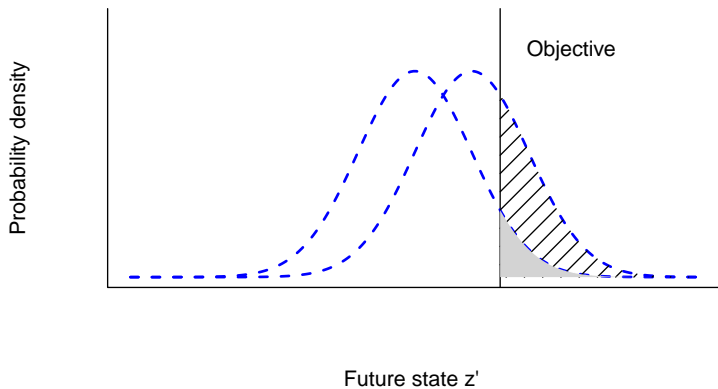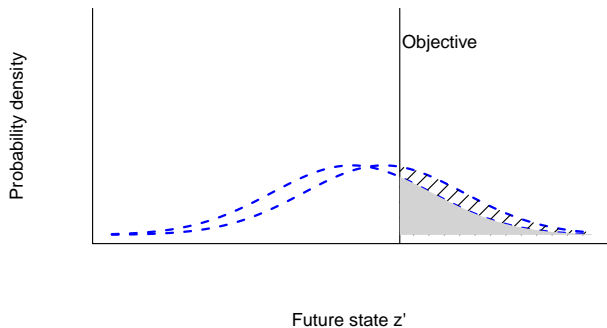
Papers using forecasting relative to goals

- ▶ Ketz, A. C., T. L. Johnson, R. J. Monello, and N. T. Hobbs. 2016. Informing management with monitoring data: the value of Bayesian forecasting. Ecosphere 7:e01587-n/a.

- ▶ 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.

- ▶ 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.

More on forecasting

- M. C. Dietz. Ecological Forecasting. Princeton University Press, Princeton New Jersey, USA, 2017.

- Workshop July 28 - August 2
  https://ecoforecast.wordpress.com/summer-course/

JAGS code for posterior and joint distributions

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

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

```
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 for time series data

Test statistic:

$$\frac{1}{T-1} \sum_{t=2}^{T} \mid y_t - y_{t-1} \mid \qquad (4)$$

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 autocorrelation 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)
```