Bayesian Dynamic Models

Bayesian Models for Ecologists

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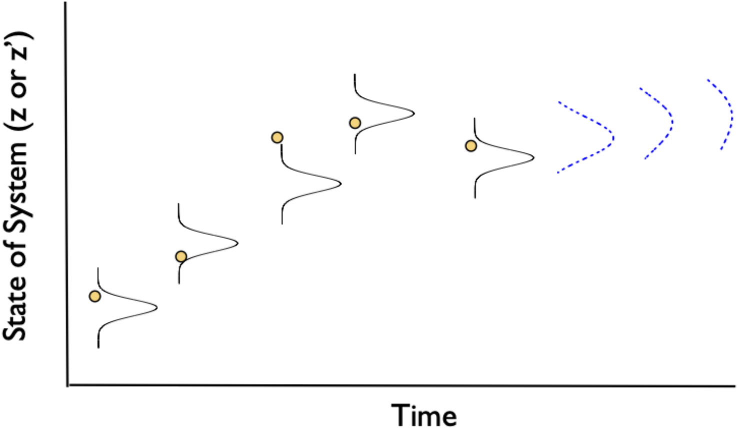
Roadmap

- Overview
- Model types with examples
  - discrete time
    - single state
    - multiple states
  - continuous time (briefly)
- Autocorrelation
- Break to start on lab problem
- Forecasting
- Forecasts for decision analysis
- Continue lab problem

Dynamic hierarchical models (aka state space models)

$$[y_t|\theta_d, z_t]$$
$$[z_t|\theta_p, z_{t-1}]$$

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.


State of System (z or z')
Time

A broadly applicable approach to modeling dynamic processes in ecology

$$[\mathbf{z}, \theta_{process,} \theta_{data}|\mathbf{y}] \propto \prod_{t=2}^{T} [y_t|\theta_{data}, z_t]\,[z_t|\theta_{process}, z_{t-1}]\,[\theta_{process}]\,[\theta_{data}], [z|y_1]$$

- Data from monitoring studies enter through the likelihood
- Data from process studies enter through the priors
- A natural approach to combining understanding accumulated at multiple scales of time and space and for including different types of uncertainty.

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.

When can we separate process variance from observation variance?

- Replication of the observation for the latent state with sufficient n
- Calibration model with properly estimated 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

$$
\begin{aligned}
\text{Deterministic model} &= g(\boldsymbol{\theta}_{process}, z_{t-1}, \mathbf{x}_{t-1}) \\
[\mathbf{z}, \boldsymbol{\theta}_{process}, \boldsymbol{\theta}_{data}, \sigma_p^2, \sigma_d^2 | \mathbf{y}] &\propto \prod_{t=2}^{T} [y_t | \boldsymbol{\theta}_{data}, z_t, \sigma_d^2] \\
&\times [z_t | g(\boldsymbol{\theta}_{process}, z_{t-1}, \mathbf{x}_{t-1}), \sigma_p^2] \\
&\times [z_1 | y_1, \sigma_d^2][\theta_{process}][\boldsymbol{\theta}_{data}][\sigma_p^2][\sigma_d^2]
\end{aligned}
$$

Data

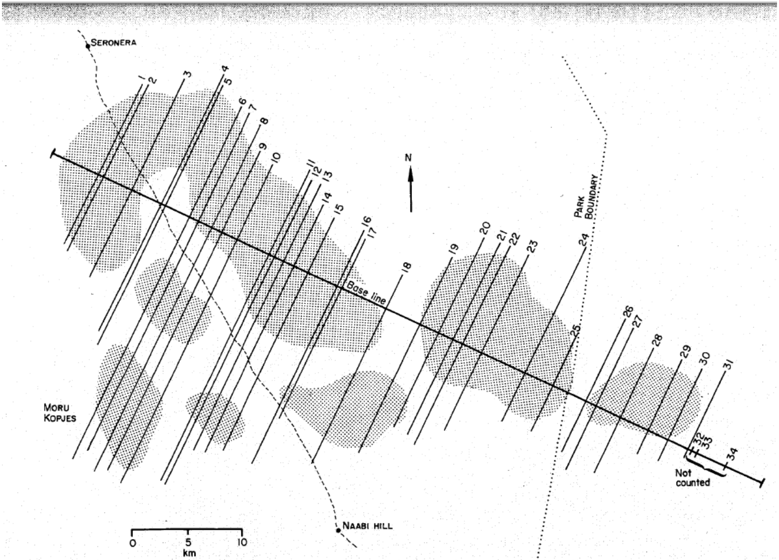


Fig. 2. The orientation of the base-line and of the random transects in the May 1971 sample count. Shading shows approximate positions of the main wildebeest herds.

Serengeti wildebeest model

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

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

$$\times \underbrace{\prod_{t=2}^{48} \left[z_t | g\left(\boldsymbol{\beta}, z_{t-1}, x_{t-1}\right), \sigma_p^2\right]}_{\text{process model}} \times \underbrace{\left[\beta_0\right]\left[\beta_1\right]\left[\beta_2\right]\left[\beta_3\right]\left[\sigma_p^2\right]\left[z_1 | y_1\right]}_{\text{parameter models}}$$

- $\mathbf{y}$ is a vector of years with non missing data. It is the mean of counts on multiple transects; $\mathbf{y.sd}_t$ is the corresponding vector of standard deviations of the mean counts.
- $y_t \sim \text{normal}(z_t, y.sd_t)$
- $z_t \sim \text{lognormal}\left(\log\left(g\left(\boldsymbol{\beta}, z_{t-1}, x_{t-1}\right)\right), \sigma_p^2\right)$
- $\beta_0 \sim \text{normal}\left(.234, .136^2\right)$ informative prior
- $\beta_{i \in 1,2,3} \sim \text{normal}(0, 1000)$
- $\sigma_p^2 \sim \text{gamma}\left(.001, .001\right)$

Exercises

- Draw the DAG
- Interpret the coefficients
    - If covaraites are not transformed
    - If covariates are centered
    - If covariates are standardized
- What is this Δt? Why do we need it in the model?

What is

$t = \forall \in \mathbf{y.i}$?

$t = \forall \in y.i$ = all t in the vector $\mathbf{y.i}$. For example:

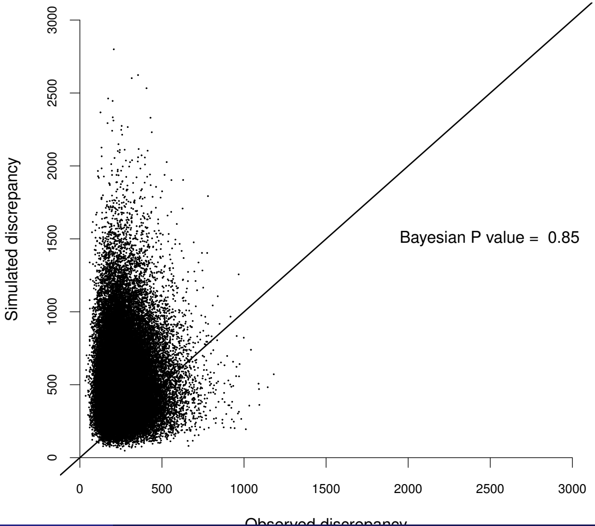
i	$y.i$
1	2
2	5
3	6
4	8
5	12

It is a vector of non-missing values for years. Use the double bracket index trick to match the y_t to the z_t, e.g.

```
for(i in 1: length(y.i){
  y[y.i[i]]~ dlnorm(z[y.i[i],y.sd[y.i[i]])
}
```

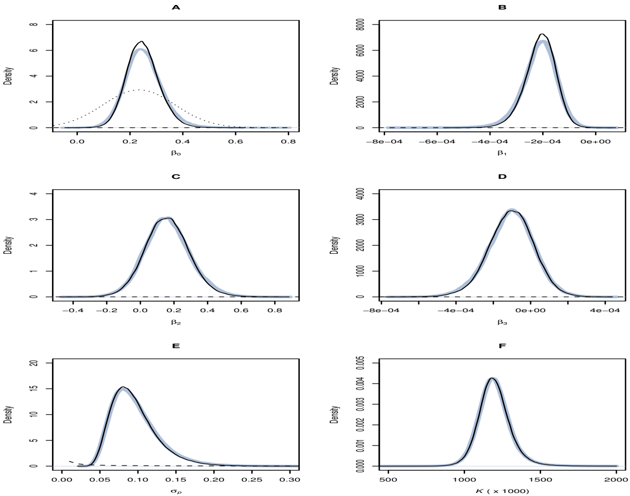
Or you could simply add NA for the missing years population estimates *if* you have values for the rainfall covariates for all years

Posterior predictive check



Marginal posteriors

Black: with informative priors on β_0,Grey: flat prior on β_0,Dotted: informative prior on β_0,Dashed: vague priors



Example of using allometric scaling for informed priors

Hobbs, N. T. 2024. A general, resource-based explanation for density dependence in populations of large herbivores. Ecological Monographs. http://doi.org/10.1002/ecm.1600

Deterministic matrix model

Process model:

$$\begin{pmatrix} z_1 \\ z_2 \\ z \\ . \\ z_n \end{pmatrix}_t = \mathbf{\Theta} \begin{pmatrix} z_1 \\ z_2 \\ z_3 \\ . \\ z_n \end{pmatrix}_{t-1} \quad (1)$$

where $\mathbf{\Theta}$ is an $n \times n$ matrix governing the transitions among states. The product $\mathbf{\Theta z}_t$ defines a system of n linked, difference equations. We can learn a great deal about the dynamics of the system from analyzing the properties of $\mathbf{\Theta}$, its eigenvalues, eignvectors, characteristic polynomials, etc. We can make inference on these using derived quantities.

Posterior and joint distribution

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

$$\prod_{t=2}^{T} [\mathbf{y}_t | \boldsymbol{\theta}_{data}, \mathbf{z}_t] \, [\mathbf{z}_t | \boldsymbol{\Theta}, \mathbf{z}_{t-1}] \, [\boldsymbol{\Theta}], [\boldsymbol{\theta}_{data}][\mathbf{z}_1 | \mathbf{y}_1]$$

Example: Ann Raiho matrix model[1]

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

[1] A. Raiho, M. B. Hooten, S. Bates, and N. T. Hobbs. Forecasting the effects of fertility control on overabundant ungulates. PLOS ONE, 10(12):e0143122. doi:10.1371/journal.pone.0143122, 2015.

$$\begin{aligned}
f &= \text{number of recruits per female surviving to census} \\
\phi_j &= \text{probability that a juvenile (aged 6 months) survives to 18 months} \\
\phi_d &= \text{annual survival probabilty of adult females} \\
\phi_b &= \text{annual survival probability of adult males} \\
m &= \text{proportion of juveniles surviving to adults that are female}
\end{aligned}$$

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

The posterior and joint distribution

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

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

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

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

$$\times \text{priors}$$

Models of high dimension can be fit with sufficient data

November 2015 MODELING OF BISON POPULATION DYNAMICS 537

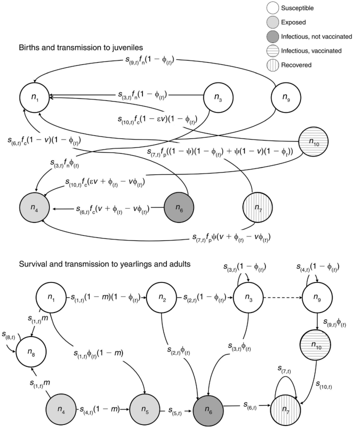


Fig. 4. We added two stages to the model to represent effects of vaccination for brucellosis in the Yellowstone bison population. Stage $n_{(9,t)}$ represents seronegative adult females that have been vaccinated. Stage $n_{(10,t)}$ represents vaccinated adult females that have been exposed. The dashed line represents animals that are vaccinated during a time step. Other stages are defined in Table 2 and parameters are defined in Table 3. The vaccine reduces the probability that exposed individuals can transmit an infection horizontally or vertically, but it does not reduce the probability that an animal can become infected. The random variable ε represents the proportional reduction in probability of vertical and horizontal transmission that results from vaccination. The survival vector (**s**) allows annual removals to be included in the model (Eq. 3); however, these were set at zero for the vaccination scenario.

Systems of differential equations

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

Implementing the process model usually needs a numerical solver to align the states with the data.

Continuous time models

- Must 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.

The problem:

Assume for simplicity that the state is observed perfectly, i.e, $y_t = z_t$. The simplest model of the change in state with time is

$$y_t = \alpha y_{t-1} + \varepsilon_t \tag{2}$$

where $\varepsilon_t \sim \text{normal}(0, \sigma^2)$. We might introduce effects of predictor variables using

$$y_t = g(\boldsymbol{\theta}, \mathbf{x}_t) + \alpha y_{t-1} + \varepsilon_t. \tag{3}$$

What if ε_t depends on previous errors, that is, $e_t = h(e_{t-1})$? In this case, there is structural variation in the data, also called temporal dependence. The assumptions of independent errors does not hold. We have two choices:

1. Improve $g(\boldsymbol{\theta}, \mathbf{x}_t)$ so that the deterministic model accounts for the temporal dependence via the covariates or by increasing the lag in state variable, i.e. $y_t = g(\boldsymbol{\theta}, \mathbf{x}_t) + \alpha y_{t-1} + \gamma y_{t-2} + \varepsilon_t$.
2. Model the temporal dependence in the errors directly.

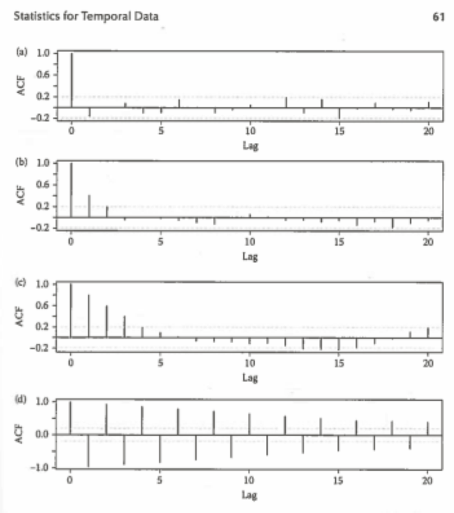
Detecting temporal dependence

The empirical autocorrelation function (ACF):

$$\rho_g = \frac{\sum_{i=1}^{n-g}(\varepsilon_i - \bar{\varepsilon})(\varepsilon_{i+g} - \bar{\varepsilon})}{\sum_{i=1}^{N}(\varepsilon_i - \bar{\varepsilon})^2}$$

where n is the number of steps in the time series and g is the "lag," the number of steps examined for temporal dependence,
$-1 \leq \rho_g \leq 1$
The notation ACF(g) means the correlation between points separated by g time periods.

ACF plots


Statistics for Temporal Data
61
(a)
(b)
(c)
(d)
ACF
Lag
1.0
0.6
0.2
-0.2
0.0
-1.0
0
5
10
15
20

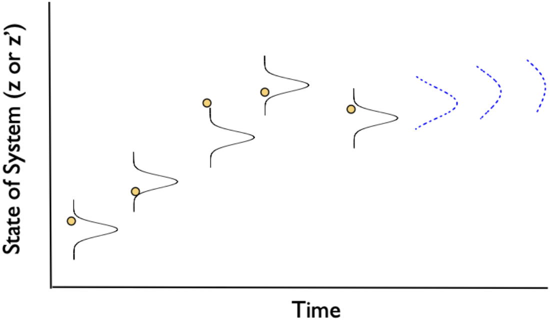
ACF in MCMC

$\mu_t = g(\boldsymbol{\theta}, z_{t-1}, \mathbf{x}_{t-1})$

1. Compute residuals at each MCMC iteration, $e_t^{(k)} = y_t - \mu_t^{(k)}$
2. Sample from MCMC output for $e_t^{(k)}$, use `acf()` function in R to find posterior distributions of ρ_g. Make statements like "Mean autocorrelation was .21 (BCI = .23,.18) at lag 3, revealing minimal temporal dependence in the residuals."

Bayesian forecasting future states z'

$$\underbrace{[z'_{T+1}|\mathbf{y}]}_{\text{predictive process distribution}} = \int_{\theta_1 \ldots \theta_P} \int_{z_1 \ldots} \int_{z_T} [z'_{T+1}|\mathbf{z}, \boldsymbol{\theta}_{process}, \mathbf{y}] \underbrace{[\mathbf{z}, \boldsymbol{\theta}_{process}, \boldsymbol{\theta}_{data}}_{\text{posterior distributi}}$$



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	$z_{n,1}$	$z_{n,2}$	$\cdots$	$z_{n,T}$	$z'_{n,T+1}$	$z'_{n,T+2}$	$\cdots$	$z'_{n,T+F}$

n = number of iterations

T = final time with data

F = number of forecasts beyond data

Posterior and joint distribution with forecasts

$$\mu_t = g(\boldsymbol{\theta}_{process}, z_{t-1}, \mathbf{x}_{t-1})$$

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

$$\prod_{t=2}^{T} [y_t | \boldsymbol{\theta}_{data}, z_t] \prod_{t=2}^{T+F} [z_t | \mu_t] [\boldsymbol{\theta}_{process}, \boldsymbol{\theta}_{data}] [z_1]$$

JAGS code for posterior and joint distributions

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

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

```
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:

$$\frac{1}{T-1}\sum_{t=2}^{T} |\, y_t - y_{t-1} \,| \tag{4}$$

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

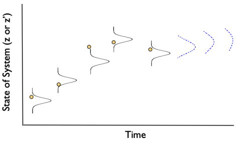
```
#Derived quantities for model evaluation

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)
```

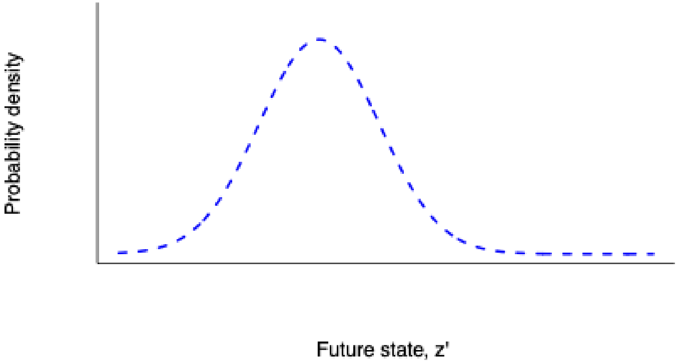
Forecasting and decision analysis

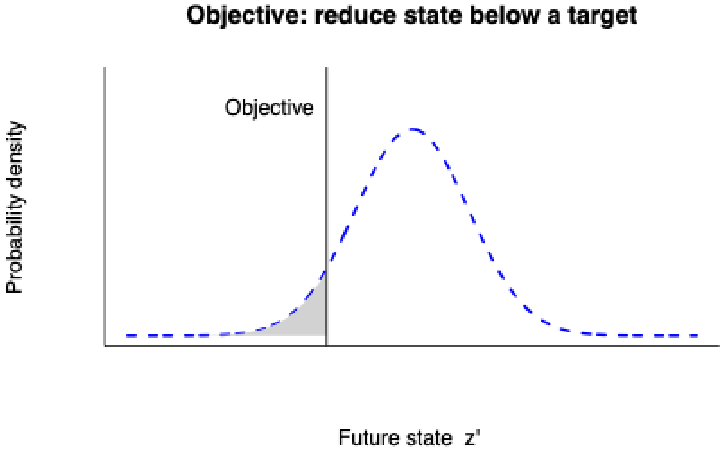
The fundamental problem of management:

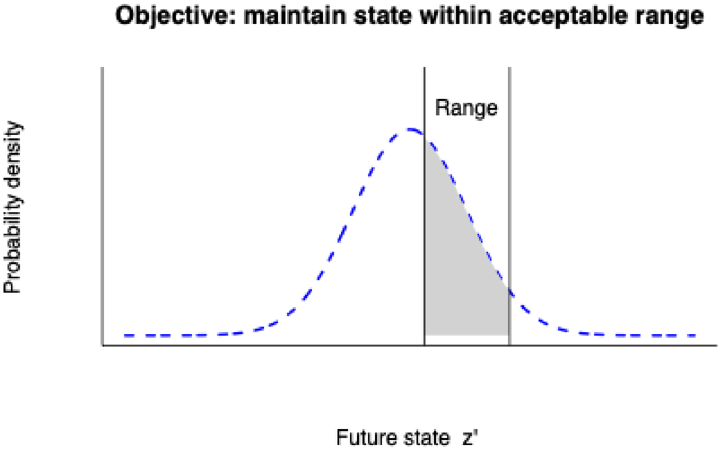
What actions can we take today that will allow us to meet goals for the future?

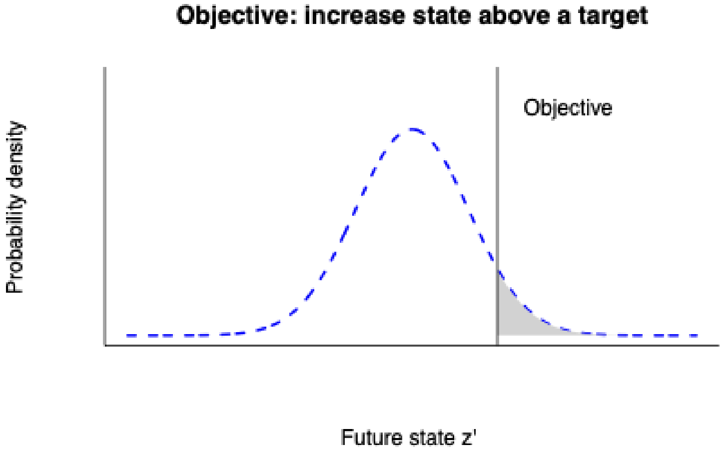


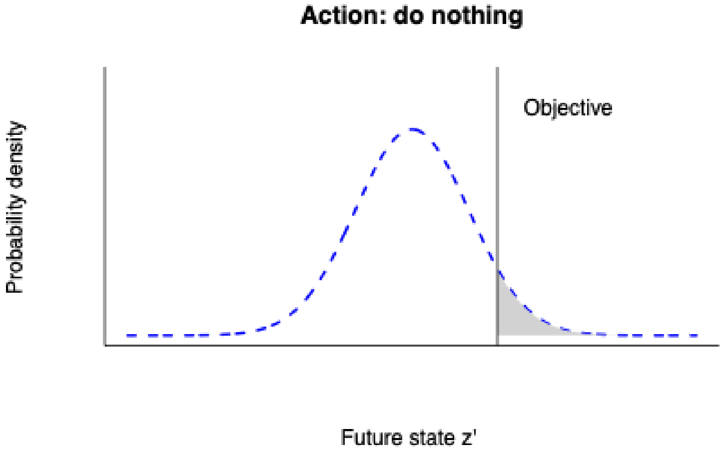
Predictive process distribution of z'

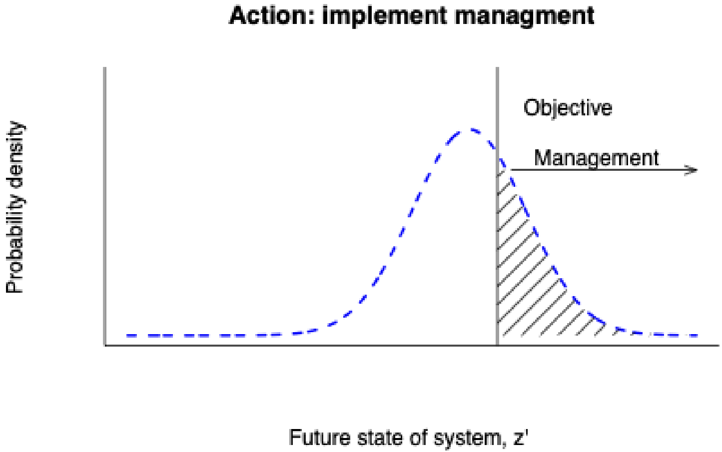


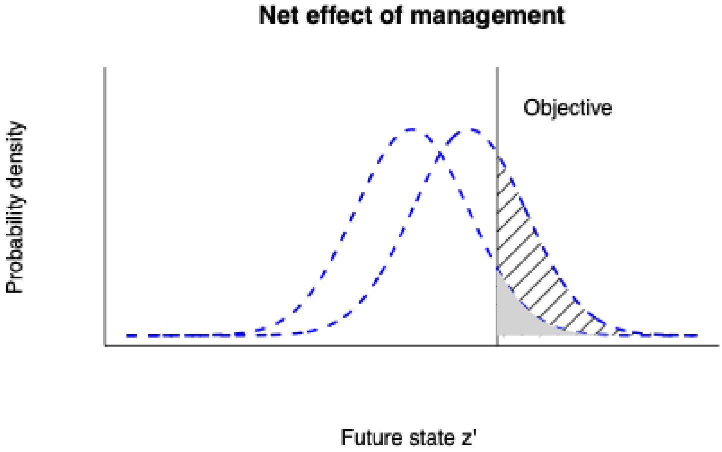

Objective: reduce state below a target
Objective
Probability density
Future state z'

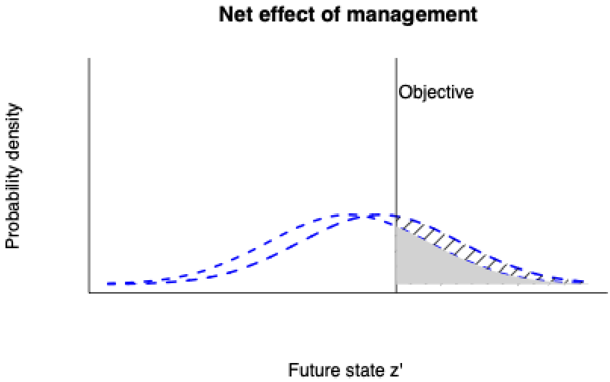

Objective: maintain state within acceptable range
Range
Probability density
Future state z'


Objective: increase state above a target
Objective
Probability density
Future state z'


Action: do nothing
Objective
Probability density
Future state z'


Action: implement managment
Objective
Management
Probability density
Future state of system, z'


Net effect of management
Objective
Probability density
Future state z'


Net effect of management
Objective
Probability density
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/`