Model Checking

Models for Socio-Environmental Data

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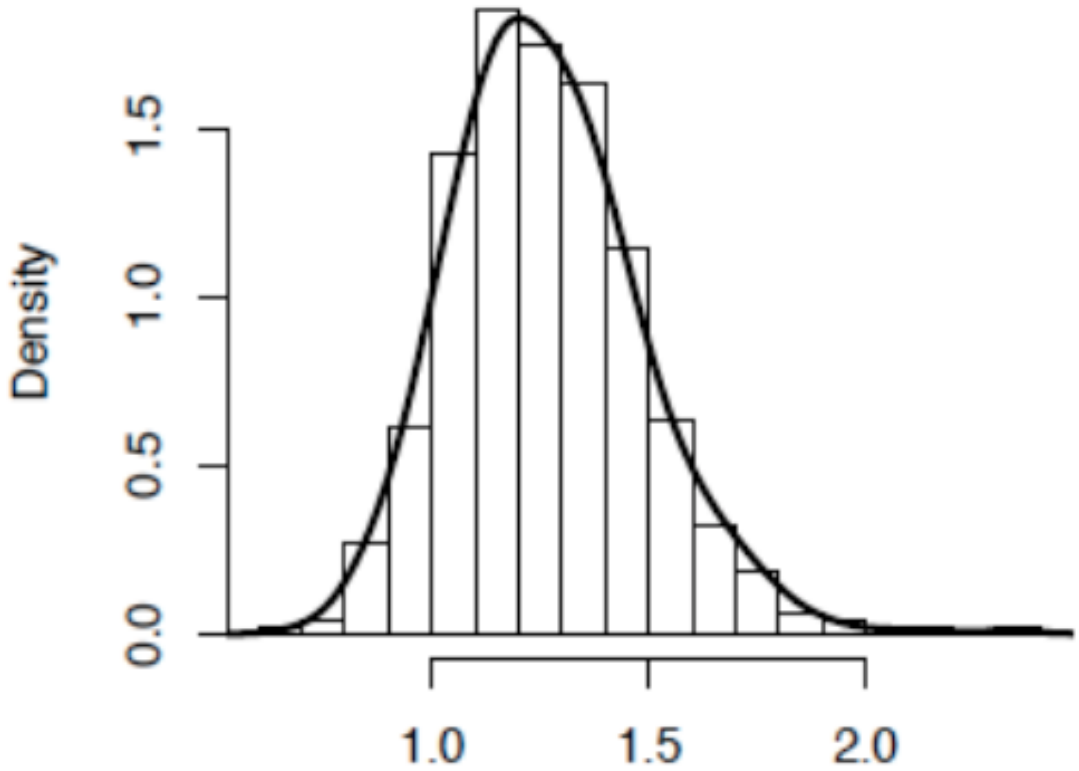
What is the first question you should ask after fitting a model?

- *Are the predictions of the model consistent with the data?*
- Is the deterministic model a reasonable representation of the process?
- Have you made the right choices for distributions to represent uncertainties?



What is model checking?

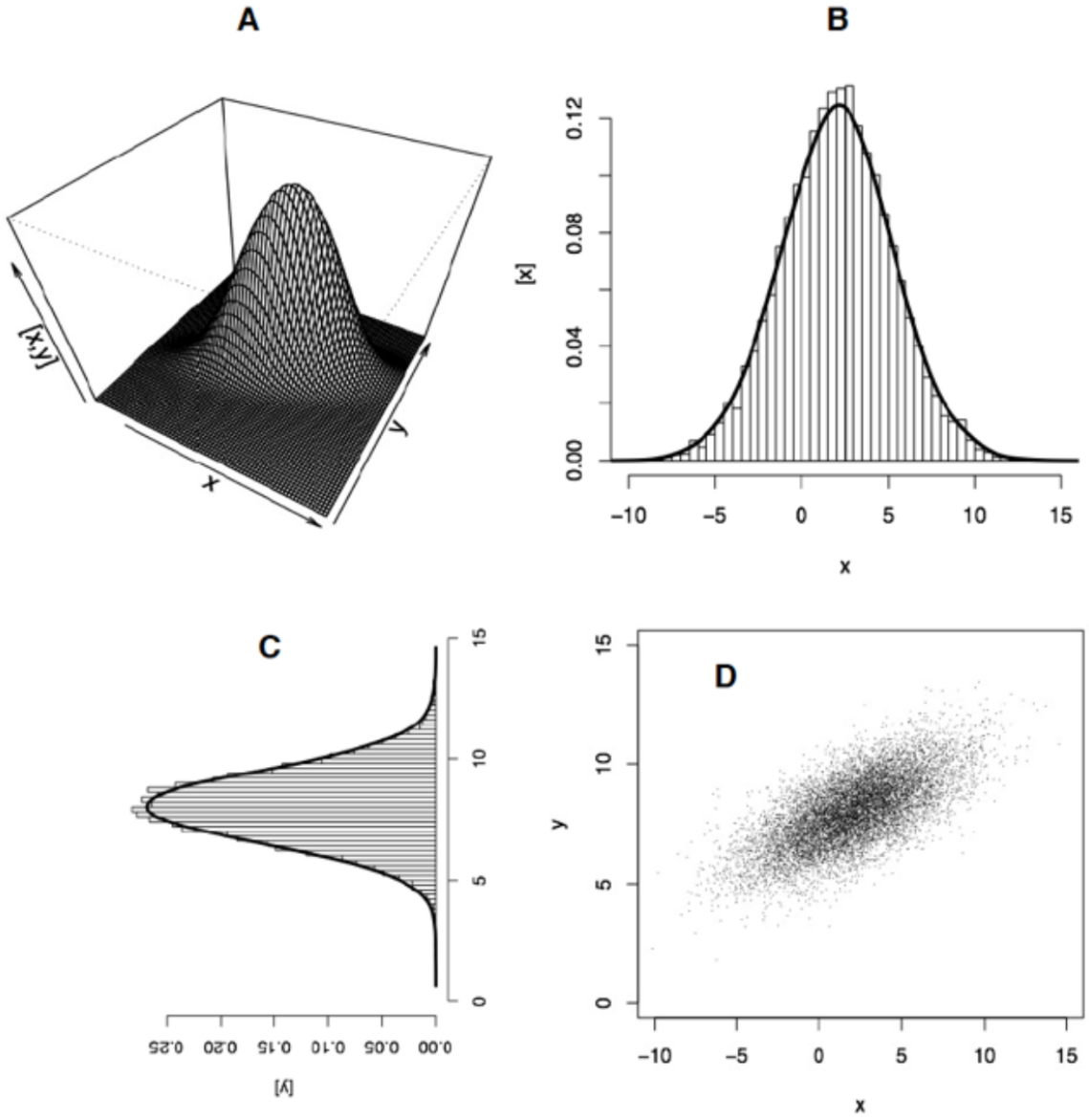
Model-based inference depends fundamentally on the assumption that your model can give rise to the data. Model checking is the process of evaluating whether this assumption is true.

Recall the marginal distribution

Recall, if the probability density function $[A, B]$ specifies the joint probability of the continuous random variables A and B then,

- $\int [A, B] dB$ is the marginal probability of A and
- $\int [A, B] dA$ is the marginal probability of B.
- This idea applies to any number of jointly distributed random variables. We simply integrate over all but one.

Marginal distributions



Posterior predictive checks

- Recall the *posterior predictive distribution* of new, unobserved data:

$$[y^{new} \mid y] = \underbrace{\int_{\theta_1} \ldots \int_{\theta_n} [y^{new} \mid \theta_1 \ldots \theta_n][\theta_1 \ldots \theta_n \mid y] d\theta_1 \ldots d\theta_n}_{\textbf{Posterior Predictive Distribution}}$$

- It is called posterior because it is conditional on the observed y and predictive because it is a prediction of y^{new}, given modeled parameter estimates.
- Posterior predictive checks show the probability of a new y conditional on θ, which is conditional on the data in hand, y.
- This is a marginal distribution because we are integrating over the θ.

$$[y^{new} \mid y] = \underbrace{\int_{\theta_1} \dots \int_{\theta_n} [y^{new} \mid \theta_1 \dots \theta][\theta_1 \dots \theta_n \mid y] d\theta_1 \dots d\theta_n}_{\textbf{Posterior Predictive Distribution}}$$

Consider,

$$\mu_i = g(\theta_1, \theta_2, \theta_3, \mathbf{x}_i) \tag{1}$$

$$y_i \sim \text{normal}(\mu_i, \sigma^2) \tag{2}$$

Also see box 8.1 in Hobbs and Hooten

A new data set at each iteration

k	θ_1	θ_1	θ_3	$i=1$	$i=2$	$i=3$	...	$i=Y$
1	.42	3.3	20.3	$y^{new}_{1,1}$	$y^{new}_{1,2}$	$y^{new}_{1,3}$	$\cdots$	$y^{new}_{1,Y}$
2	.41	2.3	18.5	$y^{new}_{2,1}$	$y^{new}_{1,2}$	$y^{new}_{1,3}$	$\cdots$	$y^{new}_{1,Y}$
3	.46	3.1	16.6	$y^{new}_{3,1}$	$y^{new}_{1,2}$	$y^{new}_{1,3}$	$\cdots$	$y^{new}_{1,Y}$
$\vdots$	$\vdots$	$\vdots$	$\vdots$	$\vdots$	$\vdots$	$\vdots$		$\vdots$
K	.39	3.4	22.1	$y^{new}_{n,1}$	$y^{new}_{n,2}$	$y^{new}_{n,3}$	$\cdots$	$y^{new}_{1,Y}$

This is easier done than said.

- We have a model $g(\theta, x)$ that predicts a response y. We approximate the posterior distribution, $[\theta \mid y]$.
- For any given value of x_i, we can simulate the posterior predictive distribution y^{new} by making a draw from $[y^{new} \mid g(\theta, x), \sigma^2]$.
- In MCMC this means making draws from the data model at each iteration; each draw is conditional on the current parameter values.
- We can simulate a new by repeating these draws for all values of the x.
- Accumulating many of these draws defines the posterior predictive distribution in exactly the same way that many draws allow us to define the posterior distribution of the parameters.

$$g(b_0, b_1, x_i) = b_0 + b_1 x_i$$

$$[b_0, b_1, \tau \mid \mathbf{y}] \propto \prod_{i=1}^{n} \text{normal}\left(y_i \mid g(b_0, b_1, x_i)_i, \tau\right) \times$$

$$\text{normal}\left(b_0 \mid 0.0001\right) \text{normal}(b_1 \mid 0, .0001) \text{gamma}\left(\tau \mid .01 .01\right)$$

```
model{
b0 ~ dnorm(0,.0001)
b1 ~ dnorm(0,.0001)
tau ~ dgamma(.01,.01)
sigma<-1/sqrt(tau)
for(i in 1:length(y)){
  mu[i] <- b0 + b1*x[i]
  y[i] ~ dnorm(mu[i],tau)
  #posterior predictive distribution of y.new[i]
  y.new[i] ~ dnorm(mu[i],tau)
  }
}
```

The Checking Part

- $T(y, \theta)$ is a test statistic (e.g., mean, standard deviation, CV, quantile, or sums of squares discrepancy) calculated from the observed data.
- $T(y^{new}, \theta)$ is the corresponding statistic from the simulated, which is generated from the posterior predictive distribution.
- We calculate:

$$P_b = \Pr(T(y^{new}, \theta) \geq T(y, \theta) \mid y)$$

- If P_B is very large or very small, then the difference between the observed data and the simulated data cannot be attributed to chance. **This indicates lack of fit**.

Candidates for test statistics

- mean
- variance
- coefficient of variation
- quantiles
- maximum, minimum
- discrepancy
- chi-square
- deviance

R. A. Fischer's Ticks

We want to know (for some reason) the average number of ticks on sheep.

- We round up 60 sheep and count ticks on each one. (What fun!)
- Does a Poisson distribution fit the distribution of the data?

$$[\lambda \mid \mathbf{y}] \propto \prod_{i=1}^{60} \text{Poisson}[y_i \mid \lambda][\lambda]$$

- For each value of λ in the MCMC chain, we generate a new data set, y^{new}, by sampling from:

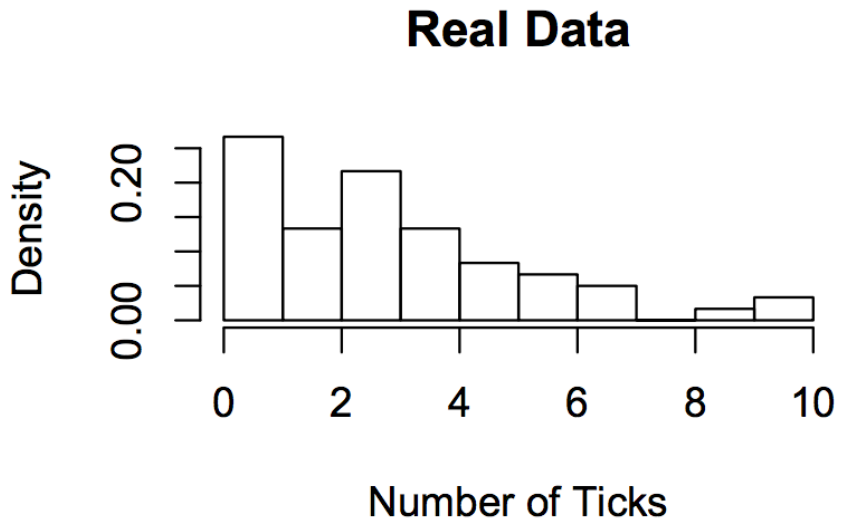
$$y_i^{new} \sim \text{Poisson}(\lambda)$$

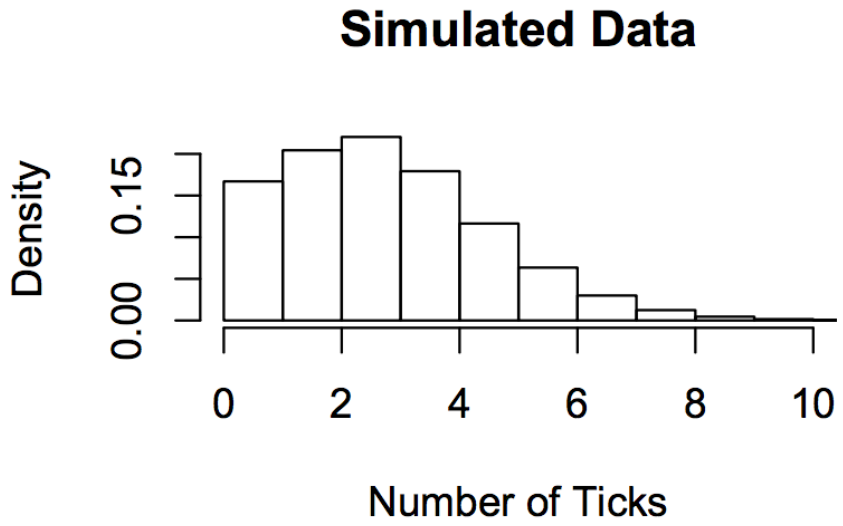
By the way, what heroic assumption are we making here? What might be a better model that, theoretically, could obviate the need for this assumption?

Code

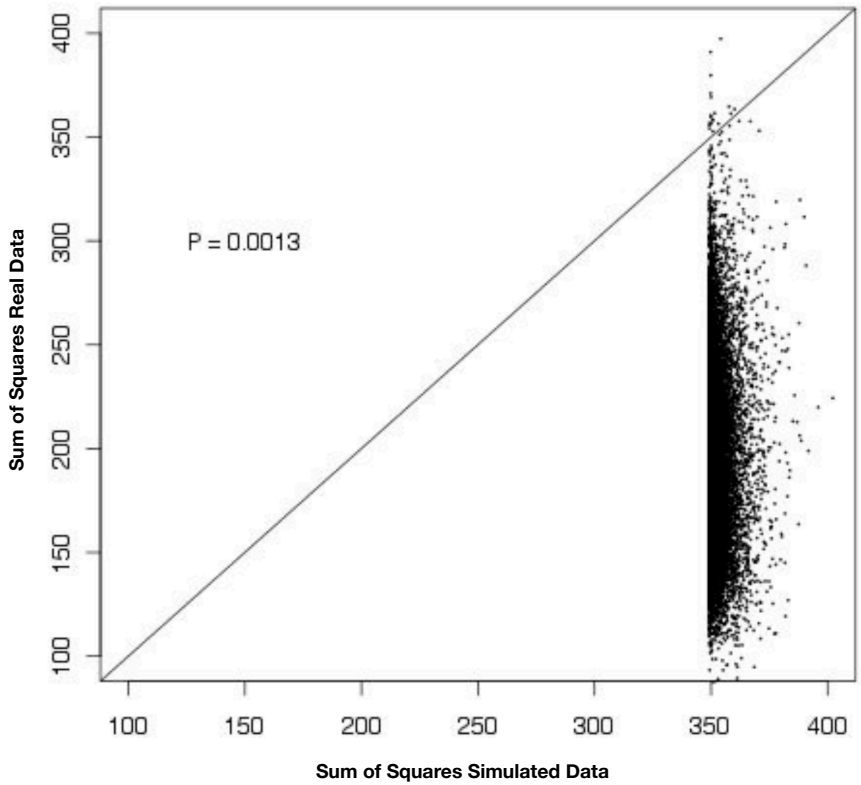
```
model{
lambda ~ dgamma(0.001,0.001)
for(i in 1:60){
     y[i] ~ dpois(lambda)
     y.new[i] ~ dpois(lambda)  #simulate a new data set of 60 points
}
cv.y <- sd(y[ ])/mean(y[ ])
cv.y.new <- sd(y.new[])/mean(y.new[ ])
pvalue.cv <- step(cv.y.new-cv.y)  # find Bayesian P value--the mean of
many 0's and 1's returned by the step function, one for each iteration in
the chain. The function step(z) returns a 1 if z > 0, returns 0
otherwise.
mean.y <-mean(y[])
mean.y.new <-mean(y.new[])
pvalue.mean <-step(mean.y.new - mean.y)
for(j in 1:60){
     sq[j] <- (y[j]-lambda)^2
     sq.new[j] <- (y.new[j]-lambda)^2
}
fit <- sum(sq[])
fit.new <- sum(sq.new[])
pvalue.fit <- step(fit.new-fit)
} #end of model
```

Simple Model





Posterior Predictive Check



- P value for CV= .0013
- P value for mean = .51
- This is a two-tailed probability, *values close to 0 and 1 indicate lack of fit*.

How could you modify this model to allow "extra" variance?

- Draw a Bayesian network and write out the posterior and joint distributions.
- Don't use the negative binomial, please.

Hierarchical model

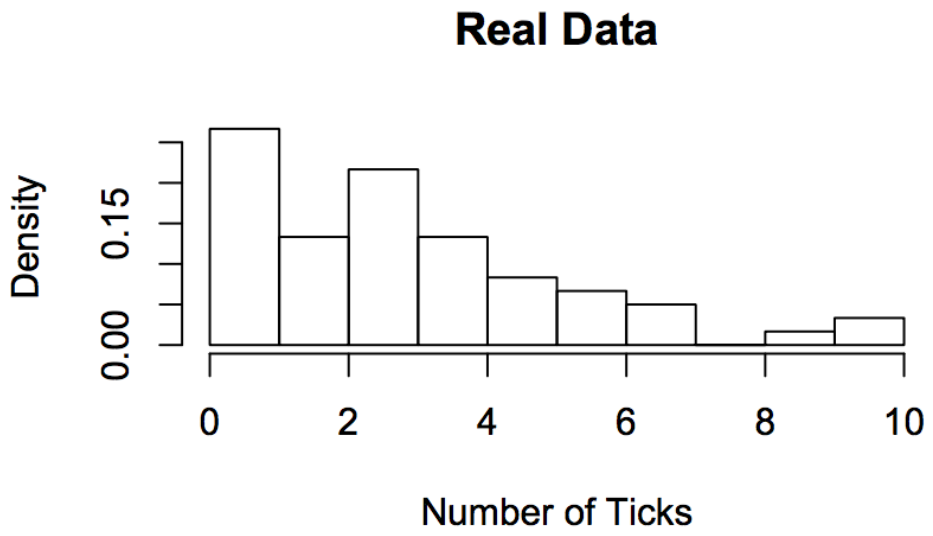
$$[a, b, \lambda \mid \mathbf{y}] \propto \prod_{i=1}^{60} [y_i \mid \lambda_i][\lambda_i \mid a, b][a][b]$$

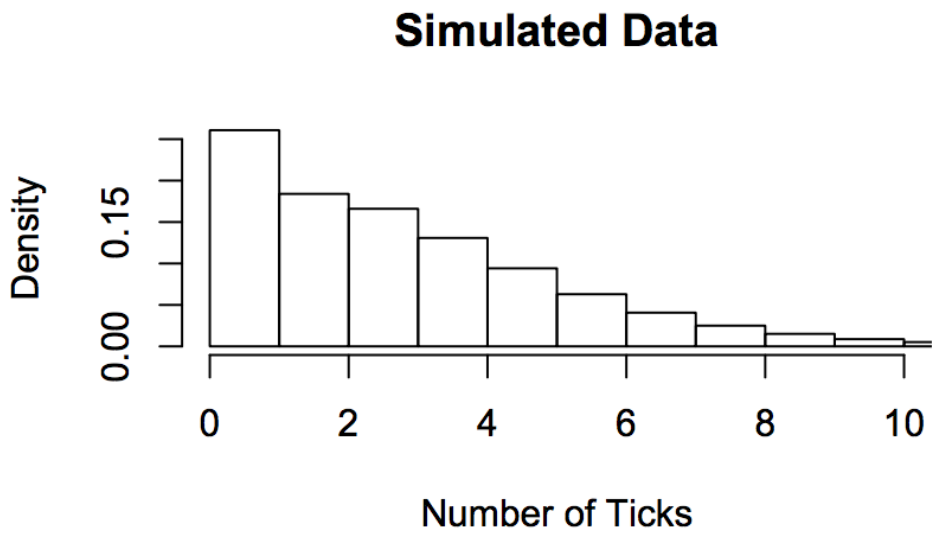
```
model{
a~ dgamma(.001,.001)
b~ dgamma(.001,.001)
for(i in 1:60){
     lambda[i] ~ dgamma(a,b)
     y[i] ~ dpois(lambda[i])
     y.sim[i] ~ dpois(lambda[i])
}
cv.y <- sd(y[ ])/mean(y[ ])
cv.y.sim <- sd(y.sim[])/mean(y.sim[ ])
pvalue.cv <- step(cv.y.sim-cv.y)  # find Bayesian P
 value--the mean of many 0's and 1's returned by
 the step function, one for each step in the chain
mean.y <-mean(y[])
mean.y.sim <-mean(y.sim[])
pvalue.mean <-step(mean.y.sim - mean.y)
for(j in 1:60){
     sq[j] <- (y[j]-lambda[j])^2
     sq.new[j] <- (y.sim[j]-lambda[j])^2
 }
 fit <- sum(sq[])
 fit.new <- sum(sq.new[])
 pvalue.fit <- step(fit.new-fit)
} #end of model
```

Hierarchical model

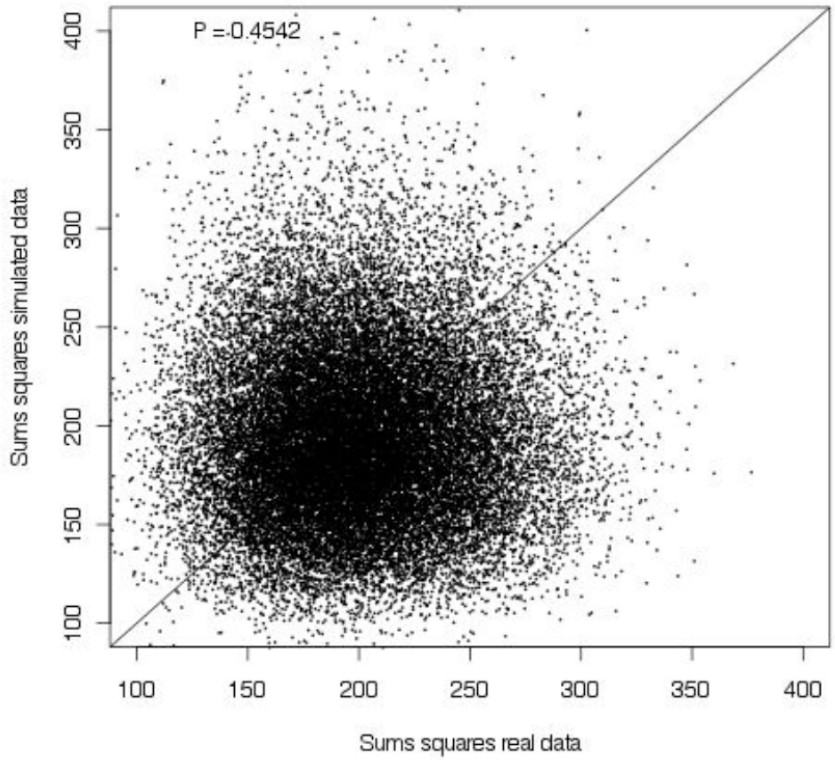
$$[a, b, \boldsymbol{\lambda}|\mathbf{y}] \propto \prod_{i=1}^{60} [y_i|\lambda_i]\,[\lambda_i|a, b]\,[a]\,[b]$$

Include pvalue.fit in variable names list for `coda.samples` or `jags.samples`. Report the mean of pvalue.fit


Real Data
Density
0.00
0.15
0
2
4
6
8
10
Number of Ticks


Simulated Data
Density
0.00
0.15
0
2
4
6
8
10
Number of Ticks

Posterior Predictive Checks



- P value for CV= .45
- P value for mean = .5

Reporting your posterior predictive checks

Posterior predictive checks revealed little evidence of lack of fit between model estimates and data for five data sets (Table 4). Bayesian P values were between 0.12 and 0.88 for 14 out of 15 test statistics for each of the three models. There was some evidence of poor fit of data simulated from the model to observations of the mean of yearling serology for all three models. (Hobbs et al. 2015)

TABLE 4. Bayesian P values for lack of fit between data simulated from posterior predictive distributions and observations for five data sets.

Model and data set	Discrepancy	Mean	SD
Frequency dependent			
Total population size	0.51	0.5	0.51
Proportion juvenile	0.57	0.64	0.93
Juvenile serology	0.8	0.75	0.81
Yearling serology	0.13	0.058	0.19
Adult serology	0.59	0.69	0.54
Density dependent			
Total population size	0.51	0.5	0.48
Proportion juvenile	0.57	0.69	0.95
Juvenile serology	0.88	0.84	0.88
Yearling serology	0.19	0.084	0.28
Adult serology	0.59	0.64	0.56
Combined			
Total population size	0.51	0.5	0.51
Proportion juvenile	0.57	0.64	0.93
Juvenile serology	0.8	0.75	0.81
Yearling serology	0.13	0.058	0.19
Adult serology	0.59	0.69	0.54

Notes: Bayesian P values, P_B, are defined as the probability that the test statistic calculated from simulated data is more extreme than the test statistic calculated from observed data. Lack of fit is indicated by values near 1 or 0. Test statistics were the mean of observations and simulated data, the standard deviation, and the discrepancy, calculated as $\sum_{i=1}^{n}(y_i - \mu_i)^2$ where y_i is an observation, μ_i is the model prediction of the observation, and n is the number of observations in the data set.

Additional sources

- A. Gelman and J. Hill. Data analysis using regression and multilievel / hierarchical modeling. Cambridge University Press, Cambridge, UK, 2009 Chapter 8
- P. B. Conn, D. S. Johnson, P. J. Williams, S. R. Melin, and M. B. Hooten. A guide to Bayesian model checking for ecologists. Ecological Monographs, 88(4):526–542, 2018.