Bayesian statistics – Nanjing Forestry University

Lecture 6 – Model check

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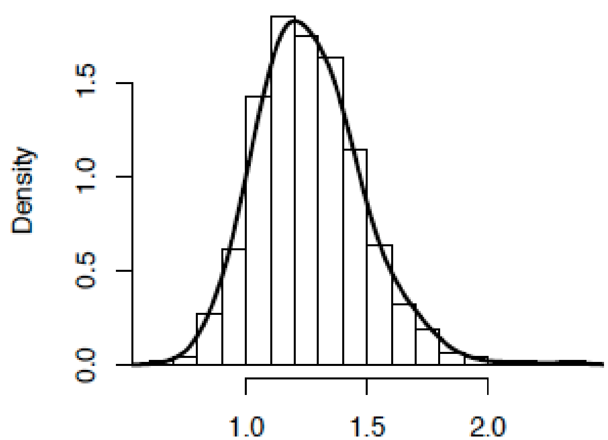
The first question we should ask after fitting a model: *Are the predictions of the model consistent with the data?*

- Is our deterministic model a reasonable representation of the process?
- Have we made the right choices of distributions to represent the uncertainties?



Marginal distributions of random variables A and B

	a_1	a_2	a_3	a_4	$\Pr(B)\downarrow$
b_1	$\frac{2}{20}$	0	$\frac{1}{20}$	$\frac{3}{20}$	$\frac{6}{20}$
b_2	0	$\frac{4}{20}$	0	$\frac{6}{20}$	$\frac{10}{20}$
b_3	$\frac{1}{20}$	$\frac{1}{20}$	$\frac{1}{20}$	0	$\frac{3}{20}$
b_4	0	0	0	$\frac{1}{20}$	$\frac{1}{20}$
$\Pr(A)\rightarrow$	$\frac{3}{20}$	$\frac{5}{20}$	$\frac{2}{20}$	$\frac{10}{20}$	$\frac{20}{20}$

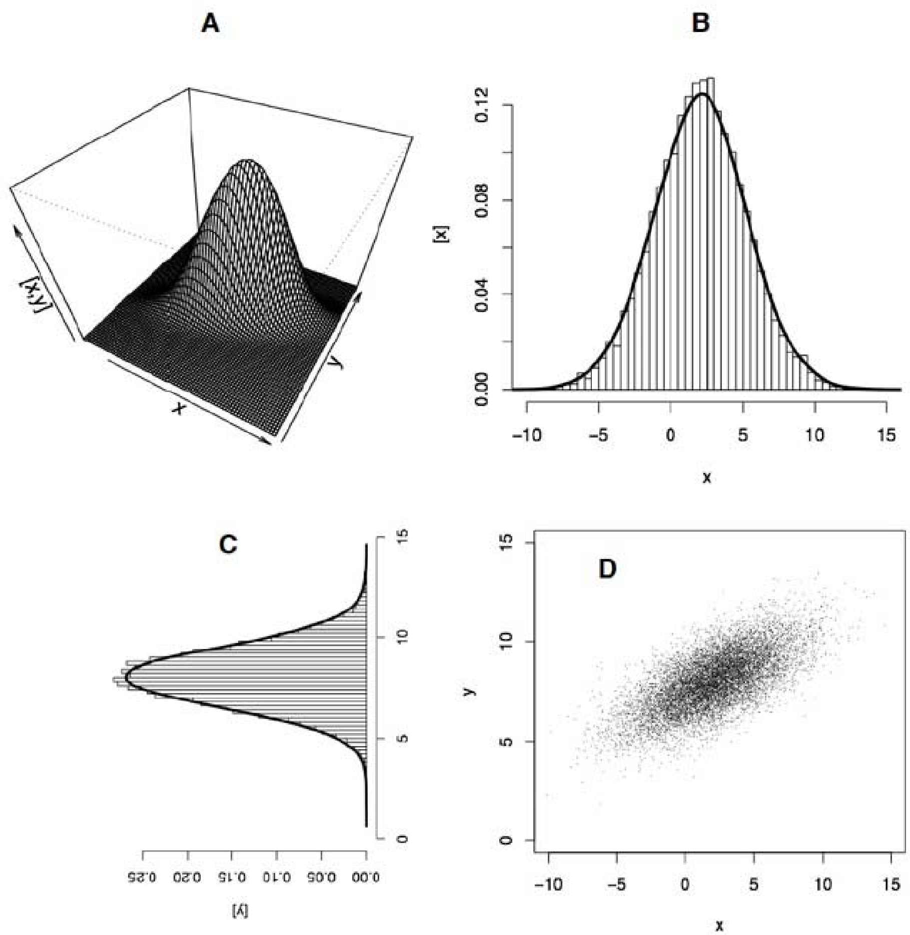
If we have a function $f(A,B)$ specifying the joint probability of the discrete random variables A and B, then

$\sum_A f(A,B)$ is the marginal probabilty of B

and

$\sum_B f(A,B)$ is the marginal probability of A.

This same idea applies to any number of jointly distributed random variables. We simply sum over all but one.


A
B
C
D
x
y
0.00
0.04
0.08
0.12
−10
−5
0
5
10
15
0.05
0.10
0.15
0.20
0.25

If we have a function $f(A,B)$ specifying the joint probability of the continuous random variables A and B, then

$$\int_B f(A,B)\,dB$$ is the marginal probabilty of A

and

$$\int_A f(A,B)\,dA$$ is the marginal probability of B.

This same idea applies to any number of jointly distributed random variables. We simply integrate over all but one.

Posterior predictive checks

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

It is called posterior because it is conditional on the observed **y** and predictive because it is a prediction for an observable y^{new}. It gives the probability of a new prediction of y conditional on $\boldsymbol{\theta}$, which, in turn, is conditional on the data in hand, **y**. Note that it is a marginal distribution because we are integrating over the $\boldsymbol{\theta}$.

$$\mu_i = g(\theta_1, \theta_2, \theta_3, x_i)$$

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

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	$y^{new}{}_{1,1}$	$y^{new}{}_{1,2}$	$y^{new}{}_{1,3}$	!	$y^{new}{}_{1,Y}$
2	.41	2.3	18.5	$y^{new}{}_{2,1}$	$y^{new}{}_{1,2}$	$y^{new}{}_{1,3}$	!	$y^{new}{}_{1,Y}$
3	.46	3.1	16.6	$y^{new}{}_{3,1}$	$y^{new}{}_{1,2}$	$y^{new}{}_{1,3}$	!	$y^{new}{}_{1,Y}$
"	"	"	"	"	"	"		"
K	.39	3.4	22.1	$y^{new}{}_{n,1}$	$y^{new}{}_{n,2}$	$y^{new}{}_{n,3}$	!	$y^{new}{}_{1,Y}$

This is easier done than said.

We have a model $g(\theta, x)$ that predicts a response y.
We estimate the posterior distribtuion, $[\theta \mid y]$.
For any given value of x_i, we can simulate the posterior predictive distribution y_i^{new} by making a draw from $[y_i^{new} \mid g(\theta, x_i), \sigma^2]$. In MCMC, this simply means making draws from the data model at each iteration because each draw is conditional on the current values of the parameters. We simulate a new dataset by repeating these draws for all values of the x.
Accumlating 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)
  }
}
```

Posterior Predictive Checks

$T(\mathbf{y},\theta)$ is a test statistic (e.g., mean, standard deviation, CV, quantile, or sums of squares discrepancy) calcuated from the observed data.

$T(\mathbf{y}^{new},\theta)$ is the corresponding statistic from the new "data" from the posterior predictive distribution.

We calcuate:

$$P_B = \Pr\left(T(\mathbf{y}^{new},\theta) \geq T(\mathbf{y},\theta) \mid \mathbf{y}\right)$$

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: (observation - prediction)^2
- chi-square: $T(y,\theta) = \sum_i = \frac{\left(y_i - \mathrm{E}\left(y_i \mid \theta\right)\right)}{\mathrm{var}(y_i \mid \theta)}$
- deviance: $T(y,\theta) = -2\log[y \mid \theta]$

R. A. Fischer's Ticks

A simple example: 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. Does a Poisson distribution fit the distribution of the data?

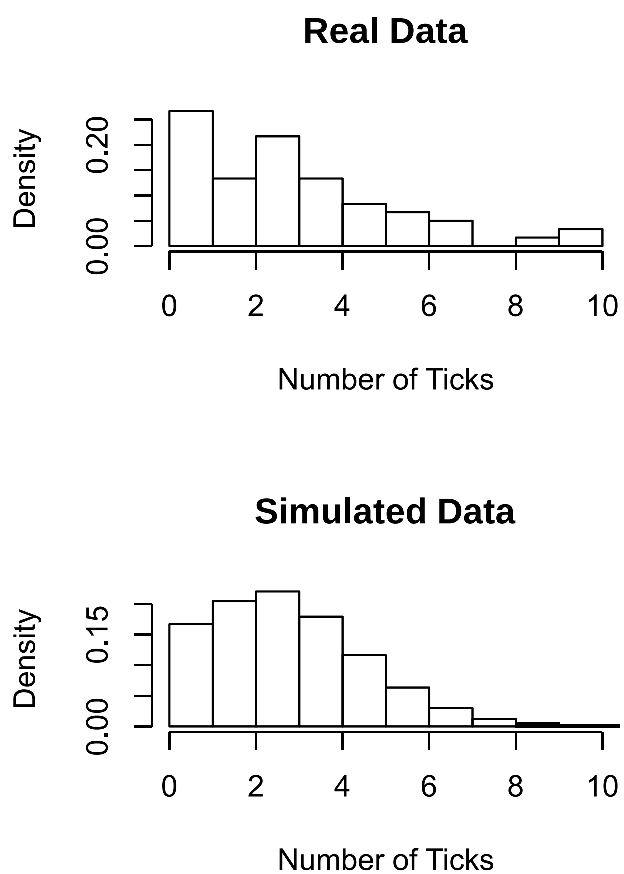
$$[\lambda \mid \mathbf{y}] \propto \prod_{i=1}^{60} \text{Poisson}\left(y_i \mid \lambda\right)[\lambda]$$

For each value of λ in the MCMC chain, we generate a new data set, $\mathbf{y}^{\text{new}}$, by sampling from

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

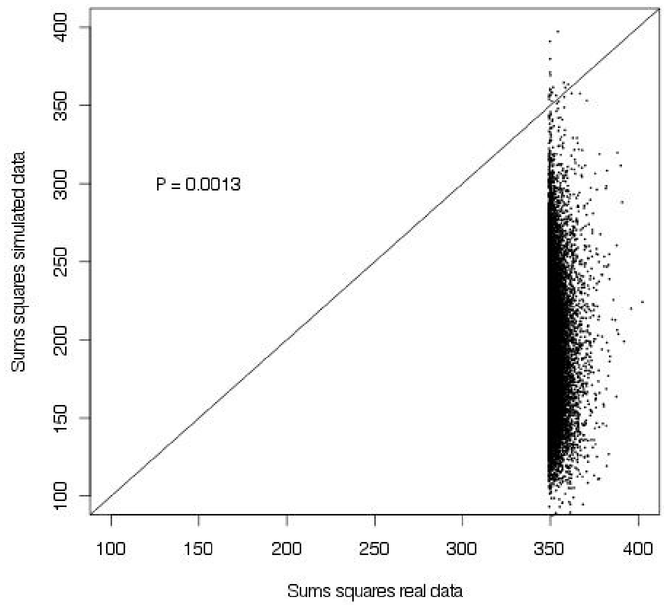
Key bit!

```
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




```
}
fit  <- sum(sq[])
fit.new <- sum(sq.new[])
pvalue.fit  <- step(fit.new-
fit)
} #end of model
```

Simple model

P value for CV= .0013
P value for mean = .51

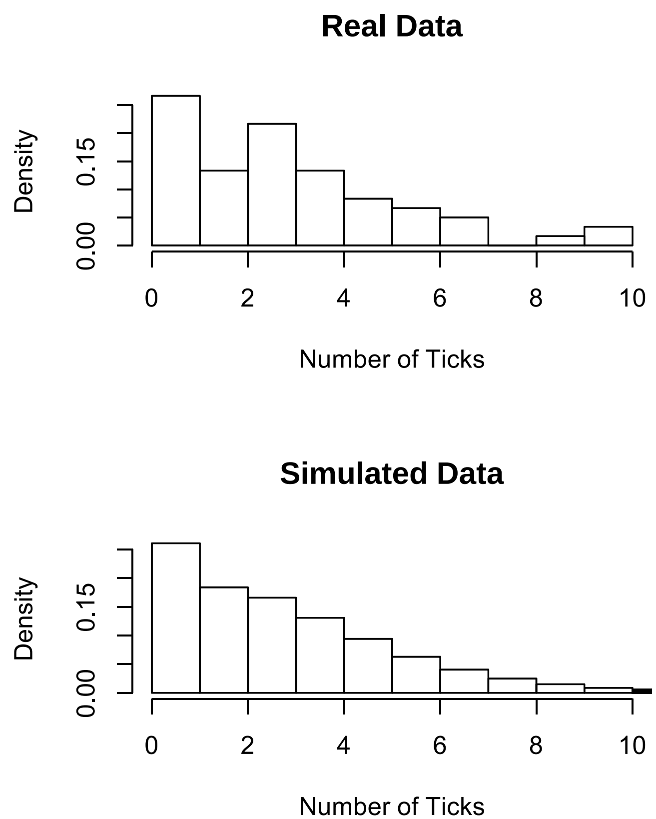
Remember, this is a two-tailed probability, so values close to 0 and 1 indicate lack of fit.

```
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

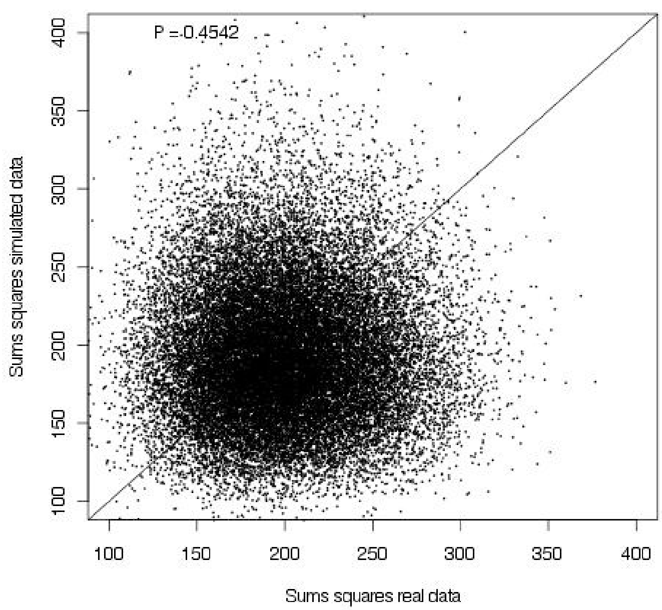
$$[a, b, \boldsymbol{\lambda}|\mathbf{y}] \propto \prod_{i=1}^{60} [y_i|\lambda_i] [\lambda_i|a, b] [a] [b]$$

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



Hierarchical model

Posterior predictive check



Hierarchical model

P value for CV= .45
P value for mean = .50