Model Checking

Bayesian Modeling for Socio-Environmental Data

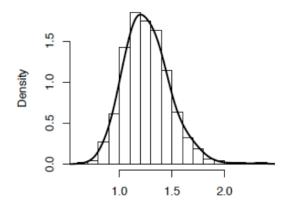
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What is the first question you should ask after fitting a model?

- 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?

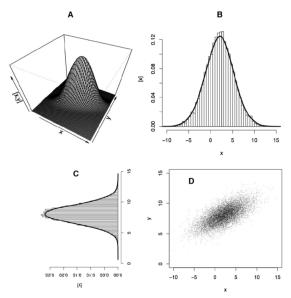
Statistical inference relies on the assumption that your model can give rise to the data. *Model checking* is the process of evaluating whether this is true.

Usefulness of the marginal distribution

Recall, if function f(A, B) specifies the joint probability of the continuous random variables A and B then,

- $\int f(A,B)dB$ is the marginal probabilty of A and
- $\int f(A,B)dA$ 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

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

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

Consider,

$$\mu_i = g(\theta_1, \theta_2, \theta_3, x_i) \tag{1}$$

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

Also see box 8.1 in Hobbs and Hooten

A new data set at each iteration

k	$oldsymbol{ heta}_1$	$oldsymbol{ heta}_1$	$ heta_3$	
1	.42	3.3	20.3	
2	.41	2.3	18.5	
3	.46	3.1	16.6	
:	÷	÷	:	
K	.39	3.4	22.1	

i = 1	i = 2	i = 3	•••	i = Y
$y_{1,1}^{new}$	$y^{new}_{1,2}$	$y_{1,3}^{new}$	•••	$y^{new}_{1,Y}$
$y^{new}_{2,1}$	$y^{new}_{1,2}$	$y^{new}_{1,3}$	•••	$y^{new}_{1,Y}$
$y^{new}_{3,1}$	$y^{new}_{1,2}$	$y^{new}_{1,3}$	•••	$y^{new}_{1,Y}$
:	:	:		:
$y_{n,1}^{new}$	$y_{n,2}^{new}$	$y_{n,3}^{new}$	•••	$y^{new}_{1,Y}$

This is easier done than said.

- We have a model $g(\theta, x)$ that predicts a response y. We estimate the posterior 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 $[y^{new} | g(\theta, x), \sigma^2]$.
- 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 dataset by repeating these draws for all values of the x.
- Accumilating 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_1x_i
[b_0,b_1,\tau \mid \mathbf{y}] \propto \prod_{i=1}^n \operatorname{normal}(y_i \mid g(b_0,b_1,x_i)_i,\tau) \times
normal(b_0 \mid 0.0001) normal(b_1 \mid 0,.0001) gamma(\tau \mid .01.01)
    model{
    b0 \sim dnorm(0..0001)
    b1 \sim dnorm(0.0001)
    tau \sim dgamma(.01,.01)
    sigma<-1/sqrt(tau)
    for(i in 1:length(y)){
       mu[i] \leftarrow b0 + b1*x[i]
       v[i] \sim 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) calcuated from the observed data.
- $T(y^{new}, \theta)$ is the corresponding statistic from the simulated, which is generated from the posterior predictive distribution.
- We calcuate:

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

 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 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?

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

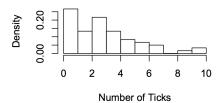
• For each value of λ in the MCMC chain, we generate a new data set, y^{new} , by sampling from:

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

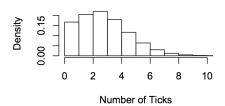
```
model{
                                                        Key bit!
lambda \sim dgamma(0.001,0.001)
for(i in 1:60){
     y[i] ~ dpois(lambda)
     y.new[i] ~ dpois(lambda) #simulate a new data set of 60 points
cv.y \leftarrow sd(y[])/mean(y[])
cv.y.new <- sd(y.new[])/mean(y.new[])</pre>
pvalue.cv <- 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[])</pre>
pvalue.mean <-step(mean.y.new - mean.y)</pre>
for(i in 1:60){
     sq[i] \leftarrow (y[i]-lambda)^2
     sq.new[j] \leftarrow (y.new[j]-lambda)^2
fit <- sum(sq□)
fit.new <- sum(sq.new[])</pre>
pvalue.fit <- step(fit.new-fit)</pre>
} #end of model
```

Simple Model

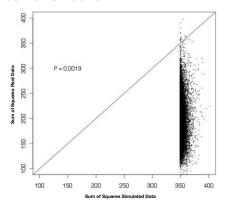
Real Data



Simulated Data



Posterior Predictive Checks



- 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.

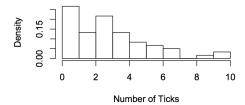
How could you modify this model to allow "extra" variance?

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

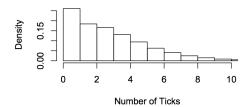
Hierarchical model

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

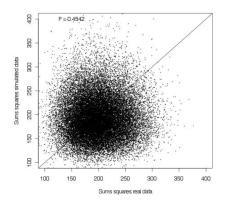
Real Data



Simulated Data



Posterior Predictive Checks



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