Bayes and R

4th Annual Bayesian Biostatistics Conference

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Why R for Bayes?

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- Easy to extend the R language
  - by writing functions
  - by creating packages
- There are nice interfaces of R with more efficient MCMC computing engines like OpenBUGS

Three Stories

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- Learning About Streakiness

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  - Using R simulation functions.

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  - Using `LearnBayes`.
  - Using `MCMCpack`

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  - Using `LearnBayes`.
  - Using `MCMCpack`
  - Using R interface to Openbugs

References

References

- Albert (2009), *Bayesian Computation with R*, 2nd edition, Springer.

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- CRAN Task View: Bayesian Inference (`http://cran.r-project.org/`)

Learning About Streakiness

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- Here is some of the data:

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...
```

- Focus on the spacings between successive hits that we put in a vector y:

```
> y
  [1]  0  1  8  3  5  1  0  4  0  7  0
 [12]  4  1  4  0  2  0  1  1  1  0  3
...
```

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- Fit the model using some prior knowledge about p
- Check the goodness of fit of the model
- We'll find that the geometric model is inappropriate – fit a new model (beta/geometric) that allows for variability in the hitting probability p
- We'll introduce some modern simulation methods for exploring a posterior distribution

A Geometric Sampling Model

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- Assume the spacings $y_1, ..., y_n$ are independent where y_i is geometric with probability p.

$$f(y_i|p) = p(1-p)^y, \;\; y = 0, 1, 2, ...$$

A Geometric Sampling Model

- Assume the spacings $y_1, ..., y_n$ are independent where y_i is geometric with probability p.

$$f(y_i|p) = p(1-p)^y, \;\; y = 0, 1, 2, ...$$

- Likelihood function $L(p)$ is joint density of the spacings viewed as a function of the parameter p.

$$L(p) = \prod_{i=1}^{n} f(y_i|p) = p^n(1-p)^s,$$

where $s = \sum y$ is the sum of the observations and the n is the sample size.

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- Next step in a Bayesian analysis is to assign a prior density $g(p)$.
- A prior reflects one's beliefs about the location of Pedroia's batting probability before sampling.
- Here's my beliefs:
  $P(p < 0.310) = 0.5$, $P(p < 0.350) = 0.8$.
- Then I find a beta prior density $g(p)$ that matches these beliefs.

```
> library(LearnBayes)
> beta.select(list(p=.5,x=.31), list(p=.8,x=.35))
[1] 30.89 68.35
```

The Posterior

The Posterior

- Observe the data. We use R to compute the sample size n and the sum of observations s.

  ```
  > n = length(y)
  > s = sum(y)
  ```

  We see $n = 213$ and $s = 438$.

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- By Bayes' rule, posterior density of p is proportional to the product of the likelihood $L(p)$ and the beta prior $g(p)$.
- Applying this recipe

$$g(p|y) \propto p^n(1-p)^s \times p^{a-1}(1-p)^{b-1}.$$

- Substituting the observed values of $n = 213$ and $s = 438$, and the beta parameter values $a = 31, b = 68$, we obtain the posterior density

$$g(p|y) \propto p^{213+31-1}(1-p)^{438+68-1}$$

which we recognize as a beta density with shape parameters $a_1 = 244$ and $b_1 = 506$.

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which we recognize as a beta density with shape parameters $a_1 = 244$ and $b_1 = 506$.
- R package contains a set of functions for plotting a beta density, computing beta probabilities and quantiles, and for simulating beta variates and these are all helpful for summarizing the posterior density.

Simulation Approach for Summarizing the Posterior

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- Use data analysis graphs and summaries of the simulated sample to learn about the parameter.

Graph the Posterior

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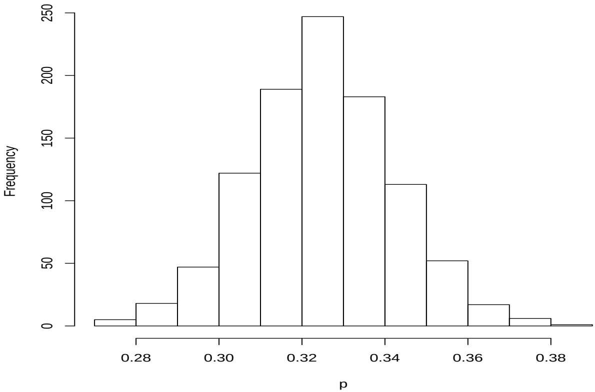
- Plot the posterior density using the R functions `hist` (can use `density` for a smoother density estimate):

  `> hist(p,main="")`



- Summarize the posterior density by finding the .05, .5, .95 quantiles of the gamma density.

```
> quantile(p,c(0.05,0.5,0.95))
```

```
       5%       50%       95%
0.2974597 0.3260421 0.3552960
```

A point estimate at p is the posterior median 0.326. A 90% interval estimate for λ is found by the 5th and 95th percentiles (0.297, 0.355).

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  A point estimate at p is the posterior median 0.326. A 90% interval estimate for λ is found by the 5th and 95th percentiles (0.297, 0.355).
- Is it likely that Pedroia's true batting ability exceeds 0.340? Answer this by computing the probability that p is larger than 0.340.

  ```
  > mean(p > 0.340)
  [1] 0.212
  ```

The Predictive Distribution

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- The predictive density can be used to predict future observation values y.

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- Suppose we wish to predict spacings $y_1^*, \ldots, y_{213}^*$ (we observed 213 spacings in the 2008 season).
- Density of these future counts is given by

$$f(y^*) = \int \prod Geom(y_i^*; p) Beta(p; 244, 506) dp$$

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- Easy to simulate values of y^* by simulation.
  1. Simulate p from Beta(244, 506)
  2. Simulate $y_1^*, \ldots, y_{213}^*$ from Geometric(p)

Prediction on R

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- Write a short function to simulate one future sample of spacings.

```
> predict = function() {
+       p = rbeta(1, 244, 506)
+       rgeom(213, p)
+ }
```

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```

- Simulate one sample.

```
> predict()
```

```
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- Answer this tabulating the observed and predicting counts.
- We'll see that the actual counts look more spread out than the predicted counts.

Comparing Predicted and Actual Counts

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- Use `table` to tabulate actual counts:

```
> table(y)

y
 0  1  2  3  4  5  6  7  8  9 12 16 18
72 56 24 13 22  8  3  4  3  3  3  1  1
```

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72 56 24 13 22  8  3  4  3  3  3  1  1
```

- Use `predict` to simulate the counts and `tabulate`:

```
> ys=predict()
> table(ys)

ys
 0  1  2  3  4  5  6  7  8  9 11 13 16
58 42 38 24 11 10  6  8  6  7  1  1  1
```

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- Do you see any differences between the predicted and actual counts?

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- See if $T_{observed}$ is consistent with this distribution.

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- See if $T_{observed}$ is consistent with this distribution.
- If $T_{observed}$ is "extreme", indicates model misfit.

The Example

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- Write function to simulate sample from y^* and compute $SD(y^*)$.

```
> model.check=function()
+ {
+ p=rbeta(1,244,506)
+ ys=rgeom(n, p)
+ sd(ys)
+ }
```

The Example

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+ {
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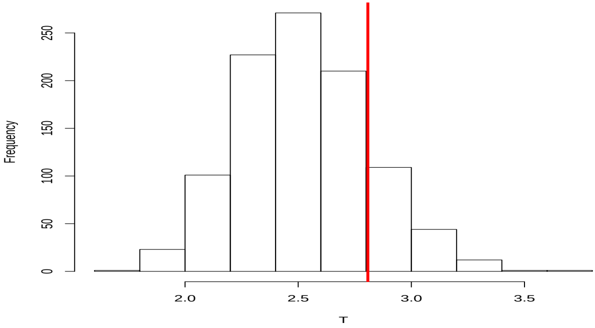
+ ys=rgeom(n, p)
+ sd(ys)
+ }
```

- Repeat this simulation 1000 times and collect values of T.

```
> T = replicate(1000, model.check())
```

- Construct histogram of T and show value of $T_{observed}$ by a vertical line.

```
> hist(T)
> abline(v = sd(y), lwd = 3, col = "red")
```



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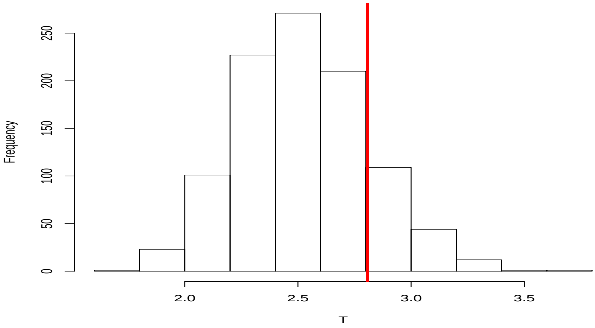

- There is more dispersion in the data than predicted from the geometric model.

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$$g(K, \eta) = \frac{1}{\eta(1-\eta)} \frac{1}{(1+K)^2}.$$

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- Want to learn about K – indicates degree of overdispersion in data.
- As K approaches ∞, model approaches Geometric(p).

Posterior of 2nd Stage Parameters

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- One can show that the marginal posterior density of (K, η) is

$$g(K, \eta | y) \propto g(K, \eta) \times \prod_{i=1}^{n} f(y_i | K, \eta),$$

where

$$f(y_i | K, \eta) = \frac{B(K\eta + 1, K(1 - \eta) + y_j)}{B(K\eta, K(1 - \eta))}$$

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- Want to summarize this distribution for inference.
- Problem: we can't use direct simulation since this is not a familiar functional form.

Summarization of the Posterior Using R

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- Write log posterior as

$$\log g(K, \eta | y) = \log g(K, \eta) + \sum_{i=1}^{n} \log f(y_i | K, \eta),$$

where

$$\begin{aligned} \log f(y_i | K, \eta) &= \log B(K\eta + 1, K(1-\eta) + y_j) \\ &- \log B(K\eta, K(1-\eta)) \end{aligned}$$

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- Write a R function that computes the logarithm of the posterior density.
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where

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- Helpful to transform posterior to $(\theta_1, \theta_2) = (logit\eta, \log K)$. (Why?)

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- Write the log posterior that is a function of (θ_1, θ_2).

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- Reexpress to $(\theta_1, \theta_2) = (logit \eta, \log K)$.
- Write the log posterior that is a function of (θ_1, θ_2).
- Don't forget the Jacobian!

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R Function to Compute Log Posterior

- `theta` is vector of parameters ($\text{logit}\eta, \log K$)
- `y` is vector of counts
- output is the value of the log posterior evaluated at `theta`

```
beta.geom=function(theta,y)
{
eta = exp(theta[1])/(1 + exp(theta[1]))
K = exp(theta[2])
N=length(y)
a=K*eta
b=K*(1-eta)
sum(lbeta(a+1,y+b))-N*lbeta(a,b) +
   theta[2] - 2 * log(1 + exp(theta[2]))
}
```

Summarizing the Posterior by the Mode

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- Use an algorithm such as Newton's method to find the posterior model.

Summarizing the Posterior by the Mode

- Use an algorithm such as Newton's method to find the posterior model.
- This algorithm is implemented in the function `laplace` in the `LearnBayes` package.

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- Approximately, posterior of θ is $\mathrm{N}(\hat{\theta}, V)$.

R Code to Find the Mode

```
> library(LearnBayes)
> # read in beta.geom function
> guess.at.mode=c(1,1)
> fit=laplace(beta.geom,guess.at.mode,y)
> fit

$mode
[1] -0.5668859  2.9022052
$var
            [,1]        [,2]
[1,]  0.01206898 -0.03539901
[2,] -0.03539901  0.28599773
$int
[1] -414.655
$converge
[1] TRUE
```

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- This approximation is a good starting point in the simulation-based methods of fitting the model.
- How accurate is this approximation?

Plot the Posterior

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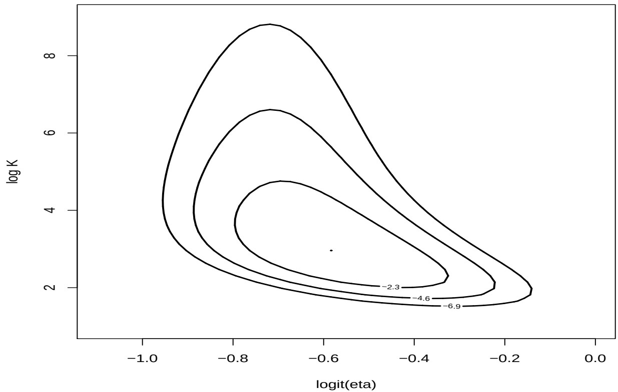
- Choose a viewing interval of (-1.1, 0) for logit η and (1, 9) for log K.

```
> mycontour(beta.geom,c(-1.1,0,1,9),y,
+    xlab="logit(eta)",ylab="log K")
```



Markov Chain Monte Carlo Fitting

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- Under general conditions, the limiting distribution of the chain will be the posterior density of interest.
- There are general-purpose Markov Chain algorithms that work for many problems.

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- Main task is to choose a reasonable neighborhood by the selection of cV, where V is an approximate variance-covariance matrix and c is a scale factor.
- Want acceptance rate of the algorithm to be approximately 20% - 40%.

R function `rwmetrop`

```
rwmetrop(logpost,proposal,start,m,par)
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- `start:` vector containing the starting value of the parameter
- `m:` the number of iterations of the chain
- `par:` data that is used in the function logpost

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- Starting value can be `fit$mode`

MCMC for the example

- `beta.geom` contains the definition of the log posterior
- Have already stored the output of `laplace` in the variable `fit`.
- Have estimate at var-cov matrix in `fit$var`.
- Starting value can be `fit$mode`
- Use a large number of iterates, say 10,000.

```
> mcmc.fit=rwmetrop(beta.geom,
+     list(var=fit$var,scale=2),
+     fit$mode,10000,y)
```

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MCMC Diagnostics

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- **Burn-in?** How many iterations does it take the chain to "reach" the posterior?
- **Good mixing?** Is the chain moving well across the posterior? Is there significant autocorrelation in the chain?
- **How many?** How many iterations should be collected?

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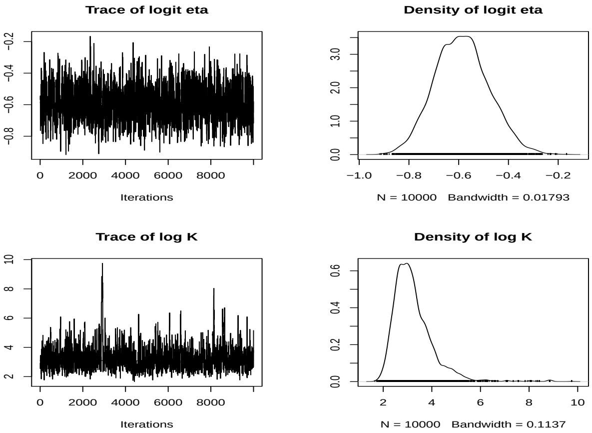
- `autocorr.plot` function produces autocorrelation plots.
- `summary` function produces summaries and correct standard errors for posterior means.

Load in coda package and create MCMC object

```
>  library(coda)
> dimnames(mcmc.fit$par)[[2]]=c("logit eta","log K")
> sim.draws=mcmc(mcmc.fit$par)
```

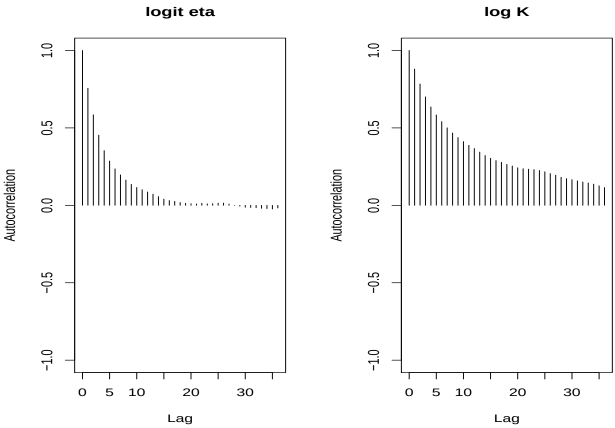
Trace and density plots

> plot(sim.draws)



Autocorrelation plots

```
> autocorr.plot(sim.draws)
```



Summaries of output with correct standard errors

```
> summary(sim.draws)

1. Empirical mean and standard deviation for each varia
   plus standard error of the mean:

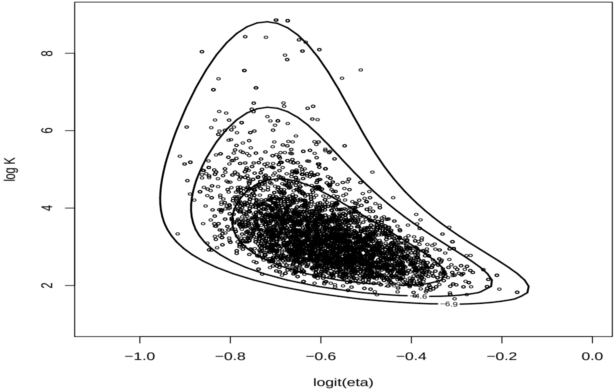
               Mean     SD Naive SE Time-series SE
logit eta -0.5873 0.1086 0.001086       0.003166
log K      3.2345 0.8462 0.008462       0.052512

2. Quantiles for each variable:

              2.5%     25%     50%     75%   97.5%
logit eta -0.788 -0.6613 -0.5897 -0.5183 -0.3674
log K      2.173  2.6858  3.0681  3.5924  5.1845
```

Demonstration that MCMC sample appears to have found posterior.

```
> mycontour(beta.geom,c(-1.1,0,1,9),y,
+   xlab="logit(eta)",ylab="log K")
> points(mcmc.fit$par,cex=.5)
```



Introduction to Gibbs Sampling

4th Annual Bayesian Biostatistics Conference

Jim Albert
Department of Mathematics and Statistics
Bowling Green State University

Web Counts

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- Record the number of visits to my website for each day for a month.
- Text file `may.june.webhits.txt` contains the day of the week and the visit count for the 31 days between May 23 and June 22 in 2009.
- I read this dataset into R and store it in the variable `data` by the read.table function.

  ```
  > data = read.table("may.june.webhits.txt",
  + header = TRUE, skip = 1)
  ```

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- Interested in estimating the ratio of the average number of visits during weekdays versus weekends.
- Can do this through a simple Poisson model

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- Let n_A and s_A denote number of counts and sum of counts for the first sample; similarly define n_B and s_B.
- Likelihood function is given by

$$L(\lambda_A, \lambda_B) = \exp(-n_A\lambda_A)\lambda_A^{s_A} \exp(-n_B\lambda_B)\lambda_A^{s_B}.$$

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- Focus is on learning about the risk ratio γ.

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- Want to simulate from joint posterior of θ, γ.

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$$[\theta|\gamma] \sim Gamma(a_0 + s_A + s_B, n_A + n_B\gamma + b_0)$$

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- Then one cycle of Gibbs sampling consists of
  - Simulate $\gamma^{(k)}$ from $Gamma(a_g + s_B, b_g + n_B\theta^{(k-1)})$.
  - Simulate $\theta^{(k)}$ from $Gamma(a_0 + s_A + s_B, n_A + n_B\gamma^{(k)} + b_0)$
- This constitutes one cycle of GS, producing $(\theta^{(k)}, \gamma^{(k)})$.

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- Compute the sample sizes `nA, nB` and the sums `yA, yB`.

Write a function to perform Gibbs Sampling.

- The list S contains the data `yA, yB` and the prior hyperparameters `a0, b0, ag, bg`.
- Compute the sample sizes `nA, nB` and the sums `yA, yB`.
- Here is the two R commands that implement one Gibbs cycle:

```
gamma=rgamma(1, shape=S$ag+s.B,
                rate=S$bg+n.B*theta)
theta=rgamma(1, shape=S$a0+s.A+s.B,
                rate=S$b0+n.A+n.B*gamma)
```

Add a reasonable starting value and loop for iter iterations.

```
theta=s.A/n.A

for (i in 1:iter)
{
 gamma=rgamma(1, shape=S$ag+s.B,
                 rate=S$bg+n.B*theta)
 theta=rgamma(1, shape=S$a0+s.A+s.B,
                 rate=S$b0+n.A+n.B*gamma)
}
```

Set up storage matrix and store the simulated draws.

```
R=matrix(0,iter,2)
theta=s.A/n.A

for (i in 1:iter)
{ gamma=rgamma(1, shape=S$ag+s.B, rate=S$bg+n.B*theta)
  theta=rgamma(1, shape=S$a0+s.A+s.B,
                  rate=S$b0+n.A+n.B*gamma)
  R[i,]=c(theta,gamma)}
return(R)
```

Add initial statements finding the sample sizes and sums.

```
n.A=length(S$yA); s.A=sum(S$yA)
n.B=length(S$yB); s.B=sum(S$yB)
R=matrix(0,iter,2)
theta=s.A/n.A
for (i in 1:iter)
{ gamma=rgamma(1, shape=S$ag+s.B, rate=S$bg+n.B*theta)
  theta=rgamma(1, shape=S$a0+s.A+s.B,
                  rate=S$b0+n.A+n.B*gamma)
  R[i,]=c(theta,gamma)}
return(R)
```

Finish function poisson.gibbs – inputs are S and iter.

```
poisson.gibbs=function(S,iter)
{ n.A=length(S$yA); s.A=sum(S$yA)
  n.B=length(S$yB); s.B=sum(S$yB)
  R=matrix(0,iter,2)
  theta=s.A/n.A
for (i in 1:iter)
{ gamma=rgamma(1, shape=S$ag+s.B, rate=S$bg+n.B*theta)
  theta=rgamma(1, shape=S$a0+s.A+s.B,
                  rate=S$b0+n.A+n.B*gamma)
  R[i,]=c(theta,gamma)}
return(R)
}
```

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- Create two datasets.
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- Source in R function.
- Run `poisson.gibbs`.
- coda the MCMC output.

Data setup

```
> options(width = 35)
> data = read.table("may.june.webhits.txt",
+     header = TRUE, skip = 1)
> weekend.counts = data$Count[data$Day ==
+     "Sat" | data$Day == "Sun"]
> weekday.counts = data$Count[data$Day ==
+     "Mon" | data$Day == "Tues" |
+     data$Day == "Wed" | data$Day ==
+     "Thur" | data$Day == "Fri"]
> stuff = list(yA = weekend.counts,
+     yB = weekday.counts, a0 = 2,
+     b0 = 1, ag = 8, bg = 8)
```

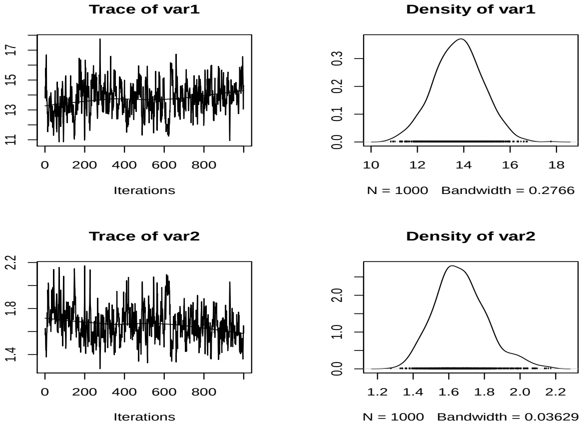
Source and run function

```
> source("poisson.gibbs.R")
> R = poisson.gibbs(stuff, 1000)
```

Some MCMC Diagnostics

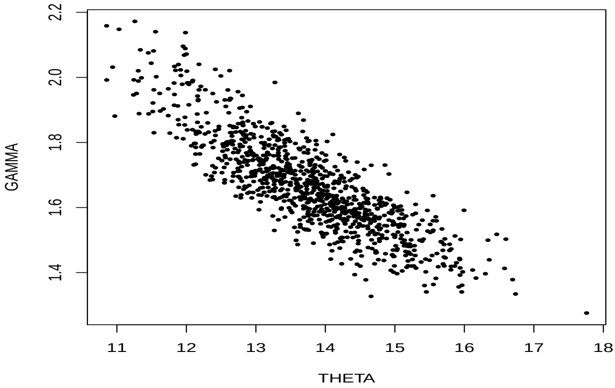
```
> library(coda)

> plot(mcmc(R))
```



Posterior of (θ, γ)

```
> plot(R, pch = 19, cex = 0.5,
+      xlab = "THETA", ylab = "GAMMA")
```



What have we learned about the risk ratio γ?

Summarize by the 5th, 50th, and 95th percentiles of the simulated draws of γ.

```
> quantile(R[, 2], c(0.05, 0.5,
+     0.95))
      5%      50%      95%
1.441356 1.656326 1.944656
```

MCMC Packages/MCMC Interfaces on R

4th Annual Bayesian Biostatistics Conference

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Website Hits

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- Using google.com/analytics, I collect the number of visits to my book's website for every day for 8 Wks (2010 data).

	Wk1	Wk2	Wk3	Wk4	Wk5	Wk6	Wk7	Wk8
Sun	11	10	12	15	8	24	14	11
Mon	23	28	27	22	23	18	28	20
Tues	18	21	27	23	27	28	25	19
Wed	51	45	32	19	15	37	34	32
Thurs	31	26	15	17	23	19	21	22
Fri	21	18	13	20	17	20	13	11
Sat	6	12	10	14	7	10	17	5

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- Use a Poisson log-linear model with an additive fit (Day + Week) to explore patterns.

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- Assign β a multivariate normal prior with mean b and precision matrix P.

Read in data matrix

```
> w=read.table("webhits2010.txt",
+   row.names=1,header=TRUE,sep="\t")
> w
      Week1 Week2 Week3 Week4 Week5 Week6 Week7 Week8
Sun      11    10    12    15     8    24    14    11
Mon      23    28    27    22    23    18    28    20
Tues     18    21    27    23    27    28    25    19
Wed      51    45    32    19    15    37    34    32
Thurs    31    26    15    17    23    19    21    22
Fri      21    18    13    20    17    20    13    11
Sat       6    12    10    14     7    10    17     5
```

Get data in ANOVA format

```
> day=factor(rep(1:7,8),labels=row.names(w))
> week=factor(rep(1:8,each=7),labels=dimnames(w)[[2]]
> count=stack(w)$values
> head(cbind(count,day,week))
```

```
     count day week
[1,]    11   1    1
[2,]    23   2    1
[3,]    18   3    1
[4,]    51   4    1
[5,]    31   5    1
[6,]    21   6    1
```

Standard glm fit

```
> fit=glm(count~day+week,family=poisson)
> fit


Coefficients:
(Intercept)       dayMon      dayTues       dayWed
    2.70098      0.58779      0.58248      0.92577
     daySat    weekWeek2    weekWeek3    weekWeek4    w
   -0.25951     -0.00623     -0.16875     -0.21387
  weekWeek7    weekWeek8
   -0.05752     -0.29391

Degrees of Freedom: 55 Total (i.e. Null);  42 Residual
Null Deviance:      220.8
Residual Deviance: 63.58       AIC: 357.7
```

Using LearnBayes

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- Write a function to compute the log posterior (uniform prior)

```
loglinearpost=function (beta, d)
{
    X=model.matrix(~day+week,data=d)
    beta=as.vector(beta)
    sum(dpois(d$count,lambda=exp(X%*%beta),log=TRUE
}
```

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}
```

- Use the functions `laplace` and `rwmetrop` to summarize the posterior.

R code for LearnBayes

```
> library(LearnBayes)
> d=list(day=day, week=week, count=count)
> fit=laplace(loglinearpost,c(2.7,rep(0,13)),d)
> proposal=list(var=fit$var,scale=0.7)
> start=fit$mode
> my.mcmc.fit=rwmetrop(loglinearpost,proposal,
+   start,10000,d)
```

Takes 57.88 seconds for 10,000 iterations of MCMC.

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- Functions are programmed in compiled C++ to maximize computational efficiency.
- My experience with `MCMCpack` is generally positive, but there are limitations in the models.

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MCMCpack function MCMCpoisson

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- Assigns a multivariate normal prior on β.
- The function returns a `mcmc` object that can be analyzed using the `coda` package.
- As an option, it returns estimate at the marginal likelihood, that can be used to compare models by Bayes factors.

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- Assuming a constant prior for β, so `b0 = 0`, `B0 = 0`
- Play with `tune` input (equivalent to `scale` in `rwmetrop`) to get reasonable acceptance rate.

```
> mcmc.fit=MCMCpoisson(count~day+week,
+     burnin = 1000, mcmc = 10000,
+     thin = 1, tune = 0.7, verbose = 0,
+     seed = NA,  beta.start = NA,
+     b0 = 0, B0 = 0, marginal.likelihood = "none")
```

```
@@@@@@@@@@@@@@@@@@@@@@@@@@@@@@@@@@@@@@@@@@@@@@@@@@@@@@
The Metropolis acceptance rate for beta was 0.20727
@@@@@@@@@@@@@@@@@@@@@@@@@@@@@@@@@@@@@@@@@@@@@@@@@@@@@@
```

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- Outputs the simulation matrix of β. So it is easy to find the marginal posterior of any function $h(\beta)$ of interest.

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- It is fast – 10,000 MCMC iterations of Poisson log-linear regression took 0.39 seconds (contrast with 57.88 seconds using `LearnBayes`)
- Outputs the simulation matrix of β. So it is easy to find the marginal posterior of any function $h(\beta)$ of interest.
- But one sacrifices some flexibility of the Bayesian approach – why should we be limited to using a normal prior?

R Interfaces with WinBUGS/OpenBUGS

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- WinBUGS is a general Windows program for implementing MCMC calculations. (Many Bayesian courses are entirely based on using WinBUGS.)
- OpenBUGS is the open-source version of WinBUGS.
- There are several R interfaces with WinBUGS and OpenBUGS. These are attractive since one can use R to get the data ready and summarize and display MCMC output.
- I'll illustrate one R package BRugs that installs OpenBUGS and the R interface.

Basic Steps to Use R Interface with OpenBUGS

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Basic Steps to Use R Interface with OpenBUGS

- Write a short script defining the Bayesian model. This script is a file in the current working directory.
- Specify the data that will be used, the parameters of the model, and initial values of the parameters in the MCMC simulation.
- A special R function `bugs` is used to perform the MCMC simulation (using the OpenBUGS engine)
- One obtains a matrix of simulated draws that one can summarize using the `coda` package.

The OpenBUGS model file “webhits.bug”

```
model
{
for (i in 1:n)
  { count[i] ~ dpois(lam[i])
     log(lam[i]) <- beta[1] + X[i,2]*beta[2] + X[i,3]*b
     X[i,4]*beta[4] + X[i,5]*beta[5] + X[i,6]*beta[6] +
     X[i,7]*beta[7] + X[i,8]*beta[8] + X[i,9]*beta[9] +
     X[i,10]*beta[10] + X[i,11]*beta[11] + X[i,12]*beta
     X[i,13]*beta[13] + X[i,14]*beta[14]
  }
for (j in 1:14)
  {  beta[j] ~ dnorm(0, 0.001)}
}
```

The R code

Specify the data, the parameters, and the initial parameter values:

```
> library(arm)
> library(BRugs)

# have already defined count and X

> n=56
> web.data = list("n","count","X")
> web.parameters = c("beta")
> web.inits = function(){
+   list(beta=fit$coef)}
```

R Code to run the MCMC

```
> web.fit = bugs(web.data, web.inits, web.parameters,
+   "webhits.bug", n.chains=1, n.iter=10000, debug=TRU
+    n.burnin=1000, program = "openbugs")
```

Now we can use coda to summarize the MCMC output:

```
> summary(mcmc(web.fit$sims.matrix))
```

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- Speed? For the example problem, it took 32 seconds for 10,000 iterations. (Between speed of `rwmetrop` and `MCMCpack`.)
- As with any MCMC simulation, have to perform diagnostics on the output.
- There are some programming tricks for special problems.
- For my introductory Bayes class, I prefer to use R procedures (like the ones in the `LearnBayes` package), since the MCMC algorithms are more transparent.

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$$T(y, \beta) = \sum_j \frac{(y_j - \lambda_j)^2}{\lambda_j},$$

  where $\lambda_j = x_j \beta$.
- Want to compare the distributions $T(y^*, \beta)$ with $T(y, \beta)$

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> X=model.matrix(~day+week)
> T.predicted=function(j)
+ {
+ lambda=exp(X%*%mcmc.fit[j,])
+ ys=rpois(length(lambda),lambda)
+ sum((ys-lambda)^2/lambda)
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> TP=sapply(1:10000,T.predicted)
```

Model checking, continued

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- The function `T.observed` simulates a value of $T(y, \beta)$ from posterior distribution.

```
> T.observed=function(j)
+ {
+ lambda=exp(X%*%mcmc.fit[j,])
+ sum((count-lambda)^2/lambda)
+ }
```

Model checking, continued

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> mean(Tobs>TP)
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```

- Conclusion: the observed data displays more variability than predicted from the Poisson model.

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- Use some alternative model such as a negative binomial regression.
- Can estimate overdispersion by the negative binomial parameter.
- Obtain better estimates at the week and day effects (more realistic standard errors).