ST440/540 Applied Bayesian Analysis
Lab activity for 3/3/2025

Announcements
- Quiz 8 due Friday
- Final project survey due Friday

A. STUDENT QUESTIONS

(1) The application of Gibbs is for Conjugate Pairs. The application for Metropolis Hastings is for Non-Conjugate Pairs. Are these statements correct?

Yes!

(2) Is it correct to say Gibbs is applicable to Parametric Distributions and MH is for Non-Parametric Distributions?

In a Bayesian analysis, we always have to specify distributions for the data and the prior, so there really isn't a notion of "nonparametric distribution". Also, even very simple distributions can lead to non-conjugacy and thus require Metropolis, e.g., Y|theta ~ Poisson(theta) and theta ~ Normal.

(3) Does MCMC sampling still work when p > n?

Yes, but only if the posterior is proper, which must be checked mathematically because MCMC will still spit out samples, they just won't be representative of a valid posterior distribution.

(4) In your derivations in homework question 2 part b, you plugged in the mean and variance for the first two derivations that were normal posterior distributions, but not alpha and beta in the inverse gamma distribution posterior for sigma^2. Was there a reason for this?

I'm not entirely sure what you're asking, but when you do the math the posterior in 2b just happens to not depend on alpha and beta. Intuitively, this happens because the full conditional distribution is conditioned on sigma (and all other parameters), and given sigma, alpha and beta are not informative about delta.

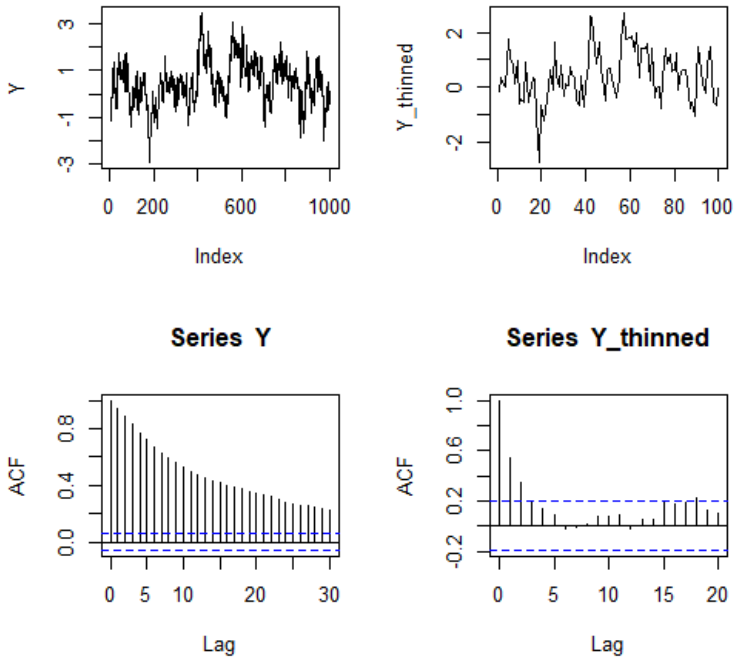
(5) Can you walk through some of the limitations for JAGS?

It's very handy which is why we will use it for the rest of the semester. Some limitations are that is a black box so you can't get in the code and optimize it for your specific problem, and generally slower than writing your own code.

(6) I feel a bit lost on the idea of autocorrelation. Does thinning mean that we are using autocorrelation = 0 (after some h iterations) to "approximate" independence for sampling? Can you clarify what might explain higher autocorrelations?

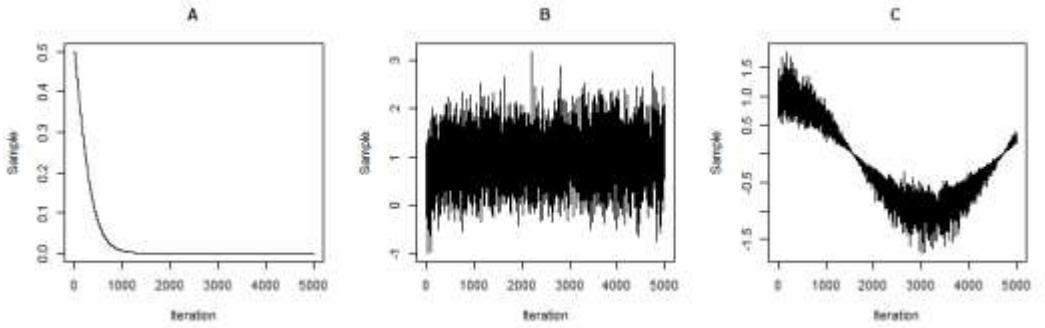
You don't need to do thinning so you can just ignore the concept if you'd like. But here is an example showing that it can reduce autocorrelation, but at the expense of having fewer samples. Autocorrelation is not the end of the world, it just means you will need to run longer chains. If the case below, I'd probably just keep the original unthinned samples.

```
n   <- 1000  # number of MCMC samples
rho <- 0.95  # Autocorrelation of the samples

# Generate fake MCMC output with autocorrelation rho
  Y <- rnorm(n)
  for(i in 2:n){Y[i] <- rnorm(1,rho*Y[i-1],sqrt(1-rho^2))}

# Thin by 10
 Y_thinned <- Y[c(1:n)%%10==1]

# Plot the chains and ACF
 plot(Y,type="l")
 plot(Y_thinned,type="l")
 acf(Y)
 acf(Y_thinned)
```



B. HOMEWORK AND QUIZ SOLUTIONS

Quiz 7: Which of these MCMC chains have converged and run long enough to give a good approximation to the posterior? Give a short sentence to justify your conclusion.

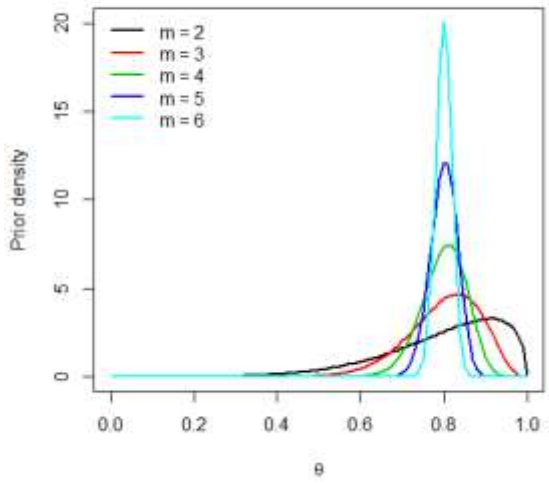


(A) It's looks like it got stuck and is not exploring the whole posterior. It is not acceptable.
(B) Looks good after about iteration 500.
(C) Clearly not converged, needs to be run much, much longer.

Chapter 3, problem 6

(a) Because the prior mean of theta is q_i, so the clutch percentage prior is centered on the overall percentage.

(b) If prior variance is controlled by m. Below is the prior with q_i = 0.8 and various m




```
theta <- seq(0,1,0.01)
q     <- 0.8
m     <- seq(2,6,1)
plot(NA,xlim=0:1,ylim=c(0,20),xlab=expression(theta),ylab="Prior density")
for(i in 1:length(m)){
  lines(theta,dbeta(theta,exp(m[i])*q,exp(m[i])*(1-q)),lwd=2,col=i)
}
```

```
legend("topleft",paste("m =",m),lwd=2,col=1:length(m),bty="n")
```

(c) The full posterior is proportional to

$$f(Y_1|\theta_1)*\ldots*f(Y_n|\theta_n)*\pi(\theta_1|m)*\ldots*\pi(\theta_n|m)*\pi(m)$$

For the full conditional of theta1 all terms that don't involve theta1 can be absorbed into the proportionality constant, and so the full conditional distribution for theta1 is proportional to

$$f(Y_1|\theta_1)\,\pi(\theta_1|m)$$

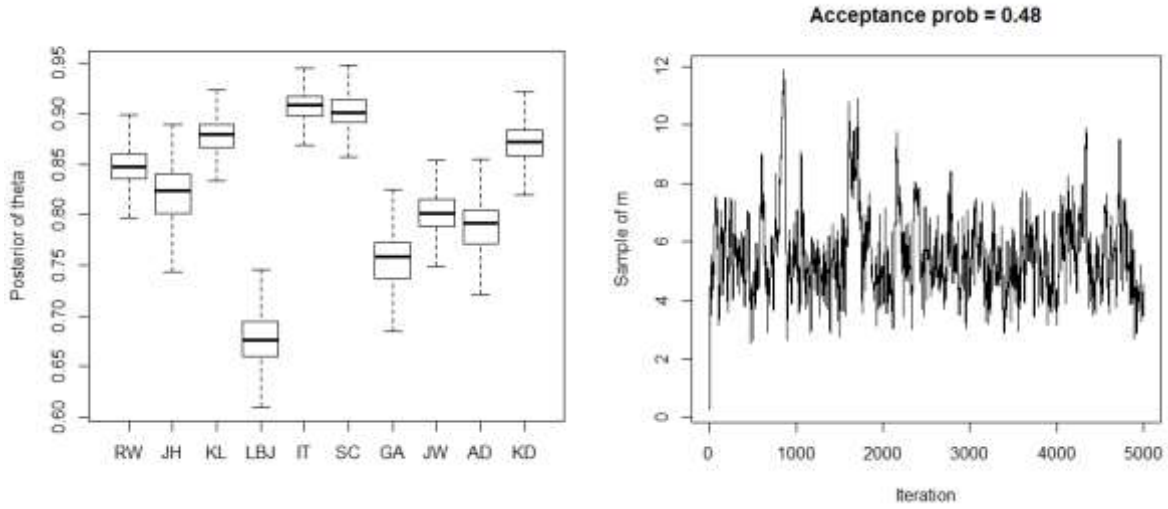
We are left with a binomial likelihood and beta prior. So, following the usual beta-binomial conjugacy results with a=exp(m)*q1 and b = exp(m)*(1-q1) we have that

$$\theta_1|Y1 \sim \text{Beta}(Y1+\exp(m)*q1, n1-Y1-\exp(1-q1)).$$

(d) Here is the code. It uses a Gibbs step for theta and Metropolis for m. Because m can be any real number (this is why we decided to use exp(m) rather than m in the beta prior) we use a Gaussian candidate distribution.

```
N      <- 10
Y      <- c(64,72,55,27,75,24,28,66,40,13)
n      <- c(75,95,63,39,83,26,41,82,54,16)
q      <- c(0.845,0.847,0.880,0.674,0.909,
            0.898,0.770,0.801,0.802,0.875)
player <- c("RW","JH","KL","LBJ","IT","SC","GA","JW","AD","KD")

iters      <- 5000
burn       <- 1000
keep_theta <- matrix(0,iters,N)
keep_m     <- rep(0,N)
colnames(keep_theta) <- player

theta  <- q
m      <- 0
can_sd <- 1
for(iter in 1:iters){
   theta <- rbeta(N,Y+exp(m)*q,n-Y+exp(m)*(1-q))

   can <- rnorm(1,m,can_sd)
   R   <- sum(dbeta(theta,exp(can)*q,exp(can)*(1-q),log=TRUE))-
          sum(dbeta(theta,  exp(m)*q,  exp(m)*(1-q),log=TRUE))+
          dnorm(can,0,sqrt(10),log=TRUE)-
          dnorm(  m,0,sqrt(10),log=TRUE)
   if(log(runif(1))<R){m <- can}

   keep_theta[iter,] <- theta
   keep_m[iter]      <- m
}

acc_rate <- mean(keep_m[2:iters]!=keep_m[2:iters-1])
boxplot(keep_theta[burn:iters,],ylab="Posterior of theta",outline=FALSE)
```

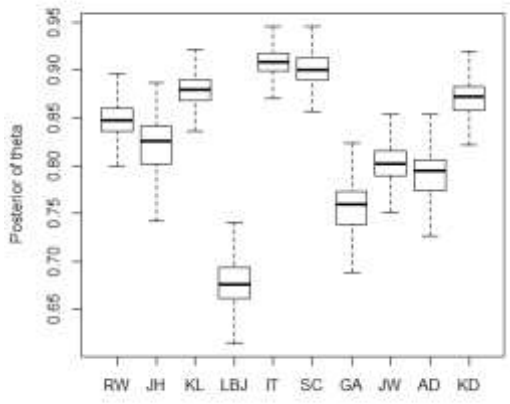
```
plot(keep_m,type="l",xlab="Iteration",ylab="Sample of m",
     main=paste("Acceptance prob =",round(acc_rate,2)))
```

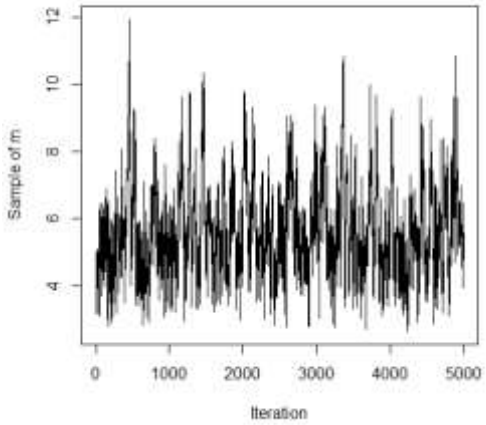


Convergence looks pretty good for m, theta is even better.

(e) Here is the JAGS code

```
library(rjags)

model_string <- textConnection("model{
   for(i in 1:10){
     Y[i]     ~ dbin(theta[i],n[i])
     theta[i] ~ dbeta(q[i]*exp(m),(1-q[i])*exp(m))
   }
   m  ~  dnorm(0, 0.1)
}")

data  <- list(n=n,Y=Y,q=q)
inits <- list(theta=q,m=0)
model <- jags.model(model_string,data = data,
         inits=inits, n.chains=1,quiet=TRUE)
update(model, 1000, progress.bar="none")
params  <- c("theta","m")
samples <- coda.samples(model,
           variable.names=params,
           n.iter=5000, progress.bar="none")
samples <- as.matrix(samples[[1]])
m       <- samples[,1]
theta   <- samples[,-1]
colnames(theta) <- player
boxplot(theta,ylab="Posterior of theta",outline=FALSE)
plot(m,type="l",xlab="Iteration",ylab="Sample of m")
```





The results are the same of the previous question.

(f) The advantage of coding it yourself is you have more control over the algorithm, disadvantages are that it generally takes longer to code and is more prone to error.

C. DISCUSSION QUESTIONS

(0) Discuss the solution to Chapter 3, problem 6d and 6e

(1) Describe to the class the error messages on

https://www4.stat.ncsu.edu/~bjreich/BSMdata/errors.html

(i) Forget to pass a variable as data

(ii) Missing values

(iii) Defining a variables twice

(iv) Priors with invalid range or initial values

(v) Passing variables that are not used

(vi) Sending an invalid list of parameters to keep

(2) Write the following model in JAGS code:

https://www4.stat.ncsu.edu/~bjreich/BSMdata/MH_concussion.html

The model is $Y_i \sim \text{Poisson}(N\lambda_i)$ where $\lambda_i = \exp(\beta_1 + i\beta_2)$ and the priors are $\beta_1, \beta_2 \sim \text{Normal}(0, \tau)$.

```
model{
 for(i in 1:4){
   Y[i] ~ dpois(lambda[i])
   log(lambda[i]) <- beta1+beta2*i
 }
 beta1 ~ dnorm(0,0.1) # setting prior variance to tau=10.
 beta2 ~ dnorm(0,0.1)
}
```

(3) The analyses linked below compare four different Bayesian software packages

https://www4.stat.ncsu.edu/~bjreich/BSMdata/software.html

https://www4.stat.ncsu.edu/~bjreich/BSMdata/software2.html

Rank (keeping in mind that this a very small example) the four packages in terms of

(a) Speed per iteration – JAGS was fastest (STAN is faster for harder problems)

(b) Convergence – JAGS was easier to tell it converged, OpenBUGS plots were confusing, ESS was highest for STAN

(c) User interface – STAN is complicated, others are about the same

(4) Examine the output in the analysis posted at

https://www4.stat.ncsu.edu/~bjreich/logistic_bball.html

and summarize MCMC converge for each model

(a) Linear: Convergence is pretty good, could be run a bit longer to get ESS > 100

(b) Quadratic: It seems to have converged (Geweke and R are OK) but ESS is low so it needs to run longer

(c) Cubic: All metrics indicate the chains have not converged.

(5) List 10 things you might try if MCMC doesn't converge:

1. Run it longer
2. Better initial values
3. Different candidate distribution (M-H v Metropolis)
4. Use STAN or NIMBLE
5. Change priors (beta instead for normal prior, make them tighter/reduce variance)
6. Pick prior based on data (empirical bayes, get MLEs) or fix some parameters
7. Get more data
8. **Simplify the model**!
9. Check identifiability
10. Double check code
11. Chose a fancier algorithm, like adaptive MH