MATH 559: BAYESIAN THEORY AND METHODS

MCMC FOR HIERARCHICAL REGRESSION MODELS

Simple linear regression: We consider linear regression data from m individuals, where it is considered that the simple linear regression parameters (β_0, β_1) for each individual are different, thereby necessitating a hierarchical model: if $i = 1, \ldots, m$ indexes individuals in the study, and $j = 1, \ldots, n$ indexes the observations made on each individual, then

- STAGE 1: **Observed data:**

$$Y_{ij} \sim Normal(\beta_{i0} + \beta_{i1} x_{ij}, \sigma_i^2) \qquad i = 1, \ldots, m, j = 1, \ldots, n \text{ independently}$$

- STAGE 2: **Population model:** for $i = 1, \ldots, m$ independently, assume that

$$(\beta_{i0}, \beta_{i1}) \sim Normal_2(\mu, \Sigma) \qquad \sigma_i^2 \sim InverseGamma(a/2, b/2).$$

  where $\mu \in \mathbb{R}^2$ and Σ is a 2×2 positive definite matrix, and $a, b > 0$ are fixed scalars. Notice that this is not an identical specification to that used in the non-hierarchical version of the model.

- STAGE 3: **Prior model:** the prior model in this case is the **Normal-Inverse Wishart** model (see last page)

$$\Sigma \sim InverseWishart(\nu, \Psi) \qquad \mu|\Sigma \sim Normal_2(\eta, \Sigma/\lambda)$$

  where $\eta \in \mathbb{R}^2$, $\nu > 1$ is a scalar and Ψ is a 2×2 positive definite matrix.

This prior is the standard conjugate prior for multivariate Normal problems. The Inverse Wishart prior is a conjugate prior for $d \times d$ covariance matrices. It has two hyperparameters:

- ν (a degrees of freedom parameter) which is a real-valued scalar such that $\nu > d - 1$; as ν increases;
- Ψ is a positive definite $d \times d$ "precision" matrix.

The expected value of this prior is

$$\frac{1}{\nu - d - 1} \Psi$$

provided $\nu > d + 1$, and the variance is finite if $\nu > d + 3$ – the variance decreases with ν^2.

MCMC: We now formulate a Gibbs sampler strategy:

1. For the **first stage** parameters conditional on the first stage parameters, we have a standard linear model, and the full conditional posteriors exhibit a conditional independent structure for $i = 1, \ldots, m$. However, the analysis is not quite the same as in the non-hierarchical case, and so we again use a Gibbs sampler structure. If $\mathbf{X}_i$ is the $n \times 2$ design matrix for the ith simple linear regression, $\mathbf{y}_i$ is the vector of response data, we have

   - $\beta_i|\sigma_i^2, \mu, \Sigma$: we have that the full conditional posterior is proportional to

$$\exp\left\{-\frac{1}{2\sigma_i^2}(\mathbf{y}_i - \mathbf{X}_i\beta_i)^\top(\mathbf{y}_i - \mathbf{X}_i\beta_i)\right\} \exp\left\{-\frac{1}{2}(\beta_i - \mu)^\top \Sigma^{-1}(\beta_i - \mu)\right\}$$

     and therefore

$$\pi_n(\beta_i|\sigma_i^2, \mu, \Sigma) \equiv Normal_2(\mathbf{m}_{ni}, \mathbf{M}_{ni})$$

     where

$$\mathbf{m}_{ni} = (\sigma_i^{-2}\mathbf{X}_i^\top\mathbf{X}_i + \Sigma^{-1})^{-1}(\sigma_i^{-2}\mathbf{X}_i^\top\mathbf{y}_i + \Sigma^{-1}\mu) \qquad \mathbf{M}_{ni} = (\sigma_i^{-2}\mathbf{X}_i^\top\mathbf{X}_i + \Sigma^{-1})^{-1}$$

   - $\sigma_i^2|\beta_i, \mu, \Sigma$: we have that the full conditional posterior is proportional to

$$\left(\frac{1}{\sigma_i^2}\right)^{n/2} \exp\left\{-\frac{1}{2\sigma_i^2}(\mathbf{y}_i - \mathbf{X}_i\beta_i)^\top(\mathbf{y}_i - \mathbf{X}_i\beta_i)\right\} \left(\frac{1}{\sigma_i^2}\right)^{a/2+1} \exp\left\{-\frac{b}{2}\right\}$$

     and then by inspection, we see that

$$\pi_n(\sigma_i^2|\beta_i, \mu, \Sigma) \equiv InverseGamma(a_n/2, b_{ni}/2)$$

     and

$$a_n = n + a \qquad b_{ni} = (\mathbf{y}_i - \mathbf{X}_i\beta_i)^\top(\mathbf{y}_i - \mathbf{X}_i\beta_i) + b$$

These two full conditional distributions can be sampled directly using `rmvn` from the `mvnfast` library, and the `rgamma` function (after reciprocation) respectively.

2. For the **second stage** parameters conditional on the first stage parameters, if $\beta_i = (\beta_{i0}, \beta_{i1})$ are regarded as known quantities, then independently for $i = 1, \ldots, n$

$$\beta_i | \mu, \Sigma \sim Normal_d(\mu, \Sigma).$$

We treat the β_i vectors as pseudo-data, and attempt to perform inference for the second stage "population" parameters. Here, the $NIW(\eta, \lambda, \nu, \Psi)$ prior is conjugate to the corresponding second-stage "likelihood", and it follows that the posterior distribution for μ and Σ is $NIW(\mu_n, \lambda_n, \nu_n, \Psi_n)$ where

$$\eta_n = \frac{m\overline{\beta} + \lambda\eta}{m+\lambda} \qquad \lambda_n = m + \lambda \qquad \nu_n = m + \nu$$

and

$$\Psi_n = \sum_{i=1}^{m}(\beta_i - \overline{\beta})(\beta_i - \overline{\beta})^\top + \frac{m\lambda}{m+\lambda}(\overline{\beta} - \eta)(\overline{\beta} - \eta)^\top + \Psi \qquad \overline{\beta} = \frac{1}{m}\sum_{i=1}^{m}\beta_i.$$

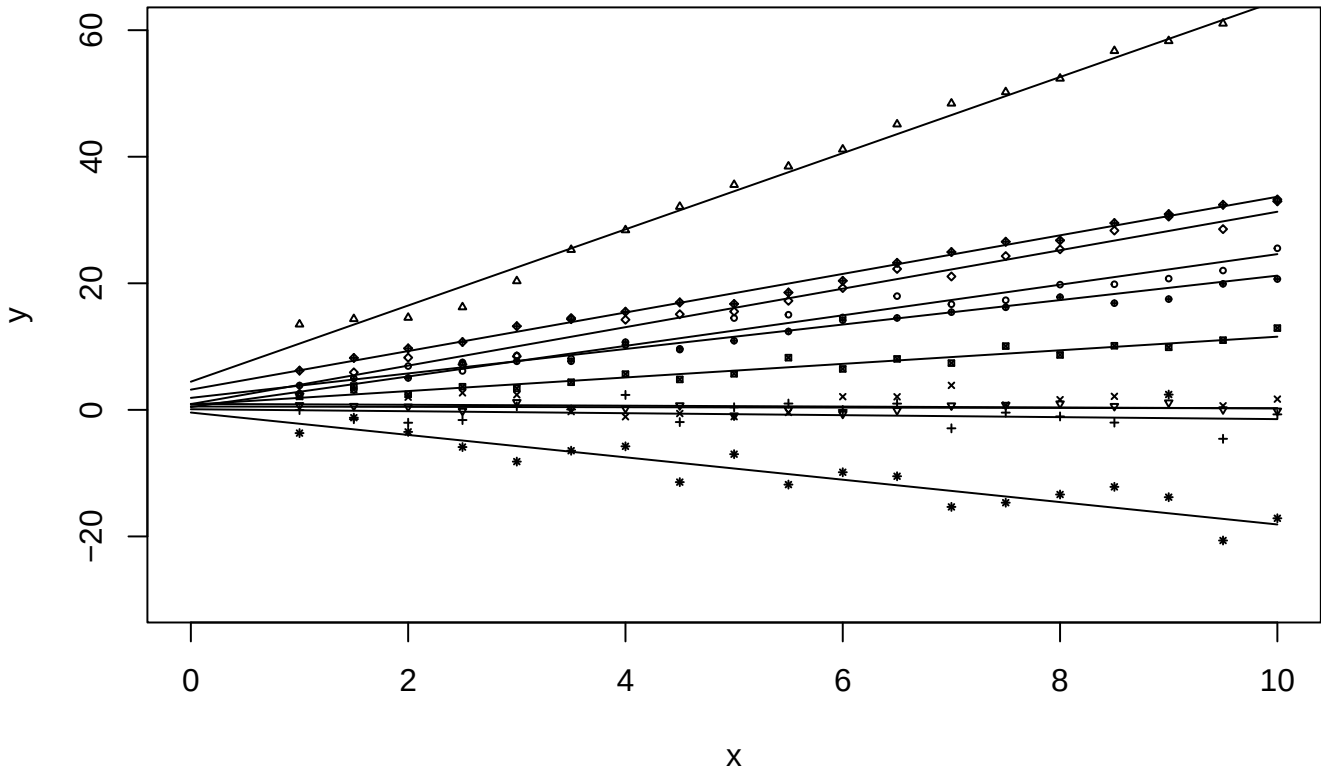
and η, ν and Ψ are hyperparameters. Then we have the results

$$\pi_n(\mu|\Sigma, -) \equiv Normal(\eta_n, \Sigma/\lambda_n) \qquad \pi_n(\Sigma|-) \equiv InverseWishart(\nu_n, \Psi_n).$$

These two full conditional distributions can be sampled directly using `rmvn` from the `mvnfast` library, and the `riwish` function from the `MCMCpack` library.

We examine the performance of the algorithm for the following simulated data.

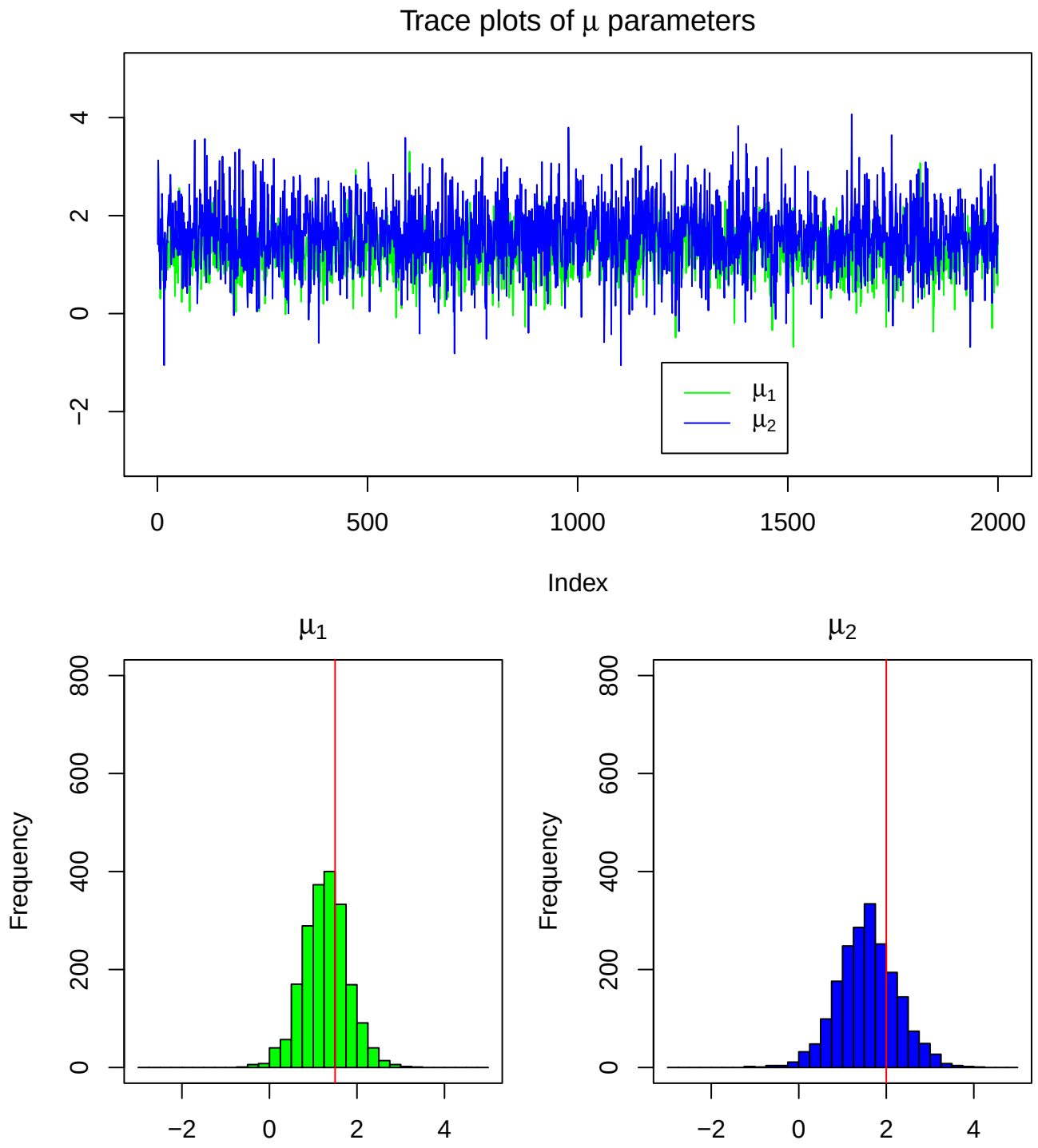
```
set.seed(2300)
#Simulation
library(mvnfast)
m<-10
mu<-c(1.5,2.0)
Sigma<-2*diag(c(1,1.5))%*% matrix(c(1,0.75,0.75,1),2,2)%*%diag(c(1,1.5))
be<-rmvn(m,mu,Sigma)
ysd<-sqrt(1/rgamma(m,2,2))

xv<-seq(0,10,by=0.01)
x<-seq(1,10.0,by=0.5)
n<-length(x)
par(mar=c(4,4,1,0))
plot(xv,xv,type='n',ylim=range(-30,60),xlab='x',ylab='y')
y<-matrix(0,nrow=m,ncol=n)
for(i in 1:m){
        muv<-be[i,1]+be[i,2]*x
        lines(xv,be[i,1]+be[i,2]*xv)
        y[i,]<-muv+rnorm(n)*ysd[i]
        points(x,y[i,],cex=0.4,pch=i)
}
```

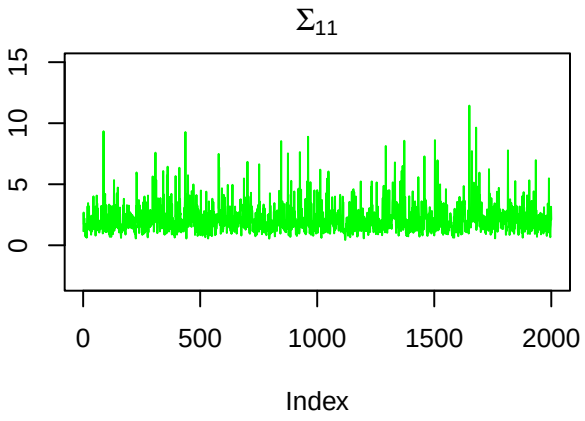


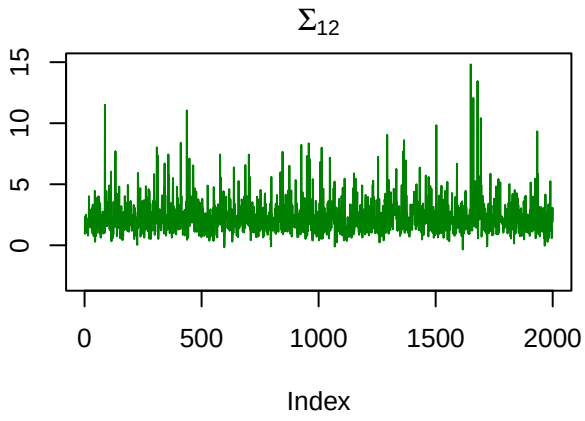
The Gibbs sampler proceeds as follows.

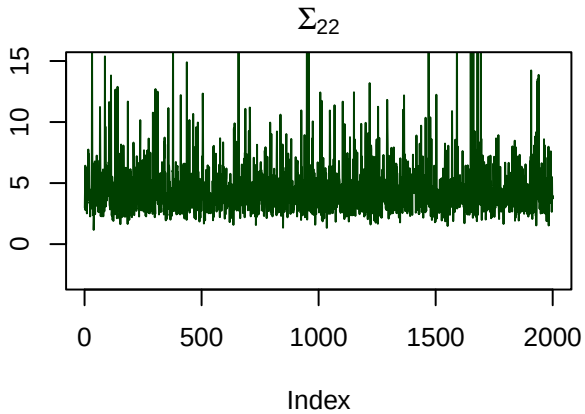
```
library(MCMCpack)
X<-cbind(1,x)
XTX<-crossprod(X)
tXy<-(t(X) %*% t(y))

a<-b<-1
eta<-c(0,0)
lambda<-0.1
nu<-4
Psi<-nu*matrix(c(1,0,0,1),2,2)

#Starting values
old.beta<-matrix(0,nrow=m,ncol=2)
old.sigsq<-rep(0,m)
for(i in 1:m){
    fit0<-lm(y[i,]~x)
    old.beta[i,]<-coef(fit0)
    old.sigsq[i]<-summary(fit0)$sigma^2
}
old.mu<-apply(old.beta,2,mean)
old.Sigma<-var(old.beta)

nsamp<-2000; nburn<-50; nthin<-1
nits<-nburn+nsamp*nthin
ico<-0

beta.samp<-array(0,c(nsamp,m,2))
sigsq.samp<-matrix(0,nrow=nsamp,ncol=m)
mu.samp<-matrix(0,nrow=nsamp,ncol=2)
Sigma.samp<-array(0,c(nsamp,2,2))
for(iter in 1:nits){
```

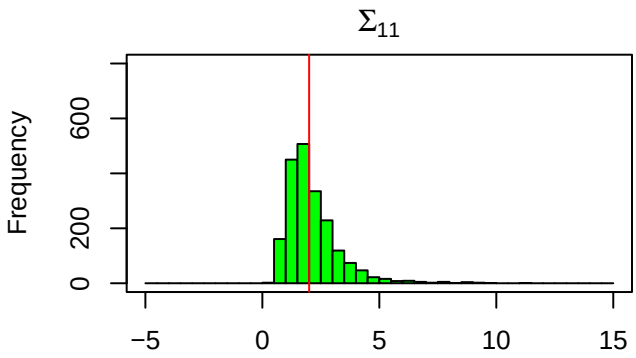
```
    #Update the betas
    old.Siginv<-solve(old.Sigma)
    ssq<-rep(0,m)
    for(i in 1:m){
        M.ninv<-((XTX/old.sigsq[i])+old.Siginv)
        M.n<-solve(M.ninv)
        m.n<-M.n %*% (old.Siginv %*% old.mu + tXy[,i]/old.sigsq[i])
        old.beta[i,]<-rmvn(1,m.n,M.n)
        ssq[i]<-sum((y[i,]-X%*%old.beta[i,])^2)
    }

    #Update the sigmas
    a.n<-a+n
    b.n<-ssq+b
    old.sigsq<-1/rgamma(m,a.n/2,b.n/2)

    #Update Sigma
    nu.n<-nu+m
    beta.bar<-apply(old.beta,2,mean)
    Psi.n<-Psi+((m*lambda)/(m+lambda))*((beta.bar-eta) %*% t(beta.bar-eta))+var(old.beta)*(m-1)
    old.Sigma<-riwish(nu.n,Psi.n)

    #Update mu given Sigma
    lambda.n<-lambda+m
    eta.n<-(m*beta.bar+lambda*eta)/(m+lambda)
    old.mu<-matrix(rmvn(1,eta.n,old.Sigma/lambda.n),ncol=1)

    if(iter > nburn & iter %% nthin == 0){
        ico<-ico+1
        beta.samp[ico,,]<-old.beta
        sigsq.samp[ico,]<-old.sigsq
        mu.samp[ico,]<-old.mu
        Sigma.samp[ico,,]<-old.Sigma
    }

}
```

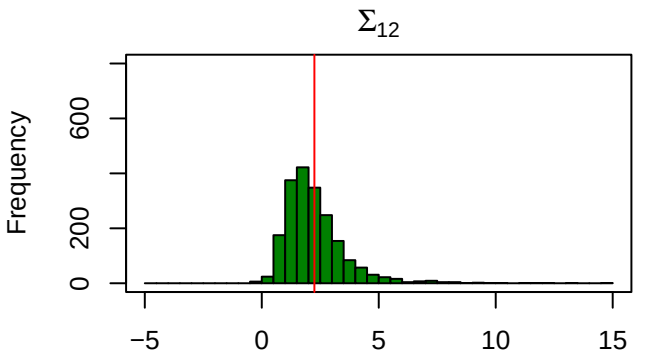

Trace plots of μ parameters
μ1
μ2
Index
μ1
μ2
Frequency
Frequency

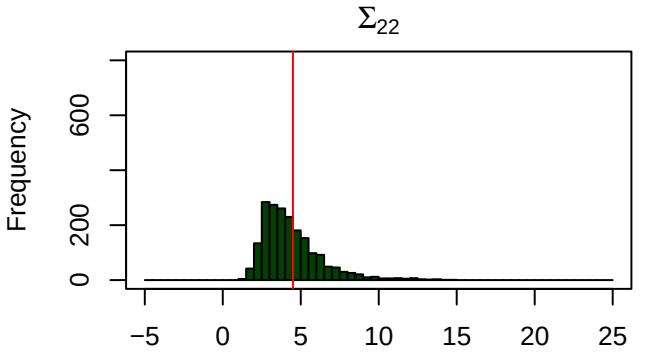

Σ_{11}
0
5
10
15
0
500
1000
1500
2000
Index

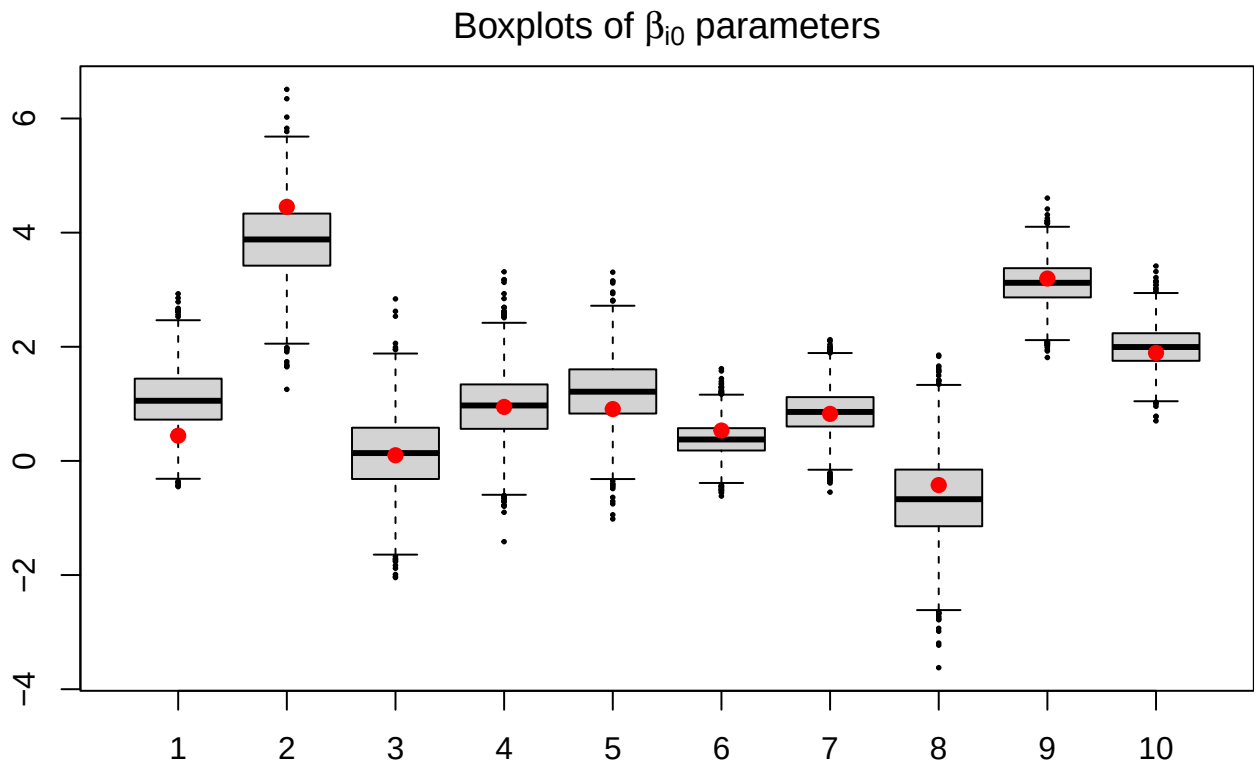

Σ_{12}
0
5
10
15
0
500
1000
1500
2000
Index

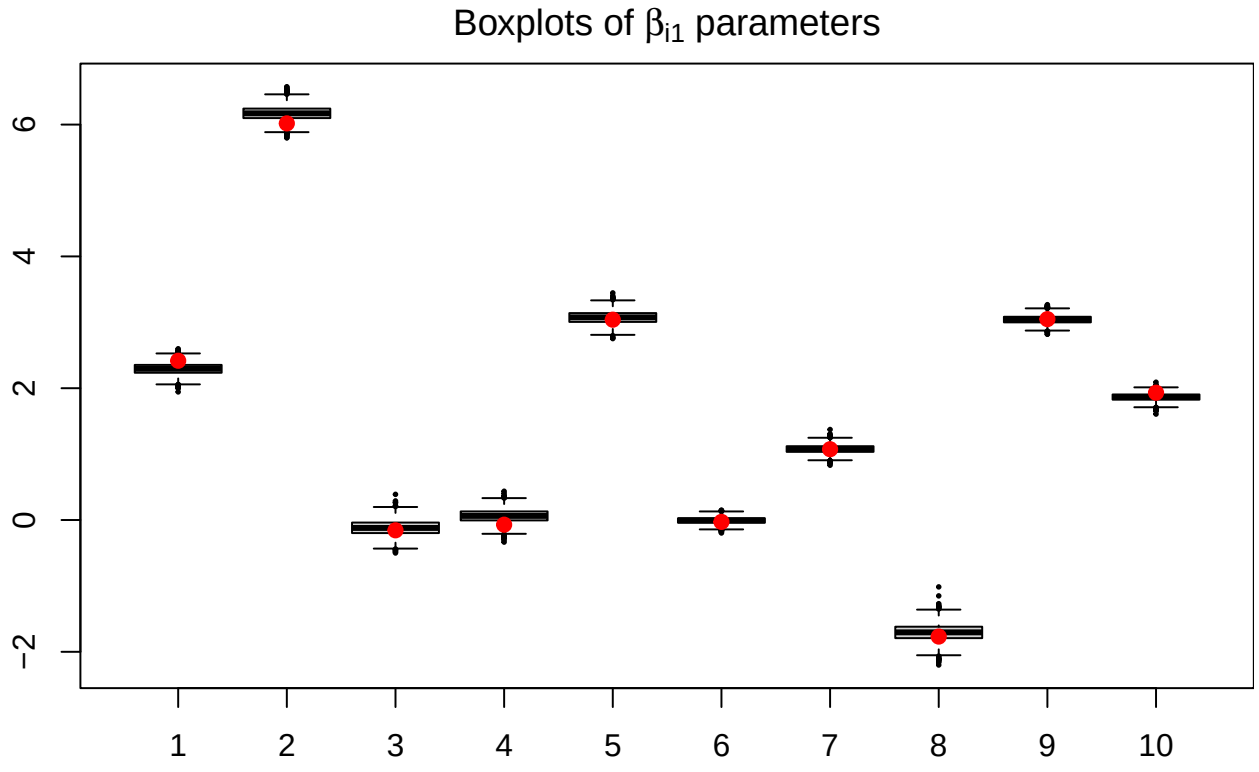

Σ_{22}
0
5
10
15
0
500
1000
1500
2000
Index


Σ_{11}
Frequency
0
200
600
−5
0
5
10
15


Σ_{12}
Frequency
0
200
600
−5
0
5
10
15


Σ_{22}
Frequency
0
200
600
−5
0
5
10
15
20
25


Boxplots of β_{i0} parameters
6
4
2
0
−2
−4
1
2
3
4
5
6
7
8
9
10


Boxplots of β_{i1} parameters
6
4
2
0
−2
1
2
3
4
5
6
7
8
9
10

THE NORMAL-INVERSE WISHART (NIW) PRIOR

This prior is the standard conjugate prior for multivariate Normal problems. The Inverse Wishart prior is a conjugate prior for $d \times d$ covariance matrices. It has two hyperparameters:

- ν (a degrees of freedom parameter) which is a real-valued scalar such that $\nu > d - 1$;
- Ψ is a positive definite $d \times d$ "precision" matrix.

The prior for Σ takes the form

$$\pi_0(\Sigma) \propto |\Sigma|^{-(\nu+d+1)/2} \exp\left\{-\frac{1}{2}\text{Tr}(\Psi\Sigma^{-1})\right\}$$

where Tr is the trace function (that is, for square matrix $\mathbf{A}$, $\text{Tr}(\mathbf{A})$ returns the sum of the diagonals of the matrix). The expected value of this distribution is the matrix

$$\frac{1}{\nu - d - 1}\Psi$$

provided $\nu > d + 1$.

The most common use of this prior is for multivariate data $\mathbf{y}_1, \ldots, \mathbf{y}_n$ arising from the model

$$\mathbf{Y}_i|\mu, \Sigma \sim Normal_d(\mu, \Sigma) \qquad i = 1, \ldots, n \text{ independently.}$$

For such data, the $NIW(\eta, \lambda, \nu, \Psi)$ prior is conjugate to the corresponding likelihood, and the posterior distribution is then $NIW(\mu_n, \lambda_n, \nu_n, \Psi_n)$ where

$$\eta_n = \frac{n\overline{\mathbf{y}} + \lambda\eta}{n + \lambda} \qquad \lambda_n = n + \lambda \qquad \nu_n = n + \nu$$

and

$$\Psi_n = \sum_{i=1}^{n}(\mathbf{y}_i - \overline{\mathbf{y}})(\mathbf{y}_i - \overline{\mathbf{y}})^\top + \frac{n\lambda}{n+\lambda}(\overline{\mathbf{y}} - \eta)(\overline{\mathbf{y}} - \eta)^\top + \Psi$$

where

$$\overline{\mathbf{y}} = \frac{1}{n}\sum_{i=1}^{n}\mathbf{y}_i$$

and η, ν and Ψ are hyperparameters. Thus

$$\pi_n(\mu|\Sigma) \equiv Normal(\eta_n, \Sigma/\lambda_n) \qquad \pi_n(\Sigma) \equiv InverseWishart(\nu_n, \Psi_n).$$

These results are the multivariate analogue of the earlier univariate result. The Inverse Wishart distribution can be regarded as a multivariate analogue of the Inverse Gamma distribution.

In `R`, sampling from the Inverse Wishart distribution is easily achieved using (for example) the `riwish` function from the `MCMCpack` library