



# LaplacesDemon Examples

Byron Hall  
STATISTICAT, LLC

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## Abstract

The **LaplacesDemon** package in R enables Bayesian inference with any Bayesian model, provided the user specifies the likelihood. This vignette is a compendium of examples of how to specify different model forms.

*Keywords:* ~Bayesian, Bayesian Inference, Laplace's Demon, LaplacesDemon, R, STATISTICAT.

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**LaplacesDemon** (Hall 2011), usually referred to as Laplace's Demon, is an R package that is available on CRAN (R Development Core Team 2010). A formal introduction to Laplace's Demon is provided in an accompanying vignette entitled "**LaplacesDemon** Tutorial", and an introduction to Bayesian inference is provided in the "Bayesian Inference" vignette.

The purpose of this document is to provide users of the **LaplacesDemon** package with examples of a variety of Bayesian methods. To conserve space, the examples are not worked out in detail, and only the minimum of necessary materials is provided for using the various methodologies. Necessary materials include the form expressed in notation, data (which is often simulated), initial values, and the `Model` function. This vignette will grow over time as examples of more methods become included. Contributed examples are welcome. Please send contributed examples in a similar format in an email to [statisticat@gmail.com](mailto:statisticat@gmail.com) for review and testing. All accepted contributions are, of course, credited.

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## 1. Autoregression, AR(1)

### 1.1. Form

$$\begin{aligned}
 y_t &\sim N(\mu_{t-1}, \tau^{-1}), \quad t = 2, \dots, (T-1) \\
 y_T^{new} &\sim N(\mu_T, \tau^{-1}) \\
 \mu_t &= \alpha + \phi y_t, \quad t = 1, \dots, T \\
 \alpha &\sim N(0, 1000) \\
 \phi &\sim N(0, 1000) \\
 \tau &\sim \Gamma(0.001, 0.001)
 \end{aligned}$$

### 1.2. Data

```

T <- 100
y <- rep(0,T)
y[1] <- 0
for (t in 2:T) {y[t] <- y[t-1] + rnorm(1,0,0.1)}
mon.names <- c("tau", paste("mu[",T,"]", sep=""))
parm.names <- c("alpha","phi","log.tau")
MyData <- list(T=T, mon.names=mon.names, parm.names=parm.names, y=y)

```

### 1.3. Initial Values

```
Initial.Values <- c(rep(0,2), log(1))
```

### 1.4. Model

```

Model <- function(parm, Data)
{
  ### Prior Parameters
  alpha.mu <- 0; alpha.tau <- 1.0E-3
  phi.mu <- 0; phi.tau <- 1.0E-3
  tau.alpha <- 1.0E-3; tau.beta <- 1.0E-3
  ### Parameters

```

```

alpha <- parm[1]; phi <- parm[2]; tau <- exp(parm[3])
### Log(Prior Densities)
alpha.prior <- dnorm(alpha, alpha.mu, 1/sqrt(alpha.tau), log=TRUE)
phi.prior <- dnorm(phi, phi.mu, 1/sqrt(phi.tau), log=TRUE)
tau.prior <- dgamma(tau, tau.alpha, tau.beta, log=TRUE)
### Log-Likelihood
mu <- alpha + phi*Data$y
LL <- sum(dnorm(Data$y[2:(Data$T-1)], mu[1:(Data$T-2)],
  1/sqrt(tau), log=TRUE))
### Log-Posterior
LP <- LL + alpha.prior + phi.prior + tau.prior
Modelout <- list(LP=LP, Dev=-2*LL, Monitor=c(tau, mu[Data$T]),
  yhat=mu, parm=parm)
return(Modelout)
}

```

## 2. Binary Logit

### 2.1. Form

$$\begin{aligned}
 y &\sim \text{Bern}(\eta) \\
 \eta &= \log[1 + \exp(\mu)] \\
 \mu &= \mathbf{X}\beta \\
 \beta_j &\sim N(0, 1000), \quad j = 1, \dots, J
 \end{aligned}$$

### 2.2. Data

```

data(demonsnacks)
N <- NROW(demonsnacks)
J <- 3
y <- ifelse(demonsnacks$Calories <= 137, 0, 1)
X <- cbind(1, as.matrix(demonsnacks[,c(7,8)]))
for (j in 2:J) {X[,j] <- CenterScale(X[,j])}
mon.names <- c("eta[1]", "mu[1]")
parm.names <- rep(NA, J)
for (j in 1:J) {parm.names[j] <- paste("beta[", j, "]", sep="")}
MyData <- list(J=J, X=X, mon.names=mon.names, parm.names=parm.names, y=y)

```

### 2.3. Initial Values

```
Initial.Values <- c(rep(0, J))
```

## 2.4. Model

```
Model <- function(parm, Data)
{
  ### Prior Parameters
  beta.mu <- rep(0,Data$J)
  beta.tau <- rep(1.0E-3,Data$J)
  ### Parameters
  beta <- parm[1:Data$J]
  ### Log(Prior Densities)
  beta.prior <- dnorm(beta, beta.mu, 1/sqrt(beta.tau), log=TRUE)
  ### Log-Posterior
  mu <- beta %*% t(Data$X)
  eta <- invlogit(mu)
  ### Log-Likelihood
  LL <- sum(dbern(Data$y, eta, log=TRUE))
  ### Log-Posterior
  LP <- LL + sum(beta.prior)
  Modelout <- list(LP=LP, Dev=-2*LL, Monitor=c(eta[1], mu[1]),
    yhat=eta, parm=parm)
  return(Modelout)
}
```

## 3. Binomial Probit

### 3.1. Form

$$y \sim \text{Bin}(p, n)$$

$$p = \phi(\mu)$$

$$\mu = \beta_1 + \beta_2 x$$

$$\beta_j \sim N(0, 1000), \quad j = 1, \dots, J$$

where  $\phi$  is the inverse CDF, and  $J=2$ .

### 3.2. Data

```
#10 Trials
exposed <- c(100,100,100,100,100,100,100,100,100,100)
deaths <- c(10,20,30,40,50,60,70,80,90,100)
dose <- c(1,2,3,4,5,6,7,8,9,10)
J <- 2 #Number of parameters
mon.names <- c("mu[1]", "mu[2]")
parm.names <- c("beta[1]", "beta[2]")
```

```
MyData <- list(J=J, n=exposed, mon.names=mon.names, parm.names=parm.names,
              x=dose, y=deaths)
```

### 3.3. Initial Values

```
Initial.Values <- c(rep(0,J))
```

### 3.4. Model

```
Model <- function(parm, Data)
{
  ### Prior Parameters
  beta.mu <- rep(0,Data$J)
  beta.tau <- rep(1.0E-3,Data$J)
  ### Parameters
  beta <- parm
  ### Log of Prior Densities
  beta.prior <- dnorm(beta, beta.mu, 1/sqrt(beta.tau), log=TRUE)
  ### Log-Likelihood
  mu <- beta[1] + beta[2]*Data$x
  mu <- ifelse(mu < -10, -10, mu); mu <- ifelse(mu > 10, 10, mu)
  p <- pnorm(mu)
  LL <- sum(dbinom(Data$y, Data$n, p, log=TRUE))
  ### Log-Posterior
  LP <- LL + sum(beta.prior)
  Modelout <- list(LP=LP, Dev=-2*LL, Monitor=mu[1:2],
                  yhat=p, parm=parm)
  return(Modelout)
}
```

## 4. Dynamic Linear Model (DLM)

The data is presented so that the time-series is subdivided into three sections: modeled ( $t = 1, \dots, T_m$ ), one-step ahead forecast ( $t = T_m + 1$ ), and future forecast [ $t = (T_m + 2), \dots, T$ ].

### 4.1. Form

$$\begin{aligned}
 y_t &\sim N(\mu_t, \tau_V^{-1}), & t = 1, \dots, T_m \\
 y_t^{new} &\sim N(\mu_t, \tau_V^{-1}), & t = (T_m + 1), \dots, T \\
 \mu_t &= \alpha + x_t \beta_t, & t = 1, \dots, T \\
 \alpha &\sim N(0, 1000) \\
 \beta_1 &\sim N(0, 1000) \\
 \beta_t &\sim N(\beta_{t-1}, \tau_W^{-1}), & t = 2, \dots, T
 \end{aligned}$$

$$\tau_V \sim \Gamma(0.001, 0.001)$$

$$\tau_W \sim \Gamma(0.001, 0.001)$$

## 4.2. Data

```
T <- 20
T.m <- 14
beta.orig <- x <- rep(0,T)
for (t in 2:T) {
  beta.orig[t] <- beta.orig[t-1] + rnorm(1,0,0.1)
  x[t] <- x[t-1] + rnorm(1,0,0.1)}
y <- 10 + beta.orig*x + rnorm(T,0,0.1)
y[(T.m+2):T] <- NA
mon.names <- rep(NA, (T-T.m))
for (i in 1:(T-T.m)) mon.names[i] <- paste("mu[", (T.m+i), "]", sep="")
parm.names <- rep(NA, T+3)
parm.names[1] <- "alpha"
for (i in 1:T) {parm.names[i+1] <- paste("beta[", i, "]", sep="")}
parm.names[(T+2):(T+3)] <- c("log.beta.w.tau", "log.v.tau")
MyData <- list(T=T, T.m=T.m, mon.names=mon.names, parm.names=parm.names,
  x=x, y=y)
```

## 4.3. Initial Values

```
Initial.Values <- rep(0,T+3)
```

## 4.4. Model

```
Model <- function(parm, Data)
{
  ### Parameters
  alpha <- parm[1]
  beta <- parm[2:(Data$T+1)]
  beta.w.tau <- exp(parm[Data$T+2])
  v.tau <- exp(parm[Data$T+3])
  ### Log(Prior Densities)
  alpha.prior <- dnorm(alpha, 0, 1/sqrt(1.0E-3), log=TRUE)
  beta.prior <- rep(0,Data$T)
  beta.prior[1] <- dnorm(beta[1], 0, 1/sqrt(1.0E-3), log=TRUE)
  beta.prior[2:Data$T] <- dnorm(beta[2:Data$T], beta[1:(Data$T-1)],
    1/sqrt(beta.w.tau), log=TRUE)
  beta.w.tau.prior <- dgamma(beta.w.tau, 0.001, 0.001, log=TRUE)
  v.tau.prior <- dgamma(v.tau, 1.0E-3, 1.0E-3, log=TRUE)
  ### Log-Likelihood
  mu <- alpha + beta*Data$x
  LL <- sum(dnorm(Data$y[1:Data$T.m], mu[1:Data$T.m], 1/sqrt(v.tau),
```

```

    log=TRUE))
### Log-Posterior
LP <- LL + alpha.prior + sum(beta.prior) + beta.w.tau.prior +
    v.tau.prior
Modelout <- list(LP=LP, Dev=-2*LL, Monitor=mu[(Data$T.m+1):Data$T],
    yhat=mu, parm=parm)
return(Modelout)
}

```

## 5. Laplace Regression

This linear regression specifies that  $y$  is Laplace-distributed, where it is usually Gaussian or normally-distributed. It has been claimed that it should be surprising that the normal distribution became the standard, when the Laplace distribution usually fits better and has wider tails (Kotz, Kozubowski, and Podgorski 2001). Another popular alternative is to use the t-distribution, though it is more computationally expensive to estimate, because it has three parameters. The Laplace distribution has only two parameters, location and scale like the normal distribution, and is computationally easier to fit. This example could be taken one step further, and the parameter vector  $\beta$  could be Laplace-distributed. Laplace's Demon recommends that users experiment with replacing the normal distribution with the Laplace distribution.

### 5.1. Form

$$\begin{aligned}
 y &\sim L(\mu, \tau^{-1}) \\
 \mu &= \mathbf{X}\beta \\
 \beta_j &\sim N(0, 1000), \quad j = 1, \dots, J \\
 \tau &\sim \Gamma(0.001, 0.001)
 \end{aligned}$$

### 5.2. Data

```

N <- 10000
J <- 5
X <- matrix(1,N,J)
for (j in 2:J) {X[,j] <- rnorm(N,runif(1,-3,3),runif(1,0.1,1))}
beta <- runif(J,-3,3)
e <- rlaplace(N,0,0.1)
y <- as.vector(beta %*% t(X) + e)
mon.names <- c("tau", "mu[1]")
parm.names <- rep(NA, J+1)
for (j in 1:J) {parm.names[j] <- paste("beta[",j,"]",sep="")}
parm.names[J+1] <- "log.tau"
MyData <- list(J=J, X=X, mon.names=mon.names, parm.names=parm.names, y=y)

```

### 5.3. Initial Values

```
Initial.Values <- c(rep(0,J), log(1))
```

### 5.4. Model

```
Model <- function(parm, Data)
{
  ### Prior Parameters
  beta.mu <- rep(0,Data$J)
  beta.tau <- rep(1.0E-3,Data$J)
  tau.alpha <- 1.0E-3
  tau.beta <- 1.0E-3
  ### Parameters
  beta <- parm[1:Data$J]
  tau <- exp(parm[Data$J+1])
  ### Log(Prior Densities)
  beta.prior <- dnorm(beta, beta.mu, 1/sqrt(beta.tau), log=TRUE)
  tau.prior <- dgamma(tau, tau.alpha, tau.beta, log=TRUE)
  ### Log-Likelihood
  mu <- beta %*% t(Data$X)
  LL <- sum(dlaplace(Data$y, mu, 1/sqrt(tau), log=TRUE))
  ### Log-Posterior
  LP <- LL + sum(beta.prior) + tau.prior
  Modelout <- list(LP=LP, Dev=-2*LL, Monitor=c(tau, mu[1]), yhat=mu,
    parm=parm)
  return(Modelout)
}
```

## 6. Linear Regression

### 6.1. Form

$$y \sim N(\mu, \tau^{-1})$$

$$\mu = \mathbf{X}\beta$$

$$\beta_j \sim N(0, 1000), \quad j = 1, \dots, J$$

$$\tau \sim \Gamma(0.001, 0.001)$$

### 6.2. Data

```
N <- 10000
J <- 5
X <- matrix(1,N,J)
for (j in 2:J) {X[,j] <- rnorm(N,runif(1,-3,3),runif(1,0.1,1))}
```

```

beta <- runif(J,-3,3)
e <- rnorm(N,0,0.1)
y <- as.vector(beta %*% t(X) + e)
mon.names <- c("tau", "mu[1]")
parm.names <- rep(NA, J+1)
for (j in 1:J) {parm.names[j] <- paste("beta[",j,"]",sep="")}
parm.names[J+1] <- "log.tau"
MyData <- list(J=J, X=X, mon.names=mon.names, parm.names=parm.names, y=y)

```

### 6.3. Initial Values

```
Initial.Values <- c(rep(0,J), log(1))
```

### 6.4. Model

```

Model <- function(parm, Data)
{
  ### Prior Parameters
  beta.mu <- rep(0,Data$J)
  beta.tau <- rep(1.0E-3,Data$J)
  tau.alpha <- 1.0E-3
  tau.beta <- 1.0E-3
  ### Parameters
  beta <- parm[1:Data$J]
  tau <- exp(parm[Data$J+1])
  ### Log(Prior Densities)
  beta.prior <- dnorm(beta, beta.mu, 1/sqrt(beta.tau), log=TRUE)
  tau.prior <- dgamma(tau, tau.alpha, tau.beta, log=TRUE)
  ### Log-Likelihood
  mu <- beta %*% t(Data$X)
  LL <- sum(dnorm(Data$y, mu, 1/sqrt(tau), log=TRUE))
  ### Log-Posterior
  LP <- LL + sum(beta.prior) + tau.prior
  Modelout <- list(LP=LP, Dev=-2*LL, Monitor=c(tau, mu[1]), yhat=mu,
    parm=parm)
  return(Modelout)
}

```

## 7. Multinomial Logit

### 7.1. Form

$$y_i \sim \text{Cat}(p_{i,1:J})$$

$$p_{i,j} = \frac{\phi_{i,j}}{\sum_{j=1}^J \phi_{i,j}}, \quad \sum_{j=1}^J p_{i,j} = 1$$

$$\phi = \exp(\mu)$$

$$\mu_{i,J} = 0$$

$$\mu_{i,j} = \mathbf{X}_{i,1:K} \beta_{j,1:K}, \quad j = 1, \dots, (J-1)$$

$$\beta_{j,k} \sim N(0, 1000) \quad j = 1, \dots, (J-1)$$

## 7.2. Data

```

y <- x01 <- x02 <- c(1:300)
y[1:100] <- 1
y[101:200] <- 2
y[201:300] <- 3
x01[1:100] <- rnorm(100, 25, 2.5)
x01[101:200] <- rnorm(100, 40, 4.0)
x01[201:300] <- rnorm(100, 35, 3.5)
x02[1:100] <- rnorm(100, 2.51, 0.25)
x02[101:200] <- rnorm(100, 2.01, 0.20)
x02[201:300] <- rnorm(100, 2.70, 0.27)
N <- length(y)
J <- 3 #Number of categories in y
K <- 3 #Number of predictors (including the intercept)
X <- matrix(c(rep(1,N),x01,x02),N,K)
mon.names <- c("mu[1]","mu[2]")
parm.names <- c("beta[1,1]","beta[1,2]","beta[1,3]","beta[2,1]",
  "beta[2,2]","beta[2,3]") ### Parameter Names [J,K]
MyData <- list(J=J, K=K, N=N, X=X, mon.names=mon.names,
  parm.names=parm.names, y=y)

```

## 7.3. Initial Values

```
Initial.Values <- c(rep(0,(J-1)*K))
```

## 7.4. Model

```

Model <- function(parm, Data)
{
  ### Prior Parameters
  beta.mu <- rep(0,(Data$J-1)*Data$K)
  beta.tau <- rep(1.0E-3,(Data$J-1)*Data$K)
  ### Parameters
  beta <- parm
  ### Log(Prior Densities)
  beta.prior <- dnorm(beta, beta.mu, 1/sqrt(beta.tau), log=TRUE)

```

```

### Log-Posterior
mu <- matrix(0,Data$N,(Data$J-1))
mu[,1] <- beta[1] + beta[2]*Data$X[,2] + beta[3]*Data$X[,3]
mu[,2] <- beta[4] + beta[5]*Data$X[,2] + beta[6]*Data$X[,3]
mu <- ifelse(mu > 700, 700, mu)
mu <- ifelse(mu < -700, -700, mu)
p <- phi <- matrix(c(exp(mu[,1]),exp(mu[,2])),rep(1,Data$N)),
  Data$N, Data$J)
for(j in 1:Data$J) {p[,j] <- phi[,j] / apply(phi,1,sum)}
### Log-Likelihood
Y <- matrix(0,Data$N,Data$J)
for (j in 1:Data$J) {Y[,j] <- ifelse(Data$y == j, 1, 0)}
LL <- sum(Y * log(p))
### Log-Posterior
LP <- LL + sum(beta.prior)
Modelout <- list(LP=LP, Dev=-2*LL, Monitor=mu[1:2],
  yhat=as.vector(phi), parm=parm)
return(Modelout)
}

```

## 8. Normal, Multilevel

This is Gelman's school example (Gelman, Carlin, Stern, and Rubin 2004). Note that **LaplaceDemon** is much slower to converge compared to this example that uses the **R2WinBUGS** package (Gelman 2009), an R package on CRAN. However, also note that Laplace's Demon (eventually) provides a better answer (higher ESS, lower DIC, etc.).

### 8.1. Form

$$\begin{aligned}
 y_j &\sim N(\theta_j, \tau_j^{-1}) \\
 \theta_j &\sim N(\theta_\mu, \theta_\tau^{-1}) \\
 \theta_\mu &\sim N(0, 1000) \\
 \theta_\tau &\sim \Gamma(0.001, 0.001) \\
 \tau_j &= sd^{-2}
 \end{aligned}$$

### 8.2. Data

```

J <- 8
y <- c(28.4, 7.9, -2.8, 6.8, -0.6, 0.6, 18.0, 12.2)
sd <- c(14.9, 10.2, 16.3, 11.0, 9.4, 11.4, 10.4, 17.6)
mon.names <- "theta.sigma"
parm.names <- 2*J+2
for (j in 1:J) {parm.names[j] <- paste("theta[",j,"",sep="")}

```

```

parm.names[J+1] <- paste("theta.mu[",j,"]",sep="")
parm.names[J+2] <- paste("log.theta.sigma[",j,"]",sep="")
MyData <- list(J=J, mon.names=mon.names, parm.names=parm.names, sd=sd, y=y)

```

### 8.3. Initial Values

```
Initial.Values <- rep(0,J+2)
```

### 8.4. Model

```

Model <- function(parm, Data)
{
  ### Hyperprior Parameters
  theta.mu.mu <- 0
  theta.mu.tau <- 1.0E-3
  ### Prior Parameters
  theta.mu <- parm[Data$J+1]
  theta.sigma <- exp(parm[Data$J+2])
  tau.alpha <- 1.0E-3
  tau.beta <- 1.0E-3
  ### Parameters
  theta <- parm[1:Data$J]; tau <- 1/(sd*sd)
  ### Log(Prior Densities)
  theta.mu.prior <- dnorm(theta.mu, theta.mu.mu,
    1/sqrt(theta.mu.tau), log=TRUE)
  tau.prior <- dgamma(tau, tau.alpha, tau.beta, log=TRUE)
  theta.prior <- dnorm(theta, theta.mu, theta.sigma, log=TRUE)
  ### Log-Likelihood
  LL <- sum(dnorm(Data$y, theta, 1/sqrt(tau), log=TRUE))
  ### Log-Posterior
  LP <- LL + theta.mu.prior + sum(theta.prior) + sum(tau.prior)
  Modelout <- list(LP=LP, Dev=-2*LL, Monitor=theta.sigma,
    yhat=theta, parm=parm)
  return(Modelout)
}

```

## 9. Poisson Regression

### 9.1. Form

$$y \sim \text{Pois}(\lambda)$$

$$\lambda = \mathbf{X}\beta$$

$$\beta_j \sim N(0, 1000), \quad j = 1, \dots, J$$

## 9.2. Data

```

N <- 10000
J <- 5
X <- matrix(runif(N*J,-2,2),N,J); X[,1] <- 1
beta <- runif(J,-2,2)
y <- as.vector(round(exp(beta %*% t(X))))
mon.names <- c("lambda[1]", "lambda[2]")
parm.names <- rep(NA,J)
for (j in 1:J) {parm.names[j] <- paste("beta[",j,"]",sep="")}
MyData <- list(J=J, X=X, mon.names=mon.names, parm.names=parm.names, y=y)

```

## 9.3. Initial Values

```
Initial.Values <- rep(0,J)
```

## 9.4. Model

```

Model <- function(parm, Data)
{
  ### Prior Parameters
  beta.mu <- rep(0,Data$J)
  beta.tau <- rep(1.0E-3,Data$J)
  ### Parameters
  beta <- parm
  ### Log(Prior Densities)
  beta.prior <- dnorm(beta, beta.mu, 1/sqrt(beta.tau), log=TRUE)
  ### Log-Likelihood
  lambda <- exp(beta %*% t(Data$X))
  LL <- sum(dpois(Data$y, lambda, log=TRUE))
  ### Log-Posterior
  LP <- LL + sum(beta.prior)
  Modelout <- list(LP=LP, Dev=-2*LL, Monitor=lambda[1:2],
    yhat=lambda, parm=parm)
  return(Modelout)
}

```

# 10. Seemingly Unrelated Regression (SUR)

The following data was used by Zellner (1962) when introducing the Seemingly Unrelated Regression methodology. In this particular example, the elements of the precision matrix  $\Omega$  are constrained. Hopefully I will soon discover, or someone can show me, a better way of maintaining positive-definiteness. Nonetheless, this form seems to work well.

### 10.1. Form

$$\begin{aligned}
Y_{t,k} &\sim N_K(\mu, \Sigma), \quad t = 1, \dots, T; \quad k = 1, \dots, K \\
\mu_{1,t} &= \alpha_1 + \alpha_2 X_{t,1} + \alpha_3 X_{t,2}, \quad t = 1, \dots, T \\
\mu_{2,t} &= \beta_1 + \beta_2 X_{t,3} + \beta_3 X_{t,4}, \quad t = 1, \dots, T \\
\Sigma &= \Omega^{-1} \\
\Omega &\sim \text{Wishart}(\nu, S), \quad 1.0E-7 \leq \Omega_{i,l} \\
S &= R^{-1} \\
\alpha_j &\sim N(0, 1000), \quad j = 1, \dots, J \\
\beta_j &\sim N(0, 1000), \quad j = 1, \dots, J
\end{aligned}$$

where each element  $i$  and  $l$  of precision matrix  $\Omega$  is constrained to the interval  $[1.0E-7, \infty)$ ,  $J=3$ ,  $K=2$ , and  $T=20$ .

### 10.2. Data

```

T <- 20
year <- c(1935, 1936, 1937, 1938, 1939, 1940, 1941, 1942, 1943, 1944, 1945, 1946,
          1947, 1948, 1949, 1950, 1951, 1952, 1953, 1954)
IG <- c(33.1, 45.0, 77.2, 44.6, 48.1, 74.4, 113.0, 91.9, 61.3, 56.8, 93.6, 159.9,
        147.2, 146.3, 98.3, 93.5, 135.2, 157.3, 179.5, 189.6)
VG <- c(1170.6, 2015.8, 2803.3, 2039.7, 2256.2, 2132.2, 1834.1, 1588.0, 1749.4,
        1687.2, 2007.7, 2208.3, 1656.7, 1604.4, 1431.8, 1610.5, 1819.4, 2079.7,
        2371.6, 2759.9)
CG <- c(97.8, 104.4, 118.0, 156.2, 172.6, 186.6, 220.9, 287.8, 319.9, 321.3, 319.6,
        346.0, 456.4, 543.4, 618.3, 647.4, 671.3, 726.1, 800.3, 888.9)
IW <- c(12.93, 25.90, 35.05, 22.89, 18.84, 28.57, 48.51, 43.34, 37.02, 37.81,
        39.27, 53.46, 55.56, 49.56, 32.04, 32.24, 54.38, 71.78, 90.08, 68.60)
VW <- c(191.5, 516.0, 729.0, 560.4, 519.9, 628.5, 537.1, 561.2, 617.2, 626.7,
        737.2, 760.5, 581.4, 662.3, 583.8, 635.2, 723.8, 864.1, 1193.5, 1188.9)
CW <- c(1.8, 0.8, 7.4, 18.1, 23.5, 26.5, 36.2, 60.8, 84.4, 91.2, 92.4, 86.0, 111.1,
        130.6, 141.8, 136.7, 129.7, 145.5, 174.8, 213.5)
Y <- matrix(c(IG, IW), T, 2)
R <- matrix(0.001, 2, 2); diag(R) <- 1
mon.names <- c("Sigma[1,1]", "Sigma[2,1]", "Sigma[1,2]", "Sigma[2,2]")
parm.names <- c("alpha[1]", "alpha[2]", "alpha[3]", "beta[1]", "beta[2]",
               "beta[3]", "log.Omega[1,1]", "log.Omega[2,1]", "log.Omega[2,2]")
MyData <- list(R=R, T=T, Y=Y, CG=CG, CW=CW, IG=IG, IW=IW, VG=VG, VW=VW,
               mon.names=mon.names, parm.names=parm.names)

```

### 10.3. Initial Values

```
Initial.Values <- c(rep(0, 6), log(as.vector(R)[c(1, 2, 4)]))
```

## 10.4. Model

```
Model <- function(parm, Data)
{
  ### Constraints
  Omega <- matrix(exp(parm[c(7,8,8,9)]),NROW(Data$R),NROW(Data$R))
  Omega <- ifelse(Omega < 1.0E-7, 1.0E-7, Omega)
  parm[7:9] <- log(as.vector(Omega)[c(1,2,4)])
  ### Prior Parameters
  alpha.mu <- rep(0,3)
  alpha.tau <- rep(1.0E-3,3)
  beta.mu <- rep(0,3)
  beta.tau <- rep(1.0E-3,3)
  ### Parameters
  alpha <- parm[1:3]
  beta <- parm[4:6]
  R <- Data$R
  S <- solve(R)
  Sigma <- solve(Omega)
  ### Log(Prior Densities)
  alpha.prior <- dnorm(alpha, alpha.mu, 1/sqrt(alpha.tau), log=TRUE)
  beta.prior <- dnorm(beta, beta.mu, 1/sqrt(beta.tau), log=TRUE)
  Omega.prior <- log(dwishart(Omega,NROW(R),S))
  ### Log-Likelihood
  mu <- matrix(0,T,2)
  mu[,1] <- alpha[1] + alpha[2]*Data$CG + alpha[3]*Data$VG
  mu[,2] <- beta[1] + beta[2]*Data$CW + beta[3]*Data$VW
  LL <- sum(dmvn(Data$Y, mu, Sigma, log=TRUE))
  ### Log-Posterior
  LP <- LL + sum(alpha.prior) + sum(beta.prior) + Omega.prior
  Modelout <- list(LP=LP, Dev=-2*LL, Monitor=as.vector(Sigma),
    yhat=as.vector(mu), parm=parm)
  return(Modelout)
}
```

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**Affiliation:**

Byron Hall

STATISTICAT, LLC

Farmington, CT

E-mail: [statisticat@gmail.com](mailto:statisticat@gmail.com)

URL: <http://www.statisticat.com/laplacesdemon.html>