LaplacesDemon Examples

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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.

LaplacesDemon (Hall 2011), usually referred to as Laplace's Demon, is an R package that is available on CRAN (R Development Core Team 2011). 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` for review and testing. All accepted contributions are, of course, credited.

Contents

1. ANOVA, One-Way

When $J = 2$, this is a Bayesian form of a t-test.

1.1. Form

$$
\begin{gathered}
y \sim N(\mu, \tau^{-1}) \\
\mu_i = \alpha + \beta[x_i], \quad i = 1, \ldots, N \\
\alpha \sim N(0, 1000) \\
\beta_j \sim N(0, 1000), \quad j = 1, \ldots, (J-1) \\
\beta_J = -\Sigma_j^{J-1} beta_j \\
\tau \sim \Gamma(0.001, 0.001)
\end{gathered}
$$

1.2. Data

```
N <- 100
J <- 5
x <- round(runif(N, 0.5, J+0.49))
alpha <- runif(1,-1,1)
```

```
beta <- runif(J,-2,2)
beta[1] <- -sum(beta[2:J])
sigma <- runif(J,0.1,0.5)
y <- rep(NA, N)
for (i in 1:N) {y[i] <- alpha + beta[x[i]] + runif(1,0,sigma[x[i]])}
mon.names <- c("LP","beta[1]","tau")
parm.names <- parm.names(list(alpha=0, beta=rep(0,J-1), log.tau=0))
MyData <- list(J=J, N=N, mon.names=mon.names, parm.names=parm.names, x=x,
    y=y)
```

1.3. Initial Values

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

1.4. Model

```
Model <- function(parm, Data)
    {
    ### Prior Parameters
    alpha.mu <- 0
    alpha.tau <- 1.0E-3
    beta.mu <- rep(0,Data$J-1)
    beta.tau <- rep(1.0E-3,Data$J-1)
    tau.alpha <- 1.0E-3
    tau.beta <- 1.0E-3
    ### Parameters
    alpha <- parm[1]
    beta <- rep(NA,Data$J)
    beta[1:(Data$J-1)] <- parm[2:Data$J]
    beta[J] <- -sum(beta[1:(Data$J-1)]) #Sum-to-zero constraint
    tau <- exp(parm[Data$J+1])
    ### Log(Prior Densities)
    alpha.prior <- dnorm(alpha, alpha.mu, 1/sqrt(alpha.tau), log=TRUE)
    beta.prior <- dnorm(beta, beta.mu, 1/sqrt(beta.tau), log=TRUE)
    tau.prior <- dgamma(tau, tau.alpha, tau.beta, log=TRUE)
    ### Log-Likelihood
    mu <- rep(NA, Data$N)
    for (j in 1:Data$J) {
        mu <- ifelse(Data$x == j, alpha + beta[j], mu)}
    LL <- sum(dnorm(Data$y, mu, 1/sqrt(tau), log=TRUE))
    ### Log-Posterior
    LP <- LL + alpha.prior + sum(beta.prior) + tau.prior
    Modelout <- list(LP=LP, Dev=-2*LL, Monitor=c(LP,beta[Data$J],tau),
        yhat=mu, parm=parm)
    return(Modelout)
    }
```

2. Autoregression, AR(1)

2.1. Form

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

2.2. 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("LP", "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)
```

2.3. Initial Values

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

2.4. 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(LP,tau,mu[Data$T]),
        yhat=mu, parm=parm)
    return(Modelout)
    }
```

3. Binary Logit

3.1. Form

$$y \sim Bern(\eta)$$

$$\eta = \log[1 + \exp(\mu)]$$

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

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

3.2. 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 <- "LP"
parm.names <- parm.names(list(beta=rep(0,J)))
MyData <- list(J=J, X=X, mon.names=mon.names, parm.names=parm.names, y=y)
```

3.3. Initial Values

```
Initial.Values <- 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[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=LP,
        yhat=eta, parm=parm)
    return(Modelout)
    }
```

4. Binomial Probit

4.1. Form

$$y \sim Bin(p, n)$$

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

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

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

where ϕ is the inverse CDF, and J=2.

4.2. 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 <- "LP"
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)
```

4.3. Initial Values

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

4.4. 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
     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=LP,
          yhat=p, parm=parm)
     return(Modelout)
     }
```

5. Contingency Table

The two-way contingency table, matrix $\mathbf{Y}$, can easily be extended to more dimensions. For this example, it is vectorized as y, and used like an ANOVA data set. Contingency table $\mathbf{Y}$ has J rows and K columns. The cell counts are fit with Poisson regression, according to intercept α, main effects β_j for each row, main effects γ_k for each column, and interaction effects $\delta_{j,k}$ for dependence effects. An omnibus (all cells) test of independence is done by estimating two models (one with δ, and one without), and a large enough Bayes Factor indicates a violation of independence when the model with δ fits better than the model without δ. In an ANOVA-like style, main effects contrasts can be used to distinguish rows or groups of rows from each other, as well as with columns. Likewise, interaction effects contrasts can be used to test independence in groups of $\delta_{j,k}$ elements. Finally, single-cell interactions can be used to indicate violations of independence for a given cell, such as when zero is not within its 95% probability interval. Although a little different, this example is similar to a method presented by Albert (1997).

5.1. Form

$$\mathbf{Y}_{j,k} \sim Pois(\lambda_{j,k}), \quad j = 1, \ldots, J, \quad k = 1, \ldots, K$$

$$\lambda_{j,k} = \exp(\alpha + \beta_j + \gamma_k + \delta_{j,k}), \quad j = 1, \ldots, J, \quad k = 1, \ldots, K$$

$$\alpha \sim N(0, 1000)$$

$$\beta_j \sim N(0, \beta_\tau^{-1}), \quad j = 1, \ldots, J$$
$$\beta_\tau \sim \Gamma(0.001, 0.001)$$
$$\gamma_k \sim N(0, \gamma_\tau^{-1}), \quad k = 1, \ldots, K$$
$$\gamma_\tau \sim \Gamma(0.001, 0.001)$$
$$\delta_{j,k} \sim N(0, \delta_\tau^{-1})$$
$$\delta_\tau \sim \Gamma(0.001, 0.001)$$

5.2. Data

```
J <- 4 #Rows
K <- 4 #Columns
Y <- matrix(c(10,20,60,20, 40,30,10,40, 10,10,40,10, 40,50,1,40), J, K,
    dimnames=list(c("Chrysler","Ford","Foreign","GM"),
    c("I-4","I-6","V-6","V-8")))
y <- as.vector(Y)
N <- length(y) #Cells
r <- rep(1:J, N/J)
c <- rep(1,K)
for (k in 2:K) {c <- c(c, rep(k, K))}
mon.names <- c("LP","beta.tau","gamma.tau","delta.tau")
parm.names <- parm.names(list(alpha=0, beta=rep(0,J), gamma=rep(0,J),
    log.b.tau=0, log.g.tau=0, log.d.tau=0, delta=matrix(0,J,K))
MyData <- list(J=J, K=K, N=N, c=c, mon.names=mon.names,
    parm.names=parm.names, r=r, y=y)
```

5.3. Initial Values

```
Initial.Values <- c(0, rep(0,J), rep(0,K), rep(0,3), rep(0,J*K))
```

5.4. Model

```
Model <- function(parm, Data)
    {
    ### Prior Parameters
    beta.tau <- exp(parm[grep("log.b.tau", Data$parm.names)])
    gamma.tau <- exp(parm[grep("log.g.tau", Data$parm.names)])
    delta.tau <- exp(parm[grep("log.d.tau", Data$parm.names)])
    ### Parameters
    alpha <- parm[grep("alpha", Data$parm.names)]
    beta <- parm[min(grep("beta", Data$parm.names)):max(
        grep("beta", Data$parm.names))]
    gamma <- parm[min(grep("gamma", Data$parm.names)):max(
        grep("gamma", Data$parm.names))]
    delta <- matrix(parm[min(grep("delta",
        Data$parm.names)):max(grep("delta", Data$parm.names))],
```

```
    Data$J, Data$K)
### Log(Prior Densities)
alpha.prior <- dnorm(alpha, 0, 1/sqrt(0.001), log=TRUE)
beta.prior <- dnorm(beta, 0, 1/sqrt(beta.tau), log=TRUE)
beta.tau.prior <- dgamma(beta.tau, 1.0E-3, 1.0E-3, log=TRUE)
gamma.prior <- dnorm(gamma, 0, 1/sqrt(gamma.tau), log=TRUE)
gamma.tau.prior <- dgamma(gamma.tau, 1.0E-3, 1.0E-3, log=TRUE)
delta.prior <- dnorm(delta, 0, 1/sqrt(delta.tau), log=TRUE)
delta.tau.prior <- dgamma(delta.tau, 1.0E-3, 1.0E-3, log=TRUE)
### Log-Likelihood
lambda <- rep(NA, Data$N)
for (i in 1:Data$N) {
    lambda[i] <- exp(alpha + beta[r[i]] + gamma[c[i]] +
         delta[r[i],c[i]])}
LL <- sum(dpois(Data$y, lambda, log=TRUE))
### Log-Posterior
LP <- LL + alpha.prior + sum(beta.prior) + beta.tau.prior +
    sum(gamma.prior) + gamma.tau.prior + sum(delta.prior) +
    delta.tau.prior
Modelout <- list(LP=LP, Dev=-2*LL, Monitor=c(LP, beta.tau,
    gamma.tau, delta.tau), yhat=lambda, parm=parm)
return(Modelout)
}
```

6. Dynamic Linear Model (DLM)

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

6.1. Form

$$y_t \sim N(\mu_t, \tau_V^{-1}), \quad t = 1, \ldots, T_m$$

$$y_t^{new} \sim N(\mu_t, \tau_V^{-1}), \quad t = (T_m + 1), \ldots, T$$

$$\mu_t = \alpha + x_t \beta_t, \quad t = 1, \ldots, T$$

$$\alpha \sim N(0, 1000)$$

$$\beta_1 \sim N(0, 1000)$$

$$\beta_t \sim N(\beta_{t-1}, \tau_W^{-1}), \quad t = 2, \ldots, T$$

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

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

6.2. 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 <- parm.names(list(alpha=0, beta=rep(0,T), log.beta.w.tau=0,
    log.v.tau=0))
MyData <- list(T=T, T.m=T.m, mon.names=mon.names, parm.names=parm.names,
    x=x, y=y)
```

6.3. Initial Values

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

6.4. 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)
    }
```

7. Factor Analysis, Confirmatory

Factor scores are in matrix $\mathbf{F}$, factor loadings for each variable are in vector λ, and f is vector that indicates which variable loads on which factor.

7.1. Form

$$\begin{gathered}
\mathbf{Y}_{i,m} \sim N(\mu_{i,m}, \tau_m^{-1}), \quad i = 1, \ldots, N, \quad m = 1, \ldots, M \\
\mu_{i,m} = \alpha_m + \lambda_m \mathbf{F}_{i,f[m]}, \quad i = 1, \ldots, N, \quad m = 1, \ldots, M \\
\mathbf{F}_{i,1:P} \sim N_P(\gamma, \Omega^{-1}), \quad i = 1, \ldots, N \\
\alpha_m \sim N(0, 1000), \quad m = 1, \ldots, M \\
\lambda_m \sim N(0, 1000), \quad m = 1, \ldots, M \\
\Omega \sim W(N, \mathbf{S}), \quad \mathbf{S} = \mathbf{I}_P
\end{gathered}$$

7.2. Data

```
data(swiss)
Y <- cbind(swiss$Agriculture, swiss$Examination, swiss$Education,
    swiss$Catholic, swiss$Infant.Mortality)
M <- NCOL(Y) #Number of variables
N <- NROW(Y) #Number of records
P <- 3 #Number of factors
f <- c(1,3,2,2,1) #Indicator f for the factor for each variable m
gamma <- rep(0,P)
S <- diag(P)
mon.names <- c("LP","mu[1,1]")
parm.names <- parm.names(list(F=matrix(0,N,P), lambda=rep(0,M),
    Omega=diag(P), alpha=rep(0,M), log.tau=rep(0,M)),
    uppertri=c(0,0,1,0,0))
MyData <- list(M=M, N=N, P=P, S=S, Y=Y, f=f, gamma=gamma,
    mon.names=mon.names, parm.names=parm.names)
```

7.3. Initial Values

```
Initial.Values <- c(rep(0, N*P), rep(0, M),
    S[upper.tri(S, diag=TRUE)], rep(0,M), rep(0,M))
```

7.4. Model

```
Model <- function(parm, Data)
    {
```

```
### Prior Parameters
alpha.mu <- rep(0, Data$M)
alpha.tau <- rep(1.0E-3, Data$M)
lambda.mu <- rep(0, Data$M)
lambda.tau <- rep(1.0E-3, Data$M)
tau.alpha <- rep(1.0E-3, Data$M)
tau.beta <- rep(1.0E-3, Data$M)
### Parameters
alpha <- parm[min(grep("alpha", Data$parm.names)):max(grep("alpha",
    Data$parm.names))]
lambda <- parm[min(grep("lambda", Data$parm.names)):max(grep("lambda",
    Data$parm.names))]
tau <- exp(parm[min(grep("log.tau", Data$parm.names)):max(grep(
    "log.tau", Data$parm.names))])
F <- matrix(parm[min(grep("F", Data$parm.names)):max(grep("F",
    Data$parm.names))], Data$N, Data$P)
Omega <- matrix(NA, Data$P, Data$P)
Omega[upper.tri(Omega, diag=TRUE)] <- parm[min(grep("Omega",
    Data$parm.names)):max(grep("Omega", Data$parm.names))]
Omega[lower.tri(Omega)] <- Omega[upper.tri(Omega)]
Sigma <- solve(Omega)
### Log(Prior Densities)
alpha.prior <- dnorm(alpha, alpha.mu, 1/sqrt(alpha.tau), log=TRUE)
lambda.prior <- dnorm(lambda, lambda.mu, 1/sqrt(lambda.tau),
    log=TRUE)
tau.prior <- dgamma(tau, tau.alpha, tau.beta, log=TRUE)
Omega.prior <- log(dwishart(Omega, Data$N, Data$S))
F.prior <- rep(NA, Data$N)
for (i in 1:Data$N) {
    F.prior[i] <- dmvn(F[i,], Data$gamma, Sigma, log=TRUE)}
### Log-Likelihood
mu <- Data$Y
for (m in 1:Data$M) { mu[,m] <- alpha[m] + lambda[m] * F[,Data$f[m]]}
LL <- sum(dnorm(Data$Y, mu, 1/sqrt(tau), log=TRUE))
### Log-Posterior
LP <- sum(LL) + sum(alpha.prior) + sum(lambda.prior) +
    sum(tau.prior) + sum(F.prior) + Omega.prior
Modelout <- list(LP=LP, Dev=-2*LL, Monitor=c(LP,mu[1,1]),
    yhat=mu, parm=parm)
return(Modelout)
}
```

8. Factor Analysis, Exploratory

Factor scores are in matrix $\mathbf{F}$ and factor loadings are in matrix Λ. Although the calculation for the recommended number of factors to explore P is also provided below (Fokoue 2004),

this example sets $P = 3$.

8.1. Form

$$\mathbf{Y}_{i,m} \sim N(\mu_{i,m}, \tau_m^{-1}), \quad i = 1, \ldots, N, \quad m = 1, \ldots, M$$
$$\mu_{i,m} = \alpha_m + \Sigma_{p=1}^{P} \nu_{i,m,p}, \quad i = 1, \ldots, N, \quad m = 1, \ldots, M$$
$$\nu_{i,m,p} = \mathbf{F}_{i,p} \Lambda_{p,m}, \quad i = 1, \ldots, N, \quad m = 1, \ldots, M, \quad p = 1, \ldots, P$$
$$\mathbf{F}_{i,1:P} \sim N_P(\gamma, \Omega^{-1}), \quad i = 1, \ldots, N$$
$$\alpha_m \sim N(0, 1000), \quad m = 1, \ldots, M$$
$$\gamma_p = 0, \quad p = 1, \ldots, P$$
$$\Lambda_{p,m} \sim N(0, 1000), \quad p = 1, \ldots, P, \quad m = 1, \ldots, M$$
$$\Omega \sim W(N, \mathbf{S}), \quad \mathbf{S} = \mathbf{I}_P$$
$$\tau_m \sim \Gamma(0.001, 0.001), \quad m = 1, \ldots, M$$

8.2. Data

data(swiss)
```
Y <- cbind(swiss$Agriculture, swiss$Examination, swiss$Education,
swiss$Catholic, swiss$Infant.Mortality)
M <- NCOL(Y) #Number of variables
N <- NROW(Y) #Number of records
P <- trunc(0.5*(2*M + 1 - sqrt(8*M + 1))) #Number of factors to explore
P <- 3 #Number of factors to explore (override for this example)
gamma <- rep(0,P)
S <- diag(P)
mon.names <- c("LP","mu[1,1]")
parm.names <- parm.names(list(F=matrix(0,N,P), Lambda=matrix(0,P,M),
    Omega=diag(P), alpha=rep(0,M), log.tau=rep(0,M)),
    uppertri=c(0,0,1,0,0))
MyData <- list(M=M, N=N, P=P, S=S, Y=Y, gamma=gamma, mon.names=mon.names,
    parm.names=parm.names)
```

8.3. Initial Values

```
Initial.Values <- c(rep(0, (N*P + P*M)),
    S[upper.tri(S, diag=TRUE)], rep(0,M), rep(0,M))
```

8.4. Model

```
Model <- function(parm, Data)
    {
    ### Prior Parameters
    alpha.mu <- rep(0, Data$M)
```

```
alpha.tau <- rep(1.0E-3, Data$M)
Lambda.mu <- 0
Lambda.tau <- 1.0E-3
tau.alpha <- rep(1.0E-3, Data$M)
tau.beta <- rep(1.0E-3, Data$M)
### Parameters
alpha <- parm[min(grep("alpha", Data$parm.names)):max(grep("alpha",
    Data$parm.names))]
tau <- exp(parm[min(grep("log.tau", Data$parm.names)):max(grep(
    "log.tau", Data$parm.names))])
F <- matrix(parm[min(grep("F", Data$parm.names)):max(grep("F",
    Data$parm.names))], Data$N, Data$P)
Lambda <- matrix(parm[min(grep("Lambda", Data$parm.names)):max(grep(
    "Lambda", Data$parm.names))], Data$P, Data$M)
Omega <- matrix(NA, Data$P, Data$P)
Omega[upper.tri(Omega, diag=TRUE)] <- parm[min(grep("Omega",
    Data$parm.names)):max(grep("Omega", Data$parm.names))]
Omega[lower.tri(Omega)] <- Omega[upper.tri(Omega)]
Sigma <- solve(Omega)
### Log(Prior Densities)
alpha.prior <- dnorm(alpha, alpha.mu, 1/sqrt(alpha.tau), log=TRUE)
tau.prior <- dgamma(tau, tau.alpha, tau.beta, log=TRUE)
Omega.prior <- dwishart(Omega, Data$N, Data$S, log=TRUE)
F.prior <- rep(NA, Data$N)
for (i in 1:Data$N) {
    F.prior[i] <- dmvn(F[i,], Data$gamma, Sigma, log=TRUE)}
Lambda.prior <- dnorm(Lambda, Lambda.mu, 1/sqrt(Lambda.tau),
    log=TRUE)
### Log-Likelihood
mu <- Data$Y
nu <- array(NA, dim=c(Data$N, Data$M, Data$P))
for (p in 1:Data$P) {nu[, ,p] <- F[,p, drop=FALSE] %*% Lambda[p,]}
for (m in 1:Data$M) {mu[,m] <- alpha[m] + apply(nu[,1,],1,sum)}
LL <- sum(dnorm(Data$Y, mu, 1/sqrt(tau), log=TRUE))
### Log-Posterior
LP <- sum(LL) + sum(alpha.prior) + sum(tau.prior) + Omega.prior +
    sum(F.prior) + sum(Lambda.prior)
Modelout <- list(LP=LP, Dev=-2*LL, Monitor=c(LP,mu[1,1]),
    yhat=mu, parm=parm)
return(Modelout)
}
```

9. 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 β could be Laplace-distributed. Laplace's Demon recommends that users experiment with replacing the normal distribution with the Laplace distribution.

9.1. Form

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

9.2. 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("LP", "tau")
parm.names <- parm.names(list(beta=rep(0,J), log.tau=0))
MyData <- list(J=J, X=X, mon.names=mon.names, parm.names=parm.names, y=y)
```

9.3. Initial Values

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

9.4. 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(LP, tau), yhat=mu,
        parm=parm)
    return(Modelout)
    }
```

10. Linear Regression

10.1. Form

$$y \sim N(\mu, \tau^{-1})$$
$$\mu = \mathbf{X}\beta$$
$$\beta_j \sim N(0, 1000), \quad j = 1, \ldots, J$$
$$\tau \sim \Gamma(0.001, 0.001)$$

10.2. 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("LP", "tau")
parm.names <- parm.names(list(beta=rep(0,J), log.tau=0))
MyData <- list(J=J, X=X, mon.names=mon.names, parm.names=parm.names, y=y)
```

10.3. Initial Values

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

10.4. 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(LP, tau), yhat=mu,
    parm=parm)
return(Modelout)
}
```

11. Linear Regression, Multilevel

11.1. Form

$$y \sim N(\mu, \tau^{-1})$$
$$\mu_i = \mathbf{X}\beta_{m[i],1:J}$$
$$\beta_{g,1:J} \sim N_J(\gamma, \Sigma), \quad g = 1, \ldots, G$$
$$\Sigma = \Omega^{-1}$$
$$\Omega \sim W(J, \mathbf{S}), \quad \mathbf{S} = \mathbf{I}_J$$
$$\gamma_j \sim N(0, 1000), \quad j = 1, \ldots, J$$
$$\tau \sim \Gamma(0.001, 0.001)$$

where m is a vector of length N, and each element indicates the multilevel group ($g = 1, \ldots, G$) for the associated record.

11.2. Data

```
N <- 30
J <- 2 ### Number of predictors (including intercept)
G <- 2 ### Number of Multilevel Groups
X <- matrix(rnorm(N,0,1),N,J); X[,1] <- 1
```

```
Sigma <- matrix(runif(J*J,-1,1),J,J)
diag(Sigma) <- runif(J,1,5)
gamma <- runif(J,-1,1)
beta <- matrix(NA,G,J)
for (g in 1:G) {beta[g,] <- rmvn(1, gamma, Sigma)}
m <- round(runif(N,0.5,(G+0.49))) ### Multilevel group indicator
y <- rep(NA,N)
for (i in 1:N) {y[i] = sum(beta[m[i],] * X[i,]) + rnorm(1,0,0.1)}
S <- diag(J)
mon.names <- c("LP","tau")
parm.names <- parm.names(list(beta=matrix(0,G,J), log.tau=0,
    gamma=rep(0,J), Omega=diag(P)), uppertri=c(0,0,0,1))
MyData <- list(G=G, J=J, N=N, S=S, X=X, m=m, mon.names=mon.names,
    parm.names=parm.names, y=y)
```

11.3. Initial.Values

```
Initial.Values <- c(rep(0,G*J), log(1), rep(0,J),
    S[upper.tri(S, diag=TRUE)])
```

11.4. Model

```
Model <- function(parm, Data)
    {
    ### Prior Parameters
    gamma.mu <- rep(0,Data$J)
    gamma.tau <- rep(1.0E-3,Data$J)
    tau.alpha <- 1.0E-3
    tau.beta <- 1.0E-3
    ### Parameters
    beta <- matrix(parm[1:(Data$G * Data$J)], Data$G, Data$J)
    gamma <- parm[min(grep("gamma", Data$parm.names)):max(grep(
        "gamma", Data$parm.names))]
    tau <- exp(parm[grep("log.tau", Data$parm.names)])
    Omega <- matrix(NA, Data$J, Data$J)
    Omega[upper.tri(Omega, diag=TRUE)] <- parm[min(grep("Omega",
        Data$parm.names)):  max(grep("Omega", Data$parm.names))]
    Omega[lower.tri(Omega)] <- Omega[upper.tri(Omega)]
    Sigma <- solve(Omega)
    ### Log(Prior Densities)
    Omega.prior <- dwishart(Omega, Data$J, Data$S, log=TRUE)
    beta.prior <- rep(0,Data$G)
    for (g in 1:Data$G) {
        beta.prior[g] <- dmvn(beta[g,], gamma, Sigma, log=TRUE)}
    gamma.prior <- dnorm(gamma, gamma.mu, 1/sqrt(gamma.tau), log=TRUE)
    tau.prior <- dgamma(tau, tau.alpha, tau.beta, log=TRUE)
    ### Log-Likelihood
```

```
mu <- Data$y
for (i in 1:Data$N) {mu[i] <- sum(beta[Data$m[i],] * Data$X[i,])}
LL <- sum(dnorm(Data$y, mu, 1/sqrt(tau), log=TRUE))
### Log-Posterior
LP <- LL + Omega.prior + sum(beta.prior) + sum(gamma.prior) +
     tau.prior
Modelout <- list(LP=LP, Dev=-2*LL, Monitor=c(LP,tau),
     yhat=mu, parm=parm)
return(Modelout)
}
```

12. Linear Regression with Full Missingness

With 'full missingness', there are missing values for both the response and at least one predictor. This is a minimal example, since there are missing values in only one of the predictors. Initial values do not need to be specified for missing values in a predictor, unless another predictor variable with missing values is used to predict the missing values of a predictor. More effort is involved in specifying a model with a missing predictor that is predicted by another missing predictor. The full likelihood approach to full missingness is excellent as long as the model is identifiable. When it is not identifiable, then imputation may be done in a previous stage. In this example, `X[,2]` is the only predictor with missing values.

12.1. Form

$$y \sim N(\mu_2, \tau_2^{-1})$$
$$\mu_2 = \mathbf{X}\beta$$
$$X_{1:N,2} \sim N(\mu_1, \tau_1^{-1})$$
$$\mu_1 = \mathbf{X}_{1:N,(1,3:J)}\alpha$$
$$\alpha_j \sim N(0, 1000), \quad j = 1, \ldots, J-1$$
$$\beta_j \sim N(0, 1000), \quad j = 1, \ldots, J$$
$$\tau_k \sim \Gamma(0.001, 0.001), \quad k = 1, \ldots, 2$$

12.2. Data

```
N <- 1000
J <- 5
X <- matrix(runif(N*J,-2,2),N,J)
X[,1] <- 1
alpha <- runif((J-1),-2,2)
X[,2] <- alpha %*% t(X[,-2]) + rnorm(N,0,0.1)
beta <- runif(J,-2,2)
y <- as.vector(beta %*% t(X) + rnorm(N,0,0.1))
```

```
y[sample(1:N, round(N*0.05))] <- NA
X[sample(1:N, round(N*0.05)),2] <- NA
mon.names <- c("LP","tau[1]","tau[2]")
parm.names <- parm.names(list(alpha=rep(0,J-1), beta=rep(0,J),
    log.tau=rep(0,2)))
MyData <- list(J=J, N=N, X=X, mon.names=mon.names, parm.names=parm.names,
    y=y)
```

12.3. Initial Values

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

12.4. Model

```
Model <- function(parm, Data)
    {
    ### Prior Parameters
    alpha.mu <- rep(0,(Data$J-1))
    alpha.tau <- rep(1.0E-3,(Data$J-1))
    beta.mu <- rep(0,Data$J)
    beta.tau <- rep(1.0E-3,Data$J)
    tau.alpha <- rep(1.0E-3,2)
    tau.beta <- rep(1.0E-3,2)
    ### Parameters
    alpha <- parm[1:(Data$J-1)]
    beta <- parm[Data$J:(2*Data$J - 1)]
    tau <- exp(parm[(2*Data$J):(2*Data$J+1)])
    ### Log(Prior Densities)
    alpha.prior <- dnorm(alpha, alpha.mu, 1/sqrt(alpha.tau), log=TRUE)
    beta.prior <- dnorm(beta, beta.mu, 1/sqrt(beta.tau), log=TRUE)
    tau.prior <- dgamma(tau, tau.alpha, tau.beta, log=TRUE)
    ### Log-Likelihood
    mu1 <- alpha %*% t(Data$X[,-2])
    X.imputed <- Data$X
    X.imputed[,2] <- ifelse(is.na(Data$X[,2]), mu1, Data$X[,2])
    LL1 <- sum(dnorm(X.imputed[,2], mu1, 1/sqrt(tau[1]), log=TRUE))
    mu2 <- beta %*% t(X.imputed)
    y.imputed <- ifelse(is.na(Data$y), mu2, Data$y)
    LL2 <- sum(dnorm(y.imputed, mu2, 1/sqrt(tau[2]), log=TRUE))
    ### Log-Posterior
    LP <- LL1 + LL2 + sum(alpha.prior) + sum(beta.prior) + sum(tau.prior)
    Modelout <- list(LP=LP, Dev=-2*LL2, Monitor=c(LP,tau),
        yhat=mu2, parm=parm)
    return(Modelout)
    }
```

13. Linear Regression with Missing Response

Initial values do not need to be specified for missing values in this response, y. Instead, at each iteration, missing values in y are replaced with their estimate in μ.

13.1. Form

$$y \sim N(\mu, \tau^{-1})$$
$$\mu = \mathbf{X}\beta$$
$$\beta_j \sim N(0, 1000), \quad j = 1, \ldots, J$$
$$\tau \sim \Gamma(0.001, 0.001)$$

13.2. Data

```
data(demonsnacks)
N <- NROW(demonsnacks)
J <- NCOL(demonsnacks)
y <- log(demonsnacks$Calories)
y[sample(1:N, round(N*0.05))] <- NA
X <- cbind(1, as.matrix(demonsnacks[,c(1,3:10)]))
for (j in 2:J) {X[,j] <- CenterScale(X[,j])}
mon.names <- c("LP","tau")
parm.names <- parm.names(list(beta=rep(0,J), log.tau=0))
MyData <- list(J=J, X=X, mon.names=mon.names, parm.names=parm.names, y=y)
```

13.3. Initial Values

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

13.4. 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$X)
y.imputed <- ifelse(is.na(Data$y), mu, Data$y)
LL <- sum(dnorm(y.imputed, mu, 1/sqrt(tau), log=TRUE))
### Log-Posterior
LP <- LL + sum(beta.prior) + tau.prior
Modelout <- list(LP=LP, Dev=-2*LL, Monitor=c(LP,tau),
    yhat=mu, parm=parm)
return(Modelout)
}
```

14. Multinomial Logit

14.1. Form

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

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

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

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

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

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

14.2. 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 <- "LP"
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)
```

14.3. Initial Values

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

14.4. 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=LP,
          yhat=p, parm=parm)
     return(Modelout)
     }
```

15. Normal, Multilevel

This is Gelman's school example (Gelman, Carlin, Stern, and Rubin 2004). Note that **LaplacesDemon** 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.).

15.1. Form

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

15.2. 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 <- c("LP","theta.sigma")
parm.names <- parm.names(list(theta=rep(0,J), theta.mu=0,
    log.theta.sigma=0))
MyData <- list(J=J, mon.names=mon.names, parm.names=parm.names, sd=sd, y=y)
```

15.3. Initial Values

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

15.4. 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=c(LP, theta.sigma),
        yhat=theta, parm=parm)
    return(Modelout)
    }
```

16. Poisson Regression

16.1. Form

$$y \sim Pois(\lambda)$$
$$\lambda = \exp(\mathbf{X}\beta)$$
$$\beta_j \sim N(0, 1000), \quad j = 1, \ldots, J$$

16.2. 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 <- "LP"
parm.names <- parm.names(list(beta=rep(0,J)))
MyData <- list(J=J, X=X, mon.names=mon.names, parm.names=parm.names, y=y)
```

16.3. Initial Values

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

16.4. 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=LP,
    yhat=lambda, parm=parm)
return(Modelout)
}
```

17. Seemingly Unrelated Regression (SUR)

The following data was used by Zellner (1962) when introducing the Seemingly Unrelated Regression methodology.

17.1. Form

$$Y_{t,k} \sim N_K(\mu_{t,k}, \Sigma), \quad t = 1, \ldots, T; \quad k = 1, \ldots, K$$
$$\mu_{1,t} = \alpha_1 + \alpha_2 X_{t,1} + \alpha_3 X_{t,2}, \quad t = 1, \ldots, T$$
$$\mu_{2,t} = \beta_1 + \beta_2 X_{t,3} + \beta_3 X_{t,4}, \quad t = 1, \ldots, T$$
$$\Sigma = \Omega^{-1}$$
$$\Omega \sim Wishart(K, \mathbf{S}), \quad \mathbf{S} = \mathbf{I}_K$$
$$\alpha_j \sim N(0, 1000), \quad j = 1, \ldots, J$$
$$\beta_j \sim N(0, 1000), \quad j = 1, \ldots, J$$

where J=3, K=2, and T=20.

17.2. 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)
S <- diag(NCOL(Y))
mon.names <- c("LP","Sigma[1,1]","Sigma[2,1]","Sigma[1,2]","Sigma[2,2]")
parm.names <- parm.names(list(alpha=rep(0,3), beta=rep(0,3),
    Omega=diag(2)), uppertri=c(0,0,1))
MyData <- list(S=S, T=T, Y=Y, CG=CG, CW=CW, IG=IG, IW=IW, VG=VG, VW=VW,
    mon.names=mon.names, parm.names=parm.names)
```

17.3. Initial Values

```
Initial.Values <- c(rep(0,3), rep(0,3), S[upper.tri(S, diag=TRUE)])
```

17.4. Model

```
Model <- function(parm, Data)
    {
    ### 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]
    Omega <- matrix(parm[c(7,8,8,9)], NROW(Data$S), NROW(Data$S))
    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 <- dwishart(Omega, NROW(Data$S), Data$S, log=TRUE)
    ### Log-Likelihood
    mu <- matrix(0,Data$T,2)
    mu[,1] <- alpha[1] + alpha[2]*Data$CG + alpha[3]*Data$VG
    mu[,2] <- beta[1] + beta[2]*Data$CW + beta[3]*Data$VW
    LL <- rep(0, Data$T)
    for (t in 1:Data$T) {
        LL[t] <- sum(dmvn(Data$Y[t,], mu[t,], Sigma, log=TRUE))}
    ### Log-Posterior
    LP <- sum(LL) + sum(alpha.prior) + sum(beta.prior) + Omega.prior
    Modelout <- list(LP=LP, Dev=-2*sum(LL),
        Monitor=c(LP, as.vector(Sigma)), yhat=mu, parm=parm)
    return(Modelout)
    }
```

18. Variable Selection

In this example, variable selection is applied to linear regression, though the method is widely applicable. The familiar regression effects vector β is now reserved for effect size, and a γ vector is added that indicates inclusion of each effect. For more information on variable selection methods, see (O'Hara and Sillanpaa 2009). The example below also shows how to apply constraints to β.

18.1. Form

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

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

$$\theta_j = \gamma_j \beta_j, \quad j = 1, \ldots, J$$

$$(\beta_j | \gamma_j) \sim N(0, \beta_\tau^{-1}) \quad T(-10, 10), \quad j = 1, \ldots, J$$

$$\beta_\tau \sim N(0, 1000)$$

$$\gamma_j = \frac{1}{1 + \exp(-\delta_j)}, \quad j = 1, ..., J$$

$$\delta_j \sim N(0, 10), \quad j = 1, \ldots, J$$

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

18.2. Data

```
data(demonsnacks)
N <- NROW(demonsnacks)
J <- NCOL(demonsnacks)
y <- log(demonsnacks$Calories)
X <- cbind(1, as.matrix(demonsnacks[,c(1,3:10)]))
for (j in 2:J) {X[,j] <- CenterScale(X[,j])}
mon.names <- c("LP", "beta.tau", "tau", parm.names(list(gamma=rep(0,J))))
parm.names <- parm.names(list(beta=rep(0,J), delta=rep(0,J),
    log.beta.tau=0, log.tau=0))
MyData <- list(J=J, X=X, mon.names=mon.names, parm.names=parm.names, y=y)
```

18.3. Initial Values

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

18.4. Model

```
Model <- function(parm, Data)
    {
    ### Hyperprior Parameters
    beta.tau.alpha <- 1.0E-3
```

```
beta.tau.beta <- 1.0E-3
delta.mu <- rep(0,Data$J)
delta.tau <- rep(1.0E-1,Data$J)
### Prior Parameters
beta.mu <- rep(0,Data$J)
beta.tau <- exp(parm[grep("log.beta.tau", Data$parm.names)])
delta <- parm[(Data$J+1):(2*Data$J)]
tau.alpha <- 1.0E-3
tau.beta <- 1.0E-3
### Parameters
beta <- parm[1:Data$J]
beta <- ifelse(beta > 10, 10, beta)
beta <- ifelse(beta < -10, -10, beta)
parm[1:Data$J] <- beta
gamma <- round(invlogit(delta))
tau <- exp(parm[grep("log.tau", Data$parm.names)])
### Log(Prior Densities)
beta.prior <- rep(0,Data$J)
beta.prior <- dtrunc(beta, "norm", a=-10, b=10, mean=beta.mu,
    sd=1/sqrt(beta.tau), log=TRUE)
beta.prior <- ifelse(gamma == 0, 0, beta.prior)
beta.tau.prior <- dgamma(beta.tau, beta.tau.alpha, beta.tau.beta,
    log=TRUE)
delta.prior <- dnorm(delta, delta.mu, 1/sqrt(delta.tau), log=TRUE)
tau.prior <- dgamma(tau, tau.alpha, tau.beta, log=TRUE)
### Log-Likelihood
theta <- beta * gamma
mu <- theta %*% t(Data$X)
LL <- sum(dnorm(y, mu, 1/sqrt(tau), log=TRUE))
### Log-Posterior
LP <- LL + sum(beta.prior) + sum(delta.prior) + beta.tau.prior +
    tau.prior
Modelout <- list(LP=LP, Dev=-2*LL, Monitor=c(LP,beta.tau,tau,gamma),
    yhat=mu, parm=parm)
return(Modelout)
}
```

19. Zero-Inflated Poisson (ZIP)

19.1. Form

$$y \sim Pois(\Lambda_{1:N,2})$$

$$z \sim Bern(\Lambda_{1:N,1})$$

$$z_i = 1 \quad when \quad y_i = 0, \quad else \quad z_i = 0, \quad i = 1, \ldots, N$$

$$\Lambda_{i,2} = 0 \quad if \quad \Lambda_{i,1} \geq 0.5, \quad i = 1, \ldots, N$$
$$\Lambda_{1:N,1} = \log[1 + \exp(\mathbf{X}_1 \alpha)]$$
$$\Lambda_{1:N,2} = \exp(\mathbf{X}_2 \beta)$$
$$\alpha_j \sim N(0, 1000), \quad j = 1, \ldots, J_1$$
$$\beta_j \sim N(0, 1000), \quad j = 1, \ldots, J_2$$

19.2. Data

```
N <- 1000
J1 <- 4
J2 <- 3
X1 <- matrix(runif(N*J1,-2,2),N,J1); X1[,1] <- 1
X2 <- matrix(runif(N*J2,-2,2),N,J2); X2[,1] <- 1
alpha <- runif(J1,-1,1)
beta <- runif(J2,-1,1)
p <- as.vector(invlogit(alpha %*% t(X1) + rnorm(N,0,0.1)))
mu <- as.vector(round(exp(beta %*% t(X2) + rnorm(N,0,0.1))))
y <- ifelse(p > 0.5, 0, mu)
z <- ifelse(y == 0, 1, 0)
mon.names <- "LP"
parm.names <- parm.names(list(alpha=rep(0,J1), beta=rep(0,J2)))
MyData <- list(J1=J1, J2=J2, N=N, X1=X1, X2=X2, mon.names=mon.names,
    parm.names=parm.names, y=y, z=z)
```

19.3. Initial Values

```
Initial.Values <- rep(0,J1+J2)
```

19.4. Model

```
Model <- function(parm, Data)
    {
    ### Prior Parameters
    alpha.mu <- rep(0, Data$J1)
    alpha.tau <- rep(1.0E-3, Data$J1)
    beta.mu <- rep(0, Data$J2)
    beta.tau <- rep(1.0E-3, Data$J2)
    ### Parameters
    alpha <- parm[1:Data$J1]
    beta <- parm[min(grep("beta", Data$parm.names)):max(grep(
        "beta", Data$parm.names))]
    ### 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)
    ### Log-Likelihood
```

```
Lambda <- matrix(NA, Data$N, 2)
Lambda[,1] <- invlogit(alpha %*% t(Data$X1))
Lambda[,2] <- exp(beta %*% t(Data$X2))
Lambda[,2] <- ifelse(Lambda[,1] >= 0.5, 0, Lambda[,2])
LL1 <- sum(dbern(Data$z, Lambda[,1], log=TRUE))
LL2 <- sum(dpois(Data$y, Lambda[,2], log=TRUE))
### Log-Posterior
LP <- LL1 + LL2 + sum(alpha.prior) + sum(beta.prior)
Modelout <- list(LP=LP, Dev=-2*LL2, Monitor=LP,
    yhat=Lambda[,2], parm=parm)
return(Modelout)
}
```

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