Applied Bayesian Analysis : NCSU ST 540

Midterm2

 $Bruce\ Campbell$

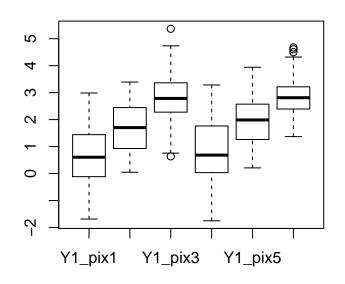
This section is a test section where we generate and fit a vector autoregressive model - $VAR(1) \in \mathbf{R}^6$ given by

$$y_t = \nu + \rho * y_{t-1} + \epsilon$$

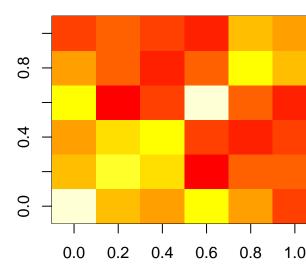
$$\epsilon \sim N(0, \Sigma)$$

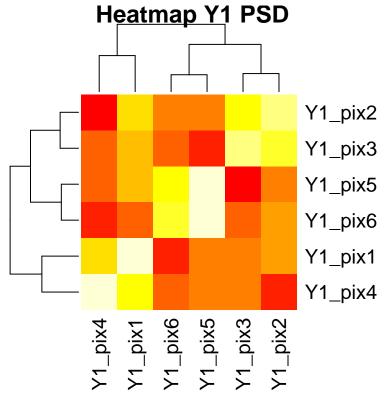
We use the y1 data to calculate a NaN firendly sample covariance and then we find the nearest positive semidefinite matrix to use to generate data for the model.

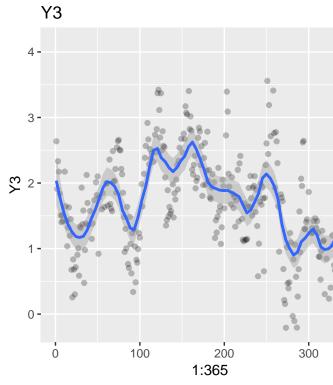
Data Visualization



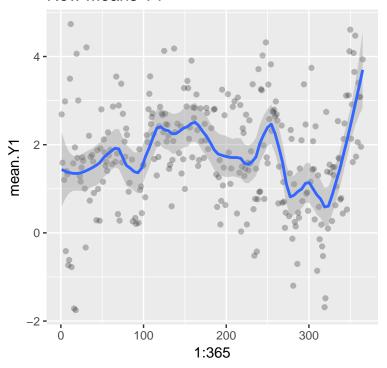
Y1 : Nearst PSD to pairwise complete obs cov ma





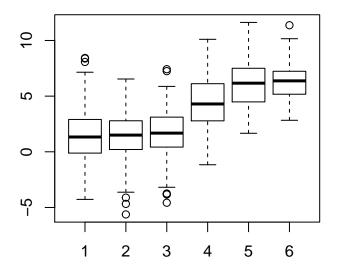


Row Means Y1



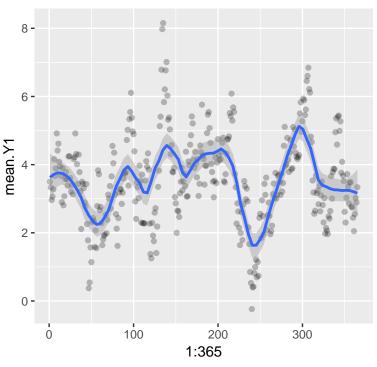
Test Data

```
rho = 0.9
nu = matrix((1:6) * 0.1, p, 1)
y = matrix(NA, N, p)
y[1, ] = (1:6)
for (t in 2:N) {
    y[t, ] = mvrnorm(1, nu + rho * y[t -
        1, ], empirical_sigma)
for (t in 2:N) {
    y[t, ] = mvrnorm(1, nu + rho * y[t -
       1, ], empirical_sigma)
}
Y1.test <- y
Y2.test <- y[, 1]
Y3.test <- rowMeans(y)
# redaction proportions
Y1.redaction.prop <- 0.8
Y2.redaction.prop <- 0.1
Y3.redaction.prop <- 0.1
Y1.test.redacted <- Y1.test
```



```
ggplot(data.frame(mean.Y1 = rowMeans(Y1.test,
    na.rm = TRUE)), aes(x = 1:365, y = mean.Y1)) +
    geom_point(alpha = 0.25) + geom_smooth(method = "loess",
    span = 0.22) + ggtitle("TEST DATA : Row Means Y1.test")
```

TEST DATA: Row Means Y1.test



```
library(R2OpenBUGS)
n.chains = 2
n.thin = 2
n.burnin = 5000
n.samples = 20000
x <- as.matrix(Y1)</pre>
stacks_dat <- list(Y1 = Y1, Y2 = Y2, Y3 = Y3,
    p = 6, N = 365
mlr_model <- function() {</pre>
    for (i in 1:N) {
        \# x[i,1] \sim dnorm(theta[i,1], inv.var)
        Y2[i] ~ dnorm(theta[i, 1], inv.var)
        Y3[i] ~ dnorm(thetaBar[i], inv.var)
        thetaBar[i] <- 1/6 * (theta[i,
            1] + theta[i, 2] + theta[i,
            3] + theta[i, 4] + theta[i,
            5] + theta[i, 6])
    }
    inv.var ~ dgamma(0.01, 0.01)
    for (i in 1:N) {
```

```
for (j in 1:p) {
            theta[i, j] ~ dnorm(Y1[i, 1],
                inv.var)
        }
    }
    # Missing data model for x
    for (i in 1:N) {
        Y1[i, 1:p] ~ dmnorm(Y1_mn[], Y1_prec[,
            ])
    }
    # Priors for missing-data model
    # parameters
    for (j in 1:p) {
        Y1_mn[j] ~ dnorm(0, 0.01)
    Y1_prec[1:p, 1:p] ~ dwish(R[, ], k)
    Y1_cov[1:p, 1:p] <- inverse(Y1_prec[,
        ])
    k < -p + 0.1
    for (j1 in 1:p) {
        for (j2 in 1:p) {
            R[j1, j2] \leftarrow 0.1 * equals(j1,
                j2)
        }
    } #R is diagonal
}
mlr_inits <- function() {</pre>
    list(I = diag(p), tau = 0.01)
}
samps <- bugs(data = stacks_dat, inits = mlr_inits,</pre>
    parameters.to.save = c("theta"), model.file = mlr_model,
    codaPkg = TRUE, debug = FALSE, n.chains = n.chains,
    n.burnin = n.burnin, n.iter = n.samples,
    n.thin = n.thin, DIC = F)
out.coda <- read.bugs(samps)</pre>
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```

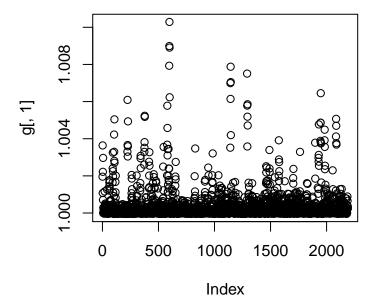
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## Abstracting theta[365,4] ... 15000 valid values
## Abstracting theta[365,5] ... 15000 valid values
## Abstracting theta[365,6] ... 15000 valid values
# save(out.coda,file =
# 'out.coda_OPENBUGS_Imputation.RData')
if (n.chains > 1) {
    g <- matrix(NA, nrow = nvar(out.coda),
        ncol = 2)
    for (v in 1:nvar(out.coda)) {
        g[v, ] <- gelman.diag(out.coda[,
            v])$psrf
    }
    count.coeff.gt \leftarrow sum(g[, 1] > 1.1)
    count.coeff.gt
    plot(g[, 1], main = "Gelman-Rubin ")
}
```

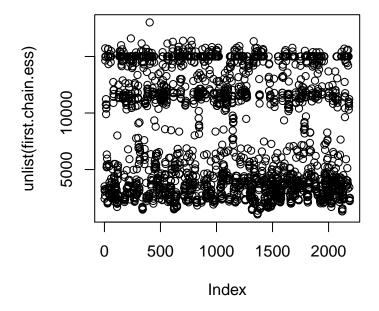
Gelman-Rubin



```
chains.ess <- lapply(out.coda, effectiveSize)

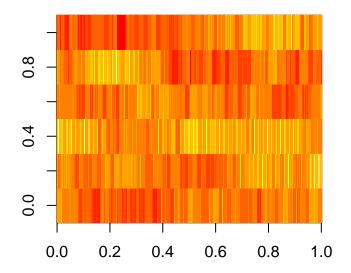
first.chain.ess <- chains.ess[1]
plot(unlist(first.chain.ess), main = "Effective Sample Size")</pre>
```

Effective Sample Size

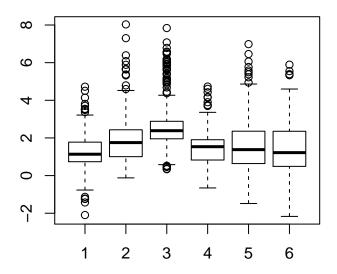


```
chain <- out.coda[[1]]</pre>
# imputedY1 <- Y1 for( i in</pre>
# 1:ncol(chain) ) { colname <-</pre>
# colnames(chain)[i] idx
\# \leftarrow gsub('x', '', colname) idx
\# <-gsub(' \setminus \{[', '', idx)\}
# idx<-gsub('\\]','',idx)
\# strsplit(idx,',') idi \leftarrow
# as.numeric(strsplit(idx,',')[[1]][1])
# idj <-
# as.numeric(strsplit(idx,',')[[1]][2])
# if(grepl('Sigma',colname) ) {
# print(paste('skipping
# ',colname,sep='')) next } samples <-</pre>
# chain[,i] imputedY1[idi,idj]
# <-mlv(samples)$M }</pre>
theta.posterior.modes <- list()</pre>
for (i in 1:ncol(chain)) {
    colname <- colnames(chain)[i]</pre>
    if (grepl("theta", colname)) {
         samples <- chain[, i]</pre>
         theta.posterior.modes[colname] <- mlv(samples)$M</pre>
    } else {
         next
```

```
}
}
theta.posterior <- matrix(unlist(theta.posterior.modes),
    ncol = 6, byrow = FALSE)
image(theta.posterior)</pre>
```



boxplot(theta.posterior)



```
# image(Y1, main='Y1')

# image(imputedY1, main='Imputed')

# write.csv(unscaled.theta.map,file =
# 'unscaled-theta-map.csv')
```