Lecture 12 - Key

Latent Variable Methods

Latent variable methods are a cornerstone of many Bayesian statistical procedures. Typically for modeling convenience a latent (unobservable) normal random variable is assumed to underlie more complicated scenarios. A few common examples are:

- Probit Regression,
- Ordinal Regression,
- Censored Data, and
- State Space Models.

Probit Regression

Probit regression is a binary GLM that uses the probit link rather than a logit link. The model can be written as:

$$\begin{aligned} y_i &\sim Bernoulli(p_i) && (1) \\ \Phi(p_i) &= X\tilde{\beta}, && (2) \end{aligned}$$

where $\Phi()$ is the CDF of a standard normal random variable. Typically Bayesians will use the probit link with a data augmentation step that facilitates Gibbs sampling of a latent random variable. Specifically, let z_i be a random variable distributed as $N(X\tilde{\beta}, 1)$, with the constraint that if $y_i = 1$, then $z_i > 0$ and if $y_i = 0$ then $z_i < 0$. The idea is that there is a continuous random variable that underlies the binary process. If the continuous process is greater than zero then the observed process results in one.

Ordinal Regression

Ordinal regression is a specific type of multinomial regression model for categorical data. Likert scale questions are a common example of this type of response. Similar to probit regression, we assume there is a continuous latent variable that underlies the categorical response. In the probit case, our threshold was set at zero. In this case there are $n - 1$ thresholds for the n distinct categorical values. In this model the threshold values are learned from the data.

Censored Data

Censored data is common in many statistical settings including biostatistics and reliability. The basic idea is that all values of the data cannot be measured, and the data has to be censored. In some situations certain values cannot be measured as they are below a devices detection level; however, the values are actually zero. Thus there is some truncation of the variable, for example $\$ < .1\$$. This is an example of lower censoring. Upper censoring can also occur, a common example is survival analysis. Typically the response of interest is the time until death. If the subject is still living at the end of the study, the result will be $\$ > x\$$, where x is the time the subject was alive during the study. Similar to the previous examples a latent variable is assumed to underlie this process.

State-Space Modeling

Another example of latent variable modeling is state space models. A common example is:

$$\begin{aligned} \text{observation equation} \qquad y_t &= x_t + \epsilon_t \qquad (3) \\ \text{evolution (state) equation} \qquad x_t &= x_{t-1} + \gamma_t, \qquad (4) \end{aligned}$$

where y_t is the observed response at time t and x_t is the latent process that evolves in time. This type of model is often thought of as signal plus noise, where the signal is the latent value $\tilde{x}_{1:t}$ and the observed signal *with noise* is $\tilde{y}_{1:t}$.

Probit Regression Exercise

Data Simulation

```
set.seed(11192018)
num.pts <- 1000
beta <- c(1,1)
X <- rnorm(num.pts)
X.comb <- cbind(rep(1,num.pts),X)
X.beta <- X.comb %*% beta
probs <- pnorm(X.beta)
Y <- rbinom(num.pts, 1, probs)
```

Model Fitting

```
num.mcmc <- 10000
beta.samples <- matrix(1, nrow = num.mcmc, ncol = 2)
upper <- lower <- rep(0, num.pts)
upper[Y == 1] <- Inf
lower[Y == 0] <- -Inf
cov.beta <- solve(t(X.comb) %*% X.comb + diag(2))

for (iter in 2:num.mcmc){
  # sample latent z
  z <- rtruncnorm(num.pts, a = lower, b = upper, mean = X.comb %*% beta.samples[iter -1,], sd = 1)

  # sample beta
  exp.beta <- cov.beta %*% t(X.comb) %*% z
  beta.samples[iter, ] <- rmnorm(1, mean = exp.beta, varcov = cov.beta)
}


glm(Y~X, family = binomial(link = 'probit'))
```

```
##
## Call:  glm(formula = Y ~ X, family = binomial(link = "probit"))
##
## Coefficients:
## (Intercept)            X
##      0.9843       1.0406
##
## Degrees of Freedom: 999 Total (i.e. Null);  998 Residual
## Null Deviance:       1152
## Residual Deviance: 804.3     AIC: 808.3
```

```
colMeans(beta.samples)
```

```
## [1] 0.9791879 1.0358753
```

Q identify the priors for this model. Do these seem reasonable? **Q** are you satisfied that the sampler is working? **Q** conduct a posterior predictive check for this situation.

Data Analysis

Return to the seattle housing data set and fit a probit model to understand patterns that cause a house to sell for more than $400,000.

```r
library(readr)
seattle <- read_csv('http://www.math.montana.edu/ahoegh/teaching/stat532/data/SeattleBinaryHousing.csv')
```

```
## Parsed with column specification:
## cols(
##   GR.400k = col_integer(),
##   price = col_double(),
##   sqft_living = col_integer(),
##   sqft_lot = col_integer(),
##   zipcode = col_integer()
## )
```

Hierarchical GLMs

Now suppose we are interested in the number of students in each school that past the test rather than overall mean test score. Then consider this following model.

$$\begin{aligned} p(y|\tilde{p}_j, n_j) &\sim Binomial(n_j, p_j) \\ p_j &= \text{logit}^{-1}(\tilde{x}_j^T \tilde{\theta}_j) \\ p(\theta_j|\tilde{\mu}, \Sigma) &= MVN(\tilde{\mu}, \Sigma) \end{aligned}$$

where n_j the number of students taking the exam for school j is known.

Q: Now what do we need for priors?

$$\begin{aligned} \Sigma &\sim InvWishart(\eta_0/2, \eta_0\tau_0^2/2) \\ \tilde{\mu} &\sim MVN(\tilde{\mu}_0, \Lambda_0) \end{aligned}$$

Q: How do we take posterior samples?

- Gibbs step for $\tilde{\mu}$ and Σ
- Metropolis step for $\tilde{\theta}$

Now write out the model using a probit link.

$$\begin{aligned} p(y|\tilde{p}_j, n_j) &\sim Binomial(n_j, p_j) \\ p_j &= \Phi(\tilde{x}_j^T \tilde{\theta}_j) \\ p(\theta_j|\tilde{\mu}, \Sigma) &= MVN(\tilde{\mu}, \Sigma) \end{aligned}$$

where n_j the number of students taking the exam for school j is known.

Q: Now what do we need for priors?

$$\begin{aligned} \Sigma &\sim InvWishart(\eta_0/2, \eta_0\tau_0^2/2) \\ \tilde{\mu} &\sim MVN(\tilde{\mu}_0, \Lambda_0) \end{aligned}$$

Q: How do we take posterior samples?

- Sample latent variables (z) (Gibbs)
- Sample μ (Gibbs)
- Sample $Sigma$ (Gibbs)
- Sample θ (Gibbs)

Hierarchical Probit Code Example

Hierarchical Probit Function

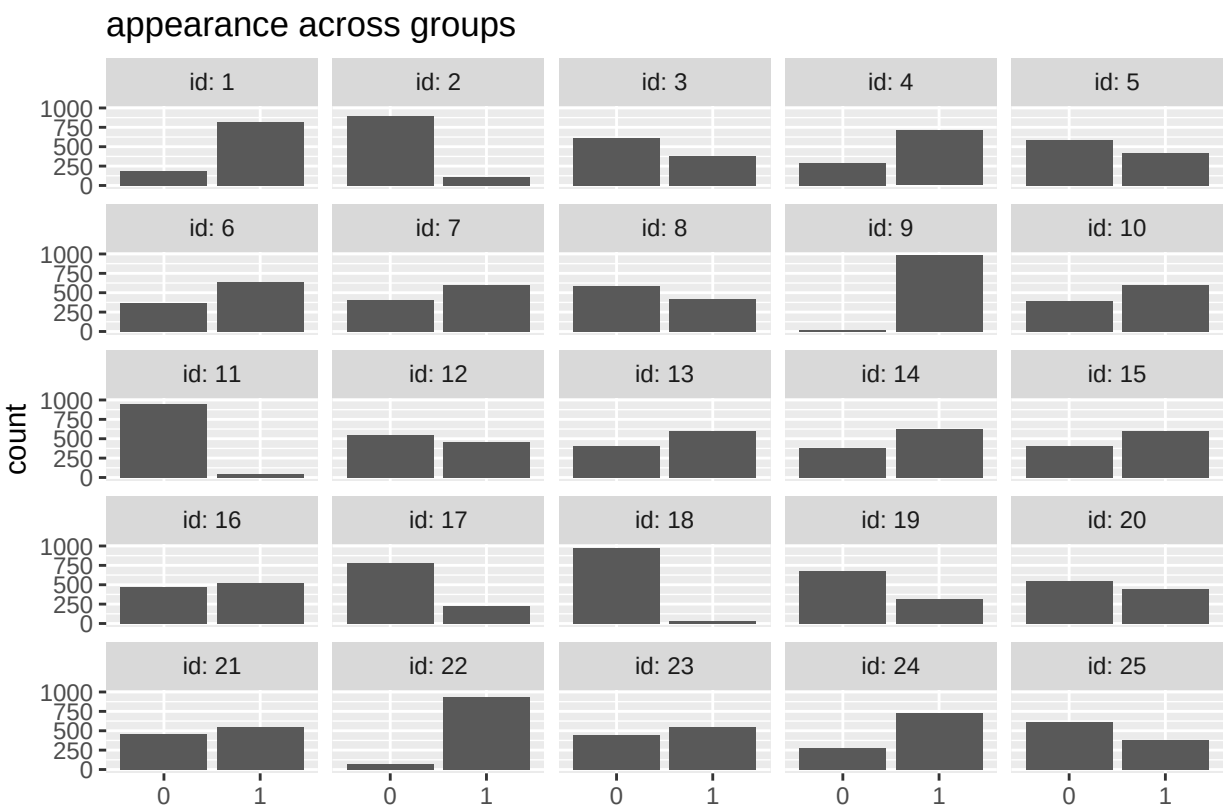
```
Hierachical_Probit <- function(Y, X, id, cum_n, num.mcmc = 1000){
  # Gibbs Sampler for Hierarchical Binary Data
  m <- length(unique(id))
  p <- ncol(X)
  N <- length(Y)

  #initialize storage
  beta.samples <- array(0, dim=c(m, p, num.mcmc))
  theta.samples <- matrix(0, num.mcmc, p)
  Sigma.samples <-  array(0, dim=c(p, p, num.mcmc))
  Sigma.samples[,,1] <- diag(p)
  X.beta <- rep(0,N)

  # priors
  Lambda <- diag(p) * 1
  Lambda.inv <- solve(Lambda)
  mu.0 <- rep(0,p)
  nu.0 <- p + 2
  S.0 <- diag(p)

  # bounds for latent variables
  upper <- lower <- rep(Inf, N)
  upper[Y == 0] <- 0
  lower[Y == 0] <- -Inf
  lower[Y == 1] <- 0

  for (iter in 2:num.mcmc){
    ## Sample latent Z
    X.beta[1:cum_n[1]] <- X[(1):(cum_n[1]),] %*% beta.samples[1, , iter - 1]
    for (group.var in 2:m){
      X.beta[(cum_n[group.var - 1] + 1):(cum_n[group.var])] <-
        X[(cum_n[group.var - 1] + 1):(cum_n[group.var]),] %*% beta.samples[group.var, , iter - 1]
    }
    z <- rtruncnorm(N,a = lower, b = upper, mean = X.beta, sd = 1)

    ## sample betas
    Sigma.inv <- solve(Sigma.samples[,,iter - 1])

    x.tmp <- X[(1):(cum_n[1]),]
    z.tmp <- matrix(z[(1):(cum_n[1])], ncol = 1)
    var.beta <- solve(t(x.tmp) %*% x.tmp + Sigma.inv)
    exp.beta <- var.beta %*% (t(x.tmp) %*% z.tmp + Sigma.inv %*% theta.samples[iter-1,] )
    beta.samples[1, , iter] <- rmnorm(n = 1, mean = exp.beta, varcov = var.beta)
    for (group.var in 2:m){
      x.tmp <- X[(cum_n[group.var - 1] + 1):(cum_n[group.var]),]
      z.tmp <- matrix(z[(cum_n[group.var - 1] + 1):(cum_n[group.var])], ncol = 1)
      var.beta <- solve(t(x.tmp) %*% x.tmp + Sigma.inv)
      exp.beta <- var.beta %*% (t(x.tmp) %*% z.tmp + Sigma.inv %*% theta.samples[iter-1,] )
      beta.samples[group.var, , iter] <- rmnorm(n = 1, mean = exp.beta, varcov = var.beta)
    }
```

```
    ## sample theta
    var.theta <- solve(m * Sigma.inv + Lambda.inv)
    exp.theta <- var.theta %*% (Sigma.inv %*% colSums(beta.samples[, , iter]) + Lambda.inv %*% mu.0)
    theta.samples[iter, ] <- rmnorm(n = 1, mean = exp.theta, varcov = var.theta)

    ## sample Sigma
    Sigma.df <- nu.0 + m
    S.theta <- matrix(0, p, p)
    for (group.var in 1:m){
      S.theta <- S.theta + (beta.samples[group.var,,iter] - theta.samples[iter,]) %*%
        t(beta.samples[group.var,,iter] - theta.samples[iter,])
    }
    Sigma.scale <- (S.0 + S.theta)
    Sigma.samples[, , iter] <- riwish(Sigma.df, Sigma.scale)
  }
  colnames(theta.samples) <- colnames(X)
  dimnames(beta.samples)[[2]] <- colnames(X)
  return(list(beta.samples = beta.samples, theta.samples = theta.samples,
              Sigma.samples = Sigma.samples))
}
```

Simulate Hierarchical Binary Data

```
set.seed(11192018)
m = 25 # number of groups
n_m = rep(1000, m) # observations per group
N = sum(n_m) # total observations
cum_n <- cumsum(n_m)

p = 2 # number of predictors
theta <- c(0,1)
sigma <- diag(c(1,1))
beta <- rmnorm(m, mean = theta, varcov = sigma) # individual parameters

### simulate data
X <- matrix(c(rep(1,N),rnorm(N)), nrow=N, ncol=2)
Y <- Xbeta <- probs <- id <- rep(0,N)

Xbeta[1:cum_n[1]] <- X[1:cum_n[1],] %*% beta[1,]
probs[1:cum_n[1]] <- pnorm(Xbeta[1:cum_n[1]])
Y[1:cum_n[1]] <- rbinom(n_m[1],1,probs[1:cum_n[1]])
id[1:cum_n[1]] <- 1
for (group.var in 2:m){
  Xbeta[(cum_n[group.var - 1] + 1):(cum_n[group.var])] <-
    X[(cum_n[group.var - 1] + 1):(cum_n[group.var]),] %*% beta[group.var,]
  probs[(cum_n[group.var - 1] + 1):(cum_n[group.var])] <-
    pnorm(Xbeta[(cum_n[group.var - 1] + 1):(cum_n[group.var])])
  Y[(cum_n[group.var - 1] + 1):(cum_n[group.var])] <-
    rbinom(n_m[group.var],1,probs[(cum_n[group.var - 1] + 1):(cum_n[group.var])])
  id[(cum_n[group.var - 1] + 1):(cum_n[group.var])] <- group.var
}

sim <- data.frame(Y = as.factor(Y), id = factor(id), X=X[,2])
```

```
ggplot(data=sim, aes(Y)) + geom_bar() + facet_wrap(~id,labeller = "label_both") +
  ggtitle('appearance across groups') + xlab('')
```



Analysis

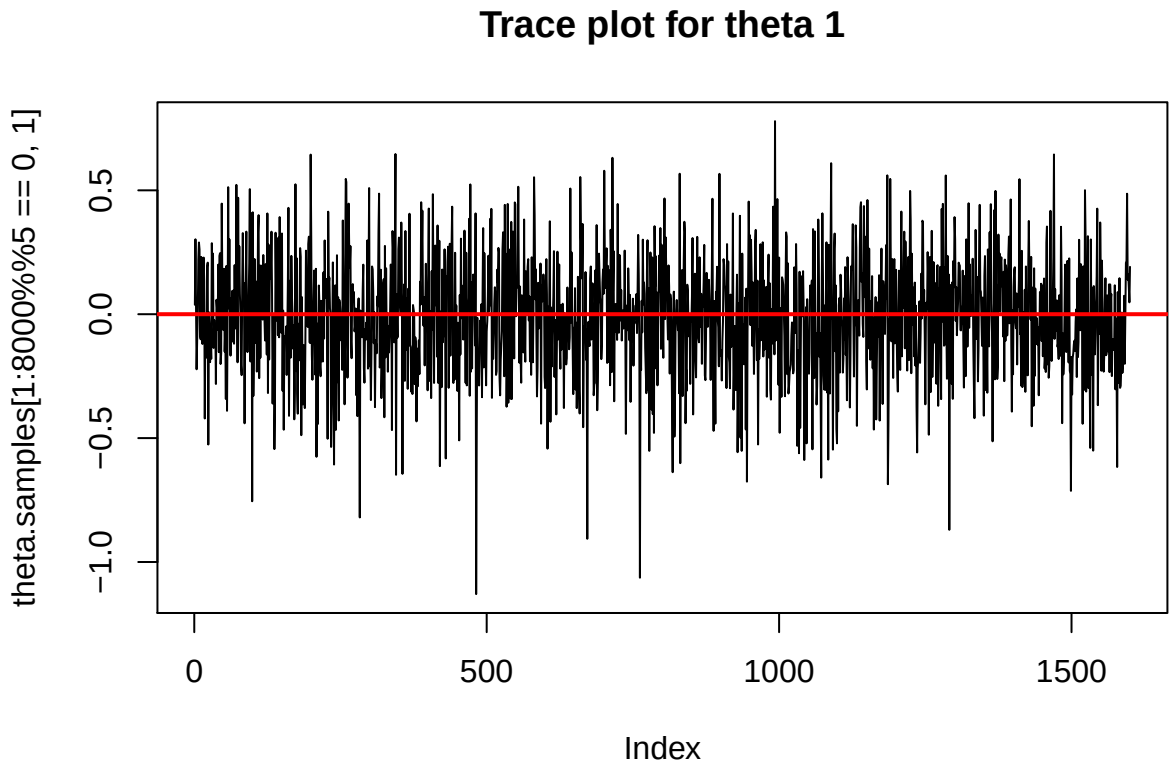
```
tmp.vals <- Hierachical_Probit(Y, X, id, cum_n, num.mcmc = 8000)

beta.samples <- tmp.vals$beta.samples
kable(beta[1:5,])
```

1.5518078	1.3253271
-1.3374766	-0.2498975
-0.8016554	2.8507909
0.6242745	0.6837699
-0.1829387	0.0563786

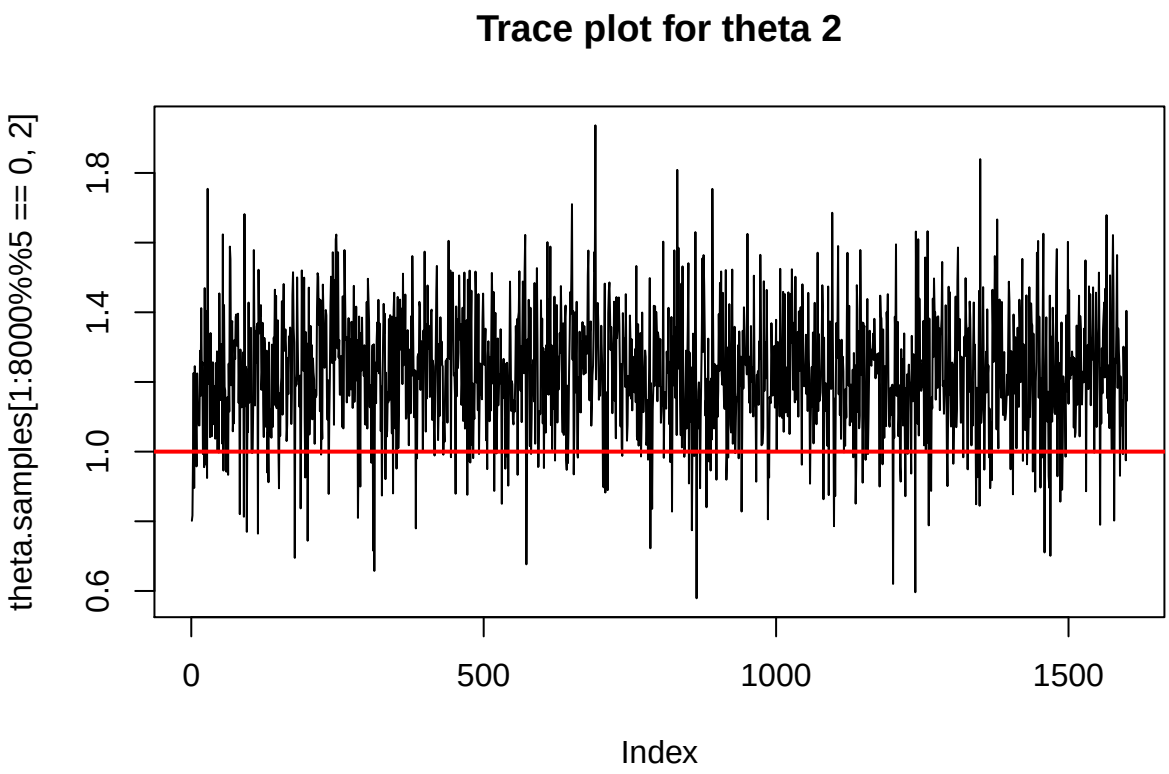
```
kable(rbind(rowMeans(beta.samples[1,,]), rowMeans(beta.samples[2,,]), rowMeans(beta.samples[3,,]),
            rowMeans(beta.samples[4,,]), rowMeans(beta.samples[5,,])))
```

1.5588356	1.2915988
-1.3127492	-0.3074197
-0.8878574	2.7410966
0.6461163	0.6376512
-0.2214625	0.0334960

```r
theta.samples <- tmp.vals$theta.samples
plot(theta.samples[1:8000 %% 5 == 0,1], type = 'l', main = 'Trace plot for theta 1')
abline(h = theta[1], col= 'red', lwd = 2)
```




```r
plot(theta.samples[1:8000 %% 5 == 0,2], type = 'l', main = 'Trace plot for theta 2')
abline(h = theta[2], col= 'red', lwd = 2)
```


Trace plot for theta 2
theta.samples[1:8000%%5 == 0, 2]
0.6
1.0
1.4
1.8
0
500
1000
1500
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