Mixed effect probit regression

Genotypic fungal resistance

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April 25, 2016

Outline

- Probit regression
- Bayesian probit regression
  - Data augmentation
- Bayesian mixed effect probit regression
- Extensions
  - Ordinal categorical data
  - Nominal categorical data
  - Bayesian logistic regression

Probit regression

Consider the model

$$Y_i \overset{ind}{\sim} Ber(\theta_i)$$

where, for the ith observation,

- Y_i is binary indicating *success* and
- θ_i is the probability of success.

A probit regression model assumes

$$\theta_i = \Phi(X_i^\top \beta)$$

where

- X_i are the explanatory variables for the ith observation,
- Φ is the standard normal cumulative distribution function, and
- β is the vector of parameters to be estimated.

Low birth weight

```
      low               age              lwt          race       smoke            ptl              ht
 Min.   :0.0000   Min.   :14.00   Min.   : 80.0   1:96   Min.   :0.0000   Min.   :0.0000   Min.   :0.00000
 1st Qu.:0.0000   1st Qu.:19.00   1st Qu.:110.0   2:26   1st Qu.:0.0000   1st Qu.:0.0000   1st Qu.:0.00000
 Median :0.0000   Median :23.00   Median :121.0   3:67   Median :0.0000   Median :0.0000   Median :0.00000
 Mean   :0.3122   Mean   :23.24   Mean   :129.8          Mean   :0.3915   Mean   :0.1958   Mean   :0.06349
 3rd Qu.:1.0000   3rd Qu.:26.00   3rd Qu.:140.0          3rd Qu.:1.0000   3rd Qu.:0.0000   3rd Qu.:0.00000
 Max.   :1.0000   Max.   :45.00   Max.   :250.0          Max.   :1.0000   Max.   :3.0000   Max.   :1.00000
       ui              ftv              bwt
 Min.   :0.0000   Min.   :0.0000   Min.   : 709
 1st Qu.:0.0000   1st Qu.:0.0000   1st Qu.:2414
 Median :0.0000   Median :0.0000   Median :2977
 Mean   :0.1481   Mean   :0.7937   Mean   :2945
 3rd Qu.:0.0000   3rd Qu.:1.0000   3rd Qu.:3487
 Max.   :1.0000   Max.   :6.0000   Max.   :4990
```

```
m = glm(low~., family=binomial(link=probit), data=birthwt[,-10]); summary(m)
```

```
Call:
glm(formula = low ~ ., family = binomial(link = probit), data = birthwt[,
    -10])

Deviance Residuals:
    Min       1Q   Median       3Q      Max
-1.8848  -0.8271  -0.5217   0.9903   2.2445

Coefficients:
            Estimate Std. Error z value Pr(>|z|)
(Intercept) -1.31431    0.24893  -5.280 1.29e-07 ***
age         -0.09774    0.11482  -0.851  0.39466
lwt         -0.27281    0.12217  -2.233  0.02555 *
race2        0.74961    0.31431   2.385  0.01708 *
race3        0.52183    0.25557   2.042  0.04117 *
smoke        0.56910    0.23469   2.425  0.01531 *
ptl          0.31968    0.20835   1.534  0.12495
ht           1.11161    0.41664   2.668  0.00763 **
ui           0.46517    0.27930   1.665  0.09581 .
ftv          0.02832    0.10161   0.279  0.78050
---
Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1

(Dispersion parameter for binomial family taken to be 1)

    Null deviance: 234.67  on 188  degrees of freedom
Residual deviance: 201.03  on 179  degrees of freedom
AIC: 221.03

Number of Fisher Scoring iterations: 5
```

Bayesian probit regression

Consider the model

$$\begin{aligned} Y_i &\overset{ind}{\sim} Ber(\theta_i) \\ \theta_i &= \Phi(X_i^\top \beta) \end{aligned}$$

with prior

$$\beta \sim N(b, B)$$

The posterior distribution is

$$\begin{aligned} p(\beta|y) &\propto p(y|\beta)p(\beta) \\ &\propto \left[\prod_{i=1}^n \Phi(X_i'\beta)^{y_i}[1-\Phi(X_i'\beta)]^{1-y_i}\right] e^{-(\beta-b)^\top B^{-1}(\beta-b)/2} \end{aligned}$$

But neither $p(\beta|y)$ nor $p(\beta_p|y, \beta_{-p})$ are a known distribution.

Data augmentation

An alternative construction of the model is

$$\begin{aligned} Y_i &= \mathrm{I}(Z_i > 0) \\ Z_i &\overset{ind}{\sim} N(X_i'\beta, 1) \end{aligned}$$

Note that

$$\begin{aligned} \theta_i &= P(Y_i = 1) \\ &= P(Z_i > 0) \\ &= P(X_i'\beta + \epsilon > 0) && \epsilon \sim N(0,1) \\ &= P(\epsilon > -X_i'\beta) \\ &= P(\epsilon < X_i'\beta) && \text{symmetry of standard normal} \\ &= \Phi(X_i'\beta) \end{aligned}$$

Thus, this is equivalent to the probit regression model.

Posterior distribution

Now, the likelihood is

$$p(y|Z) \propto \prod_{i=1}^{n} [\mathrm{I}(Z_i > 0)\mathrm{I}(y_i = 1) + \mathrm{I}(Z_i \leq 0)\mathrm{I}(y_i = 0)]$$

and

$$Z_i \overset{ind}{\sim} N(X_i'\beta, 1) \qquad \beta \sim N(b, B)$$

Therefore the *complete data likelihood* is

$$p(y, Z|\beta) \propto \prod_{i=1}^{n} N(Z_i|X_i'\beta, 1)\,[\mathrm{I}(Z_i > 0)\mathrm{I}(y_i = 1) + \mathrm{I}(Z_i \leq 0)\mathrm{I}(y_i = 0)]$$

Thus the posterior distribution is

$$p(\beta, Z|y) \propto p(y|Z, \beta)p(Z, \beta) = p(y|Z)p(Z|\beta)p(\beta) = p(y, Z|\beta)p(\beta)$$

and we will derive the full conditionals for $p(\beta|Z, y)$ and $p(Z|\beta, y)$.

Full conditional for β

The full conditional for β is

$$\begin{aligned} p(\beta|\ldots) &\propto p(y|Z)p(Z|\beta)p(\beta) \\ &\propto p(Z|\beta)p(\beta) \\ &= \left[\prod_{i=1}^{n} N(Z_i|X_i'\beta, 1)\right] N(\beta|b, B) \\ &= N(Z|X\beta, \mathrm{I})N(\beta|b, B) \end{aligned}$$

and thus $\beta|\ldots \sim N(\hat{\beta}, \hat{\Sigma}_\beta)$ with

$$\begin{aligned} \hat{\Sigma}_\beta &= [B^{-1} + X^\top X]^{-1} \\ \hat{\beta} &= \hat{\Sigma}_\beta[B^{-1}b + X^\top Z] \end{aligned}$$

Full conditional for Z

The full conditional for Z is

$$\begin{aligned} p(Z|\ldots) &\propto p(y|Z)p(Z|\beta)p(\beta) \\ &\propto p(y|Z)p(Z|\beta) \\ &= \prod_{i=1}^{n} N(Z_i|X_i'\beta,1)\left[\mathrm{I}(Z_i>0)\mathrm{I}(y_i=1)+\mathrm{I}(Z_i\leq 0)\mathrm{I}(y_i=0)\right] \end{aligned}$$

Thus the Z_i are conditionally independent with distribution

$$p(Z_i|y_i,\beta) = \begin{cases} N(Z_i|X_i'\beta,1)\mathrm{I}(Z_i>0) & \text{if } y_i=1 \\ N(Z_i|X_i'\beta,1)\mathrm{I}(Z_i\leq 0) & \text{if } y_i=0 \end{cases}$$

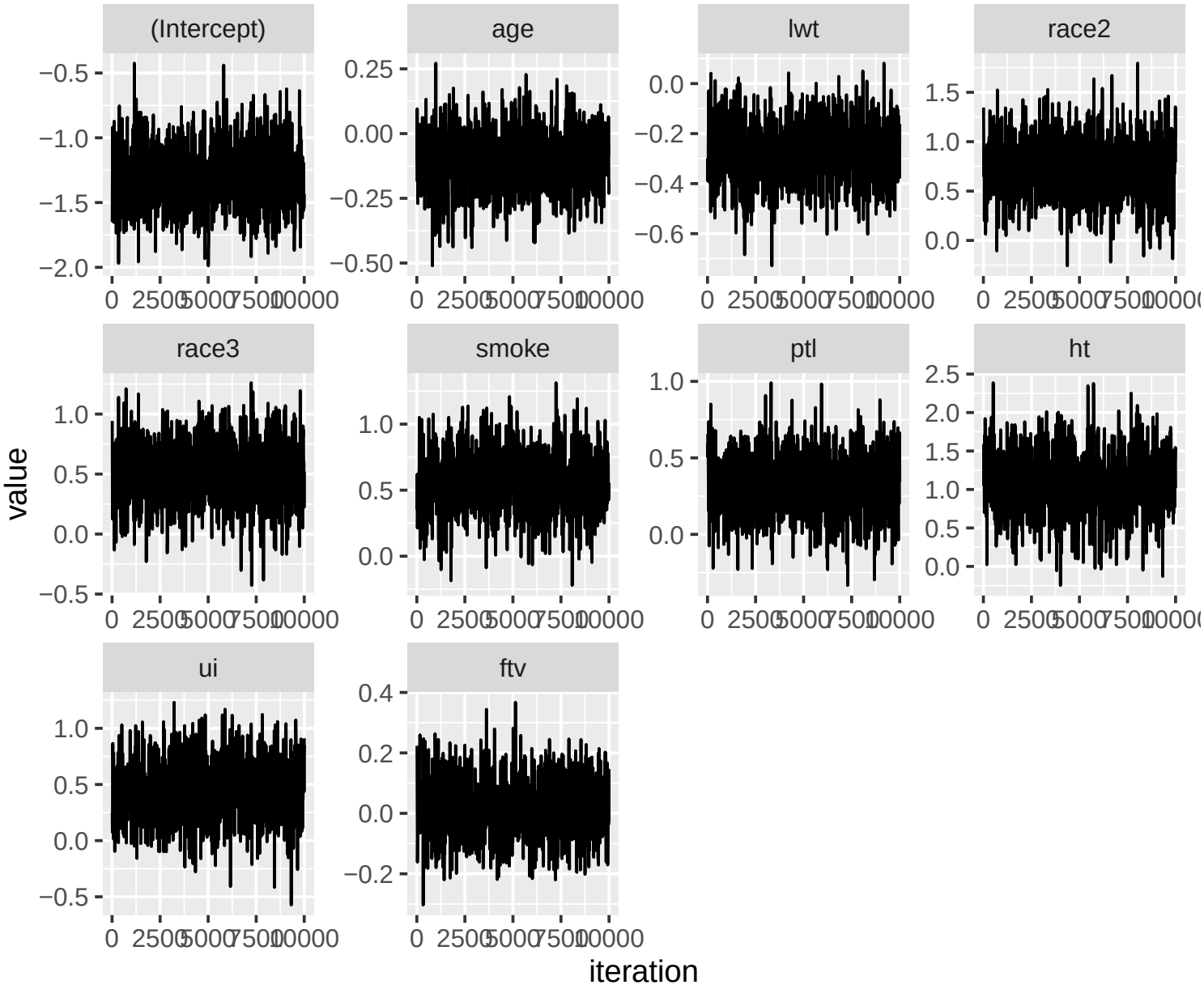
These can be drawn using the modified inverse cdf method.

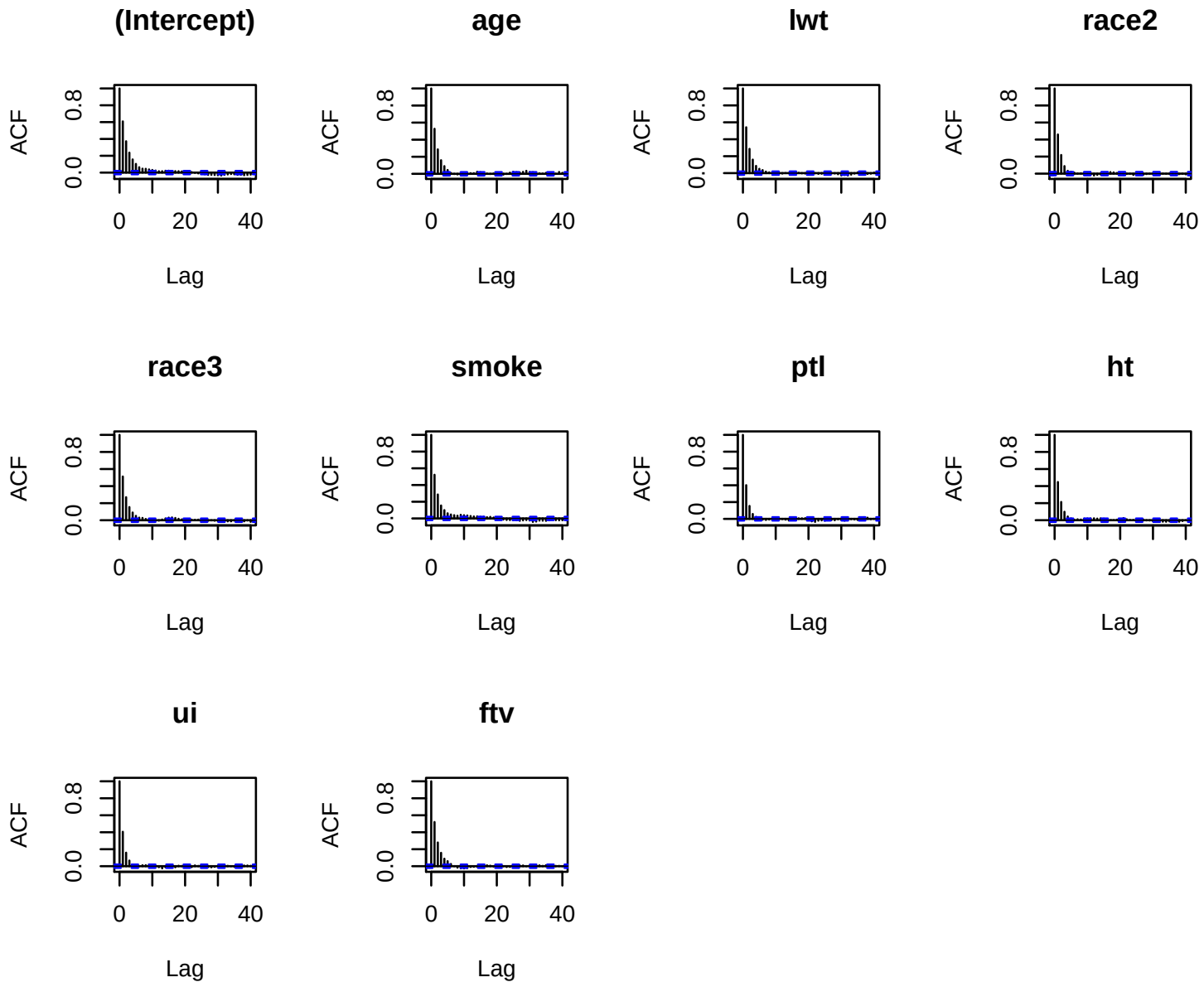
```
mcmc = function(n_iter, y, X, beta0, Sigma_beta) {
  n = nrow(X)
  p = ncol(X)

  # Precalculate quantities
  y = (as.numeric(y)==1)
  n1 = sum( y)
  n0 = sum(!y)
  XX = t(X)%*%X
  Si = solve(Sigma_beta)
  Sib = Si%*%beta0

  # Saving structures
  beta_keep       = matrix(NA, n_iter, p)
  Z_keep          = matrix(NA, n_iter, n)

  # Initial values
  m = glm(y~X-1, family=binomial(probit))
  beta = coef(m)
  Z = rep(NA,n)

  for (i in 1:n_iter) {
    # Sample Z
    Xb = X%*%beta
    cut = pnorm(0,Xb)
    Z[ y] = qnorm(runif(n1, cut[ y], 1), Xb[ y], 1)
    Z[!y] = qnorm(runif(n0, 0, cut[!y]), Xb[!y], 1)

    # Sample beta
    S_hat = solve(Si+XX)
    b_hat = S_hat %*% (Sib+t(X)%*%Z)
    beta = mvrnorm(1, b_hat, S_hat)

    # Record values
    beta_keep[i,] = beta
    Z_keep[i,] = Z
```

Run the MCMC

```
X = model.matrix(m) # Constructs the design matrix
p = ncol(X)
n_iter = 10000
system.time(out <- mcmc(n_iter, birthwt$low, X, rep(0,p), 3*diag(p)))
```

```
   user  system elapsed
  2.957   0.009   2.969
```


(Intercept)
age
lwt
race2
race3
smoke
ptl
ht
ui
ftv
value
iteration


(Intercept)
age
lwt
race2
race3
smoke
ptl
ht
ui
ftv
ACF
0.0
0.8
0
20
40
Lag

Credible intervals

```
Source: local data frame [10 x 4]

      variable   ess    lb    ub
        (fctr) (dbl) (dbl) (dbl)
1  (Intercept)  2958 -1.75 -0.81
2          age  2773 -0.33  0.12
3          lwt  2516 -0.52 -0.05
4        race2  4766  0.11  1.32
5        race3  3389 -0.01  0.98
6        smoke  3069  0.09  1.01
7          ptl  5416 -0.07  0.72
8           ht  3692  0.26  1.87
9           ui  4269 -0.08  0.98
10         ftv  2910 -0.18  0.22
```

Probit regression with random effects

Consider the probit regression model

$$\begin{aligned} Y_i &= \mathrm{I}(Z_i > 0) \\ Z &\sim N(\tilde{X}\tilde{\beta}, 1) \end{aligned}$$

where

$$\tilde{X} = [X \quad Zm] \qquad \tilde{\beta} = (\beta, \alpha)^\top$$

where X is the design matrix for fixed effects and Zm is the design matrix for the random effects. A common assumption is that the random effects are $u \sim N(0, \sigma^2 \mathrm{I})$. Thus the distribution on $\tilde{\beta}$ is

$$\tilde{\beta} = \begin{pmatrix} \beta \\ \alpha \end{pmatrix} \sim N\left(\begin{bmatrix} b \\ 0 \end{bmatrix}, \begin{bmatrix} B & 0 \\ 0 & \sigma^2 \mathrm{I} \end{bmatrix} \right)$$

where the precision is

$$\begin{bmatrix} B & 0 \\ 0 & \sigma^2 \mathrm{I} \end{bmatrix}^{-1} = \begin{bmatrix} B^{-1} & 0 \\ 0 & \frac{1}{\sigma^2} \mathrm{I} \end{bmatrix}$$

Full posterior

The full posterior is

$$p(Z, \beta, \alpha, \sigma^2 | y) \propto p(y|Z)p(Z|\tilde{\beta})p(\tilde{\beta}|\sigma^2)p(\sigma^2)$$

We have already derived the full conditionals

- $p(\tilde{\beta}|\ldots)$
- $p(Z|\ldots)$

but we need the full conditional for σ^2 to implement a Gibbs sampler.

Full conditional for σ^2

If we choose $\sigma \sim Unif(0, 10)$ and there are U random effects, then

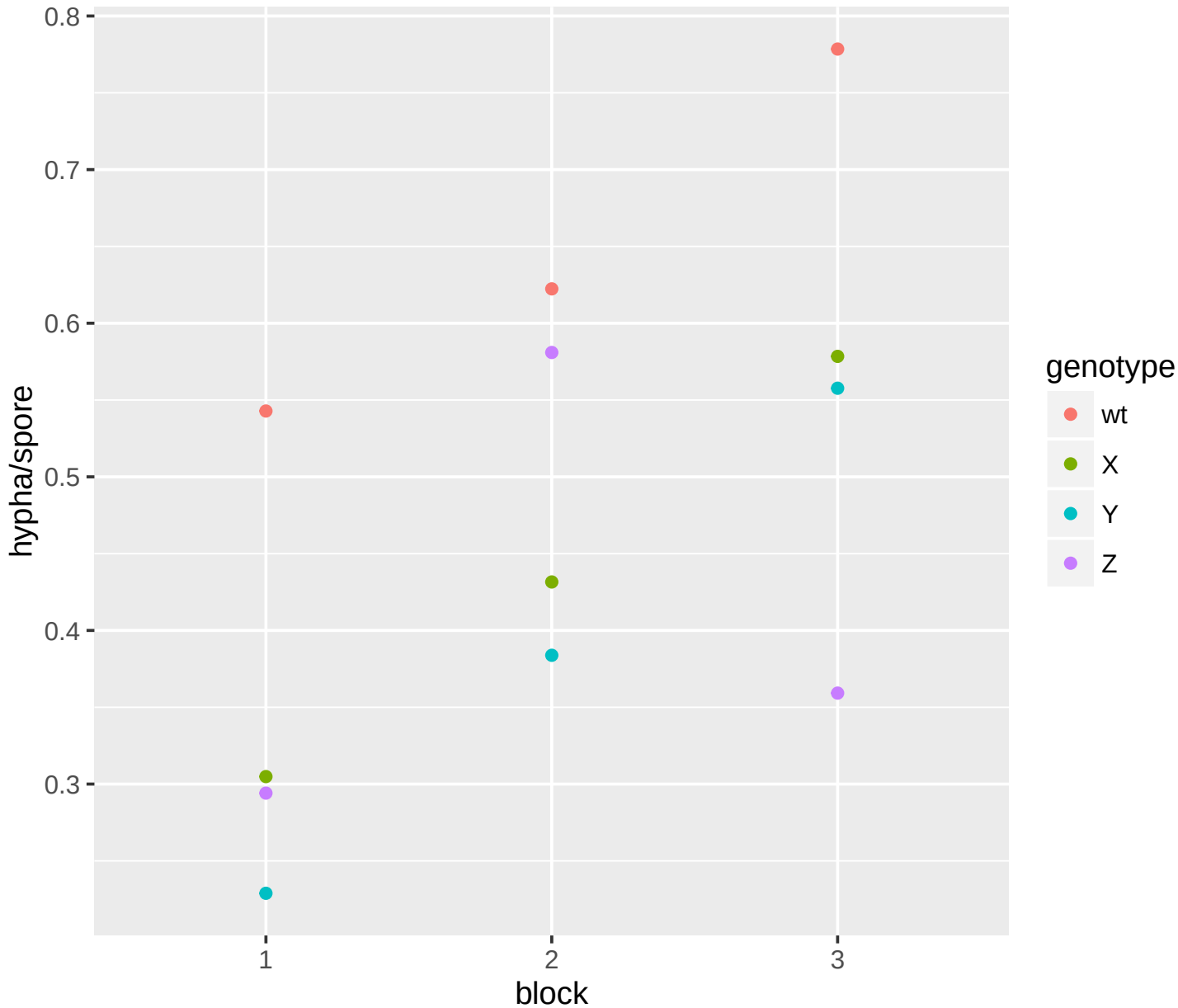
$$\begin{aligned}
p(\sigma^2|\ldots) &\propto p(y|Z)p(Z|\tilde{\beta})p(\tilde{\beta}|\sigma^2)p(\sigma^2) \\
&= p(\tilde{\beta}|\sigma^2)p(\sigma^2) \\
&\propto p(\alpha|\sigma^2)p(\sigma^2) \\
&\propto \prod_{i=1}^{U} N(\alpha_i|0, \sigma^2)\frac{1}{\sigma}\mathrm{I}(0 < \sigma^2 < 100) \\
&\propto (\sigma^2)^{-U/2} e^{-\frac{1}{2\sigma^2}\alpha'\alpha}(\sigma^2)^{-1/2}\mathrm{I}(0 < \sigma^2 < 100) \\
&= (\sigma^2)^{-\frac{U-1}{2}-1} e^{-\frac{\alpha'\alpha}{2\sigma^2}}\mathrm{I}(0 < \sigma^2 < 100)
\end{aligned}$$

Thus $\sigma^2 \sim IG([U-1]/2, \alpha'\alpha/2)$ truncated to be smaller than 100. This can be drawn using the modified inverse cdf method.

Genotypic resistance to corn fungus

	X	genotype	block	spore	hypha	prop	pot
1	1	X	1	82	25	0.3048780	X1
6	6	X	2	95	41	0.4315789	X2
11	11	X	3	102	59	0.5784314	X3
16	16	Y	1	83	19	0.2289157	Y1
21	21	Y	2	99	38	0.3838384	Y2
26	26	Y	3	104	58	0.5576923	Y3
31	31	Z	1	102	30	0.2941176	Z1
36	36	Z	2	105	61	0.5809524	Z2
41	41	Z	3	103	37	0.3592233	Z3
46	46	wt	1	140	76	0.5428571	wt1
51	51	wt	2	143	89	0.6223776	wt2
56	56	wt	3	158	123	0.7784810	wt3

Corn fungus data set

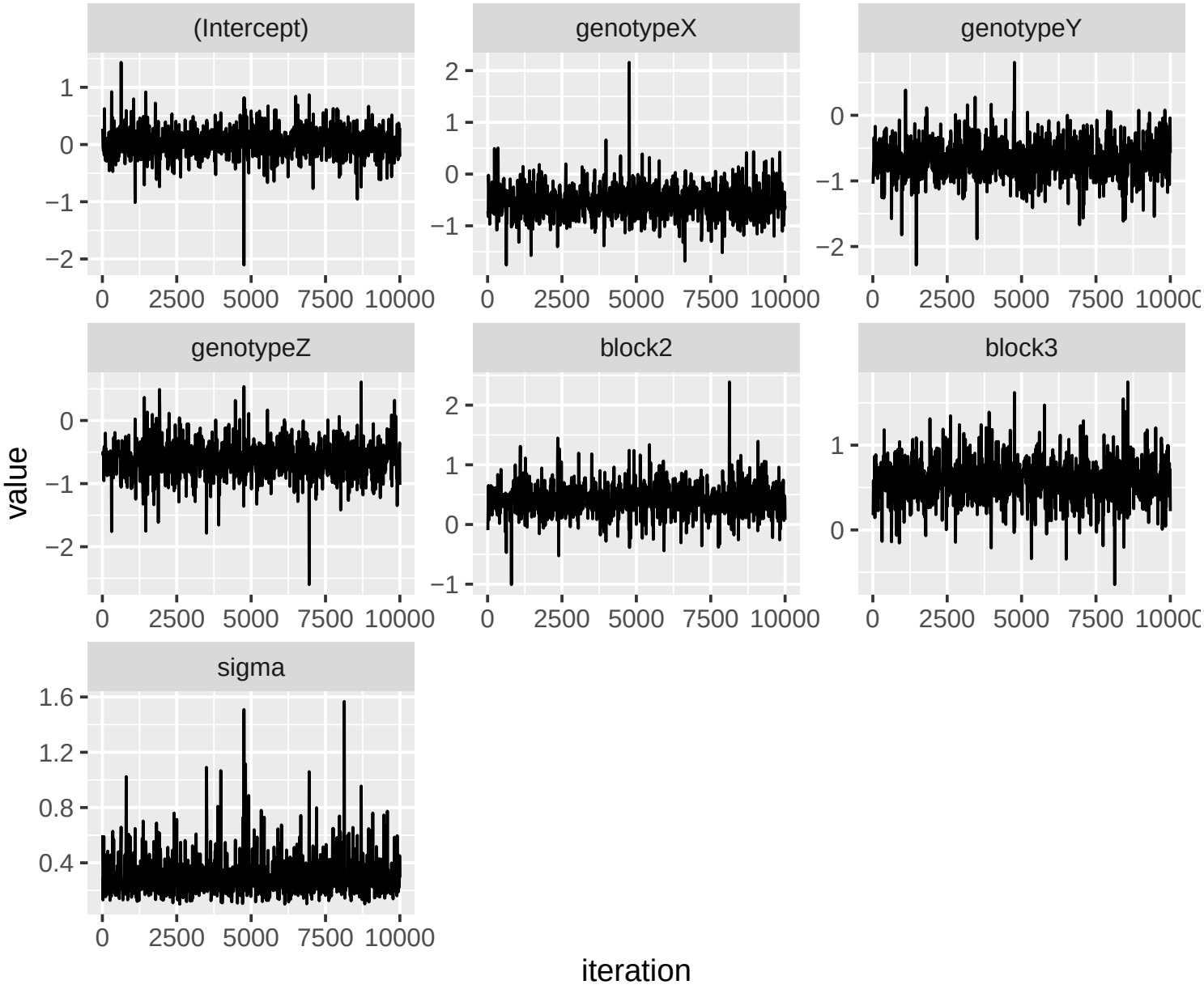


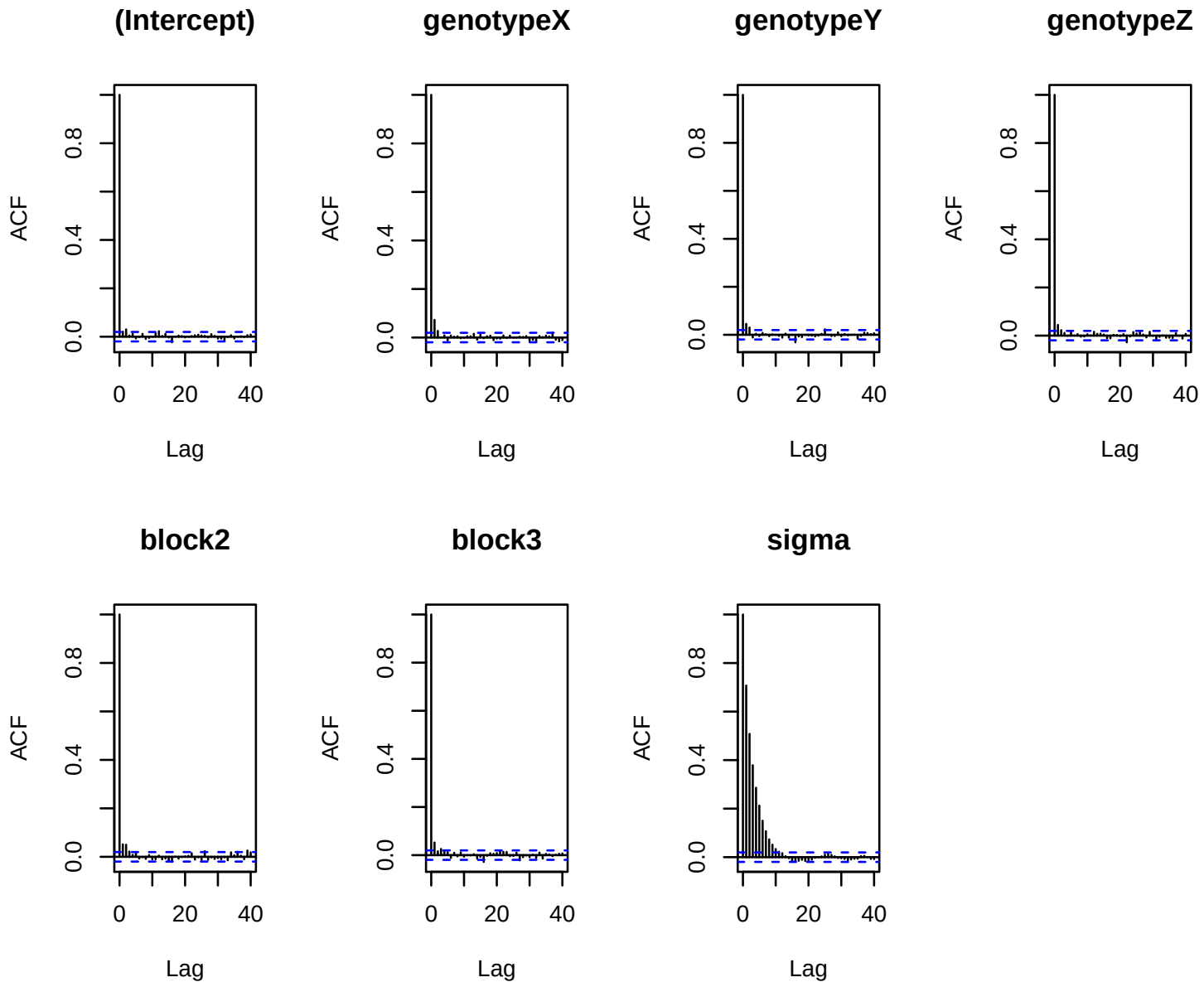
```
Generalized linear mixed model fit by maximum likelihood (Laplace Approximation) ['glmerMod']
 Family: binomial  ( probit )
Formula: cbind(hypha, spore - hypha) ~ block + genotype + (1 | pot)
   Data: d
Control: glmerControl(optimizer = "bobyqa")

     AIC      BIC   logLik deviance df.resid
    95.3     98.7    -40.6     81.3        5

Scaled residuals:
     Min       1Q   Median       3Q      Max
-1.45760 -0.35765  0.05486  0.36506  1.32376

Random effects:
 Groups Name        Variance Std.Dev.
 pot    (Intercept) 0.01773  0.1331
Number of obs: 12, groups:  pot, 12

Fixed effects:
            Estimate Std. Error z value Pr(>|z|)
(Intercept)  0.05126    0.12429   0.412 0.680040
block2       0.42497    0.13027   3.262 0.001106 **
block3       0.60818    0.13006   4.676 2.92e-06 ***
genotypeX   -0.55654    0.14700  -3.786 0.000153 ***
genotypeY   -0.68630    0.14725  -4.661 3.15e-06 ***
genotypeZ   -0.62691    0.14500  -4.324 1.53e-05 ***
---
Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1

Correlation of Fixed Effects:
          (Intr) block2 block3 gntypX gntypY
block2    -0.530
block3    -0.526  0.522
genotypeX -0.520 -0.019 -0.027
genotypeY -0.514 -0.027 -0.035  0.454
genotypeZ -0.535 -0.012 -0.012  0.460  0.459
```

```
mcmc = function(n_iter, y, X, Zm, beta0, Sigma_beta) {
  require(Matrix)
  n = nrow(X)
  p = ncol(X)
  q = ncol(Z)

  # Initial values
  m = glm(y~0+X, family=binomial(probit))
  beta = c(coef(m),rnorm(q))
  Z = rep(NA,n)

  # Precalculate quantities
  y = (as.numeric(y)==1)
  n1 = sum( y)
  n0 = sum(!y)
  X  = cbind(X,Zm)
  XX = t(X)%*%X
  Si = solve(Sigma_beta)
  Sib = Si%*%beta0
  a = (q-1)/2

  # Saving structures
  beta_keep  = matrix(NA, n_iter, p)
  alpha_keep = matrix(NA, n_iter, q)
  sigma_keep = rep(NA, n_iter)

  for (i in 1:n_iter) {
    # Sample Z
    Xb = X%*%beta
    cut = pnorm(0,as.numeric(Xb))
    Z[ y] = qnorm(runif(n1, cut[ y], 1), Xb[ y], 1)
    Z[!y] = qnorm(runif(n0, 0, cut[!y]), Xb[!y], 1)

    # Sample sigma
    alpha = beta[p+1:q]
    b = sum(alpha^2)/2
```

```
# Turn into binary data
dd = ddply(d, .(genotype,block,pot), function(x) {
  data.frame(y=c(rep(1,x$hypha),rep(0,x$spore-x$hypha)))
})

m = glmer(y~genotype+block+(1|pot), family=binomial(probit), dd)

X = model.matrix(m)
Z = as.matrix(getME(m,"Z"))
p = ncol(X)
n_iter = 10000
system.time(out <- mcmc(n_iter, dd$y, X, Z, rep(0,p), 10*diag(p)))
```

```
   user  system elapsed
 99.387   0.023  99.528
```


(Intercept)
genotypeX
genotypeY
genotypeZ
block2
block3
sigma
value
iteration
0
2500
5000
7500
10000


(Intercept)
genotypeX
genotypeY
genotypeZ
block2
block3
sigma
ACF
0.0
0.4
0.8
0
20
40
Lag

Credible intervals

```
Source: local data frame [7 x 4]

     variable   ess    lb    ub
       (fctr) (dbl) (dbl) (dbl)
1 (Intercept)  8747 -0.45  0.55
2   genotypeX  9417 -1.12  0.05
3   genotypeY 10051 -1.25 -0.09
4   genotypeZ  9572 -1.17 -0.03
5      block2  9012 -0.09  0.93
6      block3  8831  0.08  1.09
7       sigma  1688  0.13  0.68
```

Contrasts to compare other genotypes

```
t(with(betas, data.frame("X-Y" = quantile(genotypeX-genotypeY, c(.025,.975)),
                         "Y-Z" = quantile(genotypeY-genotypeZ, c(.025,.975)),
                         "X-Z" = quantile(genotypeX-genotypeZ, c(.025,.975)), check.names=FALSE)))
```

```
          2.5%     97.5%
X-Y -0.4448574 0.7118965
Y-Z -0.6486938 0.5173782
X-Z -0.5104321 0.6529829
```

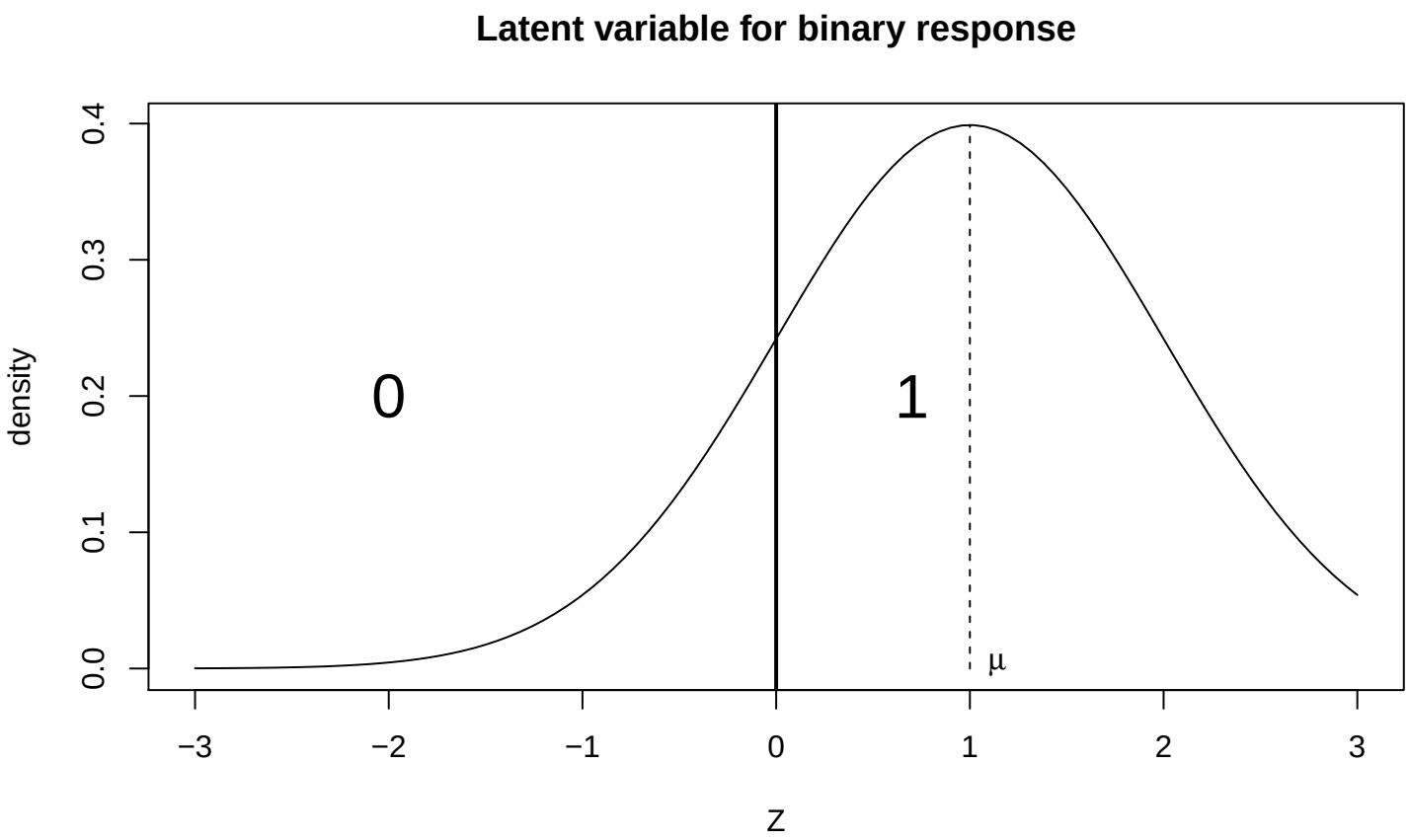
t priors

Suppose we want $\beta_j \overset{ind}{\sim} t_{v_j}(b_j, B_j)$. We can write this prior hierarchically via

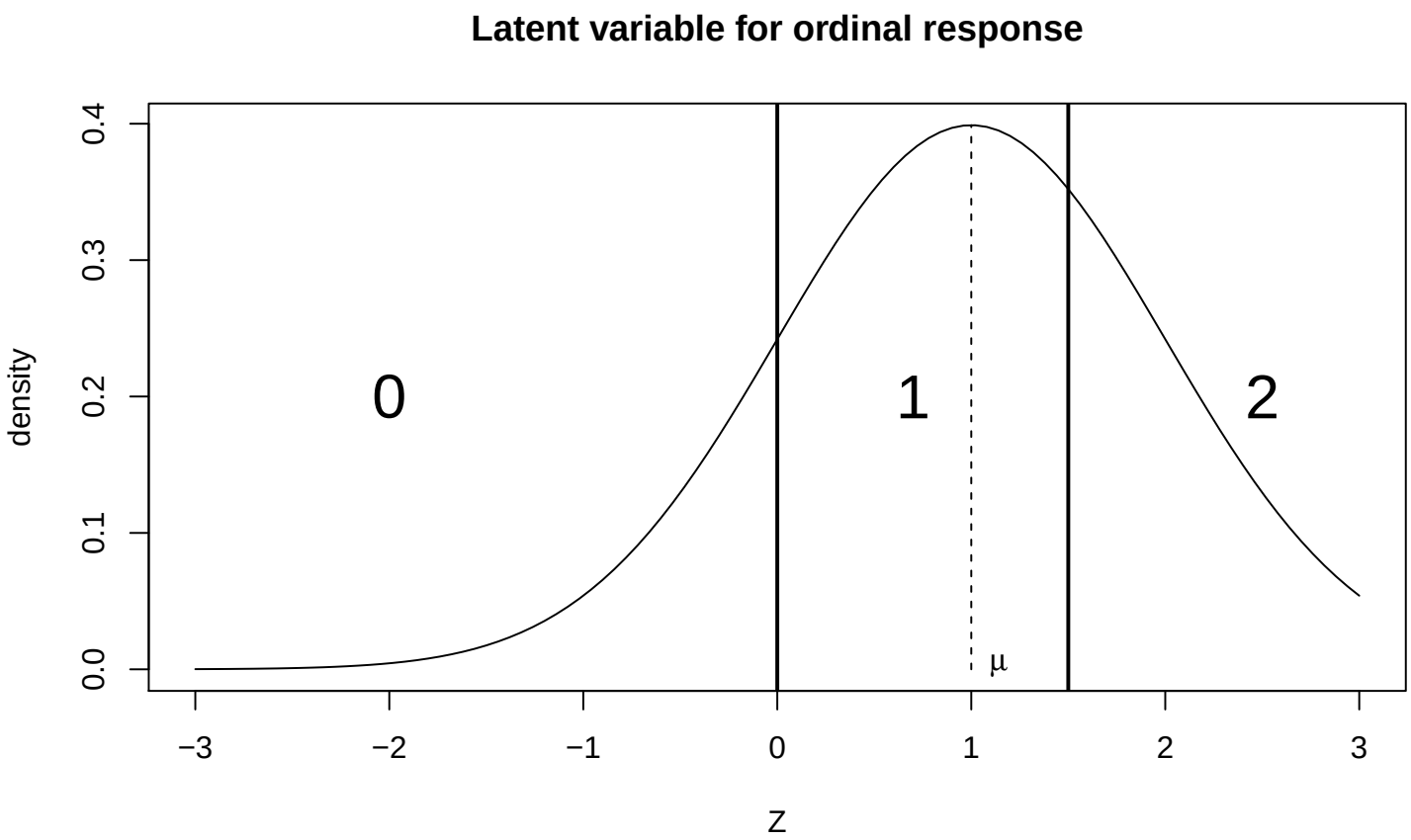
$$\beta_j|\tau_j^2 \overset{ind}{\sim} N(b_j, \tau_j^2), \qquad \tau_j^2 \sim \text{Inv}(v_j, B_j).$$

Now the MCMC can proceed exactly as before, but with the additional full conditional for $(\tau_1^2, \ldots, \tau_J^2)$ which will be independent inverse χ^2 distributions.

Binary response



Ordinal response with 3 categories



Unordered categorical response

Suppose Y_i is random variable with support $1, \ldots, K$ and

$$Pr(Y_i = k) = \theta_{ik}$$

where θ_{ik} may depend on explanatory variables for both i and k. For example, an individual is shopping for fruit then perhaps the age of the individual and the price of the fruits will affect the shopper's choice.

We can model this using data augmentation by introducing a latent utility Z_{ik} for each shopper-fruit combination. Then the response is

$$Y_i = \text{argmax}_k Z_{ik}$$

and there is great flexibility in how the Z_{ik} are modeled.

Bayesian logistic regression

$$
\begin{aligned}
Y_i &= \mathrm{I}(Z_i > 0) \\
Z_i &\overset{ind}{\sim} Logistic(X_i'\beta, 1)
\end{aligned}
$$

```
Warning: data was combined!
N: 183, P: 10
Burn-in complete: 0.06 sec. for 500 iterations.
Expect approx. 0.12 sec. for 1000 samples.
Sampling complete: 0.13 sec. for 1000 iterations.
            X1    lb    ub
1  (Intercept) -3.26 -1.43
2          age -0.57  0.24
3          lwt -0.98 -0.14
4        race2  0.27  2.42
5        race3  0.05  1.82
6        smoke  0.24  1.84
7          ptl -0.13  1.25
8           ht  0.68  3.46
9           ui -0.19  1.75
10         ftv -0.32  0.41
```