Mixed effect probit regression

Genotypic fungal resistance

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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 *i*th 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 *i*th 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

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

Note that

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

Thus, this is equivalent to the probit regression model.

Posterior distribution

Now, the likelihood is

$$p(y|\zeta) \propto \prod_{i=1}^{n} \left[\mathrm{I}(\zeta_i > 0)\mathrm{I}(y_i = 1) + \mathrm{I}(\zeta_i \le 0)\mathrm{I}(y_i = 0)\right]$$

and

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

Therefore the *complete data likelihood* is

$$p(y, \zeta|\beta) \propto \prod_{i=1}^{n} N(\zeta_i|X_i'\beta, 1) \left[\mathrm{I}(\zeta_i > 0)\mathrm{I}(y_i = 1) + \mathrm{I}(\zeta_i \le 0)\mathrm{I}(y_i = 0)\right]$$

Thus the posterior distribution is

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

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

Full conditional for β

The full conditional for β is

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

and thus $\beta|\ldots \sim N(\hat\beta,\hat\Sigma_\beta)$ with

$$\begin{array}{rl} \hat\Sigma_\beta & = [B^{-1}+X^\top X]^{-1} \\ \hat\beta & = \hat\Sigma_\beta[B^{-1}b+X^\top\zeta] \end{array}$$

Full conditional for ζ

The full conditional for ζ is

$$\begin{array}{rcl} p(\zeta|\ldots) & \propto & p(y|\zeta)p(\zeta|\beta)p(\beta) \\ & \propto & p(y|\zeta)p(\zeta|\beta) \\ & = & \prod_{i=1}^n N(\zeta_i|X_i'\beta,1)\left[\mathrm{I}(\zeta_i>0)\mathrm{I}(y_i=1)+\mathrm{I}(\zeta_i\le 0)\mathrm{I}(y_i=0)\right] \end{array}$$

Thus the ζ_i are conditionally independent with distribution

$$p(\zeta_i|y_i,\beta) = \left\{ \begin{array}{ll} N(\zeta_i|X_i'\beta,1)\mathrm{I}(\zeta_i>0) & \text{if } y_i=1 \\ N(\zeta_i|X_i'\beta,1)\mathrm{I}(\zeta_i\le 0) & \text{if } y_i=0 \end{array}\right.$$

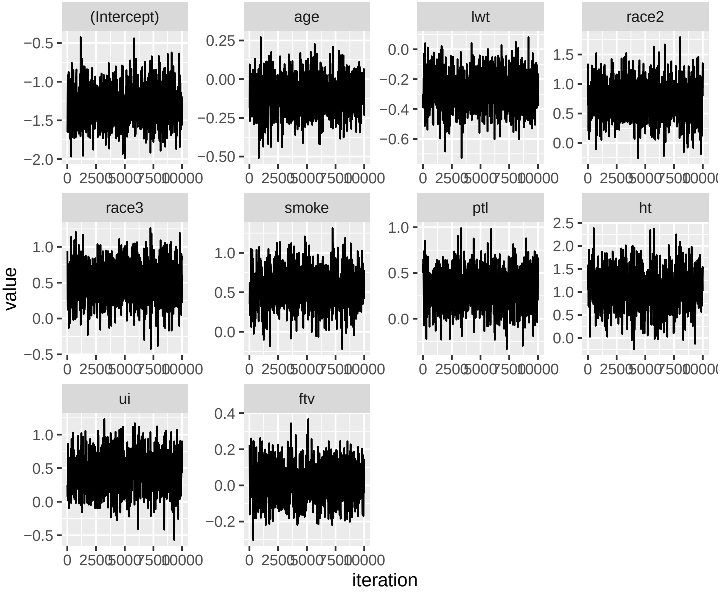
These can be drawn using the modified inverse cdf method.

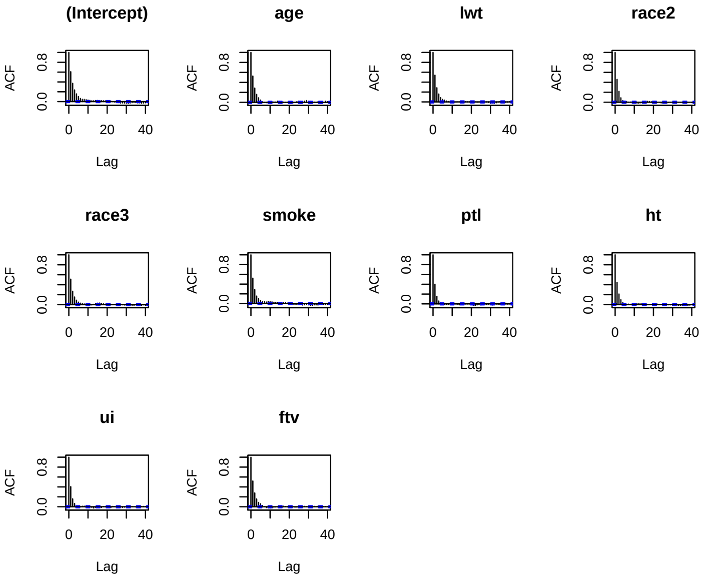
```
mcmc = function(n_iter, y, X, beta0, Sigma_beta) {
  n = nrow(X)
  p = ncol(X)

  # 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)
  zeta_keep          = matrix(NA, n_iter, n)

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

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

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

    # Record values
    beta_keep[i,] = beta
    zeta_keep[i,]    = zeta
```

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 
  2.763   0.009   2.775 
```


(Intercept)
age
lwt
race2
race3
smoke
ptl
ht
ui
ftv
value
iteration
−0.5
−1.0
−1.5
−2.0
0.25
0.00
−0.25
−0.50
0.0
−0.2
−0.4
−0.6
1.5
1.0
0.5
0.0
−0.5
2.5
2.0
0.4
0.2
−0.2
0
2500
5000
7500
10000


(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

$$\begin{array}{rl} Y_i & = \mathrm{I}(\zeta_i > 0) \\ \zeta & \sim N(\tilde{X}\tilde{\beta}, 1) \end{array}$$

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 $\alpha \sim N(0, \sigma^2\mathrm{I})$. Thus the distribution on $\tilde{\beta}$ is

$$\tilde{\beta} = \left(\begin{array}{c} \beta \\ \alpha \end{array} \right) \sim N\left(\left[\begin{array}{c} b \\ 0 \end{array} \right], \left[\begin{array}{cc} B & 0 \\ 0 & \sigma^2\mathrm{I} \end{array} \right] \right)$$

where the precision is

$$\left[\begin{array}{cc} B & 0 \\ 0 & \sigma^2\mathrm{I} \end{array} \right]^{-1} = \left[\begin{array}{cc} B^{-1} & 0 \\ 0 & \frac{1}{\sigma^2}\mathrm{I} \end{array} \right]$$

Full posterior

The full posterior is

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

We have already derived the full conditionals

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

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

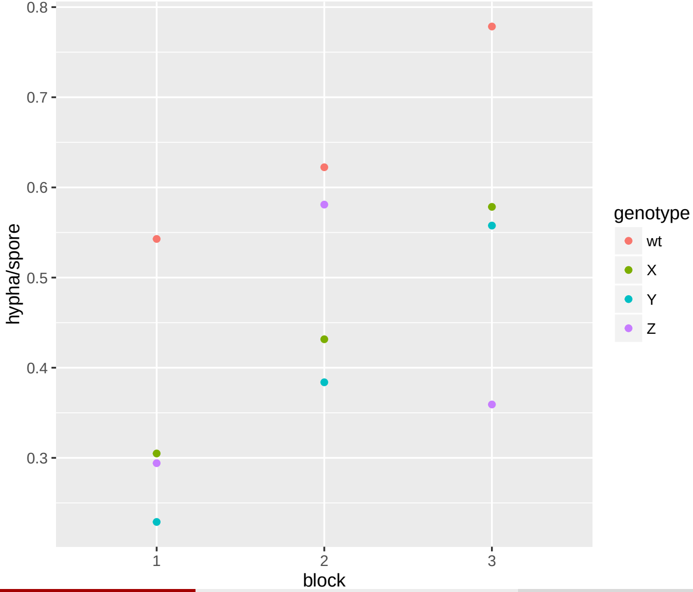
$$\begin{array}{rl} p(\sigma^2|\ldots) & \propto p(y|\zeta)p(\zeta|\tilde\beta)p(\tilde\beta|\sigma^2)p(\sigma^2) \\ & = p(\tilde\beta|\sigma^2)p(\sigma^2) \\ & \propto p(\alpha|\sigma^2)p(\sigma^2) \\ & \propto \prod_{i=1}^U N(\alpha_i|0,\sigma^2)\frac{1}{\sigma}\mathrm{I}(0<\sigma^2<100) \\ & \propto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

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

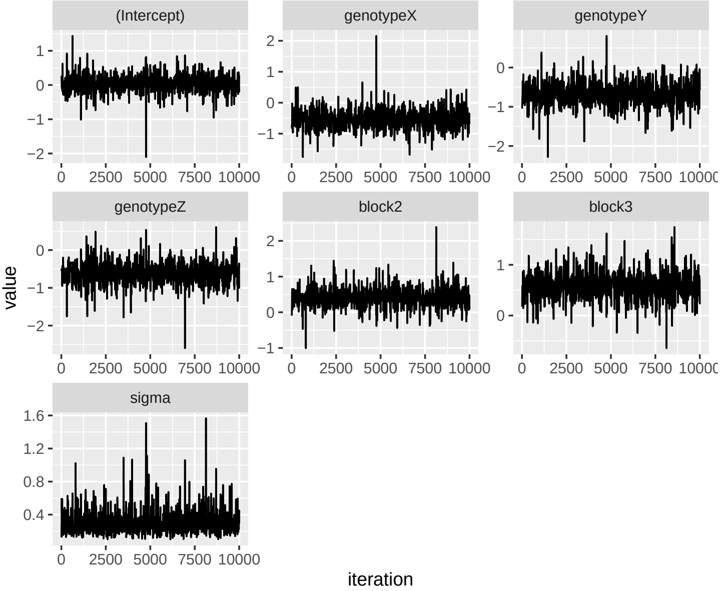


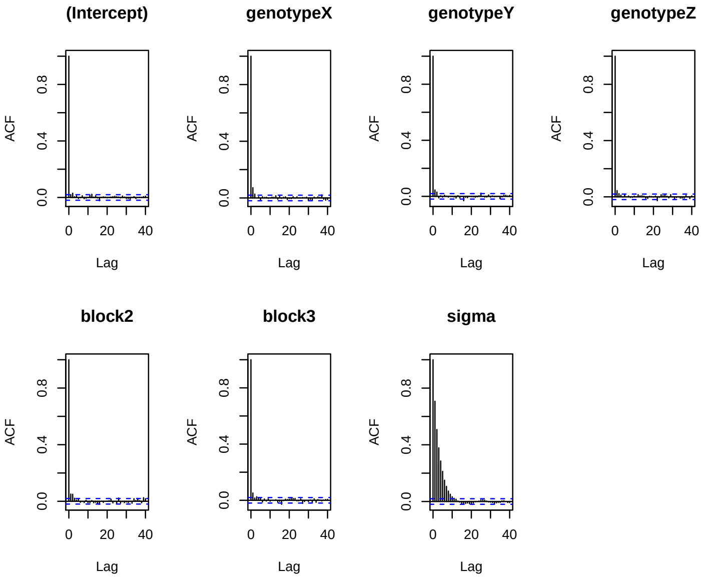
```
Generalized linear mixed model fit by maximum likelihood (Laplace Approximation) ['glmerMod']
 Family: binomial  ( probit )
Formula: cbind(hypha, spore - hypha) ~ block + genotype + (1 | pot)
   Data: d
Control: glmerControl(optimizer = "bobyqa")

     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
```

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

  # Initial values
  m = glm(y~0+X, family=binomial(probit))
  beta = c(coef(m),rnorm(q))
  zeta = 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 zeta
    Xb = X%*%beta
    cut = pnorm(0,as.numeric(Xb))
    zeta[ y] = qnorm(runif(n1, cut[ y], 1), Xb[ y], 1)
    zeta[!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 
 95.382   0.011  95.514 
```


(Intercept)
genotypeX
genotypeY
genotypeZ
block2
block3
sigma
value
iteration
0
2500
5000
7500
10000
1
0
−1
−2
2
1.6
1.2
0.8
0.4


(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
```

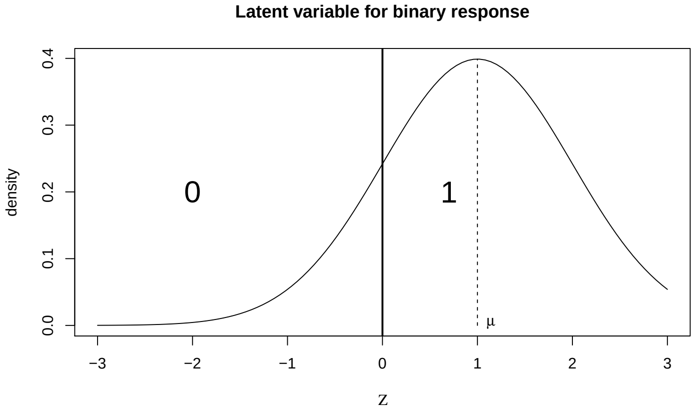
t priors

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

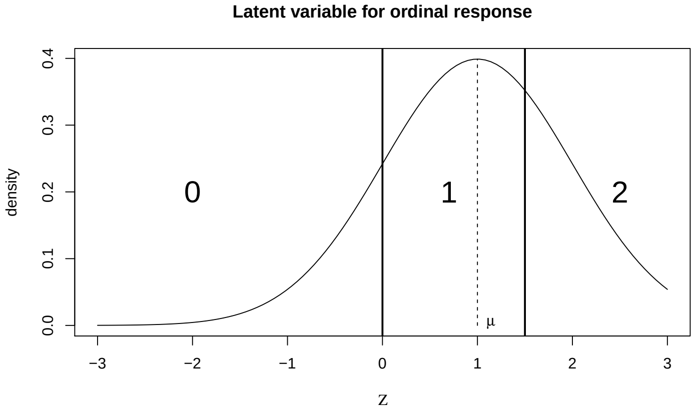
$$\beta_j|\tau_j^2 \overset{ind}{\sim} N(b_j, \tau_j^2), \qquad \tau_j^2 \sim \text{Inv} - \chi^2(v_j, B_j).$$

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 ζ_{ik} for each shopper-fruit combination. Then the response is

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

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

Bayesian logistic regression

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

```
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
```