Explanation of notation used in manuscript (Heredity 108: 134-146) and WinBUGS code

$\beta_{0,i}$=beta[i,1]

$\beta_{1,i}$=beta[i,2]

$\beta_{2,i}$=beta[i,3]

μ_0=intercept1

μ_1=intercept2

μ_2=intercept3

$\sum_{j=1}^{p} I_{j(0)} B_{j(0)} x_{i,j}$=gbv1

$\sum_{j=1}^{p} I_{j(1)} B_{j(1)} x_{i,j}$=gbv2

$\sum_{j=1}^{p} I_{j(2)} B_{j(2)} x_{i,j}$=gbv3

$I_{j(0)} B_{j(0)}$=alpha1[k]

$I_{j(1)} B_{j(1)}$=alpha2[k]

$I_{j(2)} B_{j(2)}$=alpha3[k]

$I_{j(0)}$=x1[k]

$I_{j(1)}$=x2[k]

$I_{j(2)}$ =x3[k]

$B_{j(0)}$=a1[k]

$B_{j(1)}$=a2[k]

$B_{j(2)}$=a3[k]

$x_{i,j}$=z[i,j]

$\sigma^2_{\epsilon_{i(0)}}$=sigma[1]

$\sigma^2_{\epsilon_{i(1)}}$=sigma[2]

$\sigma^2_{\epsilon_{i(2)}}$=sigma[3]

ρ_{10}=roo21

ρ_{20}=roo31

ρ_{21}=roo32

N_{y0} =NQTL1

N_{y1}=NQTL2

N_{y2} =NQTL3

σ_{g10}=gcov12

σ_{g20}=gcov13

σ_{g21}=gcov23

r_{10}=gcor12

r_{20}=gcor13

r_{21}=gcor23

h_{y0}^2 =her[1]

h_{y1}^2 =her[2]

h_{y2}^2 =her[3]

$\rho_{10} \times \hat{\sigma}_{y0}$=rcov12

$\rho_{21} \times \hat{\sigma}_{y1}$=rcov23

$\rho_{20} \times \hat{\sigma}_{y0}$=rcov13

Simulated data

Phenotypic residual variance 0.1

no block effect

Marker inits in mark inits.txt file

to monitor:

- alpha1[k], alpha2[k], alpha3[k]
- x1[k], x2[k], x3[k]
- NQTL1, NQTL2, NQTL3
- her[1], her[2], her[3]
- gcov12, 13, 23
- gcor12, 13, 23
- sigma
- intercept1, intercept2, intercept3
- rcov12, rcov13, rcov23

```
model
{

for(j in 1 : loc) {
  for(k in 1 : 2 ){
    p[ j, k ] <- 1/2
  }
}

for(i in 1 : ind) {
  for(j in 1 : loc ) {
    mark[i, j ]  ~ dcat( p[ j, 1:2] )
  }
}

for(i in 1 : ind) {
  for(j in 1 : loc ) {
    Z[i, j ] <- mark[i,j] - 1
  }
```

```
}



for (i in 1:ind) {
                                        for(j in 2:years) {
                                                                Y[i, j] ~ dnorm(mu[i,j], 10)
                                                                mu[i, j] <- beta[i, 1] + beta[i, 2] * age[j] + beta[i,3 ] * pow(age[j],2) + beta[i,4]* Y[i,j-1]
                                        }
                        gbv1[i]<- inprod(alpha1[], Z[i,])
                        gbv2[i]<- inprod(alpha2[], Z[i,])
                        gbv3[i]<- inprod(alpha3[], Z[i,])
                                        my[i,1]<-intercept1 + gbv1[i]
                                        my[i,2]<-intercept2 + gbv2[i]+roo21*beta[i,1]
                                        my[i,3]<-intercept3 + gbv3[i]+roo31*beta[i,1]+roo32*beta[i,2]
                                        my[i,4]<-0
                                        for(j in 1:3){
                                                                beta[i,j]~dnorm(my[i,j], tau[j])
                                        }
                                        beta[i,4]<-0
                }



intercept1~dnorm(0,0.001)
intercept2~dnorm(0,0.001)
intercept3~dnorm(0,0.001)

roo21~dnorm(0,0.001)
roo31~dnorm(0,0.001)
roo32~dnorm(0,0.001)

tau[1] ~dgamma(1.0E-3,1.0E-3)
sigma[1] <- 1/tau[1]
tau[2] ~dgamma(1.0E-3,1.0E-3)
sigma[2] <- 1/tau[2]
tau[3] ~dgamma(1.0E-3,1.0E-3)
```

```
sigma[3] <- 1/tau[3]
#tau[4] ~dgamma(1.0E-3,1.0E-3)
#sigma[4] <- 1/tau[4]

for(j in 1:loc){
  a1[j]~dnorm(0,prec1[j])
  lntau1[j] ~ dunif(-5,50)
  prec1[j]<-exp(lntau1[j])
  var1[j]<-1/prec1[j]
}

for(j in 1:loc){
  a2[j]~dnorm(0,prec2[j])
  lntau2[j] ~ dunif(-5,50)
  prec2[j]<-exp(lntau2[j])
  var2[j]<-1/prec2[j]
}

for(j in 1:loc){
  a3[j]~dnorm(0,prec3[j])
  lntau3[j] ~ dunif(-5,50)
  prec3[j]<-exp(lntau3[j])
  var3[j]<-1/prec3[j]
}


#lntautot~ dunif(-2,50)
#prectot<-exp(lntautot)
#sigma2tot<-1/prectot

#for(j in 1:years) {
#    tautot[j]~dgamma(1.0E-2,1.0E-2)
#    sigma2tot[j]<-1/tautot[j]
#   tau.block[j]~dgamma(1.0E-3,1.0E-3)
#   sigma2.block[j]<-1/tau.block[j]
```

```
# }


for(k in 1:loc) {
                        p1[k]<-1/loc
                        x1[k]~dbern(p1[k])
                        alpha1[k]<-x1[k]*a1[k]
                        varalpha1[k]<-x1[k]*var1[k]
                        }
for(k in 1:loc) {
                        p2[k]<-1/loc
                        x2[k]~dbern(p2[k])
                        alpha2[k]<-x2[k]*a2[k]
                        varalpha2[k]<-x2[k]*var2[k]
                        }
for(k in 1:loc) {
                        p3[k]<-1/loc
                        x3[k]~dbern(p3[k])
                        alpha3[k]<-x3[k]*a3[k]
                        varalpha3[k]<-x3[k]*var3[k]
                        }
NQTL1<-sum(x1[1:loc])
NQTL2<-sum(x2[1:loc])
NQTL3<-sum(x3[1:loc])

varb[1]<-sd(beta[1:ind,1])*sd(beta[1:ind,1])
varb[2]<-sd(beta[1:ind,2])*sd(beta[1:ind,2])
varb[3]<-sd(beta[1:ind,3])*sd(beta[1:ind,3])

vareff[1]<-sd(gbv1[1:ind])*sd(gbv1[1:ind])
vareff[2]<-sd(gbv2[1:ind])*sd(gbv2[1:ind])
vareff[3]<-sd(gbv3[1:ind])*sd(gbv3[1:ind])

her[1] <- (varb[1]-sigma[1])/varb[1]
her[2] <- (varb[2]-sigma[2])/varb[2]
her[3] <- (varb[3]-sigma[3])/varb[3]
```

```
for(i in 1:ind) {
                        prod12[i]<-beta[i,1]*beta[i,2]
                        prod13[i]<-beta[i,1]*beta[i,3]
                        prod23[i]<-beta[i,2]*beta[i,3]
                        }
cov12<-(sum(prod12[1:ind])-sum(beta[1:ind,1])*sum(beta[1:ind,2])/ind)/(ind-1)
cov13<-(sum(prod13[1:ind])-sum(beta[1:ind,1])*sum(beta[1:ind,3])/ind)/(ind-1)
cov23<-(sum(prod23[1:ind])-sum(beta[1:ind,2])*sum(beta[1:ind,3])/ind)/(ind-1)

gcor12<-gcov12/(sd(beta[1:ind,1])*sd(beta[1:ind,2]))
gcor13<-gcov13/(sd(beta[1:ind,1])*sd(beta[1:ind,3]))
gcor23<-gcov23/(sd(beta[1:ind,2])*sd(beta[1:ind,3]))

gcov12 <- cov12-rcov12
gcov13 <- cov13-rcov13
gcov23 <- cov23-rcov23

rcov12<-roo21*sd(beta[1:ind,1])
rcov13<-roo31*sd(beta[1:ind,1])
rcov23<-roo32*sd(beta[1:ind,2])
}
```