```
########################################################
#       Genetics Research
#
#       Genetic analysis of complex traits via Bayesian variable
#       selection: the utility of a mixture of uniform priors
#
#          Timo Knürr, Esa Läärä and Mikko Sillanpää
#
#       OpenBUGS script
########################################################


# Before use:
#     1. change the script by removing/adding comment signs (#)
#        before the appropriate lines, if a binary outcome is analyzed
#     2. remove the comment signs for one of the three methods IGAS, SSVS or MU
#     3. specify appropriate constants

model{

# data model:
for (i in 1:N){
     ########################
      #quantitative outcome: #
     ########################
     Y[i]~dnorm(mu[i], inv.sigma2)
      mu[i] <- alpha + X.beta[i]
     ########################
     # binary outcome:      #
     ########################
      # Z[i]~dbern(q[i])
     # logit(q[i])<- alpha + X.beta[i]

     for (m in 1:M){
      x.beta[i,m]<- X[i,m]*beta[m]
      }
      X.beta[i] <- sum(x.beta[i,1:M])
}

#prior for missing values:
for (i in 1:N){
     for (m in 1:M){
     X[i,m] ~ dbern(0.5)
     }
}

#prior for residual variance (only if quantitative outcome is analyzed):
inv.sigma ~ dgamma(s1,s2)

#prior for common intercept:
alpha ~dnorm (0, a)
```

```
#prior for effect size parameters:

########
# IGAS #
########
#for (m in 1:M){
#     beta[m]<- S[m]*theta[m]
#     theta[m] ~ dnorm(0,inv.tau2[m])
#     inv.tau2[m]~dgamma(u1,u2)
#     S[m]~dbern(p1)
#}

########
# SSVS #
########
#for (m in 1:M){
#     beta[m] ~ dnorm(0, inv.varbeta[S1[m]])
#     S[m]~dbern(p1)
#     S1[m]<-S[m]+1
#}

######
# MU #
######
#for (m in 1:M){
#     beta[m]~dunif(m.l,l)
#     dummy[m]<-0
#     dummy[m]~dgeneric(phi[m])
#    phi[m] <- log( help1*(step(beta[m]+l)-step(beta[m]-l)) +
(help2-help1)*(step(beta[m]+b)-step(beta[m]-b))  )
#}
#help1<-p1/(2*l-2*b)
#help2<-(1-p1)/(2*b)
#m.l<- -l


# constants to be specified for all models:
p1<- ...          # 1-p0, i.e. prior inclusion probability of a marker
a<-  ...               # variance of the common intercept alpha

# constants to be specified for quantitative outcome:
s1<- ...               # first parameter in the inverse-gamma prior of the residual
variance
s2<- ...               # second parameter

# constants for IGAS:
#u1<- ...             # first parameter in the inverse-gamma prior of
marker-specific tau2
#u2<- ...             # second parameter
# constants for SSVS:
#inv.varbeta[1]<- ...   # 1/t2 (inverse of spike-variance)
#inv.varbeta[2]<- ...   # 1/(c2t2)  (inverse of slab-variance)
# constants for MU:
#l<- ...              # limit for absolute effect size
#b<- ...              # border value of effect size
```

}