File S2: Implementation of the core model in OpenBUGS

This document describe how to sample from the posterior distributions of the parameters under the core model (Figure 1A) using the freely available OpenBUGS software(Thomas *et al.*, 2009). For the sake of simplicity, only the model for allele count data is presented (Figure 1A1). In addition, following the same notations as in the main text, it is assumed that, like in the BAYENV software (Coop *et al.*, 2010), $a_\pi = b_\pi = 1$ and $\rho = J$.

1 Code of the MCMC algorithm in the BUGS language

```
model
{
for(i in 1:I){
  for(j in 1:J){
   YY[i,j]~dbin(a_tr[i,j],NN[i,j])
   a_tr[i,j]<-min(1,max(0,alpha[i,j]))
     }
}
 for(i in 1:I){
  for(j in 1:J){
   pi_mat[i,j]<-p[i]
   for(k in 1:J){mat_mnv[i,j,k]<-Lambda[j,k]/(p[i]*(1-p[i]))}
         }
    alpha[i,1:J] ~ dmnorm(pi_mat[i,1:J],mat_mnv[i,1:J,1:J])
    }
  Lambda[1:J,1:J]~dwish(RR[1:J,1:J],J)
  for(i in 1:I){p[i]~dunif(0,1)}
  Omega[1:J,1:J] <- inverse(Lambda[1:J,1:J])
}
```

Warning: In the BUGS language, writing $\boldsymbol{X} \sim \mathrm{dwish}\left(R, \nu\right)$ for a matrix with rank K means $f\left(X\right) = |\boldsymbol{R}|^{\frac{\nu}{2}}|\boldsymbol{X}|^{\frac{\nu-K-1}{2}}\exp\left(-\frac{1}{2}\mathrm{tr}\left(\boldsymbol{R}\boldsymbol{X}\right)\right)$ (Ntzoufras, 2011, p91) i.e. $\boldsymbol{R}$ is the inverse-scale (or shape) matrix. Hence the definition of the RR matrix in the script above.

2 Preparing the data using R(R Core Team, 2015)

The following R script (that uses the function *writeDatafileR* by Terry Elrod: `http://www.public.iastate.edu/~alicia/stat544/writeDatafileR.txt`) allows preparing input files for OpenBUGS:

```
YY=as.matrix(read.table("YY"))
NN=as.matrix(read.table("NN"))
nsnp=nrow(YY) ; npop=ncol(YY)
RR=diag(npop,npop,npop)
zz=list(I=nsnp,J=npop,YY=YY,NN=NN,RR=RR)
writeDatafileR(zz,towhere="data.openbugs")
##init values
pi=rowSums(YY)/rowSums(NN)
invT=diag(10,npop,npop)
zz=list(p=pi,invT=invT)
writeDatafileR(zz,towhere="inits.openbugs")
```

where `YY` and `NN` are files containing count data for the reference allele and in total respectively (SNP by rows and population by column).

3 Running OPENBUGS in batch mode:

The model may be ran in batch mode under OPENBUGS using the following script (e.g., using the command `OpenBUGS script.txt >res.log`):

```
modelCheck('./coremodel.txt')
modelData('./data.openbugs')
modelCompile(1)
modelSetRN(1)
modelInits('./inits.openbugs',1)
modelGenInits()
modelUpdate(5000)
samplesSet(Lambda)
samplesSet(Omega)
samplesSet(p)
samplesSet(a_tr)
samplesSet(deviance)
summarySet(Lambda)
summarySet(Omega)
summarySet(p)
summarySet(a_tr)
summarySet(deviance)
dicSet()
modelUpdate(1000,25,1)
summaryStats('*')
dicStats()
modelQuit('y')
```

References

Coop, G., D. Witonsky, A. D. Rienzo, and J. K. Pritchard, 2010 Using environmental correlations to identify loci underlying local adaptation. Genetics 185: 1411–1423.

Ntzoufras, I., 2011 *Bayesian Modeling Using WinBUGS*. Wiley Series in Computational Statistics. Wiley.

R Core Team, 2015 *R: A Language and Environment for Statistical Computing*. R Foundation for Statistical Computing, Vienna, Austria.

Thomas, A., B. O'Hara, U. Ligges, and S. Sturtz, 2009 Making bugs open. R News 6: 12–17.