Simulation to compare DIC and WAIC

Chapter 5.5: Model selection criteria

In the simulation experiment below, we generate data from a known model and evaluate the performance of DIC and WAIC at finding the true data-generating model. The data are simulated to resemble the *gambia* data in the *geoR* package. The response Y_i is binary and generated from the random effects logistic regression model

$$\text{logit}[\text{Prob}(Y_i = 1)] = \beta_1 + X_i\beta_2 + \theta_{v_i},$$

where v_i is the village index of observation i and $\theta_v \sim \text{Normal}(0, \sigma^2)$ is the random effect for village v. Data are generated with $n = 100$ observations, ten villages each with ten observations, $\beta_1 = 0$, $\beta_2 = 1$ and $X_i \sim \text{Normal}(0, 1)$. We vary the random effect variance σ^2 to determine how large it must be before the model selection criteria consistently favor the random effects model. For each simulated data set we fit two models

1. No random effects: $\theta_v = 0$

2. Gaussian random effects: $\theta_v \sim \text{Normal}(0, \sigma^2)$

The priors are $\beta_1, \beta_2 \sim \text{Normal}(0, 100)$ and $\sigma^2 \sim \text{InvGamma}(0.1, 0.1)$. When data are generated with $\sigma = 0$ then model 1 is correct, and when $\sigma > 2$ model 2 is correct. For each model we record the DIC and WAIC for each dataset, and report the number of datasets for which each metric favors the correct model.

Define the simulation settings

```
n     <- 100
v     <- rep(1:10,10)
beta1 <- 0
beta2 <- 1
sigma <- c(0.0,0.25,0.5,0.75,1.0)
ns    <- length(sigma)
N     <- 100 # number of simulated datasets

DIC    <- array(0,c(N,2,ns))
dimnames(DIC)[[1]] <- paste("Dataset",1:N)
dimnames(DIC)[[2]] <- c("No RE","RE")
dimnames(DIC)[[3]] <- paste("Sigma =",sigma)

WAIC  <- DIC
```

Prep for JAGS

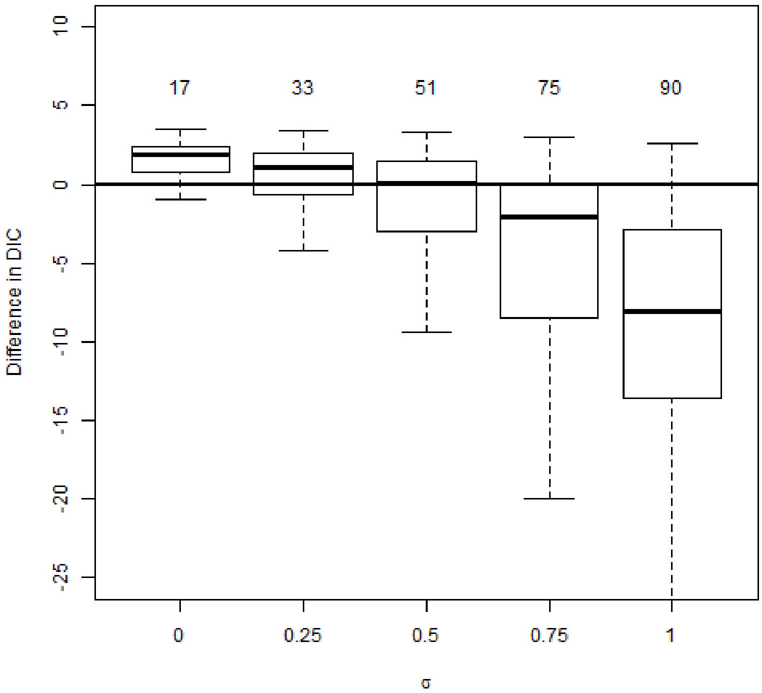
```
library(rjags)
burn   <- 1000
iters  <- 11000
chains <- 2

# Define the simple logistic regression model
mod1 <- "model{
  for(i in 1:n){
    Y[i]          ~ dbern(pi[i])
    logit(pi[i]) <- beta[1]+ X[i]*beta[2]
    like[i]      <- dbin(Y[i],pi[i],1) # For WAIC computation
  }
  for(j in 1:2){beta[j] ~ dnorm(0,0.01)}
}"

# Define the random effecs logistic regression model
mod2 <- "model{
  for(i in 1:n){
    Y[i]          ~ dbern(pi[i])
    logit(pi[i]) <- beta[1] + X[i]*beta[2] + theta[v[i]]
    like[i]      <- dbin(Y[i],pi[i],1) # For WAIC computation
  }
  for(j in 1:2){beta[j] ~ dnorm(0,0.01)}
  for(j in 1:10){theta[j] ~ dnorm(0,tau)}
  tau   ~ dgamma(0.1,0.1)
}"
```

Run the simulation

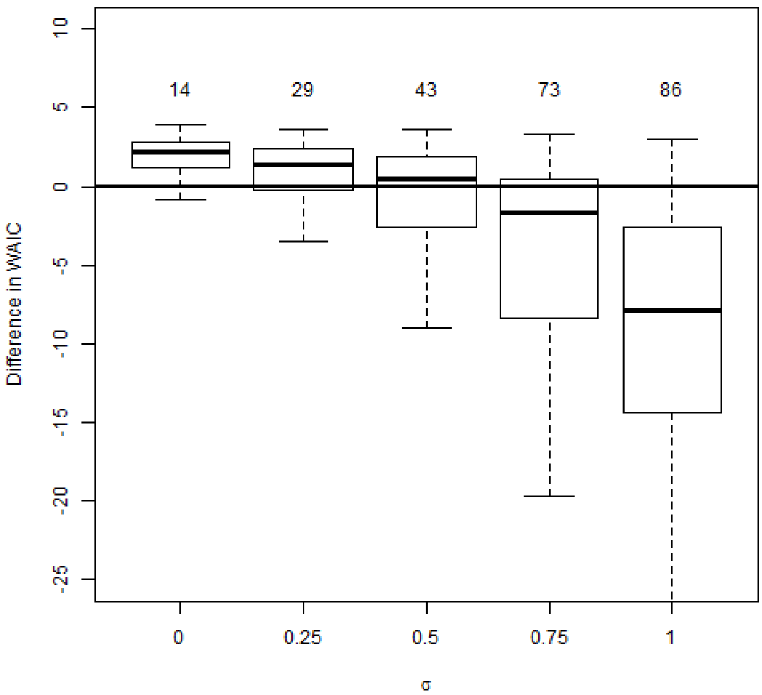
```
for(s in 1:ns){for(sim in 1:N){

 # Generate data
  set.seed(2*0820+sim)

  X     <- rnorm(n)
  theta <- rnorm(max(v),0,sigma[s])
  prob  <- 1/(1+exp(-beta1-beta2*X-theta[v]))
  Y     <- rbinom(n,1,prob)

 # Model 1 - No random effects

  mod    <- textConnection(mod1)
  data   <- list(Y=Y,X=X,n=n)
  model  <- jags.model(mod,data = data, n.chains=chains,quiet=TRUE)
  update(model, burn, progress.bar="none")
  samps  <- coda.samples(model, variable.names=c("like"),
                       n.iter=iters, progress.bar="none")

  # Compute DIC
  dic           <- dic.samples(model,n.iter=iters,progress.bar="none")
  DIC[sim,1,s]  <- sum(dic$dev)+sum(dic$pen)

  # Compute WAIC
  like          <- rbind(samps[[1]],samps[[2]]) # Combine samples from the two chains
  fbar          <- colMeans(like)
  Pw            <- sum(apply(log(like),2,var))
  WAIC[sim,1,s] <- -2*sum(log(fbar))+2*Pw


 # Model 2: Random effects model

  mod    <- textConnection(mod2)
  data   <- list(Y=Y,X=X,n=n,v=v)
  model  <- jags.model(mod,data = data, n.chains=chains,quiet=TRUE)
  update(model, burn, progress.bar="none")
  samps  <- coda.samples(model, variable.names=c("like"),
                       n.iter=iters, progress.bar="none")

  # Compute DIC
  dic           <- dic.samples(model,n.iter=iters,progress.bar="none")
  DIC[sim,2,s]  <- sum(dic$dev)+sum(dic$pen)

  # Compute WAIC
  like          <- rbind(samps[[1]],samps[[2]])
  fbar          <- colMeans(like)
  Pw            <- sum(apply(log(like),2,var))
  WAIC[sim,2,s] <- -2*sum(log(fbar))+2*Pw

}}
```

Compile the results

```
DIC_diff      <- DIC[,2,]-DIC[,1,]
DIC_pick_RE   <- colMeans(DIC_diff<0,na.rm=TRUE)

WAIC_diff     <- WAIC[,2,]-WAIC[,1,]
WAIC_pick_RE  <- colMeans(WAIC_diff<0,na.rm=TRUE)

SIG           <- matrix(sigma,N,ns,byrow=TRUE)
boxplot(DIC_diff~SIG,ylim=c(-25,10),outline=FALSE,
        xlab=expression(sigma),ylab="Difference in DIC")
abline(0,0,lwd=2)
text(1:ns,rep(5,ns),round(100*DIC_pick_RE),pos=3)
```




```
boxplot(WAIC_diff~SIG,ylim=c(-25,10),outline=FALSE,
        xlab=expression(sigma),ylab="Difference in WAIC")
abline(0,0,lwd=2)
text(1:ns,rep(5,ns),round(100*WAIC_pick_RE),pos=3)
```



Summary: Both $WAIC$ and DIC reliably select the correct model. When data are generated with $\sigma = 0$ the model without random effects is true and the random effects models is only selected for 10-20% of the simulated datasets. On the other hand, when data are generated with $\sigma > 0$ both metrics select the random effects model with high probability.