Model selection for the Gambia data

Chapter 5.5: Model selection criteria

The *gambia* data in the *geoR* package includes data for 1332 children in the Gambia. The binary response Y_i is the indictor that child i tested positive for malaria. Child i lives in village $v_i \in \{1, \ldots, 65\}$. We use five covariates in X_{ij}:

1. Age: age of the child, in days
2. Netuse: indicator variable denoting whether (1) or not (0) the child regularly sleeps under a bed-net
3. Treated: indicator variable denoting whether (1) or not (0) the bed-net is treated (coded 0 if netuse=0)
4. Green: satellite-derived measure of the greenness of vegetation in the immediate vicinity of the village (arbitrary units)
5. PCH: indicator variable denoting the presence (1) or absence (0) of a health center in the village

We use the random effects logistic regression model

$$\text{logit}[\text{Prob}(Y_i = 1)] = \alpha + \sum_{j=1}^{p} X_{ij}\beta_j + \theta_{v_i},$$

where θ_v is the random effect for village v. We compare three models for the village random effects via DIC and WAIC:

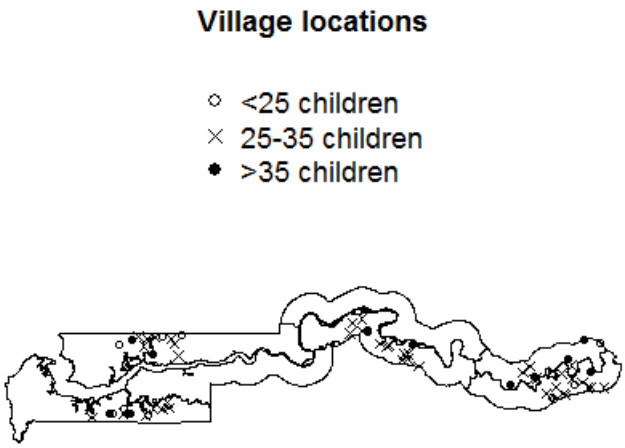
1. No random effects: $\theta_v = 0$
2. Gaussian random effects: $\theta_v \sim \text{Normal}(0, \tau^2)$
3. Double-exponential random effects: $\theta_v \sim \text{DE}(0, \tau^2)$

Load the data

```
library(geoR)

Y <- gambia[,3]
X <- scale(gambia[,4:8])
s <- gambia[,1:2]
n <- length(Y)
p <- ncol(X)

# Compute the village ID

S <- unique(s) # Lat/long of the villages
m <- nrow(S)
village <- rep(0,n)
members <- rep(0,m)
for(j in 1:m){
   d             <- (s[,1]-S[j,1])^2 + (s[,2]-S[j,2])^2
   village[d==0] <- j
   members[j]    <- sum(d==0)
}

size <- ifelse(members<25,1,2)
size <- ifelse(members>35,3,size)
table(size)
```

```
## size
##  1  2  3
## 11 42 12
```

```
pch  <- c(1,4,19)

plot(gambia.borders, type="l",
     asp=1,axes=F,cex.main=1.5,
     xlab="",ylab="",main="Village locations")
points(S[,1],S[,2],pch=pch[size])
legend("top",c("<25 children","25-35 children",">35 children"),pch=pch,cex=1.5,bty="n")
```



Prep for JAGS

```
library(rjags)
burn   <- 1000
iters  <- 5000
chains <- 2
```

Model 1: No random effects

```
mod <- textConnection("model{
  for(i in 1:n){
    Y[i]          ~ dbern(pi[i])
    logit(pi[i]) <- beta[1]        + X[i,1]*beta[2] + X[i,2]*beta[3] +
                    X[i,3]*beta[4] + X[i,4]*beta[5] + X[i,5]*beta[6]
    like[i]      <- dbin(Y[i],pi[i],1) # For WAIC computation
  }
  for(j in 1:6){beta[j] ~ dnorm(0,0.01)}
}")

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, n.thin = 5, progress.bar="none")

# Compute DIC
DIC    <- dic.samples(model,n.iter=iters,n.thin = 5, progress.bar="none")

# 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   <- -2*sum(log(fbar))+2*Pw

DIC
```

```
## Mean deviance:  2520
## penalty 6.076
## Penalized deviance: 2526
```

```
WAIC;Pw
```

```
## [1] 2525.59
```

```
## [1] 6.029153
```

Model 2: Gaussian random effects

```
mod <- textConnection("model{
  for(i in 1:n){
    Y[i]          ~ dbern(pi[i])
    logit(pi[i]) <- beta[1]        + X[i,1]*beta[2] + X[i,2]*beta[3] +
                    X[i,3]*beta[4] + X[i,4]*beta[5] + X[i,5]*beta[6] +
                    theta[village[i]]
    like[i]      <- dbin(Y[i],pi[i],1) # For WAIC computation
  }
  for(j in 1:6){beta[j] ~ dnorm(0,0.01)}
  for(j in 1:65){theta[j] ~ dnorm(0,tau)}
  tau   ~ dgamma(0.1,0.1)
}")

data   <- list(Y=Y,X=X,n=n,village=village)
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, n.thin = 5,progress.bar="none")

# Compute DIC
DIC    <- dic.samples(model,n.iter=iters,n.thin = 5,progress.bar="none")

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

DIC
```

```
## Mean deviance:  2278
## penalty 54.85
## Penalized deviance: 2333
```

```
WAIC;Pw
```

```
## [1] 2333.474
```

```
## [1] 53.43145
```

Model 3: Double-exponential random effects

```
mod <- textConnection("model{
  for(i in 1:n){
    Y[i]          ~ dbern(pi[i])
    logit(pi[i]) <- beta[1]        + X[i,1]*beta[2] + X[i,2]*beta[3] +
                    X[i,3]*beta[4] + X[i,4]*beta[5] + X[i,5]*beta[6] +
                    theta[village[i]]
    like[i]      <- dbin(Y[i],pi[i],1) # For WAIC computation
  }
  for(j in 1:6){beta[j] ~ dnorm(0,0.01)}
  for(j in 1:65){theta[j] ~ ddexp(0,tau)}
  tau   ~ dgamma(0.1,0.1)
}")

data   <- list(Y=Y,X=X,n=n,village=village)
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, n.thin = 5,progress.bar="none")

# Compute DIC
DIC    <- dic.samples(model,n.iter=iters,n.thin = 5,progress.bar="none")

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

DIC
```

```
## Mean deviance:  2276
## penalty 56.91
## Penalized deviance: 2333
```

```
WAIC;Pw
```

```
## [1] 2333.153
```

```
## [1] 54.29588
```

Summary: Both $WAIC$ and DIC show strong support for including village random effects but cannot distinguish between Gaussian and double-exponential random effect distributions.