MCMC for Generalized Linear Mixed Models with glmmBUGS

by Patrick Brown and Lutong Zhou

Abstract The **glmmBUGS** package is a bridging tool between Generalized Linear Mixed Models (GLMMs) in R and the BUGS language. It provides a simple way of performing Bayesian inference using Markov Chain Monte Carlo (MCMC) methods, taking a model formula and data frame in R and writing a BUGS model file, data file, and initial values files. Functions are provided to reformat and summarize the BUGS results. A key aim of the package is to provide files and objects that can be modified prior to calling BUGS, giving users a platform for customizing and extending the models to accommodate a wide variety of analyses.

Introduction

There are two steps in model fitting that are much more time consuming in WinBUGS than in R. First, unbalanced multi-level data needs to be formatted in a way that BUGS can handle, including changing categorical variables to indicator variables. Second, a BUGS model file must be written. The **glmmBUGS** package addresses these issues by allowing users to specify models as formulas in R, as they would in the `glm` function, and provides everything necessary for fitting the model with WinBUGS or OpenBUGS via the **R2WinBUGS** package (Sturtz et al., 2005).

The **glmmBUGS** package creates the necessary BUGS model file, starting value function, and suitably formatted data. Improved chain mixing is accomplished with a simple reparametrization and the use of sensible starting values. Functions are provided for formatting and summarizing the results. Although a variety of models can be implemented entirely within **glmmBUGS**, the package intends to provide a basic set of data and files for users to modify as necessary. This allows the full flexibility of BUGS model specification to be exploited, with much of the initial "grunt work" being taken care of by **glmmBUGS**.

Examples

Independent random effects

Consider the bacteria data from the **MASS** package:

```
> library(MASS)
> data(bacteria)
> head(bacteria)
```

```
  y ap hilo week  ID     trt
1 y  p   hi    0 X01 placebo
2 y  p   hi    2 X01 placebo
3 y  p   hi    4 X01 placebo
4 y  p   hi   11 X01 placebo
5 y  a   hi    0 X02   drug+
6 y  a   hi    2 X02   drug+
```

The variables to be considered are: `y`, the presence or absence of bacteria in a sample coded as `"y"` and `"n"` respectively; `week`, the time of the observation; `ID`, the subject identifier; and `trt` giving the treatment group as `"placebo"`, `"drug"`, or `"drug+"`.

A generalized linear mixed model is applied to the data with:

$$\begin{aligned} Y_{ij} &\sim \text{Bernoulli}(p_{ij}) \\ \text{logit}(p_{ij}) &= \mu + x_{ij}\beta + V_i \\ V_i &\sim iid\ \text{N}(0,\sigma^2) \end{aligned} \tag{1}$$

where: Y_{ij} indicates the presence or absence of bacteria of the ith person at week j; covariates x_{ij} are week and indicator variables for treatment; p_{ij} denotes the probability of bacteria presence; V_i is the random effect for the ith patient, assumed to be normal with mean 0 and variance σ^2. To improve the mixing of the Markov chain, a reparametrized model is fitted with:

$$\begin{aligned} Y_{ij} &\sim \text{Bernoulli}(p_{ij}) \\ \text{logit}(p_{ij}) &= R_i + w_{ij}\gamma \\ R_i &\sim \text{N}(\mu + g_i\alpha,\sigma^2). \end{aligned} \tag{2}$$

Here g_i is the (indicator variable for) treatment group for subject i and w_{ij} is the week that observation j was taken. Note that the two models are the same, with $V_i = R_i - \mu - g_i\alpha$, $\beta = (\gamma,\alpha)$ and $x_{ij} = (w_{ij},g_i)$. The model in (1) has strong negative dependence between the posterior samples of V_i and μ, whereas R_i and μ in (2) are largely independent.

As BUGS only allows numeric data, and cannot have the '+' sign in variable names, the data are recoded as follows:

```
> bacterianew <- bacteria
> bacterianew$yInt = as.integer(bacterianew$y ==
+     "y")
> levels(bacterianew$trt) <- c("placebo",
+     "drug", "drugplus")
```

The primary function in the package is `glmmBUGS`, which does the preparatory work for fitting the model in (2) with:

```
> library(glmmBUGS)
> bacrag <- glmmBUGS(formula = yInt ~
+     trt + week, data = bacterianew,
+     effects = "ID", modelFile = "model.bug",
+     family = "bernoulli")
```

This specifies yInt as a Bernoulli-valued response, trt and week as fixed-effect covariates, and the "ID" column for the random effects. The result is a list with three elements:

ragged is a list containing the data to be passed to WinBUGS;

pql is the result from fitting the model with the glmmPQL function in **MASS** package.

startingValues is a list of starting values for the parameters and random effects, which is obtained from the glmmPQL result.

In addition, two files are written to the working directory

'model.bug' is the BUGS model file

'getInits.R' contains the R code for a function to generate random starting values.

To accommodate unbalanced designs, the data are stored as ragged arrays, as described in the section "Handling unbalanced datasets" of the WinBUGS manual (Spiegelhalter et al., 2004). The ragged result has a vector element "SID" indicating the starting position of each individual's observations in the dataset. The covariates are split into elements "XID" and "Xobservations" for the individual-level and observation-level covariates respectively:

```
> names(bacrag$ragged)

[1] "NID"           "SID"
[3] "yInt"          "XID"
[5] "Xobservations"
```

The model file consists of an outer loop over ID levels and an inner loop over observations. The details of how the model is implemented are best understood by examining the 'model.bug' file and consulting the WinBUGS manual.

At this stage the user is expected to modify the files and, if necessary, the data to refine the model, set appropriate priors, and ensure suitability of starting values. Before using the bugs function in the **R2WinBUGS** package to sample from the posterior, the starting value function getInits must be prepared. First, the file 'getInits.R' (which contains the source for getInits) should be edited and sourced into R. Next, the list containing the PQL-derived starting values must be assigned the name startingValues, as getInits will be accessing this object every time it is run.

```
> source("getInits.R")
> startingValues = bacrag$startingValues
> library(R2WinBUGS)
> bacResult = bugs(bacrag$ragged, getInits,
+     model.file = "model.bug", n.chain = 3,
+     n.iter = 2000, n.burnin = 100,
+     parameters.to.save = names(getInits()),
+     n.thin = 10)
```

Post WinBUGS commands

After running WinBUGS, a series of functions in the **glmmBUGS** package can be used to manipulate and check the simulation results. The restoreParams function is used to restore the original parametrization from (1) and assign the original names to the group or subject identifiers.

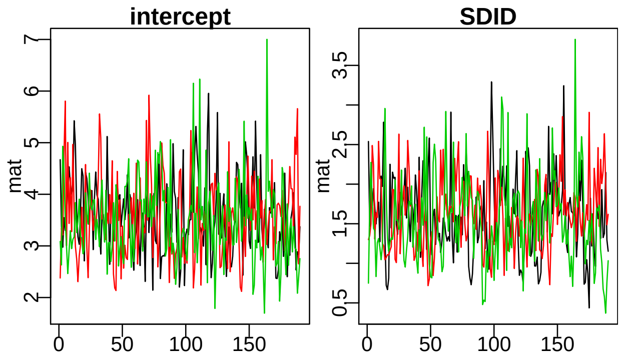
```
> bacParams = restoreParams(bacResult,
+     bacrag$ragged)
> names(bacParams)

[1] "intercept" "SDID"      "deviance"
[4] "RID"       "betas"
```

The result is a set of posterior samples for μ (intercept), σ (SDID), all the V_i (RID), and β (betas). Posterior means and credible intervals are obtained with the summaryChain function.

```
> bacsummary = summaryChain(bacParams)
> names(bacsummary)

[1] "scalars" "RID"     "betas"

> signif(bacsummary$betas[, c("mean",
+     "2.5%", "97.5%")], 3)

               mean   2.5%   97.5%
observations -0.159 -0.263 -0.0614
trtdrug      -1.500 -3.240  0.0164
trtdrugplus  -0.920 -2.740  0.6060

> bacsummary$scalars[, c("mean", "2.5%",
+     "97.5%")]

              mean     2.5%    97.5%
intercept 3.547556 2.243375 5.219125
SDID      1.597761 0.737010 2.716975
```

In order to check the convergence of the simulations, we use the checkChain function to produce trace plots of the intercept and σ parameters.

```
> checkChain(bacParams, c("intercept",
+     "SDID"))
```



A spatial example

The `ontario` dataset contains expected and observed cases of molar cancer by census sub-division in Ontario, Canada.

```
> data(ontario)
> head(ontario)

         CSDUID observed logExpected
3501005 3501005       61    2.118865
3501011 3501011       50    1.971265
3501012 3501012      117    3.396444
3501020 3501020       65    1.919814
3501030 3501030       37    1.779957
3501042 3501042       16    1.182329
```

Consider the following model (see Rue and Held, 2005):

$$\begin{aligned} Y_i &\sim \text{Poisson}(\lambda_i E_i) \\ \log(\lambda_i) &= \mu + U_i + V_i \\ U_i &\sim \text{GMRF}(\sigma_U^2) \\ V_i &\sim \text{iid N}(0, \sigma_V^2) \end{aligned} \quad (3)$$

where Y_i and E_i are the observed and expected number of cancer cases in census division i; λ_i is the cancer incidence rate; the U_i are spatial random effects, a Gaussian Markov random field with variance σ_U^2; and V_i are spatially independent random effects with variance σ_V^2.

This model is reparametrised with $R_i = U_i + \mu + V_i$ in place of V_i. An adjacency matrix is required for the spatial random effect. This was computed from the spatial boundary files with the `poly2nb` function from the **spdep** package and is stored as the object `popDataAdjMat`. The model can be fitted with `glmmBUGS` as follows:

```
> data(popDataAdjMat)
> forBugs = glmmBUGS(formula = observed +
+     logExpected ~ 1, spatial = popDataAdjMat,
+     effects = "CSDUID", family = "poisson",
+     data = ontario)
```

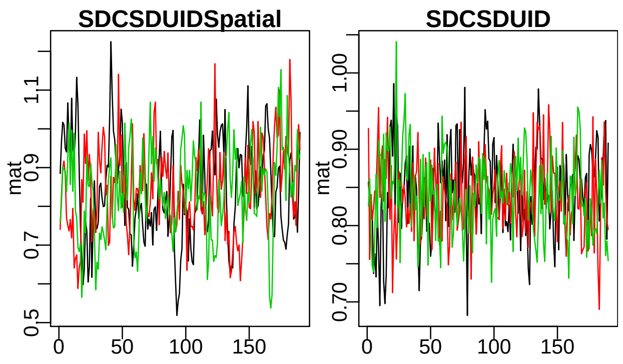
Note that the expected counts are needed on the log scale, and are passed as a second argument on the left side of the model equation to denote their being offset parameters without a coefficient. The random effect is at the census sub-division level (`CSDUID`), with `popDataAdjMat` giving the dependency structure. Posterior samples can be generated as follows:

```
> startingValues = forBugs$startingValues
> source("getInits.R")
> onResult = bugs(forBugs$ragged, getInits,
+     model.file = "model.bug", n.chain = 3,
+     n.iter = 2000, n.burnin = 100,
+     parameters.to.save = names(getInits()),
+     n.thin = 10)
> ontarioParams = restoreParams(onResult,
+     forBugs$ragged)
> names(ontarioParams)
```

```
[1] "intercept"         "SDCSDUID"
[3] "SDCSDUIDSpatial"   "deviance"
[5] "RCSDUID"           "RCSDUIDSpatial"
[7] "FittedRateCSDUID"
```

There are posterior simulations for two variance parameters, σ_U (`SDCSDUIDSPATIAL`) and σ_V (`SDCSDUID`). Samples for the random effects are given for U_i (`RCSDUIDSpatial`), $U_i + V_i$ (`RCSDUID`), and λ_i (`FittedRateCSDUID`). Trace plots are shown below for σ_U and σ_V, the standard deviations of the spatial and non-spatial random effects.

```
> checkChain(ontarioParams, c("SDCSDUIDSpatial",
+     "SDCSDUID"))
```



These trace plots show poor mixing, and the Markov chain should be re-run with longer chains and more thinning.

The posterior means for the relative risk λ_i for Toronto and Ottawa (Census Subdivisions 3506008 and 3530005) are extracted with:

```
> ontarioSummary = summaryChain(ontarioParams)
> ontarioSummary$FittedRateCSDUID[c("3506008",
+     "3520005"), "mean"]


    3506008     3520005
0.119725007 0.008148696
```

The posterior probability of each region having a relative risk twice the provincial average is computed with

```
> postProb = apply(ontarioParams$RCSDUID,
+     3, function(x) mean(x > log(2)))
```

The `"RCSDUID"` element of `ontarioParams` is a three dimensional array, with entry i,j,k being iteration i of chain j for region k. The `apply` statement computes the proportion of log-relative risks over log(2) for each region (the third dimension).

The results can be merged into the original spatial dataset, as described in the documentation for the **diseasemapping** package. Figure 1 shows a map of the posterior probabilities.

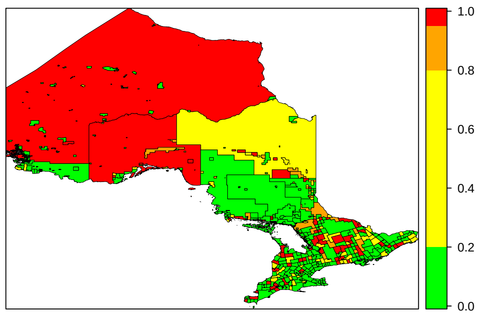


Figure 1: Posterior probabilities of Ontario census sub-divisions having twice the provincial average risk of molar cancer.

Additional features

The `reparam` argument to the `glmmBUGS` function reparametrizes the intercept, and a set of covariates for a new baseline group is provided. Recall that in the bacteria example the `ragged` object passed to WinBUGS divides covariates into observation and ID level effects. `ragged$Xobservations` is a vector and `ragged$XID` is a matrix of two columns, which contains the week variable and indicator variables for the treatments respectively. The `reparam` argument should accordingly be a list with one or more of elements `"observations"` containing the week or `"ID"` containing the two treatment indicators. Setting `reparam=list(observations=2)` would make week 2 the baseline week, rather than week zero. This argument is useful when using spline functions as covariates, as the intercept parameter which WinBUGS updates can be set to the curve evaluated in the middle of the dataset.

The `prefix` argument allows a character string to precede all data and variable names. This can be used to combine multiple model files and datasets into a single BUGS model, and modifying these files to allow dependence between the various components. For instance, one random effects model for blood pressure could be given `prefix='blood'`, and a model for body mass given `prefix='mass'`. To allow for dependence between the individual-level random effects for blood pressure and mass, the two data sets and starting values produced by the `glmmBUGS` function can be combined, and the two model files concatenated and modified. Were it not for the prefix, some variable names would be identical in the two datasets and combining would not be possible.

Finally, multi-level models can be accommodated by passing multiple variable names in the `effects` argument. If the bacteria data were collected from students nested within classes nested within schools, the corresponding argument would be `effects = c("school","class","ID")`.

Currently unimplemented features that would enhance the package include: random coefficients (specified with an `lmer`-type syntax); survival distributions (with `"Surv"` objects as responses); and geostatistical models for the random effects. As WinBUGS incorporates methods for all of the above, these tasks are very feasible and offers of assistance from the community would be gratefully accepted.

Summary

There are a number of methods and R packages for performing Bayesian inference on generalized linear mixed models, including **geoRglm** (Christensen and Ribeiro, 2002), **MCMCglmm** (Hadfield, 2009) and **glmmGibbs** (Myles and Clayton, 2001). Particularly noteworthy is the **INLA** package which avoids the use of MCMC by using Laplace approximations, as described in Rue et al. (2009). Despite this, many researchers working with R (including the authors) continue to use WinBUGS for model fitting. This is at least partly due to the flexibility of the BUGS language, which gives the user nearly full control over specification of distributions and dependence structures. This package aims to retain this flexibility by providing files to be edited before model fitting is carried out, rather than providing a large number of options for, i.e. prior distributions. More model-specific packages such as **INLA** are entirely adequate (and perhaps preferable) for the two examples presented here. Those who wish to have full control over priors or build more complex models, for example multivariate or errors-in-covariate models, will likely appreciate the head start which the **glmmBUGS** package can provide for these tasks.

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