

Small Area Estimation with R

Unit 6: Non-linear models

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- So far, we have only considered models with a Normal response
- Generalized Linear Models have been used to tackle Small Area Estimation problems
- Problems may arise when combining individual and aggregate models
- Specific methods will be required to combine information efficiently (see, for example, Jackson et al., 2006, 2008)
- We will show examples using a Bayesian approach

Disease mapping

- Health authorities collect mortality (and morbidity) data on a regular basis
- The aim of disease mapping is to estimate the relative risk of a certain disease
- In addition, to the observed number of cases, and expected number is computed on the population and, possibly, some known risk factors
- Spatial random effects are often considered because risks are assumed to vary smoothly
- Temporal effects can be included if the data cover several periods of time

Example: SIDS in North Carolina

- Cressie and Chan (1989) have studied the mortality in children by Sudden Infant Death Syndrome in 1974-78 and 1979-84
- The administrative aggregation of the data is county level
- In addition, the number of births and the proportion of non-white births are available and can be used to compute the expected number of cases
- These data are available in package `spdep`: `data(mc.sids)`

BYM propose a model that includes spatial and non-spatial random effects to account for different types of unmeasured variables:

$$O_i \sim Po(\mu_i)$$

$$\log(\mu_i) = \log(E_i) + \alpha + \beta X_i + u_i + v_i$$

$$u_i \sim N(0, \sigma_u^2)$$

$$v_i | v_{-i} \sim N(\sum_{j \sim i} v_j / n_j, \sigma_v^2 / n_j)$$

WinBUGS model

```
model
{
  for(i in 1:N)
  {
    observed[i] ~ dpois(mu[i])
    log(theta[i]) <- alpha + beta*nonwhite[i] + u[i] + v[i]
    mu[i] <- expected[i]*theta[i]

    u[i] ~ dnorm(0, precu)
  }

  v[1:N] ~ car.normal(adj[], weights[], num[], precv)

  alpha ~ dflat()
  beta ~ dnorm(0, 1.0E-5)
  precu ~ dgamma(0.001, 0.001)
  precv ~ dgamma(0.1, 0.1)

  sigmau<-1/precu
  sigmav<-1/precv
}
```

Example: SIDS in North Carolina

The following code is used to set the data and run the model to fit

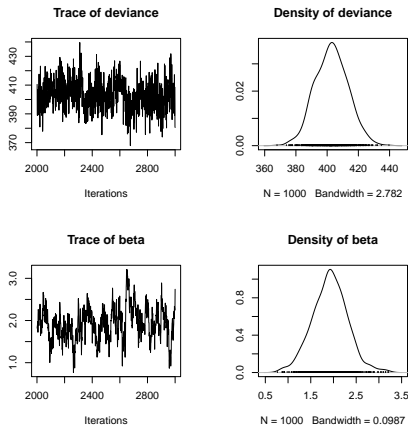
```
> library(maptools)
> library(spdep)
> library(rgdal)
> #Read data from shapefile
> nc <- readShapePoly(system.file("etc/shapes/sids.shp", package="spdep")[1],
+   ID="FIPSNO")#, proj4string=CRS("+proj=longlat +ellps=clrk66"))
> rn <- sapply(slot(nc, "polygons"), function(x) slot(x, "ID"))
> ncCC89nb <- read.gal(system.file("etc/weights/ncCC89.gal", package="spdep")[1],
+   region.id=rn)
> nc.nb<-nb2WB(ncCC89nb)
> #Prepare data set
> nc$Observed<-nc$SID74
> nc$Population<-nc$BIR74#Population at risk; number of births
> r<-sum(nc$Observed)/sum(nc$Population)
> nc$Expected<-nc$Population*r
> N<-length(nc$Observed)
> #Computed Standardised Mortality Ratio
> nc$SMR<-nc$Observed/nc$Expected
> #Proportion of non-white births
> nc$nwprop<-nc$NWBIR74/nc$BIR74
> d<-list(N=N, observed=nc$Observed, expected=nc$Expected,
+   nonwhite=nc$nwprop,#log(nwprop/(1-nwprop)),
+   adj=nc.nb$adj, weights=nc.nb$weights, num=nc.nb$num)
> inits<-list(u=rep(0,N), v=rep(0,N), alpha=0, beta=0, precu=.001, precv=.001)
```

Example: SIDS in North Carolina

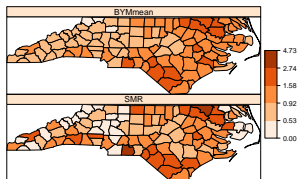
```
> library(R2WinBUGS)
> bymmodelfile<-paste(getwd(), "/BYM-model.txt", sep="")
> wdir<-paste(getwd(), "/BYM", sep="")
> if(!file.exists(wdir)){dir.create(wdir)}
> #BugsDir <- "/Users/virgiliogomezgislab/.wine/dosdevices/c:/Program Files/WinBUGS14"
> BugsDir <- "/Users/virgil/.wine/dosdevices/c:/Program Files/WinBUGS14"
> MCMCres<- bugs(data=d, inits=list(inits),
+   working.directory=wdir,
+   parameters.to.save=c("theta", "alpha", "beta", "u", "v", "sigmau", "sigmav"),
+   n.chains=1, n.iter=30000, n.burnin=20000, n.thin=10,
+   model.file=bymmodelfile,
+   bugs.directory=BugsDir,
+   WINEPATH="/usr/local/bin/winepath")
> #Load the data obtained by running WinBUGS in Windows
> nc$BYMmean<-MCMCres$mean$theta
> nc$BYMumean<-MCMCres$mean$u
> nc$BYMvmean<-NA
> nc$BYMvmean[nc.nb$num>0]<-MCMCres$mean$v
>
```


Example: SIDS in North Carolina

```
> library(coda)
> ncoutput<-read.coda("BYM/coda1.txt", "BYM/codaIndex.txt")
> #par(mfrow=c(2,4))
> #plot(ncoutput[,c("deviance", "alpha", "beta", "theta[94]")],auto.layout=FALSE)
> plot(ncoutput[,c("deviance", "beta")])
```



Example: SIDS in North Carolina



```
> library(RColorBrewer)
> brks<-quantile(nc$SMR, seq(0,1,1/5))
> #Used method proposed by Nicky Best
> logSMR<-log(nc$SMR[nc$SMR>0])
> nsteps <- 5
> step<-(max(logSMR)-min(logSMR))/nsteps
> brks<-exp(min(logSMR)+(0:nsteps)*step)
> brks[1]<-0
> cols <- brewer.pal(5, "Oranges")
> atcol<-(0:5)*max(nc$SMR)/5
> colorkey<-list(labels=as.character(c(formatC(brks, format="f",
+ at=atcol, height=.5)
> print(spplot(nc, c("SMR", "BYMmean"), at=brks, col.regions=cols,
+ axes=TRUE, colorkey=colorkey))
```

Estimation of unemployment

- The survey records the unemployment status of the population in the sample
- Other socio-economic covariates can be recorded
- A logictic regression can be used to model the probability of being unemployed in the area
- In order to produce small area estimates, the model must be fit using area level covariates
- The Office for National Statistics (UK) uses the following model

$$y_{ij} \sim \text{Binom}(p_i, N_i); j = 1, \dots, n_i$$

$$\text{logit}(p_i) = \alpha + \beta X_i; i = 1, \dots, K$$

Unemployment in Sweden

- We have simulated a data set mimicking a survey on the population
- The target variable is the employment status: 1-employed, 0-unemployed
- The covariates, which are based on the area level, are
 - Age (average age)
 - Sex (proportion of males)
 - Higher education status (proportion of persons with higher education)
- Unit level covariates are not used in this model because combining them with area level covariates is not straightforward
- If the model is fit with unit level covariates and the small area estimates are computed by 'plugging-in' the area level covariates a bias is introduced

WinBUGS model

```
model
{
  for(i in 1:totssize)
  {

    emp[i]~dbern(p[i])

    logit(pp[i])<-alpha+bage*AGE[area[i]]+bsex*SEX[area[i]]+beduc*EDUC[area[i]]+u[area[i]]+v[area[i]]

    p[i]<-max(0.000000001, min(pp[i], 0.999999999))

  }

  for(i in 1:N)
  {
    u[i] ~ dnorm(0, precu)

    logit(rateemp[i])<-alpha+bage*AGE[i]+bsex*SEX[i]+beduc*EDUC[i]+u[i]+v[i]
    rateunemp[i]<- 1-rateemp[i]
  }

  v[1:N] ~ car.normal(adj[], weights[], num[], precv)

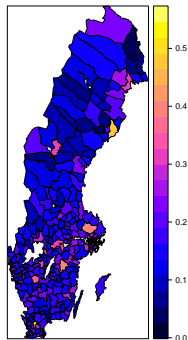
  precu ~ dgamma (a0,b0)
  precv ~ dgamma (a1,b1)

  alpha ~ dflat()
  bage ~ dflat()
  bsex ~ dflat()
  beduc ~ dflat()
}
```

Example: Unemployment in Sweden

```
> dunemp<-source("Unemployment/WBdata/datasp.txt")$value
> dsp<-source("Unemployment/WBdata/spdata.txt")$value
> initsunemp1<-source("Unemployment/ints/initssp-1.txt")$value
> initsunemp2<-source("Unemployment/ints/initssp-2.txt")$value
> bymmodelfile<-paste(getwd(), "/Unemployment/models/modelsp.txt", sep="")
> wdir<-paste(getwd(), "/BYM-Unemp", sep="")
> if(!file.exists(wdir)){dir.create(wdir)}
> #BugsDir <- "/Users/virgiliogomezgislab/.wine/dosdevices/c:/Program Files/WinBUGS14"
> BugsDir <- "/Users/virgil/.wine/dosdevices/c:/Program Files/WinBUGS14"
> MCMCresunemp<- bugs(data=c(dunemp, dsp), inits=list(initsunemp1, initsunemp2),
+   working.directory=wdir,
+   parameters.to.save=c("p", "alpha", "bage", "bsex", "beduc"),
+   n.chains=2, n.iter=3000, n.burnin=2000, n.thin=1,
+   model.file=bymmodelfile,
+   bugs.directory=BugsDir,
+   WINEPATH="/usr/bin/winepath")
>
> load("MCMCresunemp.RData")
```

Example: Unemployment in Sweden



```
> library(maptools)
> Sweden<-readShapePoly(fn="Sweden_municipality")
> Sweden<-unionSpatialPolygons(Sweden,Sweden$KOD83_91)
> Sweden<-SpatialPolygonsDataFrame(Sweden,
+   data.frame(unemp=1-unique(MCMCresunemp$mean$p)), mat
> print(spplot(Sweden, "unemp", cuts=20))
>
```

- Besag, J., J. C. York, and A. Mollié (1991). Bayesian image restoration, with two applications in spatial statistics. *Annals of the Institute of Statistical Mathematics* **43**, 1–59.
- Cressie, N, Chan NH (1989) Spatial modelling of regional variables. *Journal of the American Statistical Association* **84**: 393–401
- Ghosh, M. and J. N. K. Rao (1994). Small area estimation: An appraisal. *Statistical Science* **9**(1), 55–76.
- Jackson, C. et al. (2006). Improving ecological inference using individual-level data. *Statistics in Medicine* **25**(12), 2136–2159.
- Jackson, C. et al. (2008). Hierarchical related regression for combining aggregate and individual data in studies of socio-economic disease risk factors. *JRSS, Series A* 171(1), 159–178.