

# Example 8.3

Disease mapping: from foundations to multidimensional modeling

*Martinez-Beneito M.A. and Botella-Rocamora P.*

This document reproduces the analysis made at Example 8.3 of the book: “Disease mapping: from foundations to multidimensional modeling” by Martinez-Beneito M.A. and Botella-Rocamora P., published by CRC press in 2019. You can watch the analysis made with full detail at this pdf document, or even execute it if you want with the material available at <https://github.com/MigueBeneito/DMBook>. Anyway, this pdf file should be enough for following most of the details of the analysis made for this example.

The statistical analysis below has been run in **R**, by additionally using the library **Rmarkdown**, so be sure that you have this software installed if you want to reproduce by yourself the content of this document. In that case we advise you to download first the annex material at <https://github.com/MigueBeneito/DMBook>, open with **Rstudio** the corresponding **.Rproj** file that you will find at the folder corresponding to this example and compile the corresponding **.Rmd** document. This will allow you to reproduce the whole statistical analysis below.

This document has been executed with real data that are not provided in order to preserve their confidentiality. Slightly modified data are provided instead, as described in Chapter 1 of the book. Thus, when reproducing this document you will not obtain exactly the same results, although they should be very close to those shown here.

## Libraries and data loading

```
# Libraries loading
#-----
if (!require(RColorBrewer)) {
  install.packages("RColorBrewer")
  library(RColorBrewer)
}
if (!require(rgdal)) {
  install.packages("rgdal")
  library(rgdal)
}
if (!require(spdep)) {
  install.packages("spdep")
  library(spdep)
}
if (!require(pbugs)) {
  if (!require(devtools)) {
    install.packages("devtools")
    devtools::install_github("fisabio/pbugs")
  } else {
    install_github("fisabio/pbugs")
  }
}

# Data loading
#-----
# For reproducing the document, the following line should be changed to
# load('../Data/Obs.SANOVA-mod.Rdata') since that file contains the modified
```

```

# data making it possible to reproduce this document.
load("../Data/Obs.SANOVA.Rdata")
# load('../Data/Obs.SANOVA-mod.Rdata')
load("../Data/Exp.SANOVA.Rdata")
# Cartography
load("../Data/AIDS.Rdata")

```

## Adjacency matrix in WinBUGS format

```

carto.val.wb = nb2WB(poly2nb(carto.val, snap = 1))

```

## Definition of a design matrix for the contrasts between spatial patterns

```

matH = matrix(nrow = 8, ncol = 8)
# Joint pattern
matH[, 1] = c(1, 1, 1, 1, 1, 1, 1, 1)
# Differences between diseases
matH[, 2] = c(1, 1, 1, 1, -1, -1, -1, -1)
# Differences between sexes
matH[, 3] = c(1, 1, -1, -1, 1, 1, -1, -1)
# Differences between periods
matH[, 4] = c(1, -1, 1, -1, 1, -1, 1, -1)
# Interaction disease-sex
matH[, 5] = c(1, 1, -1, -1, -1, -1, 1, 1)
# Interaction disease-period
matH[, 6] = c(1, -1, -1, 1, 1, -1, -1, 1)
# Interaction sex-period
matH[, 7] = c(1, -1, -1, 1, -1, 1, 1, -1)
# Interaction disease-sex-period
matH[, 8] = c(1, -1, 1, -1, -1, 1, -1, 1)
# Normalization of H columns
matH <- 1/sqrt(8) * (matH)

```

## SANOVA inference in WinBUGS

```

SANOVAModel <- function() {
  for (i in 1:nAreas) {
    for (j in 1:nPatterns) {
      Obs[i, j] ~ dpois(lambda[i, j])
      log(lambda[i, j]) <- log(Exp[i, j]) + log.theta[i, j]
      log.theta[i, j] <- mu[j] + Phi[i, j]
      Phi[i, j] <- inprod2(BYM[i, ], Ht[, j])
      BYM[i, j] <- sd.sp[j] * spat[j, i] + sd.het[j] * unstruct[i, j]
      unstruct[i, j] ~ dnorm(0, 1)

      sSMR[i, j] <- 100 * exp(mu[j] + Phi[i, j])
    }
  }
}

```

```

    for (j in 1:nPatterns) {
      spat[j, 1:nAreas] ~ car.normal(adj[], weights[], num[], 1)
      # Prior distributions
      mu[j] ~ dflat()
      sd.sp[j] ~ dunif(0, 5)
      sd.het[j] ~ dunif(0, 5)
    }
  }

data = list(Obs = Obs.SANOVA, Exp = Exp.SANOVA, nAreas = dim(Obs.SANOVA)[1],
            nPatterns = dim(Obs.SANOVA)[2], adj = carto.val.wb$adj, weights = rep(1,
            length(carto.val.wb$adj)), num = carto.val.wb$num, Ht = t(mathH))
inits = function() {
  list(mu = rnorm(dim(Obs.SANOVA)[2]), sd.sp = runif(dim(Obs.SANOVA)[2]),
       sd.het = runif(dim(Obs.SANOVA)[2]), spat = matrix(rnorm(prod(dim(Obs.SANOVA))),
       nrow = dim(Obs.SANOVA)[2]), unstruct = matrix(rnorm(prod(dim(Obs.SANOVA))),
       ncol = dim(Obs.SANOVA)[2]))
}
param = c("sSMR", "mu", "sd.sp", "sd.het", "Phi", "BYM")

Resul.SANOVA = pbugs(data = data, inits = inits, parameters = param, model.file = SANOVAModel,
                    n.iter = 10000, n.burnin = 1000, DIC = F, bugs.seed = 1)
# Computing time
Resul.SANOVA$exec_time

## Time difference of 1.707286 hours

# Result summaries
summary(Resul.SANOVA$summary[, "Rhat"])

##      Min. 1st Qu.  Median    Mean 3rd Qu.    Max.
## 0.9995  1.0004  1.0015  1.0022  1.0032  1.0431

summary(Resul.SANOVA$summary[, "n.eff"])

##      Min. 1st Qu.  Median    Mean 3rd Qu.    Max.
##   110.0   700.0  1000.0   844.7  1000.0  1000.0

```

## Variance decomposition

```

par(mfrow = c(1, 1))
patterns = Resul.SANOVA$mean$BYM
var.decomp = apply(patterns, 2, var)/sum(apply(patterns, 2, var))
names(var.decomp) = c("Common", "Diseases", "Sexes", "Periodo", "Int.1", "Int.2",
                      "Int.3", "Int.4")
apply(patterns, 2, var)

## [1] 0.1416349914 0.0559966228 0.0076274207 0.0335718338 0.0029562636
## [6] 0.0005324063 0.0006499115 0.0003714150

var.decomp

##      Common  Diseases    Sexes   Periodo   Int.1   Int.2
## 0.582043593 0.230115985 0.031344594 0.137962170 0.012148652 0.002187903

```

```
##          Int.3          Int.4
## 0.002670787 0.001526316
```

## Choropleth maps

```
colors = brewer.pal(7, "BrBG")[7:1]

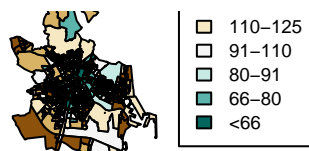
par(mfrow = c(2, 2))
par(mar = c(5, 4, 4, 2) + 0.1)
# Common
pattern = exp(Resul.SANOVA$mean$BYM[, 1])
cuts = as.numeric(cut(100 * pattern, 100 * c(-0.1, 1/1.5, 1/1.25, 1/1.1, 1.1,
      1.25, 1.5, 100)))
plot(carto.val, xlim = c(721500, 736000), ylim = c(4368000, 4378000), col = colors[cuts])
title("Common pattern", cex = 0.75)
legend(x = "bottomright", fill = colors[7:1], legend = c(">150", "125-150",
      "110-125", "91-110", "80-91", "66-80", "<66"), cex = 0.75, inset = 0.03)

# Diseases
pattern <- exp(Resul.SANOVA$mean$BYM[, 2])
cuts <- as.numeric(cut(100 * pattern, 100 * c(-0.1, 1/1.5, 1/1.25, 1/1.1, 1.1,
      1.25, 1.5, 100)))
plot(carto.val, xlim = c(721500, 736000), ylim = c(4368000, 4378000), col = colors[cuts])
title("Dif.between diseases \n (COPD vs Lung)", cex = 0.75)
legend(x = "bottomright", fill = colors[7:1], legend = c(">150", "125-150",
      "110-125", "91-110", "80-91", "66-80", "<66"), cex = 0.75, inset = 0.03)

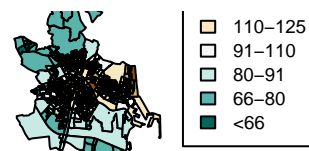
# Sex
pattern = exp(Resul.SANOVA$mean$BYM[, 3])
cuts = as.numeric(cut(100 * pattern, 100 * c(-0.1, 1/1.5, 1/1.25, 1/1.1, 1.1,
      1.25, 1.5, 100)))
plot(carto.val, xlim = c(721500, 736000), ylim = c(4368000, 4378000), col = colors[cuts])
title("Dif.between sexes", cex = 0.75)
legend(x = "bottomright", fill = colors[7:1], legend = c(">150", "125-150",
      "110-125", "91-110", "80-91", "66-80", "<66"), cex = 0.75, inset = 0.03)

# Period
pattern = exp(Resul.SANOVA$mean$BYM[, 4])
cuts = as.numeric(cut(100 * pattern, 100 * c(-0.1, 1/1.5, 1/1.25, 1/1.1, 1.1,
      1.25, 1.5, 100)))
plot(carto.val, xlim = c(721500, 736000), ylim = c(4368000, 4378000), col = colors[cuts])
title("Dif.between periods", cex = 0.75)
legend(x = "bottomright", fill = colors[7:1], legend = c(">150", "125-150",
      "110-125", "91-110", "80-91", "66-80", "<66"), cex = 0.75, inset = 0.03)
```

### Common pattern



### Dif.between diseases (COPD vs Lung)



### Dif.between sexes



### Dif.between periods

