

# Example 4.4

Disease mapping: from foundations to multidimensional modeling

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This document reproduces the analysis made at Example 4.4 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(DCluster)) {
  install.packages("DCcluster")
  library(DCluster)
}
if (!require(INLA)) {
  install.packages("INLA", repos = c(getOption("repos"), INLA = "https://inla.r-inla-download.org/R/s
    dep = TRUE)
  library(INLA)
}
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/ObsOral-mod.Rdata') since that file contains the
# modified data making it possible to reproduce this document.
load("../Data/ObsOral.Rdata")
# load('../Data/ObsOral-mod.Rdata')
load("../Data/ExpOral.Rdata")
load("../Data/Population.Rdata")
load("../Data/VR.Rdata")

```

## R function for calculating the DIC criterion of the models fitted

The function below computes the DIC criterion for disease mapping models fitted with WinBUGS. It returns DIC values comparable to those reported by INLA, in contrast to WinBUGS. See annex material for Example 4.3.

```

# Arguments: Simu.sSMRs: matrix of dimensions n.IterXn.Units where
# n.Iter are the number of MCMC iterations saved and n.Units the number
# of spatial units in the analysis. You will typically find this as a
# submatrix of the sims.matrix element of any bugs object. O: Vector of
# length n.Units with the observed deaths per spatial unit. E: Vector
# of length n.Units with the expected deaths per spatial unit.
DICPoisson = function(Simu.sSMRs, O, E) {
  mu = t(apply(Simu.sSMRs/100, 1, function(x) {
    x * E
  })))
  D = apply(mu, 1, function(x) {
    -2 * sum(O * log(x) - x - lfactorial(O))
  })
  Dmean = mean(D)
  mumean = apply(Simu.sSMRs/100, 2, mean) * E
  DinMean = -2 * sum(O * log(mumean) - mumean - lfactorial(O))
  # if(save==TRUE){return(c(Dmedia,Dmedia-DenMedia,2*Dmedia-DenMedia))}
  cat("D=", Dmean, "pD=", Dmean - DinMean, "DIC=", 2 * Dmean - DinMean,
      "\n")
}

```

## Poisson-gamma model

Model fitted by empirical Bayes methods.

```

PoisGamma <- empbaysmooth(Obs.muni, Exp.muni, maxiter = 100)
# Posterior mean of the sSMRs
PoisGamma$nu/PoisGamma$alpha

## [1] 0.9113144
# Posterior sd of the sSMRs
sqrt(PoisGamma$nu/(PoisGamma$alpha^2))

## [1] 0.2937582

```

```

# sSMR fitted for this model
PoisGamma.sSMR <- 100 * PoisGamma$smthrr
# Random sample of values of the posterior distribution for calculating
# its DIC and comparing it to alternative models.
PoisGamma.sSMR.sample <- 100 * apply(cbind(Obs.muni + PoisGamma$nu, Exp.muni +
  PoisGamma$alpha), 1, function(x) {
    rgamma(1000, x[1], x[2])
  })
# DIC
DICPoisson(PoisGamma.sSMR.sample, Obs.muni, Exp.muni)

## D= 1691.704 pD= 112.5128 DIC= 1804.217

```

## Poisson-logNormal model

```

# WinBUGS for the Poisson-logNormal model
ModelLogNormal = function() {
  for (i in 1:n) {
    O[i] ~ dpois(lambda[i])
    log(lambda[i]) <- log(E[i]) + log.theta[i]
    log.theta[i] <- mu + het[i]
    het[i] ~ dnorm(0, tau)
    sSMR[i] <- 100 * exp(log.theta[i])
    P.sSMR[i] <- step(sSMR[i] - 100)
  }
  mu ~ dflat()
  tau <- pow(sd.het, -2)
  sd.het ~ dunif(0, 10)
}

# Call to the WinBUGS model above to compute the sSMRs corresponding to
# this model.
data <- list(O = Obs.muni, E = Exp.muni, n = 540)
inits <- function() {
  list(het = rnorm(540), mu = rnorm(1))
}
param <- c("sSMR", "mu", "sd.het")
ResulLN <- pbugs(data = data, inits = inits, param = param, n.iter = 2200,
  n.burnin = 200, model.file = ModelLogNormal, bugs.seed = 1)
# Computing time
ResulLN$exec_time

```

## Time difference of 13.46477 secs

### # Result summaries

```
summary(ResulLN$summary[, "Rhat"])
```

```
##      Min. 1st Qu.  Median    Mean 3rd Qu.    Max.
## 0.9995  1.0003  1.0013  1.0018  1.0028  1.0133
```

```
summary(ResulLN$summary[, "n.eff"])
```

```
##      Min. 1st Qu.  Median    Mean 3rd Qu.    Max.
##   170.0   720.0  1000.0   854.6  1000.0  1000.0
```

```

round(ResulLN$summary[c("mu", "sd.het"), ], 1)

##          mean sd 2.5% 25% 50% 75% 97.5% Rhat n.eff
## mu      -0.1  0 -0.2 -0.1 -0.1 -0.1 -0.1  1 1000
## sd.het  0.2  0  0.2  0.2  0.2  0.3  0.3  1 1000

# DIC
DICPoisson(ResulLN$sims.matrix[, grep("sSMR", dimnames(ResulLN$sims.matrix)[[2]])],
  Obs.muni, Exp.muni)

## D= 1727.075 pD= 88.0676 DIC= 1815.143
# smoothed SMRs for Castell de Cabres and Oliva for this model
VR.cart@data[VR.cart$NOMBRE == "Castell de Cabres", ]

##          AREA PERIMETER MUNI_ MUNI_ID CODMUNI CODPROV CODAUTO CODCOMAR
## 12037 30777133 27462.59 5119 5119 12037 12 12 02
##          NOMBRE POB91 POB95 POB95M POB95F
## 12037 Castell de Cabres 24 21 11 10
PoisGamma.sSMR[which(dimnames(PopM)[[1]] == "12037")]

## [1] 100.3617
100 * Obs.muni[which(dimnames(PopM)[[1]] == "12037")]/Exp.muni[which(dimnames(PopM)[[1]] ==
  "12037")]

## 12037
## 3977.445
VR.cart@data[VR.cart$NOMBRE == "Oliva", ]

##          AREA PERIMETER MUNI_ MUNI_ID CODMUNI CODPROV CODAUTO CODCOMAR
## 46181 60080946 41274.36 6928 6928 46181 46 12 00
##          NOMBRE POB91 POB95 POB95M POB95F
## 46181 Oliva 20289 20828 10255 10573
PoisGamma.sSMR[which(dimnames(PopM)[[1]] == "46181")]

## [1] 174.5226
100 * Obs.muni[which(dimnames(PopM)[[1]] == "46181")]/Exp.muni[which(dimnames(PopM)[[1]] ==
  "46181")]

## 46181
## 214.764

```

## Alternative INLA fitting of the Poisson-logNormal model

```

# Uniform prior distribution for the standard deviation of the random
# effects
sdunif = "expression:
\tlogdens = -log_precision/2;
\treturn(logdens)"

data = data.frame(O = Obs.muni, E = Exp.muni, id.node = 1:540)
form = O ~ f(id.node, model = "iid", hyper = list(prec = list(prior = sdunif)))
resul.INLA = inla(form, family = "poisson", data = data, E = E, control.compute = list(dic = TRUE))

```

```
# Computing time
```

```
resul.INLA
```

```
##
```

```
## Call:
```

```
## c("inla(formula = form, family = \"poisson\", data = data, E = E, \" \" control.compute = list(di
```

```
##
```

```
## Time used:
```

```
## Pre-processing Running inla Post-processing Total
```

```
## 1.3918679 1.2177379 0.1219301 2.7315359
```

```
##
```

```
## Integration Strategy: Model contains 1 hyperparameters
```

```
## The model contains 1 fixed effect (including a possible intercept)
```

```
##
```

```
## Likelihood model: poisson
```

```
##
```

```
## The model has 1 random effects:
```

```
## 1.'id.node' is a IID model
```

```
# DIC
```

```
resul.INLA$dic$dic
```

```
## [1] 1817.63
```

```
# Fit with strategy='laplace' option
```

```
resul.INLA2 = inla(form, family = "poisson", data = data, E = E, control.compute = list(dic = TRUE),
```

```
control.inla = list(strategy = "laplace"))
```

```
# Computing time
```

```
resul.INLA2
```

```
##
```

```
## Call:
```

```
## c("inla(formula = form, family = \"poisson\", data = data, E = E, \" \" control.compute = list(di
```

```
##
```

```
## Time used:
```

```
## Pre-processing Running inla Post-processing Total
```

```
## 1.1048229 7.9284542 0.1299088 9.1631858
```

```
##
```

```
## Integration Strategy: Model contains 1 hyperparameters
```

```
## The model contains 1 fixed effect (including a possible intercept)
```

```
##
```

```
## Likelihood model: poisson
```

```
##
```

```
## The model has 1 random effects:
```

```
## 1.'id.node' is a IID model
```

```
# DIC
```

```
resul.INLA2$dic$dic
```

```
## [1] 1817.916
```

```
# Correlation for the sSMRs of both implementations
```

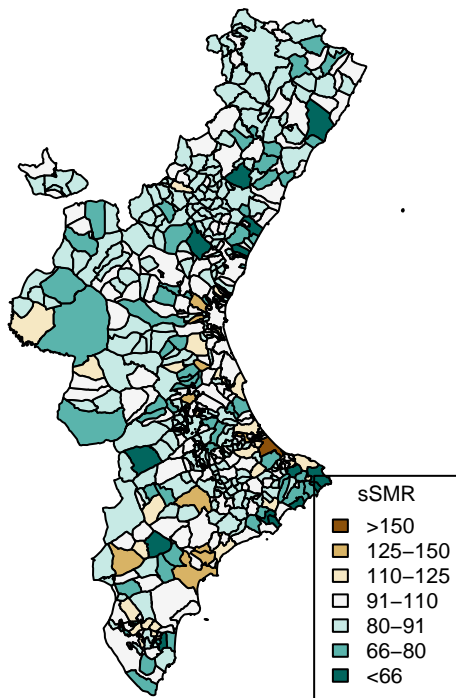
```
cor(ResulLN$mean$sSMR, resul.INLA2$summary.fitted.values[, 1])
```

```
## [1] 0.9977109
```

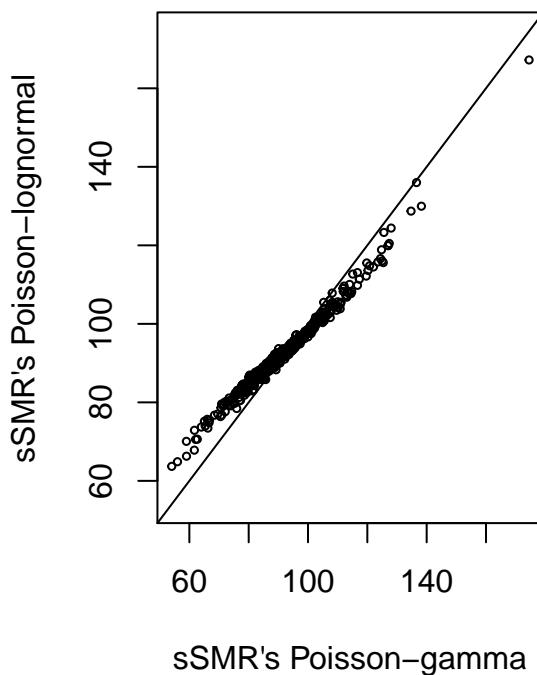
## Comparison between the Poisson-gamma and Poisson-logNormal sSMRs

```
# Figure in the example
colors <- brewer.pal(7, "BrBG")[7:1]
par(mfrow = c(1, 2))
par(mar = c(1, 1, 2, 1) + 0.1)
plot(VR.cart, col = colors[as.numeric(cut(PoisGamma.sSMR, 100 * c(-0.1,
  1/1.5, 1/1.25, 1/1.1, 1.1, 1.25, 1.5, 100))))])
title("Poisson-gamma model", 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 = 0.65, inset = 0.03,
  title = "sSMR")
par(mar = c(5, 4, 4, 2) + 0.1)
plot(PoisGamma.sSMR, ResulLN$mean$sSMR, xlab = "sSMR's Poisson-gamma",
  ylab = "sSMR's Poisson-lognormal", main = "sSMR's for both models",
  cex = 0.5, xlim = c(min(PoisGamma.sSMR), max(PoisGamma.sSMR)), ylim = c(min(PoisGamma.sSMR),
    max(PoisGamma.sSMR)))
abline(c(0, 1))
```

**Poisson-gamma model**



**sSMR's for both models**



```
# Summaries
sd(PoisGamma.sSMR)

## [1] 12.88918

sd(ResulLN$mean$sSMR)

## [1] 9.6445
```

```
cor(PoisGamma.sSMR, ResultLN$mean$sSMR)
```

```
## [1] 0.9900888
```