Example 2.1

Disease mapping: from foundations to multidimensional modeling

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This document reproduces the analysis made at Example 2.1 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.

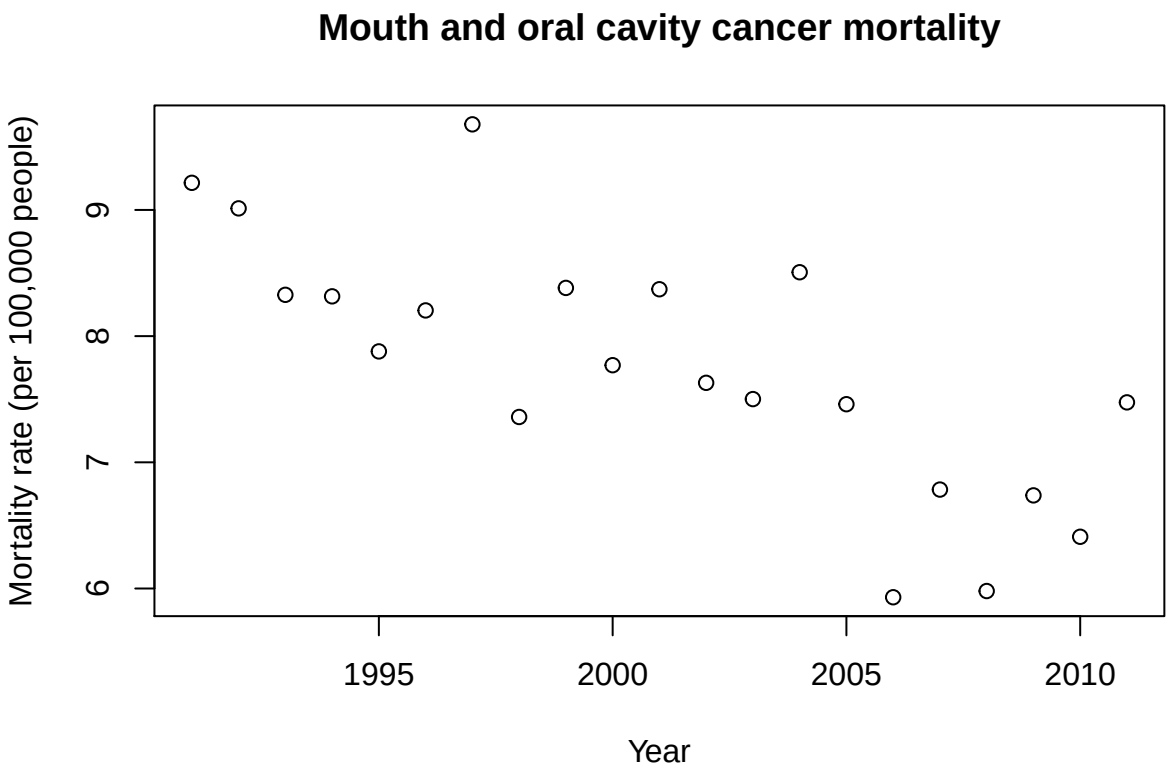
The statistical analysis below has been run in `R`, by additionally using the library `Rmarkdown`, so be sure that you have this software installed if you want to reproduce by yourself the content of this document. In that case we advise you to download first the annex material at https://github.com/MigueBeneito/DMBook, 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.

Libraries and data loading

```
# Libraries loading
#------------------

# library for numerical integration
if (!require(cubature)) {
    install.packages("cubature")
    library(cubature)
}

# Data loading
#------------
load("../Data/OralCancerTimeTrends.RData")
```

Data preparation and plotting

```
# data preparation
#-----------------
year = 1991:2011
year.centered = year - mean(year)

rates = 1e+05 * O/Pop

# data plotting
#-------------
plot(year, rates, xlab = "Year", ylab = "Mortality rate (per 100,000 people)",
    main = "Mouth and oral cavity cancer mortality")
```



Frequentist analysis

```
# Linear model
RateVsYear = lm(rates ~ year.centered)

# Summary for the linear model
summary(RateVsYear)
```

```
##
## Call:
## lm(formula = rates ~ year.centered)
##
## Residuals:
##      Min       1Q   Median       3Q      Max
## -1.20992 -0.30830 -0.03206  0.22072  1.42554
##
## Coefficients:
##               Estimate Std. Error t value Pr(>|t|)
## (Intercept)    7.75854    0.14611  53.102  < 2e-16 ***
## year.centered -0.12358    0.02413  -5.122 6.06e-05 ***
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
##
## Residual standard error: 0.6695 on 19 degrees of freedom
```

```
## Multiple R-squared:  0.5799, Adjusted R-squared:  0.5578
## F-statistic: 26.23 on 1 and 19 DF,  p-value: 6.064e-05
```

```
# Confidence intervals for the parameters in the linear model
confint(RateVsYear)
```

```
##                     2.5 %      97.5 %
## (Intercept)    7.4527395  8.06434706
## year.centered -0.1740793 -0.07307567
```

Bayesian analysis

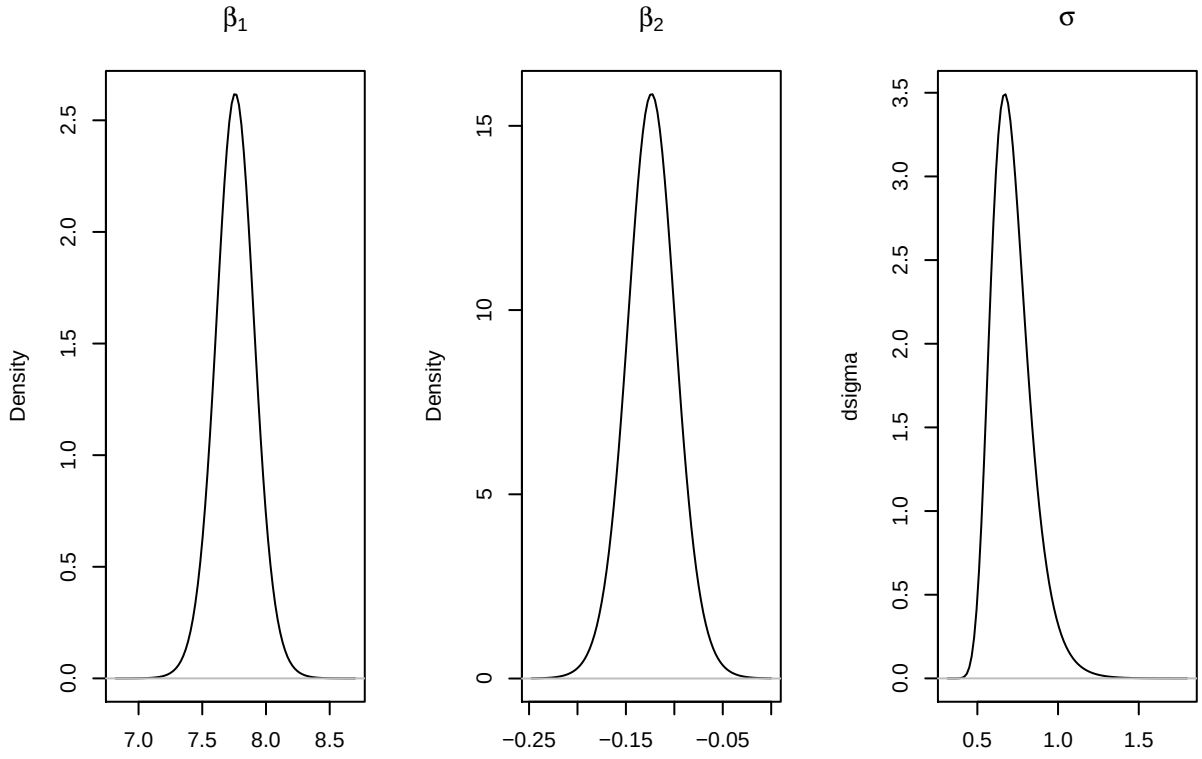
Computation of the posterior distribution of the parameters in the model

```
# Full posterior distribution without the unknown integration constant
post.full = function(y, x, beta1, beta2, sigma, sd.beta, sigma.up) {
    sigma^(-length(y)) * (sigma < sigma.up) * exp(-0.5 * ((beta1^2 + beta2^2)/(sd.beta^2) +
        sum((y - beta1 - beta2 * x)^2)/(sigma^2)))
}

# posterior distribution as a function of a single argument, as
# required for the numerical integration function adaptIntegrate
posterior = function(argum) {
    post.full(rates, year.centered, argum[1], argum[2], argum[3], 1000,
        1000)
}

# Integral of the full posterior distribution without integration
# constant as defined above.
total = hcubature(posterior, lowerLimit = c(6.8, -0.25, 0.3), upperLimit = c(8.7,
    0, 1.8))$integral

# posterior distribution for beta1 given the rest of parameters
post.beta1 = function(beta1, other) {
    posterior(c(beta1, other[1], other[2]))
}
# posterior distribution for beta2 given the rest of parameters
post.beta2 = function(beta2, other) {
    posterior(c(other[1], beta2, other[2]))
}
# posterior distribution for sigma given the rest of parameters
post.sigma = function(sigma, other) {
    posterior(c(other[1], other[2], sigma))
}

# posterior densities for a grid of values for beta1, beta2 and sigma
#------------------------------------------------------------------------

# grid of values
range.beta1 = 6.8 + (1:100) * 1.9/100
range.beta2 = -0.25 + (1:100) * 0.25/100
range.sigma = 0.3 + (1:100) * 1.5/100
```

```r
# posterior densities
dbeta1 = vector()
dbeta2 = vector()
dsigma = vector()

for (i in 1:100) {
    dbeta1[i] = hcubature(post.beta1, beta1 = range.beta1[i], lowerLimit = c(-0.25,
        0.3), upperLimit = c(0, 1.8))$integral/total
    dbeta2[i] = hcubature(post.beta2, beta2 = range.beta2[i], lowerLimit = c(6.8,
        0.3), upperLimit = c(8.7, 1.8))$integral/total
    dsigma[i] = hcubature(post.sigma, sigma = range.sigma[i], lowerLimit = c(6.8,
        -0.25), upperLimit = c(8.7, 0))$integral/total
}
pbeta1 <- dbeta1 * (1.9/100)
pbeta2 <- dbeta2 * (0.25/100)
psigma <- dsigma * (1.5/100)
```

Posterior distributions plotting

```r
par(mfrow = c(1, 3))
plot(range.beta1, dbeta1, main = expression(beta[1]), type = "l", xlab = "",
    ylab = "Density")
abline(h = 0, col = "gray")
plot(range.beta2, dbeta2, main = expression(beta[2]), type = "l", xlab = "",
    ylab = "Density")
abline(h = 0, col = "gray")
plot(range.sigma, dsigma, main = expression(sigma), type = "l", xlab = "")
abline(h = 0, col = "gray")
```



Posterior summaries

```
# Posterior mean for beta1
sum(range.beta1 * pbeta1)
```

```
## [1] 7.758545
```

```
# Posterior mean for beta2
sum(range.beta2 * pbeta2)
```

```
## [1] -0.1235778
```

```
# Posterior mean for sigma
sum(range.sigma * psigma)
```

```
## [1] 0.7182637
```

```
# 95% credible interval for beta1
c(range.beta1[sum(cumsum(pbeta1) < 0.025)], range.beta1[sum(cumsum(pbeta1) <
    0.975)])
```

```
## [1] 7.427 8.054
```

```
# 95% credible interval for beta2
c(range.beta2[sum(cumsum(pbeta2) < 0.025)], range.beta2[sum(cumsum(pbeta2) <
    0.975)])
```

```
## [1] -0.1775 -0.0750
```

```r
# 95% credible interval for sigma
c(range.sigma[sum(cumsum(psigma) < 0.025)], range.sigma[sum(cumsum(psigma) <
    0.975)])
```

```
## [1] 0.510 1.005
```