Example 9.1

Disease mapping: from foundations to multidimensional modeling

Martinez-Beneito M. and Botella-Rocamora P.

This document reproduces the analysis made at Example 9.1 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.

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

```r
if (!require(RColorBrewer)) {
    install.packages("RColorBrewer")
    library(RColorBrewer)
}
if (!require(rgdal)) {
    install.packages("rgdal")
    library(rgdal)
}
if (!require(pbugs)) {
    if (!require(devtools)) {
        install.packages("devtools")
        devtools::install_github("fisabio/pbugs")
    } else {
        install_github("fisabio/pbugs")
    }
}

# For reproducing the document, the following line should be changed to
# load('../Data/ObsMDM-mod.Rdata') since that file contains the modified
# data making it possible to reproduce this document.
load("../Data/ObsMDM.Rdata")
# load('../Data/ObsOral-mod.Rdata')
load("../Data/ExpMDM.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.

```r
# 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")
}
```

Function monitoring the convergence of the deviance of multidimensional models

```r
plot.deviance = function(resul) {
    deviances = matrix(nrow = dim(resul$sims.array)[1], ncol = dim(resul$sims.array)[2])
    for (j in 1:(dim(resul$sims.array)[2])) {
        for (i in 1:(dim(resul$sims.array)[1])) {
            sSMR = aperm(array(resul$sims.array[i, j, grep("sSMR", dimnames(resul$summary)[[1]])],
                dim = dim(Obs.md)[4:1]), 4:1)
            deviances[i, j] = -2 * sum(dpois(as.vector(Obs.md), as.vector((sSMR/100) *
                Exp.md), log = T))
        }
    }
    plot(deviances[, 1], type = "l", ylim = c(min(deviances), max(deviances)),
        ylab = "Deviance", xlab = "Iteration saved")
    for (j in 2:(dim(resul$sims.array)[2])) {
        lines(deviances[, j], col = j)
    }
}
```

Definition of some constants that will be extensively used for the rest of the analysis

```
num.simu = 30000
num.burnin = 10000

Nmuni = 540
Nper = 5
Ndiseases = 2
Nsex = 2
nGroups = c(Nmuni, Nper, Ndiseases, Nsex)  #Municipalities, Periods, Diseases, Sexes

num = VR.wb$num
adj = VR.wb$adj

# We define the data for the multidimensional models here since they will be
# common to all the models run
data = list(Obs = Obs.md, Exp = Exp.md, nGroups = nGroups, adj = adj, num = num,
    C = rep(1/num, num), M = 1/num)
```

Fully separable model

```
model1.2.3.4 = function() {
    for (k in 1:(nGroups[4])) {
        # Sex Disease Period Municipality
        for (j in 1:(nGroups[3])) {
            for (p in 1:(nGroups[2])) {
                for (i in 1:(nGroups[1])) {
                    Obs[i, p, j, k] ~ dpois(lambda[i, p, j, k])
                    log(lambda[i, p, j, k]) <- log(Exp[i, p, j, k]) + log.theta[i,
                        p, j, k]
                    log.theta[i, p, j, k] <- mu[p, j, k] + S1234[i, p, j, k]
                    # Adds dependence between sexes
                    S1234[i, p, j, k] <- inprod2(S123[i, p, j, ], structure4[,
                        k])
                    # Adds dependence between diseases
                    S123[i, p, j, k] <- inprod2(S12[i, p, , k], structure3[, j])
                    # Adds dependence between periods
                    S12[i, p, j, k] <- inprod2(tS1[k, j, , i], structure2[, p])

                    sSMR[i, p, j, k] <- 100 * exp(log.theta[i, p, j, k])
                }
                mu[p, j, k] ~ dflat()
                # Spatially dependent underlying random effects
                tS1[k, j, p, 1:(nGroups[1])] ~ car.proper(ceros[], C[], adj[],
                    num[], M[], 1, gamma)
            }
        }
    }

    # Parameters for the PCAR distributions
    for (l in 1:(nGroups[1])) {
```

```
            ceros[l] <- 0
    }
    gamma.inf <- min.bound(C[], adj[], num[], M[])
    gamma.sup <- max.bound(C[], adj[], num[], M[])
    gamma ~ dunif(gamma.inf, gamma.sup)

    # Structure matrix for the second dimension (period). Structure 2 is defined
    # as the upper Cholesky matrix of the covariance matrix of an AR1 process.
    for (pc in 1:(nGroups[2])) {
        # First Row
        structure2[1, pc] <- pow(ro, pc - 1)
        # Rest of columns
        for (pr in 2:(nGroups[2])) {
            structure2[pr, pc] <- step(pc - pr) * pow(ro, pc - pr) * pow((1 -
                ro * ro), 0.5)
        }
    }
    ro ~ dunif(-1, 1)

    # Structure matrix for the third dimension (disease):
    for (i in 1:(nGroups[3])) {
        for (j in 1:(nGroups[3])) {
            structure3[i, j] ~ dnorm(0, prec)
        }
    }

    # Structure matrix for the fourth dimension (sex):
    for (i in 1:(nGroups[4])) {
        for (j in 1:(nGroups[4])) {
            structure4[i, j] ~ dnorm(0, prec)
        }
    }

    # Prior distribution for the random effects variability
    prec <- pow(sdstruct, -2)
    sdstruct ~ dunif(0, 100)
}

inits = function() {
    list(mu = array(runif(Nper * Ndiseases * Nsex, -0.5, 0), dim = c(Nper, Ndiseases,
        Nsex)), ro = runif(1, 0, 1), structure3 = matrix(rnorm(Ndiseases * Ndiseases,
        0, 0.2), nrow = Ndiseases), structure4 = matrix(rnorm(Nsex * Nsex, 0,
        0.2), nrow = Nsex), sdstruct = runif(1, 0, 1), gamma = runif(1, 0.5,
        0.95), tS1 = array(rnorm(Nmuni * Nper * Ndiseases * Nsex, 0, 0.2), dim = c(Nsex,
        Ndiseases, Nper, Nmuni)))
}
param = c("mu", "gamma", "ro", "structure3", "structure4", "sdstruct", "sSMR")

res1.2.3.4 = pbugs(data = data, inits = inits, par = param, model = model1.2.3.4,
    n.iter = num.simu, n.burnin = num.burnin, bugs.seed = 1)
# Computing time
res1.2.3.4$exec_time
# Convergence assessment of identifiable parameters
```

```
aux = c(grep("mu", dimnames(res1.2.3.4$summary)[[1]]), grep("gamma", dimnames(res1.2.3.4$summary)[[1]])
    grep("ro", dimnames(res1.2.3.4$summary)[[1]]), grep("sdstruct", dimnames(res1.2.3.4$summary)[[1]]),
    grep("sSMR", dimnames(res1.2.3.4$summary)[[1]]))
summary(res1.2.3.4$summary[aux, "Rhat"])
summary(res1.2.3.4$summary[aux, "n.eff"])
plot.deviance(res1.2.3.4)
```

Spatial structure nested within period

```
model12.2.3.4 = function() {
    for (k in 1:(nGroups[4])) {
        # Sex Disease Period Municipality
        for (j in 1:(nGroups[3])) {
            for (p in 1:(nGroups[2])) {
                for (i in 1:(nGroups[1])) {
                    Obs[i, p, j, k] ~ dpois(lambda[i, p, j, k])
                    log(lambda[i, p, j, k]) <- log(Exp[i, p, j, k]) + log.theta[i,
                        p, j, k]
                    log.theta[i, p, j, k] <- mu[p, j, k] + S1234[i, p, j, k]
                    # Adds dependence between sexes
                    S1234[i, p, j, k] <- inprod2(S123[i, p, j, ], structure4[,
                        k])
                    # Adds dependence between diseases
                    S123[i, p, j, k] <- inprod2(S12[i, p, , k], structure3[, j])
                    # Adds dependence between periods
                    S12[i, p, j, k] <- inprod2(tS1[k, j, , i], structure2[, p])

                    sSMR[i, p, j, k] <- 100 * exp(log.theta[i, p, j, k])
                }
                mu[p, j, k] ~ dflat()
                # Spatially dependent underlying random effects
                tS1[k, j, p, 1:(nGroups[1])] ~ car.proper(ceros[], C[], adj[],
                    num[], M[], 1, gamma[p])
            }
        }
    }

    # Parameters for the PCAR distributions
    for (l in 1:(nGroups[1])) {
        ceros[l] <- 0
    }
    gamma.inf <- min.bound(C[], adj[], num[], M[])
    gamma.sup <- max.bound(C[], adj[], num[], M[])
    for (p in 1:(nGroups[2])) {
        gamma[p] ~ dunif(gamma.inf, gamma.sup)
    }

    # Structure matrix for the second dimension (period). Structure 2 is defined
    # as the upper Cholesky matrix of the covariance matrix of an AR1 process.
    for (pc in 1:(nGroups[2])) {
        # First Row
        structure2[1, pc] <- pow(ro, pc - 1)
```

```r
        # Rest of columns
        for (pr in 2:(nGroups[2])) {
            structure2[pr, pc] <- step(pc - pr) * pow(ro, pc - pr) * pow((1 -
                ro * ro), 0.5)
        }
    }
    ro ~ dunif(-1, 1)

    # Dimension 3 (Disease):
    for (i in 1:(nGroups[3])) {
        for (j in 1:(nGroups[3])) {
            structure3[i, j] ~ dnorm(0, prec)
        }
    }

    # Dimension 4 (Sex):
    for (i in 1:(nGroups[4])) {
        for (j in 1:(nGroups[4])) {
            structure4[i, j] ~ dnorm(0, prec)
        }
    }

    # Prior distribution for the random effects variability
    prec <- pow(sdstruct, -2)
    sdstruct ~ dunif(0, 100)
}

set.seed(1)
inits = function() {
    list(mu = array(runif(Nper * Ndiseases * Nsex, -0.5, 0), dim = c(Nper, Ndiseases,
        Nsex)), ro = runif(1, 0, 1), structure3 = matrix(rnorm(Ndiseases * Ndiseases,
        0, 0.2), nrow = Ndiseases), structure4 = matrix(rnorm(Nsex * Nsex, 0,
        0.2), nrow = Nsex), sdstruct = runif(1, 0, 10), gamma = runif(Nper,
        0.5, 0.95), tS1 = array(rnorm(Nmuni * Nper * Ndiseases * Nsex, 0, 0.2),
        dim = c(Nsex, Ndiseases, Nper, Nmuni)))
}
param = c("mu", "gamma", "ro", "structure3", "structure4", "sdstruct", "sSMR")

res12.2.3.4 = pbugs(data = data, inits = inits, par = param, model = model12.2.3.4,
    n.iter = num.simu, n.burnin = num.burnin, bugs.seed = 1)
# Computing time
res12.2.3.4$exec_time
# Convergence assessment of identifiable parameters
aux = c(grep("mu", dimnames(res12.2.3.4$summary)[[1]]), grep("ro", dimnames(res12.2.3.4$summary)[[1]]),
    grep("sdstruct", dimnames(res12.2.3.4$summary)[[1]]), grep("sSMR", dimnames(res12.2.3.4$summary)[[1]
summary(res12.2.3.4$summary[aux, "Rhat"])
summary(res12.2.3.4$summary[aux, "n.eff"])
plot.deviance(res12.2.3.4)
```

Spatial structure nested within disease

```r
model13.2.3.4 = function() {
    for (k in 1:(nGroups[4])) {
        # Sex Disease Period Municipality
        for (j in 1:(nGroups[3])) {
            for (p in 1:(nGroups[2])) {
                for (i in 1:(nGroups[1])) {
                    Obs[i, p, j, k] ~ dpois(lambda[i, p, j, k])
                    log(lambda[i, p, j, k]) <- log(Exp[i, p, j, k]) + log.theta[i,
                        p, j, k]
                    log.theta[i, p, j, k] <- mu[p, j, k] + S1234[i, p, j, k]
                    # Adds dependence between sexes
                    S1234[i, p, j, k] <- inprod2(S123[i, p, j, ], structure4[,
                        k])
                    # Adds dependence between diseases
                    S123[i, p, j, k] <- inprod2(S12[i, p, , k], structure3[, j])
                    # Adds dependence between periods
                    S12[i, p, j, k] <- inprod2(tS1[k, j, , i], structure2[, p])

                    sSMR[i, p, j, k] <- 100 * exp(log.theta[i, p, j, k])

                }
                mu[p, j, k] ~ dflat()
                # Spatially dependent underlying random effects
                tS1[k, j, p, 1:(nGroups[1])] ~ car.proper(ceros[], C[], adj[],
                    num[], M[], 1, gamma[j])
            }
        }
    }

    # Parameters for the PCAR distributions
    for (l in 1:(nGroups[1])) {
        ceros[l] <- 0
    }
    gamma.inf <- min.bound(C[], adj[], num[], M[])
    gamma.sup <- max.bound(C[], adj[], num[], M[])
    for (j in 1:(nGroups[3])) {
        gamma[j] ~ dunif(gamma.inf, gamma.sup)
    }

    # Structure matrix for the second dimension (period). Structure 2 is defined
    # as the upper Cholesky matrix of the covariance matrix of an AR1 process.
    for (pc in 1:(nGroups[2])) {
        # First Row
        structure2[1, pc] <- pow(ro, pc - 1)
        # Rest of columns
        for (pr in 2:(nGroups[2])) {
            structure2[pr, pc] <- step(pc - pr) * pow(ro, pc - pr) * pow((1 -
                ro * ro), 0.5)
        }
    }
    ro ~ dunif(-1, 1)
```

```r
    # Dimension 3 (Disease):
    for (i in 1:(nGroups[3])) {
        for (j in 1:(nGroups[3])) {
            structure3[i, j] ~ dnorm(0, prec)
        }
    }

    # Dimension 4 (Sex):
    for (i in 1:(nGroups[4])) {
        for (j in 1:(nGroups[4])) {
            structure4[i, j] ~ dnorm(0, prec)
        }
    }

    # Prior distribution for the random effects variability
    prec <- pow(sdstruct, -2)
    sdstruct ~ dunif(0, 100)
}

inits = function() {
    list(mu = array(runif(Nper * Ndiseases * Nsex, -0.5, 0), dim = c(Nper, Ndiseases,
        Nsex)), ro = runif(1, 0, 1), structure3 = matrix(rnorm(Ndiseases * Ndiseases,
        0, 0.2), nrow = Ndiseases), structure4 = matrix(rnorm(Nsex * Nsex, 0,
        0.2), nrow = Nsex), sdstruct = runif(1, 0, 1), gamma = runif(Ndiseases,
        0.5, 0.95), tS1 = array(rnorm(Nmuni * Nper * Ndiseases * Nsex, 0, 0.2),
        dim = c(Nsex, Ndiseases, Nper, Nmuni)))
}
param = c("mu", "gamma", "ro", "structure3", "structure4", "sdstruct", "sSMR")

res13.2.3.4 = pbugs(data = data, inits = inits, par = param, model = model13.2.3.4,
    n.iter = num.simu, n.burnin = num.burnin, bugs.seed = 1)
# Computing time
res13.2.3.4$exec_time
# Convergence assessment of identifiable parameters
aux = c(grep("mu", dimnames(res13.2.3.4$summary)[[1]]), grep("ro", dimnames(res13.2.3.4$summary)[[1]]),
    grep("sdstruct", dimnames(res13.2.3.4$summary)[[1]]), grep("sSMR", dimnames(res13.2.3.4$summary)[[1]
summary(res13.2.3.4$summary[aux, "Rhat"])
summary(res13.2.3.4$summary[aux, "n.eff"])
plot.deviance(res13.2.3.4)
```

Spatial structure nested within sex

```r
model14.2.3.4 = function() {
    for (k in 1:(nGroups[4])) {
        # Sex Disease Period Municipality
        for (j in 1:(nGroups[3])) {
            for (p in 1:(nGroups[2])) {
                for (i in 1:(nGroups[1])) {
                    Obs[i, p, j, k] ~ dpois(lambda[i, p, j, k])
                    log(lambda[i, p, j, k]) <- log(Exp[i, p, j, k]) + log.theta[i,
                        p, j, k]
```

```
                     log.theta[i, p, j, k] <- mu[p, j, k] + S1234[i, p, j, k]
                     # Adds dependence between sexes
                     S1234[i, p, j, k] <- inprod2(S123[i, p, j, ], structure4[,
                        k])
                     # Adds dependence between diseases
                     S123[i, p, j, k] <- inprod2(S12[i, p, , k], structure3[, j])
                     # Adds dependence between periods
                     S12[i, p, j, k] <- inprod2(tS1[k, j, , i], structure2[, p])

                     sSMR[i, p, j, k] <- 100 * exp(log.theta[i, p, j, k])
                  }
                  mu[p, j, k] ~ dflat()
                  # Spatially dependent underlying random effects
                  tS1[k, j, p, 1:(nGroups[1])] ~ car.proper(ceros[], C[], adj[],
                     num[], M[], 1, gamma[k])
               }
         }
      }

      # Parameters for the PCAR distributions
      for (l in 1:(nGroups[1])) {
         ceros[l] <- 0
      }
      gamma.inf <- min.bound(C[], adj[], num[], M[])
      gamma.sup <- max.bound(C[], adj[], num[], M[])
      for (k in 1:(nGroups[4])) {
         gamma[k] ~ dunif(gamma.inf, gamma.sup)
      }

      # Structure matrix for the second dimension (period). Structure 2 is defined
      # as the upper Cholesky matrix of the covariance matrix of an AR1 process.
      for (pc in 1:(nGroups[2])) {
         # First Row
         structure2[1, pc] <- pow(ro, pc - 1)
         # Rest of columns
         for (pr in 2:(nGroups[2])) {
            structure2[pr, pc] <- step(pc - pr) * pow(ro, pc - pr) * pow((1 -
               ro * ro), 0.5)
         }
      }
      ro ~ dunif(-1, 1)

      # Dimension 3 (Disease):
      for (i in 1:(nGroups[3])) {
         for (j in 1:(nGroups[3])) {
            structure3[i, j] ~ dnorm(0, prec)
         }
      }

      # Dimension 4 (Sex):
      for (i in 1:(nGroups[4])) {
         for (j in 1:(nGroups[4])) {
            structure4[i, j] ~ dnorm(0, prec)
```

```
        }
    }

    # Prior distribution for the random effects variability
    prec <- pow(sdstruct, -2)
    sdstruct ~ dunif(0, 100)
}

inits = function() {
    list(mu = array(runif(Nper * Ndiseases * Nsex, -0.5, 0), dim = c(Nper, Ndiseases,
        Nsex)), ro = runif(1, 0, 1), structure3 = matrix(rnorm(Ndiseases * Ndiseases,
        0, 0.2), nrow = Ndiseases), structure4 = matrix(rnorm(Nsex * Nsex, 0,
        0.2), nrow = Nsex), sdstruct = runif(1, 0, 1), gamma = runif(Nsex, 0.5,
        0.95), tS1 = array(rnorm(Nmuni * Nper * Ndiseases * Nsex, 0, 0.2), dim = c(Nsex,
        Ndiseases, Nper, Nmuni)))
}
param = c("mu", "gamma", "ro", "structure3", "structure4", "sdstruct", "sSMR")

res14.2.3.4 = pbugs(data = data, inits = inits, par = param, model = model14.2.3.4,
    n.iter = num.simu, n.burnin = num.burnin, bugs.seed = 1)
# Computing time
res14.2.3.4$exec_time
# Convergence assessment of identifiable parameters
aux = c(grep("mu", dimnames(res14.2.3.4$summary)[[1]]), grep("ro", dimnames(res14.2.3.4$summary)[[1]]),
    grep("sdstruct", dimnames(res14.2.3.4$summary)[[1]]), grep("sSMR", dimnames(res14.2.3.4$summary)[[1]
summary(res14.2.3.4$summary[aux, "Rhat"])
summary(res14.2.3.4$summary[aux, "n.eff"])
plot.deviance(res14.2.3.4)
```

Temporal structure nested within disease

```
model1.23.3.4 = function() {
    for (k in 1:(nGroups[4])) {
        # Sex Disease Period Municipality
        for (j in 1:(nGroups[3])) {
            for (p in 1:(nGroups[2])) {
                for (i in 1:(nGroups[1])) {
                    Obs[i, p, j, k] ~ dpois(lambda[i, p, j, k])
                    log(lambda[i, p, j, k]) <- log(Exp[i, p, j, k]) + log.theta[i,
                        p, j, k]
                    log.theta[i, p, j, k] <- mu[p, j, k] + S1234[i, p, j, k]
                    # Adds dependence between sexes
                    S1234[i, p, j, k] <- inprod2(S123[i, p, j, ], structure4[,
                        k])
                    # Adds dependence between diseases
                    S123[i, p, j, k] <- inprod2(S12[i, p, , k], structure3[, j])
                    # Adds dependence between periods
                    S12[i, p, j, k] <- inprod2(tS1[k, j, , i], structure2[, p,
                        j])

                    sSMR[i, p, j, k] <- 100 * exp(log.theta[i, p, j, k])
                }
```

```
                    mu[p, j, k] ~ dflat()
                    # Spatially dependent underlying random effects
                    tS1[k, j, p, 1:(nGroups[1])] ~ car.proper(ceros[], C[], adj[],
                        num[], M[], 1, gamma)
                }
            }
        }

        # Parameters for the PCAR distributions
        for (l in 1:(nGroups[1])) {
            ceros[l] <- 0
        }
        gamma.inf <- min.bound(C[], adj[], num[], M[])
        gamma.sup <- max.bound(C[], adj[], num[], M[])
        gamma ~ dunif(gamma.inf, gamma.sup)

        # Structure matrix for the second dimension (period). Structure 2 is defined
        # as the upper Cholesky matrix of the covariance matrix of an AR1 process.
        for (j in 1:(nGroups[3])) {
            for (pc in 1:(nGroups[2])) {
                # First Row
                structure2[1, pc, j] <- pow(ro[j], pc - 1)
                # Rest of columns
                for (pr in 2:(nGroups[2])) {
                    structure2[pr, pc, j] <- step(pc - pr) * pow(ro[j], pc - pr) *
                        pow((1 - ro[j] * ro[j]), 0.5)
                }
            }
            ro[j] ~ dunif(-1, 1)
        }

        # Structure matrix for the third dimension (disease):
        for (i in 1:(nGroups[3])) {
            for (j in 1:(nGroups[3])) {
                structure3[i, j] ~ dnorm(0, prec)
            }
        }

        # Structure matrix for the third dimension (sex):
        for (i in 1:(nGroups[4])) {
            for (j in 1:(nGroups[4])) {
                structure4[i, j] ~ dnorm(0, prec)
            }
        }

        # Prior distribution for the random effects variability
        prec <- pow(sdstruct, -2)
        sdstruct ~ dunif(0, 100)
}

inits = function() {
    list(mu = array(runif(Nper * Ndiseases * Nsex, -0.5, 0), dim = c(Nper, Ndiseases,
        Nsex)), ro = runif(Ndiseases, 0, 0.2), structure3 = matrix(rnorm(Ndiseases *
```

```r
        Ndiseases, 0, 0.2), nrow = Ndiseases), structure4 = matrix(rnorm(Nsex *
        Nsex, 0, 1), nrow = Nsex), sdstruct = runif(1, 0, 1), gamma = runif(1,
        0.5, 0.95), tS1 = array(rnorm(Nmuni * Nper * Ndiseases * Nsex, 0, 0.2),
        dim = c(Nsex, Ndiseases, Nper, Nmuni)))
}
param = c("mu", "gamma", "ro", "structure3", "structure4", "sdstruct", "sSMR")
res1.23.3.4 = pbugs(data = data, inits = inits, par = param, model = model1.23.3.4,
    n.iter = num.simu, n.burnin = num.burnin, bugs.seed = 1)
# Computing time
res1.23.3.4$exec_time
# Convergence assessment of identifiable parameters
aux = c(grep("mu", dimnames(res1.23.3.4$summary)[[1]]), grep("gamma", dimnames(res1.23.3.4$summary)[[1]]
    grep("sdstruct", dimnames(res1.23.3.4$summary)[[1]]), grep("sSMR", dimnames(res1.23.3.4$summary)[[1]
summary(res1.23.3.4$summary[aux, "Rhat"])
summary(res1.23.3.4$summary[aux, "n.eff"])
plot.deviance(res1.23.3.4)
```

Temporal structure nested within sex

```r
model1.24.3.4 = function() {
    for (k in 1:(nGroups[4])) {
        # Sex Disease Period Municipality
        for (j in 1:(nGroups[3])) {
            for (p in 1:(nGroups[2])) {
                for (i in 1:(nGroups[1])) {
                    Obs[i, p, j, k] ~ dpois(lambda[i, p, j, k])
                    log(lambda[i, p, j, k]) <- log(Exp[i, p, j, k]) + log.theta[i,
                      p, j, k]
                    log.theta[i, p, j, k] <- mu[p, j, k] + S1234[i, p, j, k]
                    # Adds dependence between sexes
                    S1234[i, p, j, k] <- inprod2(S123[i, p, j, ], structure4[,
                      k])
                    # Adds dependence between diseases
                    S123[i, p, j, k] <- inprod2(S12[i, p, , k], structure3[, j])
                    # Adds dependence between periods
                    S12[i, p, j, k] <- inprod2(tS1[k, j, , i], structure2[, p,
                      k])

                    sSMR[i, p, j, k] <- 100 * exp(log.theta[i, p, j, k])
                }
                mu[p, j, k] ~ dflat()
                # Spatially dependent underlying random effects
                tS1[k, j, p, 1:(nGroups[1])] ~ car.proper(ceros[], C[], adj[],
                  num[], M[], 1, gamma)
            }
        }
    }

    # Parameters for the PCAR distributions
    for (l in 1:(nGroups[1])) {
        ceros[l] <- 0
    }
```

```
    gamma.inf <- min.bound(C[], adj[], num[], M[])
    gamma.sup <- max.bound(C[], adj[], num[], M[])
    gamma ~ dunif(gamma.inf, gamma.sup)

    # Structure matrix for the second dimension (period). Structure 2 is defined
    # as the upper Cholesky matrix of the covariance matrix of an AR1 process.
    for (k in 1:(nGroups[4])) {
        for (pc in 1:(nGroups[2])) {
            # First Row
            structure2[1, pc, k] <- pow(ro[k], pc - 1)
            # Rest of columns
            for (pr in 2:(nGroups[2])) {
                structure2[pr, pc, k] <- step(pc - pr) * pow(ro[k], pc - pr) *
                  pow((1 - ro[k] * ro[k]), 0.5)
            }
        }
        ro[k] ~ dunif(-1, 1)
    }

    # Structure matrix for the third dimension (disease):
    for (i in 1:(nGroups[3])) {
        for (j in 1:(nGroups[3])) {
            structure3[i, j] ~ dnorm(0, prec)
        }
    }

    # Structure matrix for the third dimension (sex):
    for (i in 1:(nGroups[4])) {
        for (j in 1:(nGroups[4])) {
            structure4[i, j] ~ dnorm(0, prec)
        }
    }

    # Prior distribution for the random effects variability
    prec <- pow(sdstruct, -2)
    sdstruct ~ dunif(0, 100)
}

inits = function() {
    list(mu = array(runif(Nper * Ndiseases * Nsex, -0.5, 0), dim = c(Nper, Ndiseases,
        Nsex)), ro = runif(Nsex, 0, 1), structure3 = matrix(rnorm(Ndiseases *
        Ndiseases, 0, 0.2), nrow = Ndiseases), structure4 = matrix(rnorm(Nsex *
        Nsex, 0, 0.2), nrow = Nsex), sdstruct = runif(1, 0, 1), gamma = runif(1,
        0.5, 0.95), tS1 = array(rnorm(Nmuni * Nper * Ndiseases * Nsex, 0, 0.2),
        dim = c(Nsex, Ndiseases, Nper, Nmuni)))
}
param <- c("mu", "gamma", "ro", "structure3", "structure4", "sdstruct", "sSMR")

res1.24.3.4 = pbugs(data = data, inits = inits, par = param, model = model1.24.3.4,
    n.iter = num.simu, n.burnin = num.burnin, bugs.seed = 1)
# Computing time
res1.24.3.4$exec_time
# Convergence assessment of identifiable parameters
```

```
aux <- c(grep("mu", dimnames(res1.24.3.4$summary)[[1]]), grep("gamma", dimnames(res1.24.3.4$summary)[[1]
    grep("sdstruct", dimnames(res1.24.3.4$summary)[[1]]), grep("sSMR", dimnames(res1.24.3.4$summary)[[1]
summary(res1.24.3.4$summary[aux, "Rhat"])
summary(res1.24.3.4$summary[aux, "n.eff"])
plot.deviance(res1.24.3.4)
```

Disease structure nested within Period

```
model1.2.32.4 = function() {
    for (k in 1:(nGroups[4])) {
        # Sex Disease Period Municipality
        for (j in 1:(nGroups[3])) {
            for (p in 1:(nGroups[2])) {
                for (i in 1:(nGroups[1])) {
                  Obs[i, p, j, k] ~ dpois(lambda[i, p, j, k])
                  log(lambda[i, p, j, k]) <- log(Exp[i, p, j, k]) + log.theta[i,
                    p, j, k]
                  log.theta[i, p, j, k] <- mu[p, j, k] + S1234[i, p, j, k]
                  # Adds dependence between sexes
                  S1234[i, p, j, k] <- inprod2(S123[i, p, j, ], structure4[,
                    k])
                  # Adds dependence between diseases
                  S123[i, p, j, k] <- inprod2(S12[i, p, , k], structure3[, j,
                    p])
                  # Adds dependence between periods
                  S12[i, p, j, k] <- inprod2(tS1[k, j, , i], structure2[, p])

                  sSMR[i, p, j, k] <- 100 * exp(log.theta[i, p, j, k])
                }
                mu[p, j, k] ~ dflat()
                # Spatially dependent underlying random effects
                tS1[k, j, p, 1:(nGroups[1])] ~ car.proper(ceros[], C[], adj[],
                  num[], M[], 1, gamma)
            }
        }
    }

    # Parameters for the PCAR distributions
    for (l in 1:(nGroups[1])) {
        ceros[l] <- 0
    }
    gamma.inf <- min.bound(C[], adj[], num[], M[])
    gamma.sup <- max.bound(C[], adj[], num[], M[])
    gamma ~ dunif(gamma.inf, gamma.sup)

    # Structure matrix for the second dimension (period). Structure 2 is defined
    # as the upper Cholesky matrix of the covariance matrix of an AR1 process.
    for (pc in 1:(nGroups[2])) {
        # First Row
        structure2[1, pc] <- pow(ro, pc - 1)
        # Rest of columns
        for (pr in 2:(nGroups[2])) {
```

```
            structure2[pr, pc] <- step(pc - pr) * pow(ro, pc - pr) * pow((1 -
                ro * ro), 0.5)
        }
    }
    ro ~ dunif(-1, 1)

    # Structure matrix for the third dimension (disease):
    for (p in 1:(nGroups[2])) {
        for (i in 1:(nGroups[3])) {
            for (j in 1:(nGroups[3])) {
                structure3[i, j, p] ~ dnorm(0, prec)
            }
        }
    }

    # Structure matrix for the third dimension (sex):
    for (i in 1:(nGroups[4])) {
        for (j in 1:(nGroups[4])) {
            structure4[i, j] ~ dnorm(0, prec)
        }
    }

    # Prior distribution for the random effects variability
    prec <- pow(sdstruct, -2)
    sdstruct ~ dunif(0, 100)
}

inits = function() {
    list(mu = array(runif(Nper * Ndiseases * Nsex, -0.5, 0), dim = c(Nper, Ndiseases,
        Nsex)), ro = runif(1, 0, 1), structure3 = array(rnorm(Ndiseases * Ndiseases *
        Nper, 0, 0.2), dim = c(Ndiseases, Ndiseases, Nper)), structure4 = matrix(rnorm(Nsex *
        Nsex, 0, 0.2), nrow = Nsex), sdstruct = runif(1, 0, 1), gamma = runif(1,
        0.5, 0.95), tS1 = array(rnorm(Nmuni * Nper * Ndiseases * Nsex, 0, 0.2),
        dim = c(Nsex, Ndiseases, Nper, Nmuni)))
}
param = c("mu", "gamma", "ro", "structure3", "structure4", "sdstruct", "sSMR")

res1.2.32.4 = pbugs(data = data, inits = inits, par = param, model = model1.2.32.4,
    n.iter = num.simu, n.burnin = num.burnin, bugs.seed = 1)
# Computing time
res1.2.32.4$exec_time
# Convergence assessment of identifiable parameters
aux = c(grep("mu", dimnames(res1.2.32.4$summary)[[1]]), grep("gamma", dimnames(res1.2.32.4$summary)[[1]]
    grep("ro", dimnames(res1.2.32.4$summary)[[1]]), grep("sdstruct", dimnames(res1.2.32.4$summary)[[1]]
    grep("sSMR", dimnames(res1.2.32.4$summary)[[1]]))
summary(res1.2.32.4$summary[aux, "Rhat"])
summary(res1.2.32.4$summary[aux, "n.eff"])
plot.deviance(res1.2.32.4)
```

Disease structure nested within sex

```r
model1.2.34.4 = function() {
    for (k in 1:(nGroups[4])) {
        # Sex Disease Period Municipality
        for (j in 1:(nGroups[3])) {
            for (p in 1:(nGroups[2])) {
                for (i in 1:(nGroups[1])) {
                    Obs[i, p, j, k] ~ dpois(lambda[i, p, j, k])
                    log(lambda[i, p, j, k]) <- log(Exp[i, p, j, k]) + log.theta[i,
                      p, j, k]
                    log.theta[i, p, j, k] <- mu[p, j, k] + S1234[i, p, j, k]
                    # Adds dependence between sexes
                    S1234[i, p, j, k] <- inprod2(S123[i, p, j, ], structure4[,
                      k])
                    # Adds dependence between diseases
                    S123[i, p, j, k] <- inprod2(S12[i, p, , k], structure3[, j,
                      k])
                    # Adds dependence between periods
                    S12[i, p, j, k] <- inprod2(tS1[k, j, , i], structure2[, p])

                    sSMR[i, p, j, k] <- 100 * exp(log.theta[i, p, j, k])
                }
                mu[p, j, k] ~ dflat()

                # Spatially dependent underlying random effects
                tS1[k, j, p, 1:(nGroups[1])] ~ car.proper(ceros[], C[], adj[],
                  num[], M[], 1, gamma)
            }
        }
    }

    # Parameters for the PCAR distributions
    for (l in 1:(nGroups[1])) {
        ceros[l] <- 0
    }
    gamma.inf <- min.bound(C[], adj[], num[], M[])
    gamma.sup <- max.bound(C[], adj[], num[], M[])
    gamma ~ dunif(gamma.inf, gamma.sup)

    # Structure matrix for the second dimension (period). Structure 2 is defined
    # as the upper Cholesky matrix of the covariance matrix of an AR1 process.
    for (pc in 1:(nGroups[2])) {
        # First Row
        structure2[1, pc] <- pow(ro, pc - 1)
        # Rest of columns
        for (pr in 2:(nGroups[2])) {
            structure2[pr, pc] <- step(pc - pr) * pow(ro, pc - pr) * pow((1 -
                ro * ro), 0.5)
        }
    }
    ro ~ dunif(-1, 1)
```

```r
    # Structure matrix for the fourth dimension (disease):
    for (k in 1:(nGroups[4])) {
        for (i in 1:(nGroups[3])) {
            for (j in 1:(nGroups[3])) {
                structure3[i, j, k] ~ dnorm(0, prec)
            }
        }
    }

    # Structure matrix for the fourth dimension (sex):
    for (i in 1:(nGroups[4])) {
        for (j in 1:(nGroups[4])) {
            structure4[i, j] ~ dnorm(0, prec)
        }
    }

    # Prior distribution for the random effects variability
    prec <- pow(sdstruct, -2)
    sdstruct ~ dunif(0, 100)
}

inits <- function() {
    list(mu = array(runif(Nper * Ndiseases * Nsex, -0.5, 0), dim = c(Nper, Ndiseases,
        Nsex)), ro = runif(1, 0, 1), structure3 = array(rnorm(Ndiseases * Ndiseases *
        Nsex, 0, 0.2), dim = c(Ndiseases, Ndiseases, Nsex)), structure4 = matrix(rnorm(Nsex *
        Nsex, 0, 0.2), nrow = Nsex), sdstruct = runif(1, 0, 1), gamma = runif(1,
        0.5, 0.95), tS1 = array(rnorm(Nmuni * Nper * Ndiseases * Nsex, 0, 0.2),
        dim = c(Nsex, Ndiseases, Nper, Nmuni)))
}
param = c("mu", "gamma", "ro", "structure3", "structure4", "sdstruct", "sSMR")

res1.2.34.4 = pbugs(data = data, inits = inits, par = param, model = model1.2.34.4,
    n.iter = num.simu, n.burnin = num.burnin, bugs.seed = 1)
# Computing time
res1.2.34.4$exec_time
# Convergence assessment of identifiable parameters
aux <- c(grep("mu", dimnames(res1.2.34.4$summary)[[1]]), grep("gamma", dimnames(res1.2.34.4$summary)[[1]
    grep("ro", dimnames(res1.2.34.4$summary)[[1]]), grep("sdstruct", dimnames(res1.2.34.4$summary)[[1]]
    grep("sSMR", dimnames(res1.2.34.4$summary)[[1]]))
summary(res1.2.34.4$summary[aux, "Rhat"])
summary(res1.2.34.4$summary[aux, "n.eff"])
plot.deviance(res1.2.34.4)
```

Sex structure nested within period

```r
model1.2.3.42 = function() {
    for (k in 1:(nGroups[4])) {
        # Sex Disease Period Municipality
        for (j in 1:(nGroups[3])) {
            for (p in 1:(nGroups[2])) {
                for (i in 1:(nGroups[1])) {
                    Obs[i, p, j, k] ~ dpois(lambda[i, p, j, k])
```

```
                   log(lambda[i, p, j, k]) <- log(Exp[i, p, j, k]) + log.theta[i,
                     p, j, k]
                   log.theta[i, p, j, k] <- mu[p, j, k] + S1234[i, p, j, k]
                   # Adds dependence between sexes
                   S1234[i, p, j, k] <- inprod2(S123[i, p, j, ], structure4[,
                     k, p])
                   # Adds dependence between disease
                   S123[i, p, j, k] <- inprod2(S12[i, p, , k], structure3[, j])
                   # Adds dependence between period
                   S12[i, p, j, k] <- inprod2(tS1[k, j, , i], structure2[, p])

                   sSMR[i, p, j, k] <- 100 * exp(log.theta[i, p, j, k])
                 }
               mu[p, j, k] ~ dflat()
               # Spatially dependent underlying random effects
               tS1[k, j, p, 1:(nGroups[1])] ~ car.proper(ceros[], C[], adj[],
                 num[], M[], 1, gamma)
           }
       }
}

# Parameters for the PCAR distributions
for (l in 1:(nGroups[1])) {
    ceros[l] <- 0
}
gamma.inf <- min.bound(C[], adj[], num[], M[])
gamma.sup <- max.bound(C[], adj[], num[], M[])
gamma ~ dunif(gamma.inf, gamma.sup)

# Structure matrix for the second dimension (period). Structure 2 is defined
# as the upper Cholesky matrix of the covariance matrix of an AR1 process.
for (pc in 1:(nGroups[2])) {
    # First Row
    structure2[1, pc] <- pow(ro, pc - 1)
    # Rest of columns
    for (pr in 2:(nGroups[2])) {
        structure2[pr, pc] <- step(pc - pr) * pow(ro, pc - pr) * pow((1 -
            ro * ro), 0.5)
    }
}
ro ~ dunif(-1, 1)

# Structure matrix for the third dimension (disease):
for (i in 1:(nGroups[3])) {
    for (j in 1:(nGroups[3])) {
        structure3[i, j] ~ dnorm(0, prec)
    }
}

# Structure matrix for the third dimension (sex):
for (k in 1:(nGroups[2])) {
    for (i in 1:(nGroups[4])) {
        for (j in 1:(nGroups[4])) {
```

```r
                        structure4[i, j, k] ~ dnorm(0, prec)
                }
            }
        }

        # Prior distribution for the random effects variability
        prec <- pow(sdstruct, -2)
        sdstruct ~ dunif(0, 100)
}

inits = function() {
    list(mu = array(runif(Nper * Ndiseases * Nsex, -0.5, 0), dim = c(Nper, Ndiseases,
        Nsex)), ro = runif(1, 0, 1), structure3 = matrix(rnorm(Ndiseases * Ndiseases,
        0, 0.2), nrow = Ndiseases), structure4 = array(rnorm(Nsex * Nsex * Nper,
        0, 0.2), dim = c(Nsex, Nsex, Nper)), sdstruct = runif(1, 0, 1), tS1 = array(rnorm(Nmuni *
        Nper * Ndiseases * Nsex, 0, 0.2), dim = c(Nsex, Ndiseases, Nper, Nmuni)))
}
inits = function() {
    list(mu = array(runif(Nper * Ndiseases * Nsex, -0.5, 0), dim = c(Nper, Ndiseases,
        Nsex)), ro = runif(1, 0.7, 1), structure3 = matrix(rnorm(Ndiseases *
        Ndiseases, apply(res1.2.3.42$sims.array[, 3, grep("structure3", dimnames(res1.2.3.42$sims.array)
        2, mean), 0.2), nrow = Ndiseases), structure4 = array(rnorm(Nsex * Nsex *
        Nper, apply(res1.2.3.42$sims.array[, 3, grep("structure4", dimnames(res1.2.3.42$sims.array)[[3]]
        2, mean), 0.1), dim = c(Nsex, Nsex, Nper)), sdstruct = rnorm(1, mean(res1.2.3.42$sims.array[,
        3, "sdstruct"]), 0.1), tS1 = array(rnorm(Nmuni * Nper * Ndiseases *
        Nsex, 0, 1), dim = c(Nsex, Ndiseases, Nper, Nmuni)))
}

param = c("mu", "gamma", "ro", "structure3", "structure4", "sdstruct", "sSMR")

res1.2.3.42 = pbugs(data = data, inits = inits, par = param, model = model1.2.3.42,
    n.iter = num.simu, n.burnin = num.burnin, n.chains = 3)
# Computing time
res1.2.3.42$exec_time
# Convergence assessment of identifiable parameters
aux = c(grep("mu", dimnames(res1.2.3.42$summary)[[1]]), grep("gamma", dimnames(res1.2.3.42$summary)[[1]]
    grep("ro", dimnames(res1.2.3.42$summary)[[1]]), grep("sdstruct", dimnames(res1.2.3.42$summary)[[1]]
    grep("sSMR", dimnames(res1.2.3.42$summary)[[1]]))
summary(res1.2.3.42$summary[aux, "Rhat"])
summary(res1.2.3.42$summary[aux, "n.eff"])
plot.deviance(res1.2.3.42)
```

Sex structure nested within disease

```r
model1.2.3.43 = function() {
    for (k in 1:(nGroups[4])) {
        # Sex Disease Period Municipality
        for (j in 1:(nGroups[3])) {
            for (p in 1:(nGroups[2])) {
                for (i in 1:(nGroups[1])) {
                    Obs[i, p, j, k] ~ dpois(lambda[i, p, j, k])
                    log(lambda[i, p, j, k]) <- log(Exp[i, p, j, k]) + log.theta[i,
```

```
                 p, j, k]
             log.theta[i, p, j, k] <- mu[p, j, k] + S1234[i, p, j, k]
             # Adds dependence between sexes
             S1234[i, p, j, k] <- inprod2(S123[i, p, j, ], structure4[,
               k, j])
             # Adds dependence between diseases
             S123[i, p, j, k] <- inprod2(S12[i, p, , k], structure3[, j])
             # Adds dependence between periods
             S12[i, p, j, k] <- inprod2(tS1[k, j, , i], structure2[, p])

             sSMR[i, p, j, k] <- 100 * exp(log.theta[i, p, j, k])
           }
         mu[p, j, k] ~ dflat()
         # Spatially dependent underlying random effects
         tS1[k, j, p, 1:(nGroups[1])] ~ car.proper(ceros[], C[], adj[],
           num[], M[], 1, gamma)
       }
     }
}


# Parameters for the PCAR distributions
for (l in 1:(nGroups[1])) {
    ceros[l] <- 0
}
gamma.inf <- min.bound(C[], adj[], num[], M[])
gamma.sup <- max.bound(C[], adj[], num[], M[])
gamma ~ dunif(gamma.inf, gamma.sup)

# Structure matrix for the second dimension (period). Structure 2 is defined
# as the upper Cholesky matrix of the covariance matrix of an AR1 process.
for (pc in 1:(nGroups[2])) {
    # First Row
    structure2[1, pc] <- pow(ro, pc - 1)
    # Rest of columns
    for (pr in 2:(nGroups[2])) {
        structure2[pr, pc] <- step(pc - pr) * pow(ro, pc - pr) * pow((1 -
            ro * ro), 0.5)
    }
}
ro ~ dunif(-1, 1)

# Structure matrix for the third dimension (disease):
for (i in 1:(nGroups[3])) {
    for (j in 1:(nGroups[3])) {
        structure3[i, j] ~ dnorm(0, prec)
    }
}

# Structure matrix for the third dimension (sex):
for (k in 1:(nGroups[3])) {
    for (i in 1:(nGroups[4])) {
        for (j in 1:(nGroups[4])) {
            structure4[i, j, k] ~ dnorm(0, prec)
```

```
            }
        }
    }

    # Prior distribution for the random effects variability
    prec <- pow(sdstruct, -2)
    sdstruct ~ dunif(0, 100)
}

inits = function() {
    list(mu = array(runif(Nper * Ndiseases * Nsex, -0.5, 0), dim = c(Nper, Ndiseases,
        Nsex)), ro = runif(1, 0, 1), structure3 = matrix(rnorm(Ndiseases * Ndiseases,
        0, 0.2), nrow = Ndiseases), structure4 = array(rnorm(Nsex * Nsex * Ndiseases,
        0, 0.2), dim = c(Nsex, Nsex, Ndiseases)), sdstruct = runif(1, 0, 1),
        tS1 = array(rnorm(Nmuni * Nper * Ndiseases * Nsex, 0, 0.2), dim = c(Nsex,
            Ndiseases, Nper, Nmuni)))
}
param = c("mu", "gamma", "ro", "structure3", "structure4", "sdstruct", "sSMR")

res1.2.3.43 = pbugs(data = data, inits = inits, par = param, model = model1.2.3.43,
    n.iter = num.simu, n.burnin = num.burnin, bugs.seed = 1)
# Computing time
res1.2.3.43$exec_time
# Convergence assessment of identifiable parameters
aux = c(grep("mu", dimnames(res1.2.3.43$summary)[[1]]), grep("gamma", dimnames(res1.2.3.43$summary)[[1]]
    grep("ro", dimnames(res1.2.3.43$summary)[[1]]), grep("sdstruct", dimnames(res1.2.3.43$summary)[[1]]
    grep("sSMR", dimnames(res1.2.3.43$summary)[[1]]))
summary(res1.2.3.43$summary[aux, "Rhat"])
summary(res1.2.3.43$summary[aux, "n.eff"])
plot.deviance(res1.2.3.43)
```

```
load("Rdata/res1.2.3.4.Rdata")
load("Rdata/res12.2.3.4.Rdata")
load("Rdata/res13.2.3.4.Rdata")
load("Rdata/res14.2.3.4.Rdata")
load("Rdata/res1.23.3.4.Rdata")
load("Rdata/res1.24.3.4.Rdata")
load("Rdata/res1.2.32.4.Rdata")
load("Rdata/res1.2.34.4.Rdata")
load("Rdata/res1.2.3.42.Rdata")
load("Rdata/res1.2.3.43.Rdata")
```

```
# Model 1.2.3.4
#--------------
res1.2.3.4$exec_time
```

```
## Time difference of 16.18184 hours
```

```
# set of identifiable parameters
aux = c(grep("mu", dimnames(res1.2.3.4$summary)[[1]]), grep("gamma", dimnames(res1.2.3.4$summary)[[1]])
    grep("ro", dimnames(res1.2.3.4$summary)[[1]]), grep("sdstruct", dimnames(res1.2.3.4$summary)[[1]]),
    grep("sSMR", dimnames(res1.2.3.4$summary)[[1]]))
# Convergence assessment for the set of identifiable parameters in the model
res1.2.3.4$summary[aux, "Rhat"][which(res1.2.3.4$summary[aux, "Rhat"] > 1.1)]
```

```
## named numeric(0)
```
```
res1.2.3.4$summary[aux, "n.eff"][which(res1.2.3.4$summary[aux, "n.eff"] < 100)]
```
```
## mu[1,1,2] mu[1,2,2] mu[2,1,2] mu[2,2,2] mu[3,1,2] mu[3,2,2] mu[4,1,2]
##        70        46        61        51        76        48        43
## mu[4,2,2] mu[5,1,2] mu[5,2,2]
##        47        57        51
```
```
plot.deviance(res1.2.3.4)
```
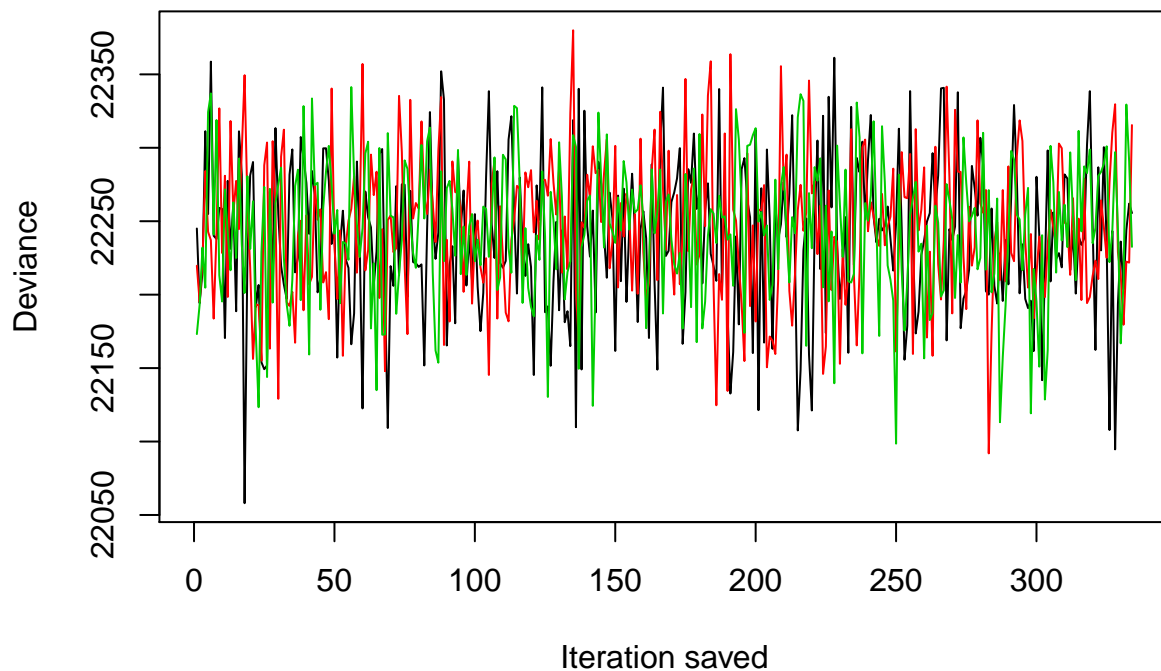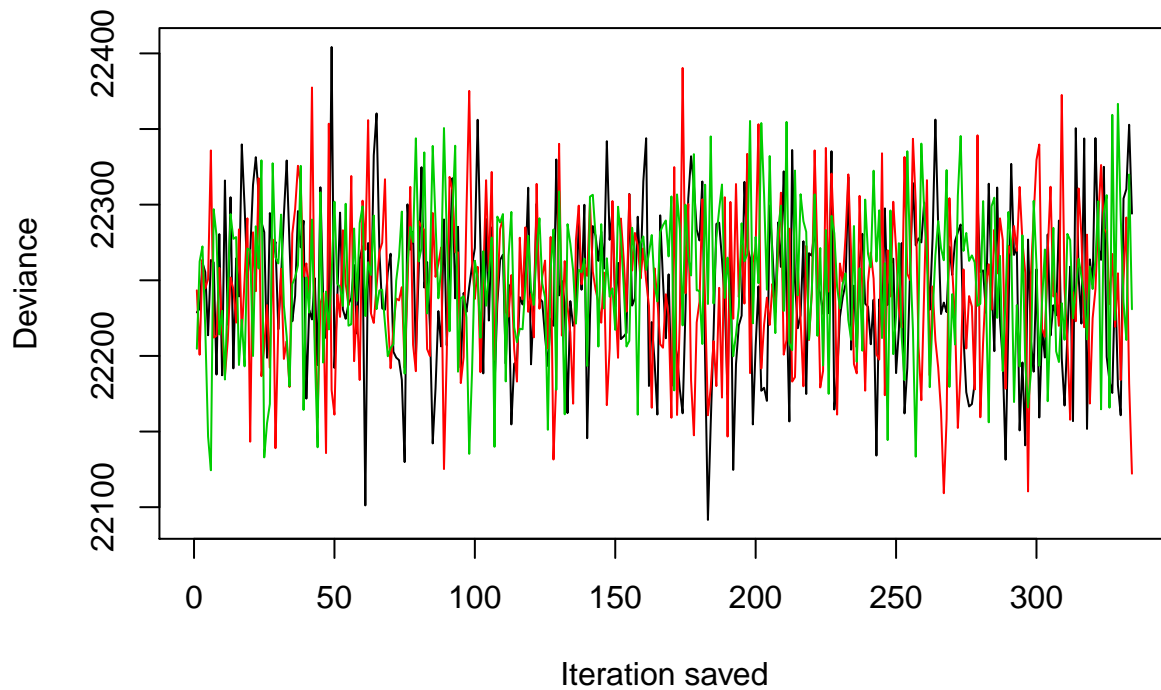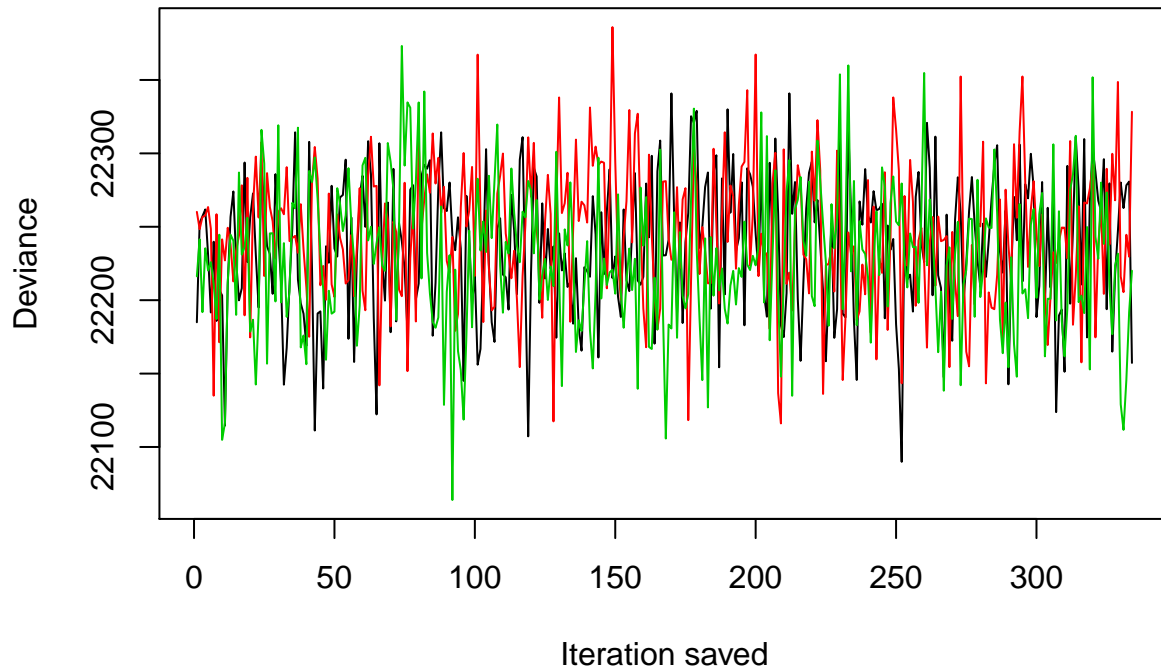


```
# Model 12.2.3.4
#----------------
res12.2.3.4$exec_time
```
```
## Time difference of 16.07526 hours
```
```
# Set of identifiable parameters
aux = c(grep("mu", dimnames(res12.2.3.4$summary)[[1]]), grep("ro", dimnames(res12.2.3.4$summary)[[1]]),
    grep("sdstruct", dimnames(res12.2.3.4$summary)[[1]]), grep("sSMR", dimnames(res12.2.3.4$summary)[[1]
# Convergence assessment for the set of identifiable parameters in the model
res12.2.3.4$summary[aux, "Rhat"][which(res12.2.3.4$summary[aux, "Rhat"] > 1.1)]
```
```
named numeric(0)
```
```
res12.2.3.4$summary[aux, "n.eff"][which(res12.2.3.4$summary[aux, "n.eff"] <
    100)]
```
```
mu[1,2,2]   mu[2,2,2]   mu[3,2,2]   mu[4,2,2]
50   45   48   47
```

```
##      mu[5,2,2]  sSMR[18,3,2,1]  sSMR[47,3,2,1]  sSMR[65,3,2,1]
##             51              85              96              65
##  sSMR[70,3,2,1]  sSMR[76,3,2,1]  sSMR[82,3,2,1]  sSMR[98,3,2,1]
##             82              82              97              97
## sSMR[130,3,2,1] sSMR[526,3,2,1]
##             81              87
```

```
plot.deviance(res12.2.3.4)
```



```
# Model 13.2.3.4
#---------------
res13.2.3.4$exec_time
```

```
## Time difference of 17.38821 hours
```

```
# Set of identifiable parameters
aux = c(grep("mu", dimnames(res13.2.3.4$summary)[[1]]), grep("ro", dimnames(res13.2.3.4$summary)[[1]]),
    grep("sdstruct", dimnames(res13.2.3.4$summary)[[1]]), grep("sSMR", dimnames(res13.2.3.4$summary)[[1]
# Convergence assessment for the set of identifiable parameters in the model
res13.2.3.4$summary[aux, "Rhat"][which(res13.2.3.4$summary[aux, "Rhat"] > 1.1)]
```

```
## named numeric(0)
```

```
res13.2.3.4$summary[aux, "n.eff"][which(res13.2.3.4$summary[aux, "n.eff"] <
    100)]
```

```
##      mu[1,1,1]       mu[1,2,1]       mu[2,1,1]       mu[2,2,1]       mu[2,2,2]
##             66              65              63              62              80
##      mu[3,1,1]       mu[3,2,1]       mu[3,2,2]       mu[4,1,1]       mu[4,1,2]
```

```
##              43              42              62              33              94
##     mu[4,2,1]      mu[4,2,2]      mu[5,1,1]      mu[5,2,1]      mu[5,2,2]
##              32              53              45              38              58
## sSMR[6,4,1,2]
##              98
```

```r
plot.deviance(res13.2.3.4)
```



```r
# Model 14.2.3.4
#---------------
res14.2.3.4$exec_time
```

```
## Time difference of 17.38963 hours
```

```r
# Set of identifiable parameters
aux = c(grep("mu", dimnames(res14.2.3.4$summary)[[1]]), grep("ro", dimnames(res14.2.3.4$summary)[[1]]),
    grep("sdstruct", dimnames(res14.2.3.4$summary)[[1]]), grep("sSMR", dimnames(res14.2.3.4$summary)[[1]
# Convergence assessment for the set of identifiable parameters in the model
res14.2.3.4$summary[aux, "Rhat"][which(res14.2.3.4$summary[aux, "Rhat"] > 1.1)]
```

```
## named numeric(0)
```

```r
res14.2.3.4$summary[aux, "n.eff"][which(res14.2.3.4$summary[aux, "n.eff"] <
    100)]
```

```
## mu[2,1,1] mu[2,2,1] mu[3,1,1] mu[3,2,1] mu[4,1,1] mu[4,2,1] mu[5,2,1]
##        73        83        45        41        69        50        67
```

```r
plot.deviance(res14.2.3.4)
```
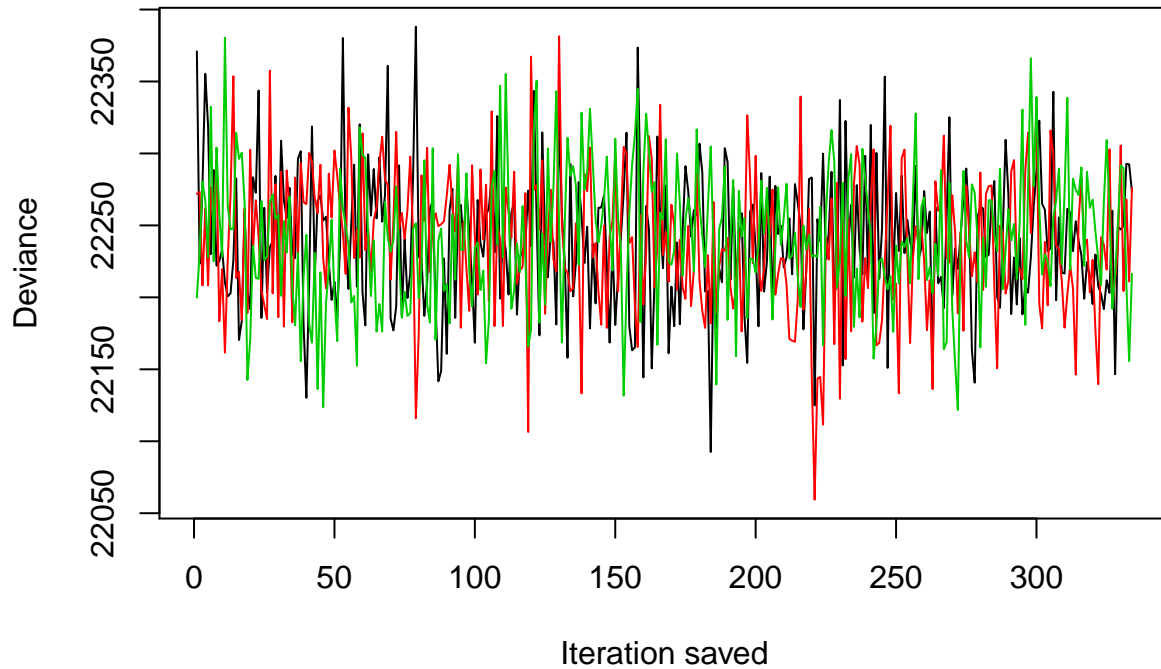


```r
# Model 1.23.3.4
#---------------
res1.23.3.4$exec_time
```

```
## Time difference of 21.54016 hours
```

```r
# Set of identifiable parameters
aux = c(grep("mu", dimnames(res1.23.3.4$summary)[[1]]), grep("gamma", dimnames(res1.23.3.4$summary)[[1]]
    grep("sdstruct", dimnames(res1.23.3.4$summary)[[1]]), grep("sSMR", dimnames(res1.23.3.4$summary)[[1]
# Convergence assessment for the set of identifiable parameters in the model
res1.23.3.4$summary[aux, "Rhat"][which(res1.23.3.4$summary[aux, "Rhat"] > 1.1)]
```

```
## named numeric(0)
```

```r
res1.23.3.4$summary[aux, "n.eff"][which(res1.23.3.4$summary[aux, "n.eff"] <
    100)]
```

```
##       mu[1,1,1]       mu[1,2,1]       mu[1,2,2]       mu[2,1,1]
##              42              47              99              87
##       mu[2,2,1]       mu[3,1,1]       mu[3,2,1]       mu[4,1,2]
##              67              72              49              86
##       mu[4,2,1]       mu[4,2,2]       mu[5,1,2]       mu[5,2,1]
##              57              89              86              53
##       mu[5,2,2] sSMR[211,3,1,2]
##              54              76
```

```r
plot.deviance(res1.23.3.4)
```
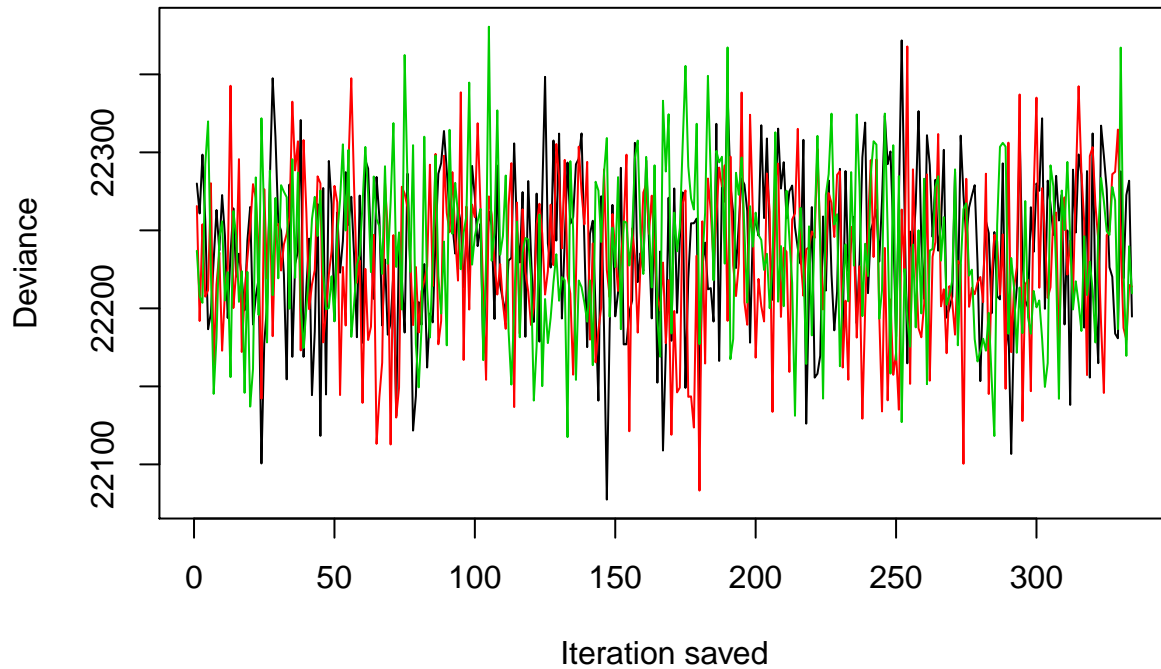


```r
# Model 1.24.3.4
#---------------
res1.24.3.4$exec_time
```

```
## Time difference of 18.59226 hours
```

```r
# Set of identifiable parameters
aux <- c(grep("mu", dimnames(res1.24.3.4$summary)[[1]]), grep("gamma", dimnames(res1.24.3.4$summary)[[1]
    grep("sdstruct", dimnames(res1.24.3.4$summary)[[1]]), grep("sSMR", dimnames(res1.24.3.4$summary)[[1]
# Convergence assessment for the set of identifiable parameters in the model
res1.24.3.4$summary[aux, "Rhat"][which(res1.24.3.4$summary[aux, "Rhat"] > 1.1)]
```

```
## mu[1,2,1] mu[2,2,1] mu[3,1,1] mu[3,2,1] mu[4,2,1] mu[5,2,1]
##  1.113622  1.115768  1.104690  1.143837  1.110951  1.104773
```

```r
res1.24.3.4$summary[aux, "n.eff"][which(res1.24.3.4$summary[aux, "n.eff"] <
    100)]
```

```
##      mu[1,1,1]      mu[1,1,2]      mu[1,2,1]      mu[1,2,2]
##             27             45             25             46
##      mu[2,1,1]      mu[2,1,2]      mu[2,2,1]      mu[2,2,2]
##             29             36             25             37
##      mu[3,1,1]      mu[3,1,2]      mu[3,2,1]      mu[3,2,2]
##             24             32             19             50
##      mu[4,1,1]      mu[4,1,2]      mu[4,2,1]      mu[4,2,2]
##             33             32             25             36
```

```
##        mu[5,1,1]        mu[5,1,2]        mu[5,2,1]        mu[5,2,2]
##               29               27               27               27
## sSMR[226,3,1,2]
##               97
```

```r
plot.deviance(res1.24.3.4)
```
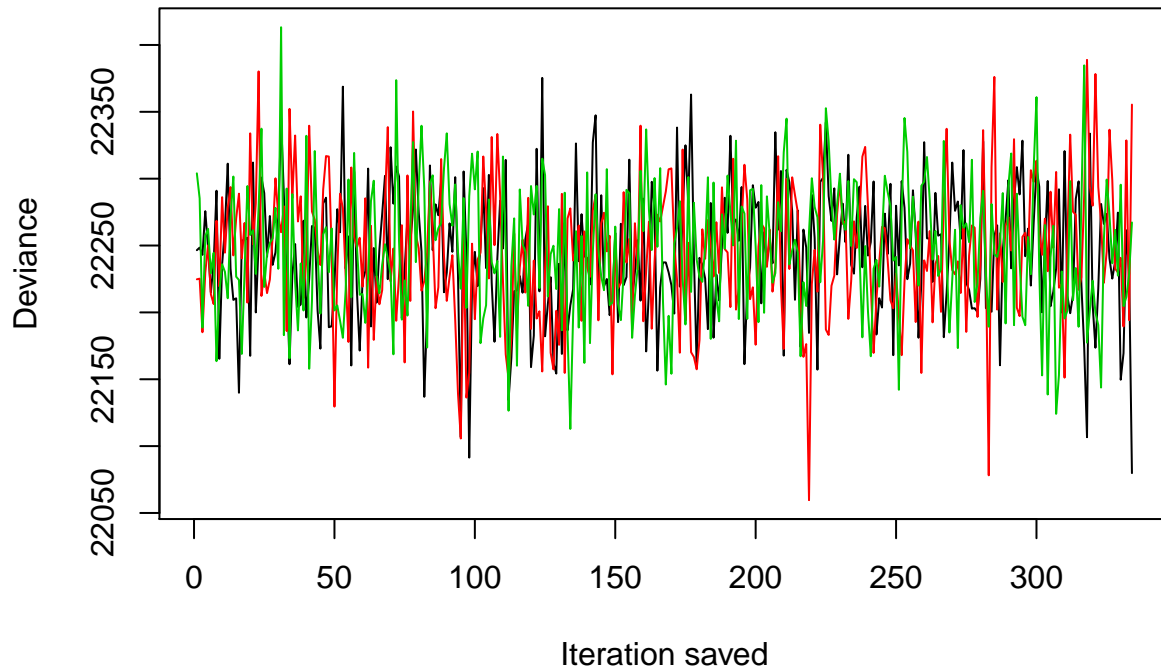


```r
# Model 1.2.32.4
#----------------
res1.2.32.4$exec_time
```

```
## Time difference of 16.08551 hours
```

```r
# Set of identifiable parameters
aux = c(grep("mu", dimnames(res1.2.32.4$summary)[[1]]), grep("gamma", dimnames(res1.2.32.4$summary)[[1]]),
    grep("ro", dimnames(res1.2.32.4$summary)[[1]]), grep("sdstruct", dimnames(res1.2.32.4$summary)[[1]]),
    grep("sSMR", dimnames(res1.2.32.4$summary)[[1]]))
# Convergence assessment for the set of identifiable parameters in the model
res1.2.32.4$summary[aux, "Rhat"][which(res1.2.32.4$summary[aux, "Rhat"] > 1.1)]
```

```
## mu[1,1,1] mu[1,1,2] mu[1,2,1] mu[1,2,2] mu[2,1,1] mu[2,1,2] mu[2,2,1]
##  1.111849  1.117250  1.151226  1.107400  1.109809  1.100279  1.165123
## mu[3,2,1] mu[4,1,1] mu[4,1,2] mu[4,2,1] mu[5,1,1] mu[5,2,1]
##  1.210639  1.118595  1.113928  1.206280  1.151116  1.203195
```

```r
res1.2.32.4$summary[aux, "n.eff"][which(res1.2.32.4$summary[aux, "n.eff"] <
    100)]
```

```
## mu[1,1,1] mu[1,1,2] mu[1,2,1] mu[1,2,2] mu[2,1,1] mu[2,1,2] mu[2,2,1]
```

```
##         23         22         18         23         27         25         19
## mu[2,2,2] mu[3,1,1] mu[3,1,2] mu[3,2,1] mu[3,2,2] mu[4,1,1] mu[4,1,2]
##         33         29         30         15         58         22         22
## mu[4,2,1] mu[4,2,2] mu[5,1,1] mu[5,1,2] mu[5,2,1]   sdstruct
##         14         71         19         36         15         90
```

```r
plot.deviance(res1.2.32.4)
```
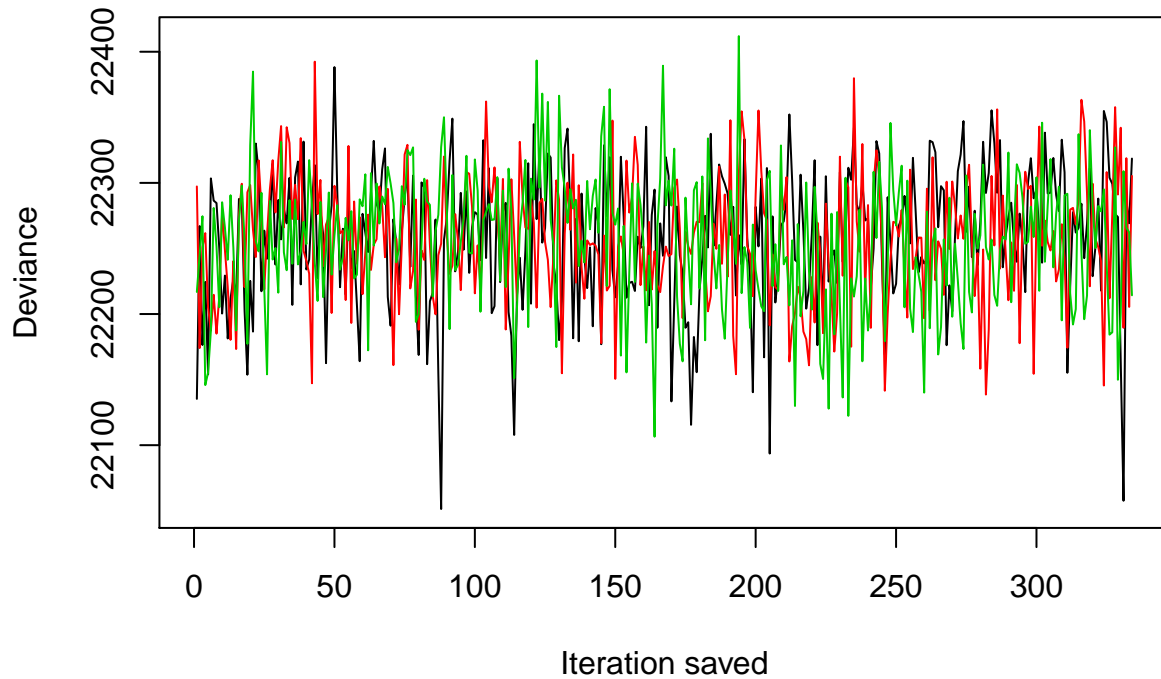


```r
# Model 1.2.34.4
#---------------
res1.2.34.4$exec_time
```

```
## Time difference of 17.07709 hours
```

```r
# Set of identifiable parameters
aux <- c(grep("mu", dimnames(res1.2.34.4$summary)[[1]]), grep("gamma", dimnames(res1.2.34.4$summary)[[1]]
    grep("ro", dimnames(res1.2.34.4$summary)[[1]]), grep("sdstruct", dimnames(res1.2.34.4$summary)[[1]]
    grep("sSMR", dimnames(res1.2.34.4$summary)[[1]]))
# Convergence assessment for the set of identifiable parameters in the model
res1.2.34.4$summary[aux, "Rhat"][which(res1.2.34.4$summary[aux, "Rhat"] > 1.1)]
```

```
## mu[1,1,1] mu[1,2,1] mu[2,1,1] mu[2,1,2] mu[2,2,1] mu[3,1,1] mu[3,2,1]
##  1.219914  1.225912  1.288188  1.109528  1.266834  1.305392  1.295803
## mu[4,1,1] mu[4,1,2] mu[4,2,1] mu[5,1,1] mu[5,1,2] mu[5,2,1] mu[5,2,2]
##  1.306648  1.143601  1.278787  1.285311  1.145286  1.247463  1.108043
##     gamma
##  1.168871
```

```
res1.2.34.4$summary[aux, "n.eff"][which(res1.2.34.4$summary[aux, "n.eff"] <
    100)]
```

```
## mu[1,1,1] mu[1,1,2] mu[1,2,1] mu[1,2,2] mu[2,1,1] mu[2,1,2] mu[2,2,1]
##        13        40        13        62        11        28        12
## mu[2,2,2] mu[3,1,1] mu[3,1,2] mu[3,2,1] mu[3,2,2] mu[4,1,1] mu[4,1,2]
##        45        10        32        11        52        10        22
## mu[4,2,1] mu[4,2,2] mu[5,1,1] mu[5,1,2] mu[5,2,1] mu[5,2,2]     gamma
##        11        54        11        23        12        34        18
```

```
plot.deviance(res1.2.34.4)
```
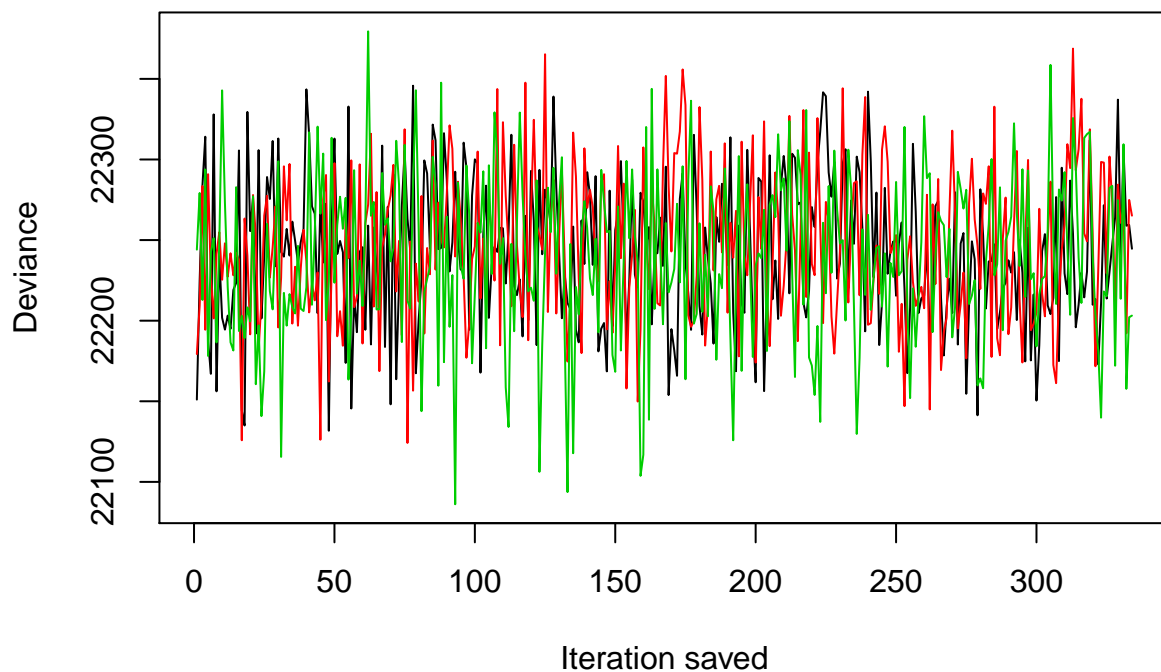


```
# Model 1.2.3.42
#---------------
res1.2.3.42$exec_time
```

```
## Time difference of 15.38796 hours
```

```
# Set of identifiable parameters
aux = c(grep("mu", dimnames(res1.2.3.42$summary)[[1]]), grep("gamma", dimnames(res1.2.3.42$summary)[[1]]
    grep("ro", dimnames(res1.2.3.42$summary)[[1]]), grep("sdstruct", dimnames(res1.2.3.42$summary)[[1]]
    grep("sSMR", dimnames(res1.2.3.42$summary)[[1]]))
# Convergence assessment for the set of identifiable parameters in the model
res1.2.3.42$summary[aux, "Rhat"][which(res1.2.3.42$summary[aux, "Rhat"] > 1.1)]
```
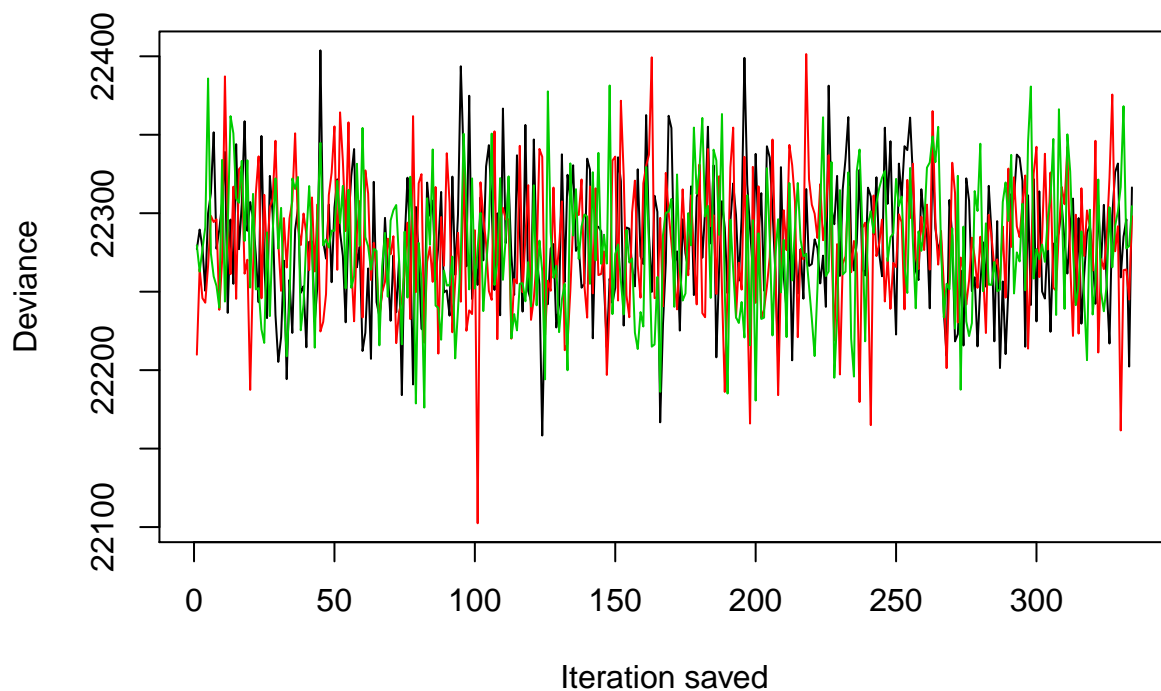
```
## mu[5,2,2]
##  1.106674
```

```
res1.2.3.42$summary[aux, "n.eff"][which(res1.2.3.42$summary[aux, "n.eff"] <
    100)]
```

```
## mu[1,1,1] mu[1,1,2] mu[1,2,1] mu[1,2,2] mu[2,1,1] mu[2,1,2] mu[2,2,1]
##        36        85        37        69        62        71        60
## mu[2,2,2] mu[3,1,1] mu[3,1,2] mu[3,2,1] mu[3,2,2] mu[4,1,1] mu[4,1,2]
##        39        75        45        78        40        86        59
## mu[4,2,1] mu[4,2,2] mu[5,1,2] mu[5,2,2]     gamma
##        90        40        29        28        53
```

```
plot.deviance(res1.2.3.42)
```



```
# Model 1.2.3.43
#---------------
res1.2.3.43$exec_time
```

```
## Time difference of 17.06298 hours
```

```
# Set of identifiable parameters
aux = c(grep("mu", dimnames(res1.2.3.43$summary)[[1]]), grep("gamma", dimnames(res1.2.3.43$summary)[[1]]
    grep("ro", dimnames(res1.2.3.43$summary)[[1]]), grep("sdstruct", dimnames(res1.2.3.43$summary)[[1]]
    grep("sSMR", dimnames(res1.2.3.43$summary)[[1]]))
# Convergence assessment for the set of identifiable parameters in the model
res1.2.3.43$summary[aux, "Rhat"][which(res1.2.3.43$summary[aux, "Rhat"] > 1.1)]
```

```
## mu[1,1,1] mu[1,2,1] mu[2,1,1] mu[2,2,1] mu[3,1,1] mu[3,2,1] mu[4,1,1]
##  1.185811  1.218294  1.207739  1.227347  1.171367  1.192079  1.158134
## mu[4,2,1] mu[5,1,1] mu[5,2,1]     gamma
```

```
##  1.172619  1.143151  1.174097  1.177149
```

```r
res1.2.3.43$summary[aux, "n.eff"][which(res1.2.3.43$summary[aux, "n.eff"] <
    100)]
```

```
##      mu[1,1,1]       mu[1,1,2]       mu[1,2,1]       mu[1,2,2]
##             25              74              23              90
##      mu[2,1,1]       mu[2,1,2]       mu[2,2,1]       mu[3,1,1]
##             20              56              19              24
##      mu[3,1,2]       mu[3,2,1]       mu[3,2,2]       mu[4,1,1]
##             73              22              98              28
##      mu[4,1,2]       mu[4,2,1]       mu[5,1,1]       mu[5,2,1]
##             76              27              25              21
##          gamma sSMR[388,1,2,1] sSMR[388,2,2,1] sSMR[388,5,2,1]
##             17              82              90              97
```

```r
plot.deviance(res1.2.3.43)
```
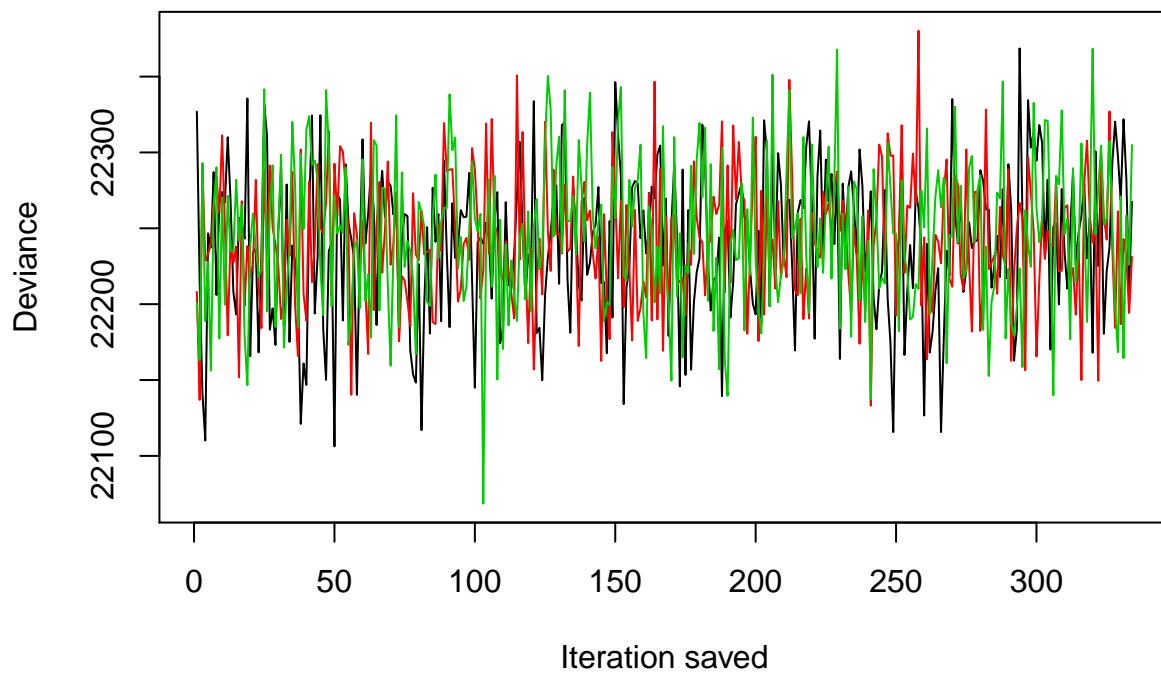

According to the convergence assessments above it would be surely worth to increase the number of MCMC iterations in order to achieve n.effs>100 and R-hats<1.1 for all the parameters in the model. Anyway, for the illustrative goals of the example and, because of the already long computing time of the current runs, we keep the current results for the rest of the example.

Illustration of the MCMC performance for some non-identifable parameters in the model

```r
# History plots for the temporal correlation parameters for the 1.23.3.4
# model, whose temporal dependence parameter varies as a function of the
# disease.
par(mfrow = c(1, 2))
# History plot for rho_1
plot(res1.23.3.4$sims.array[, 1, "ro[1]"], type = "l")
lines(res1.23.3.4$sims.array[, 2, "ro[1]"], col = 2)
lines(res1.23.3.4$sims.array[, 3, "ro[1]"], col = 3)
# History plot for rho_2
plot(res1.23.3.4$sims.array[, 1, "ro[2]"], type = "l")
lines(res1.23.3.4$sims.array[, 2, "ro[2]"], col = 2)
lines(res1.23.3.4$sims.array[, 3, "ro[2]"], col = 3)
```
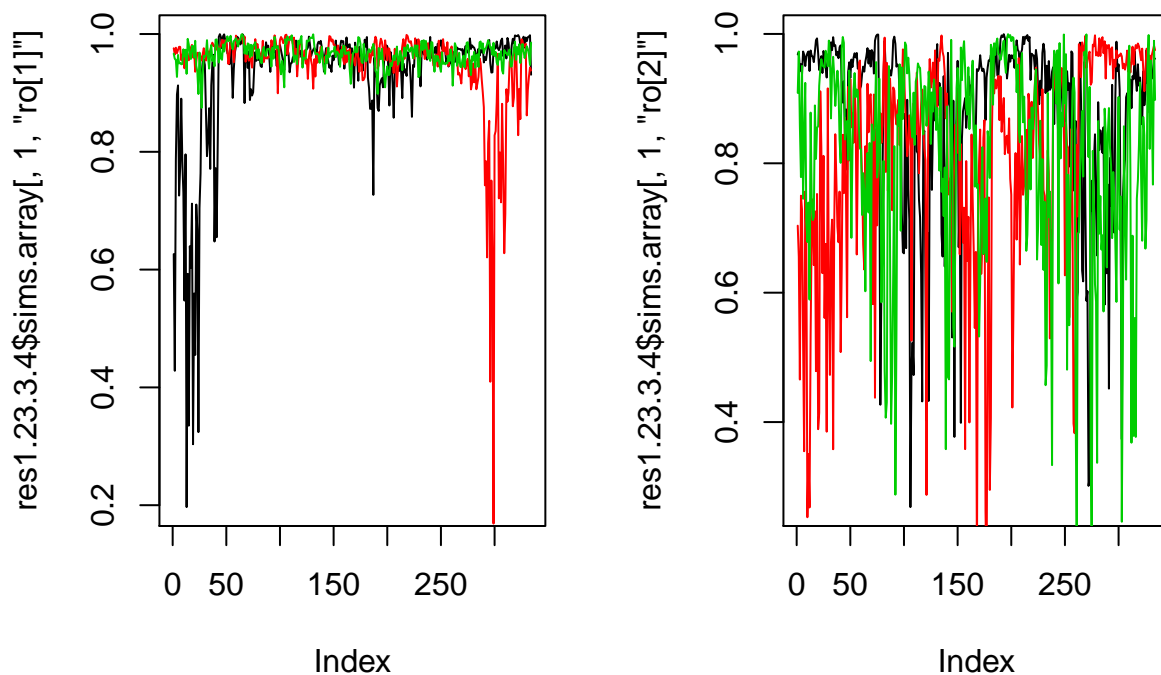


```r
# History plots for the spatial correlation parameters for the 1.2.32.4
# model.
par(mfrow = c(1, 1))
# History plot for gamma
plot(res1.2.32.4$sims.array[, 1, "gamma"], type = "l")
lines(res1.2.32.4$sims.array[, 2, "gamma"], col = 2)
lines(res1.2.32.4$sims.array[, 3, "gamma"], col = 3)
```
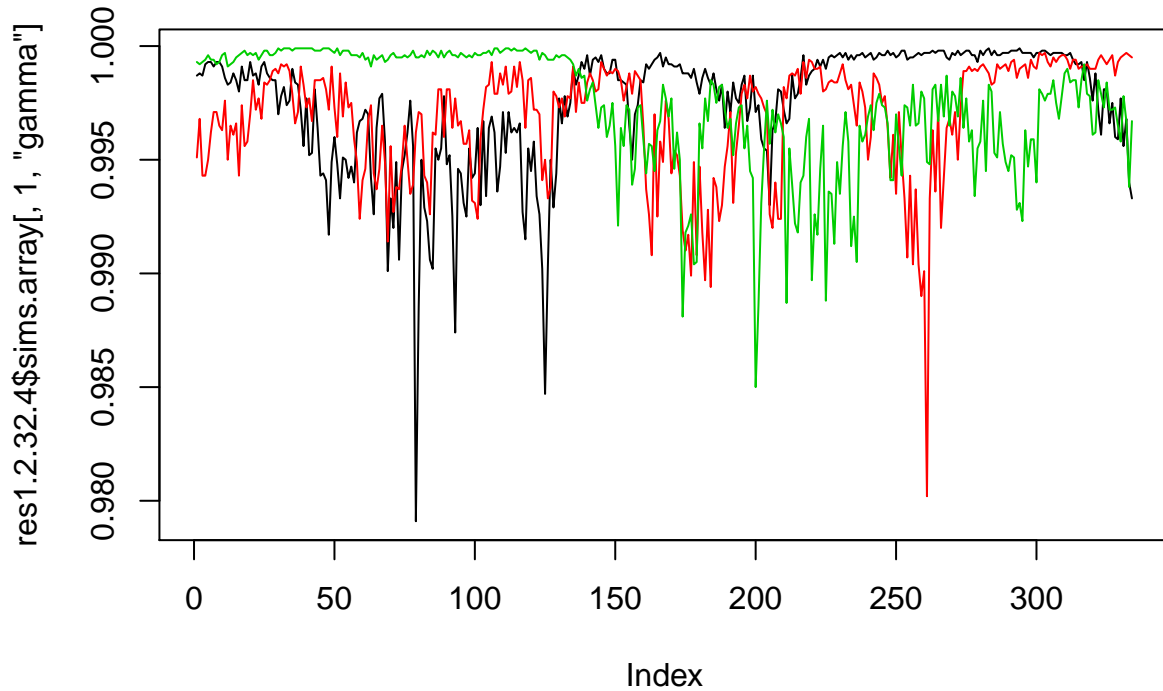
As it can be seen there seems to be two different temporal correlation parameters: one above 0.9 and a second one between 0.6 and 0.9. Nevertheless, these two parameters are switching their roles between ρ_1 and ρ_2. When one of these parameters is lower than 0.9 the other one is higher and vice-versa. Anyway these two parameters do not change their roles so frequently. This multimodality of ρ_1 and ρ_2 makes them to have an apparently defective convergence, anyway this issue should not have any impact on the sSMRs which would be combination of two different temporal processes, regardless of their order.

On the other hand, the latest plot illustrates a history plot for the spatial correlation parameter of the multidimensional model. It can be appreciated how `WinBUGS` finds some problems (high autocorrelation) for sampling this parameter. Anyway, this apparently problematic performance should have a small impact in practice since the great majority of the values drawn are above 0.99 pointing all of them a very high spatial autocorrelation. Thus, the practical differences induced by these different values, taking values on a tiny range, should be small.

DIC computation for each of the models run

```
DICPoisson(res1.2.3.4$sims.matrix[, grep("sSMR", dimnames(res1.2.3.4$sims.matrix)[[2]])],
    aperm(Obs.md, c(4, 3, 2, 1)), aperm(Exp.md, c(4, 3, 2, 1)))
```

```
## D= 22242.36 pD= 423.796 DIC= 22666.16
```

```
DICPoisson(res12.2.3.4$sims.matrix[, grep("sSMR", dimnames(res12.2.3.4$sims.matrix)[[2]])],
    aperm(Obs.md, c(4, 3, 2, 1)), aperm(Exp.md, c(4, 3, 2, 1)))
```

```
## D= 22246.3 pD= 431.9284 DIC= 22678.23
```

```
DICPoisson(res13.2.3.4$sims.matrix[, grep("sSMR", dimnames(res13.2.3.4$sims.matrix)[[2]])],
    aperm(Obs.md, c(4, 3, 2, 1)), aperm(Exp.md, c(4, 3, 2, 1)))
```

D= 22236.45 pD= 431.3733 DIC= 22667.83

```
DICPoisson(res14.2.3.4$sims.matrix[, grep("sSMR", dimnames(res14.2.3.4$sims.matrix)[[2]])],
    aperm(Obs.md, c(4, 3, 2, 1)), aperm(Exp.md, c(4, 3, 2, 1)))
```

D= 22240.01 pD= 429.9265 DIC= 22669.94

```
DICPoisson(res1.23.3.4$sims.matrix[, grep("sSMR", dimnames(res1.23.3.4$sims.matrix)[[2]])],
    aperm(Obs.md, c(4, 3, 2, 1)), aperm(Exp.md, c(4, 3, 2, 1)))
```

D= 22234.78 pD= 433.1402 DIC= 22667.92

```
DICPoisson(res1.24.3.4$sims.matrix[, grep("sSMR", dimnames(res1.24.3.4$sims.matrix)[[2]])],
    aperm(Obs.md, c(4, 3, 2, 1)), aperm(Exp.md, c(4, 3, 2, 1)))
```

D= 22245.71 pD= 423.7306 DIC= 22669.44

```
DICPoisson(res1.2.32.4$sims.matrix[, grep("sSMR", dimnames(res1.2.32.4$sims.matrix)[[2]])],
    aperm(Obs.md, c(4, 3, 2, 1)), aperm(Exp.md, c(4, 3, 2, 1)))
```

D= 22257.02 pD= 438.1466 DIC= 22695.16

```
DICPoisson(res1.2.34.4$sims.matrix[, grep("sSMR", dimnames(res1.2.34.4$sims.matrix)[[2]])],
    aperm(Obs.md, c(4, 3, 2, 1)), aperm(Exp.md, c(4, 3, 2, 1)))
```

D= 22242.42 pD= 425.5391 DIC= 22667.96

```
DICPoisson(res1.2.3.42$sims.matrix[, grep("sSMR", dimnames(res1.2.3.42$sims.matrix)[[2]])],
    aperm(Obs.md, c(4, 3, 2, 1)), aperm(Exp.md, c(4, 3, 2, 1)))
```

D= 22279.6 pD= 384.6425 DIC= 22664.24

```
DICPoisson(res1.2.3.43$sims.matrix[, grep("sSMR", dimnames(res1.2.3.43$sims.matrix)[[2]])],
    aperm(Obs.md, c(4, 3, 2, 1)), aperm(Exp.md, c(4, 3, 2, 1)))
```

D= 22242.34 pD= 425.7346 DIC= 22668.07

Exploration of the results for the 1.2.3.4(2) model

Some summary statistics

```
# Spatial dependence
round(res1.2.3.42$summary["gamma", ], 3)
```

```
##   mean     sd   2.5%    25%    50%    75%  97.5%   Rhat  n.eff
##  0.997  0.002  0.991  0.996  0.998  0.999  1.000  1.054 53.000
```

```
# Temporal dependence
round(res1.2.3.42$summary["ro", ], 3)
```

```
##     mean      sd    2.5%     25%     50%     75%   97.5%    Rhat
##    0.992   0.007   0.974   0.989   0.994   0.997   1.000   1.000
##    n.eff
## 1000.000
```

```r
# Dependence between diseases
#---------------------------
aux <- res1.2.3.42$sims.matrix[, c("structure3[1,1]", "structure3[1,2]", "structure3[2,1]",
    "structure3[2,2]")]
cors <- apply(aux, 1, function(x) {
    mat <- matrix(x, ncol = 2, byrow = TRUE)
    cov2cor(t(mat) %*% mat)
})
# Posterior mean
matrix(apply(cors, 1, mean), nrow = 2)
```

```
##           [,1]      [,2]
## [1,] 1.0000000 0.9016632
## [2,] 0.9016632 1.0000000
```

```r
# 2.5% and 97.5% posterior quantiles
quantile(cors[2, ], c(0.025, 0.975))
```

```
##      2.5%     97.5%
## 0.7964754 0.9619590
```

```r
# Dependence between sexes
#------------------------
aux <- res1.2.3.42$sims.matrix[, grep("structure4", dimnames(res1.2.3.42$sims.matrix)[[2]])]
aux.array <- array(dim = c(dim(aux)[1], 2, 2, 5))
for (i in 1:(dim(aux)[1])) {
    aux.array[i, , , ] <- aperm(array(aux[i, ], dim = c(5, 2, 2)), 3:1)
}
# Period 1
cors <- apply(aux.array, 1, function(x, period) {
    mat <- x[, , period]
    cov2cor(t(mat) %*% mat)[1, 2]
}, period = 1)
# Posterior mean
mean(cors)
```

```
## [1] 0.8190678
```

```r
# 2.5% and 97.5% posterior quantiles
quantile(cors, c(0.025, 0.975))
```

```
##      2.5%     97.5%
## 0.4115391 0.9992454
```

```r
# Period 2
cors <- apply(aux.array, 1, function(x, period) {
    mat <- x[, , period]
    cov2cor(t(mat) %*% mat)[1, 2]
}, period = 2)
# Posterior mean
mean(cors)
```

```
## [1] 0.5422862
```

```r
# 2.5% and 97.5% posterior quantiles
quantile(cors, c(0.025, 0.975))
```

```
##      2.5%     97.5%
```

```
## 0.09268655 0.88009253
```

```r
# Period 3
cors <- apply(aux.array, 1, function(x, period) {
    mat <- x[, , period]
    cov2cor(t(mat) %*% mat)[1, 2]
}, period = 3)
# Posterior mean
mean(cors)
```

```
## [1] 0.3188412
```

```r
# 2.5% and 97.5% posterior quantiles
quantile(cors, c(0.025, 0.975))
```

```
##        2.5%       97.5%
## -0.06846229   0.69574516
```

```r
# Period 4
cors <- apply(aux.array, 1, function(x, period) {
    mat <- x[, , period]
    cov2cor(t(mat) %*% mat)[1, 2]
}, period = 4)
# Posterior mean
mean(cors)
```

```
## [1] 0.109252
```

```r
# 2.5% and 97.5% posterior quantiles
quantile(cors, c(0.025, 0.975))
```

```
##        2.5%       97.5%
## -0.2421250   0.4302399
```

```r
# Period 5
cors <- apply(aux.array, 1, function(x, period) {
    mat <- x[, , period]
    cov2cor(t(mat) %*% mat)[1, 2]
}, period = 5)
# Posterior mean
mean(cors)
```

```
## [1] 0.209441
```

```r
# 2.5% and 97.5% posterior quantiles
quantile(cors, c(0.025, 0.975))
```

```
##        2.5%       97.5%
## -0.1016040   0.4950844
```

Tables 9.1 and 9.2

```r
# Table 9.1
#----------
aux <- res1.2.3.42$sims.matrix[, grep("sSMR", dimnames(res1.2.3.42$sims.matrix)[[2]])]
aux.array <- array(dim = c(dim(aux)[1], 540, 5, 2, 2))
for (i in 1:(dim(aux)[1])) {
    aux.array[i, , , , ] <- aperm(array(aux[i, ], dim = c(2, 2, 5, 540)), 4:1)
```

```
}

cor.iter <- array(dim = c(dim(aux)[1], 12, 12))
# Combinations of factors to include in Tables 9.1 and 9.2
combinations <- rbind(c(1, 1, 1), c(3, 1, 1), c(5, 1, 1), c(1, 1, 2), c(3, 1,
    2), c(5, 1, 2), c(1, 2, 1), c(3, 2, 1), c(5, 2, 1), c(1, 2, 2), c(3, 2,
    2), c(5, 2, 2))
for (i in 1:(dim(aux)[1])) {
    for (j in 1:12) {
        for (k in 1:12) {
            cor.iter[i, j, k] <- cor(aux.array[i, , combinations[j, 1], combinations[j,
                2], combinations[j, 3]], aux.array[i, , combinations[k, 1],
                combinations[k, 2], combinations[k, 3]])
        }
    }
}
# Table 9.1
round(apply(cor.iter, c(2, 3), mean), 2)
```

```
##        [,1] [,2] [,3] [,4] [,5] [,6] [,7] [,8] [,9] [,10] [,11] [,12]
##  [1,] 1.00 0.89 0.75 0.85 0.76 0.82 0.89 0.73 0.58  0.78  0.71  0.76
##  [2,] 0.89 1.00 0.95 0.58 0.44 0.53 0.83 0.87 0.79  0.57  0.44  0.52
##  [3,] 0.75 0.95 1.00 0.39 0.24 0.34 0.73 0.86 0.86  0.40  0.25  0.35
##  [4,] 0.85 0.58 0.39 1.00 0.91 0.92 0.72 0.43 0.24  0.90  0.83  0.83
##  [5,] 0.76 0.44 0.24 0.91 1.00 0.96 0.63 0.30 0.10  0.81  0.91  0.86
##  [6,] 0.82 0.53 0.34 0.92 0.96 1.00 0.69 0.38 0.19  0.83  0.87  0.90
##  [7,] 0.89 0.83 0.73 0.72 0.63 0.69 1.00 0.88 0.74  0.82  0.72  0.79
##  [8,] 0.73 0.87 0.86 0.43 0.30 0.38 0.88 1.00 0.96  0.53  0.37  0.48
##  [9,] 0.58 0.79 0.86 0.24 0.10 0.19 0.74 0.96 1.00  0.33  0.16  0.27
## [10,] 0.78 0.57 0.40 0.90 0.81 0.83 0.82 0.53 0.33  1.00  0.90  0.91
## [11,] 0.71 0.44 0.25 0.83 0.91 0.87 0.72 0.37 0.16  0.90  1.00  0.95
## [12,] 0.76 0.52 0.35 0.83 0.86 0.90 0.79 0.48 0.27  0.91  0.95  1.00
```

```
# Table 9.2
#----------
aux <- res1.2.3.4$sims.matrix[, grep("sSMR", dimnames(res1.2.3.4$sims.matrix)[[2]])]
aux.array <- array(dim = c(dim(aux)[1], 540, 5, 2, 2))
for (i in 1:(dim(aux)[1])) {
    aux.array[i, , , , ] <- aperm(array(aux[i, ], dim = c(2, 2, 5, 540)), 4:1)
}

for (i in 1:(dim(aux)[1])) {
    for (j in 1:12) {
        for (k in 1:12) {
            cor.iter[i, j, k] <- cor(aux.array[i, , combinations[j, 1], combinations[j,
                2], combinations[j, 3]], aux.array[i, , combinations[k, 1],
                combinations[k, 2], combinations[k, 3]])
        }
    }
}
# Table 9.2
round(apply(cor.iter, c(2, 3), mean), 2)
```

```
##        [,1] [,2] [,3] [,4] [,5] [,6] [,7] [,8] [,9] [,10] [,11] [,12]
```

```
## [1,]  1.00 0.93 0.85 0.47 0.46 0.44 0.88 0.79 0.68   0.46   0.45   0.42
## [2,]  0.93 1.00 0.92 0.40 0.42 0.41 0.85 0.86 0.76   0.40   0.42   0.40
## [3,]  0.85 0.92 1.00 0.32 0.34 0.38 0.78 0.82 0.85   0.32   0.34   0.37
## [4,]  0.47 0.40 0.32 1.00 0.93 0.85 0.36 0.26 0.16   0.89   0.82   0.74
## [5,]  0.46 0.42 0.34 0.93 1.00 0.92 0.34 0.27 0.18   0.82   0.88   0.80
## [6,]  0.44 0.41 0.38 0.85 0.92 1.00 0.34 0.28 0.22   0.76   0.82   0.88
## [7,]  0.88 0.85 0.78 0.36 0.34 0.34 1.00 0.93 0.84   0.43   0.42   0.41
## [8,]  0.79 0.86 0.82 0.26 0.27 0.28 0.93 1.00 0.93   0.34   0.36   0.36
## [9,]  0.68 0.76 0.85 0.16 0.18 0.22 0.84 0.93 1.00   0.25   0.27   0.32
## [10,] 0.46 0.40 0.32 0.89 0.82 0.76 0.43 0.34 0.25   1.00   0.92   0.85
## [11,] 0.45 0.42 0.34 0.82 0.88 0.82 0.42 0.36 0.27   0.92   1.00   0.92
## [12,] 0.42 0.40 0.37 0.74 0.80 0.88 0.41 0.36 0.32   0.85   0.92   1.00
```

Figure 9.1

```r
# Temporal component for each combination of disease and sex
T.i <- array(dim = c(dim(res1.2.3.42$sims.list$sSMR)[1], 5, 2, 2))
for (i in 1:dim(res1.2.3.42$sims.list$sSMR)[1]) {
    for (j in 1:2) {
        for (k in 1:2) {
            m <- mean(log(res1.2.3.42$sims.list$sSMR[i, , , j, k]/100))
            T.i[i, , j, k] <- apply(log(res1.2.3.42$sims.list$sSMR[i, , , j,
                k]/100) - m, 2, mean)
        }
    }
}
T <- exp(apply(T.i, 2:4, mean))

# Figure 9.1
plot(T[, 1, 1], type = "b", pch = 1, ylim = c(min(T), max(T)), xlab = "Period",
    ylab = "Risks time trend")
lines(T[, 1, 2], type = "b", pch = 19)
lines(T[, 2, 1], type = "b", pch = 2)
lines(T[, 2, 2], type = "b", pch = 17)
title("Model 1.2.3.4(2)")
legend("topleft", c("Oral cancer - Men", "Oral cancer - Women", "Lung cancer - Men",
    "Lung cancer - Women"), pch = c(1, 19, 2, 17), bty = "n")
```

Model 1.2.3.4(2)
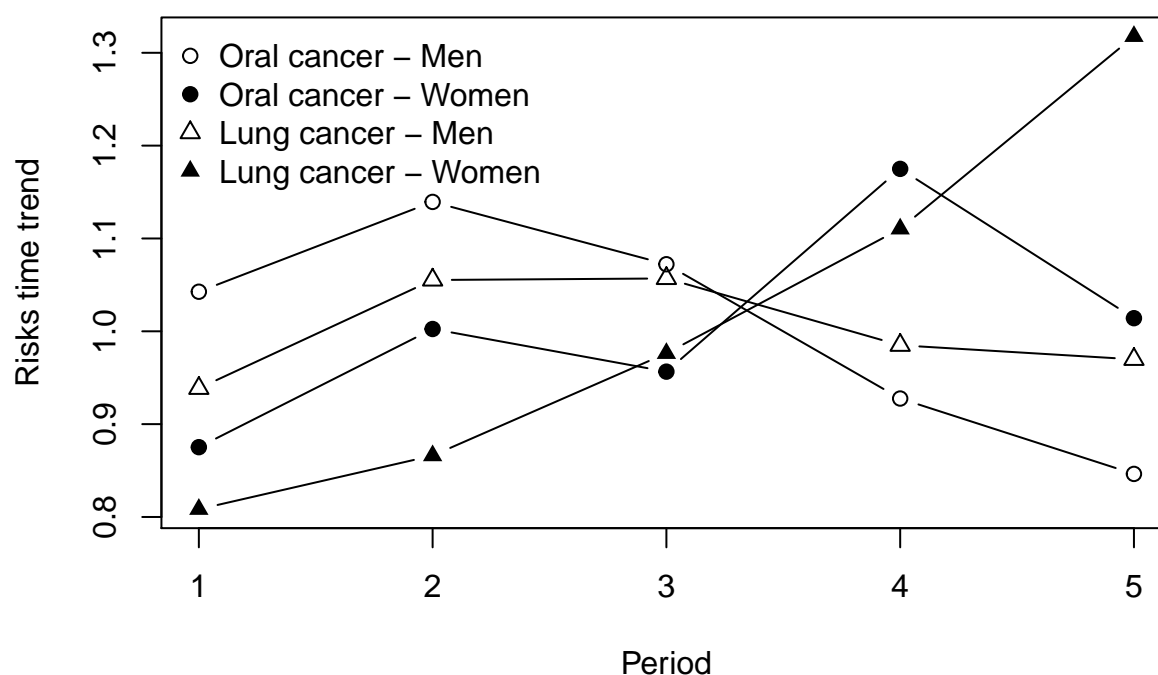
Choropleth maps

```
sSMRWithoutT.i <- array(dim = dim(res1.2.3.42$sims.list$sSMR))
for (i in 1:dim(sSMRWithoutT.i)[1]) {
    for (j in 1:dim(sSMRWithoutT.i)[2]) {
        for (k in 1:dim(sSMRWithoutT.i)[3]) {
            for (l in 1:dim(sSMRWithoutT.i)[4]) {
                for (m in 1:dim(sSMRWithoutT.i)[5]) {
                    sSMRWithoutT.i[i, j, k, l, m] <- res1.2.3.42$sims.list$sSMR[i,
                        j, k, l, m]/exp(T.i[i, k, l, m])
                }
            }
        }
    }
}
sSMRWithoutT <- apply(sSMRWithoutT.i, 2:5, mean)

diseases <- c("Oral cancer", "Lung cancer")
sexes <- c("Men", "Women")

# Choropleth maps figure for men
#-----------------------------
colors <- brewer.pal(7, "BrBG")[7:1]
cuts <- 100 * c(-0.1, 1/1.5, 1/1.25, 1/1.1, 1.1, 1.25, 1.5, 100)
```
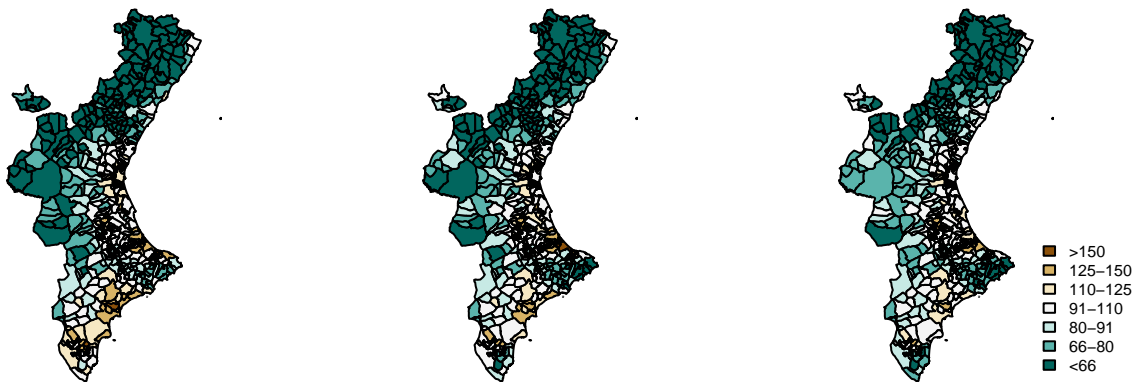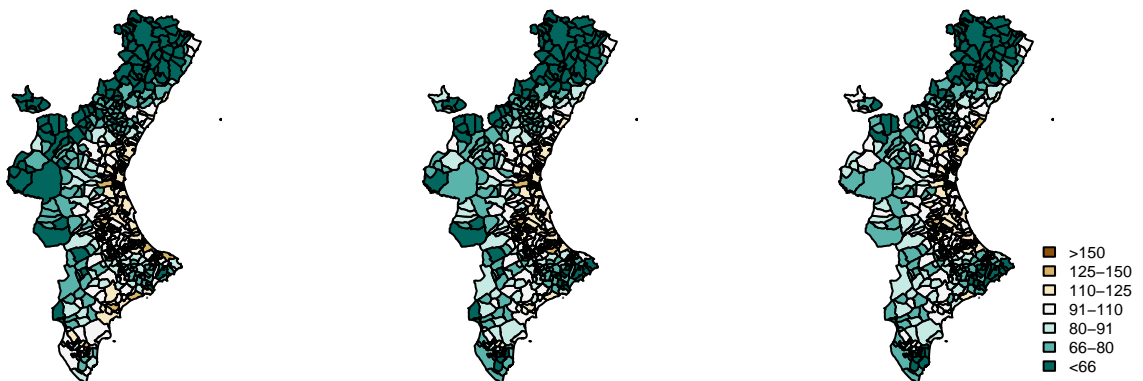
```
par(mfrow = c(2, 3))
par(mar = c(0, 0, 1, 0) + 0.1)
sex <- 1
for (dis in 1:2) {
    for (p in c(1, 3, 5)) {
        sSMRWithoutT.cut <- as.numeric(cut(sSMRWithoutT[, p, dis, sex], cuts))
        plot(VR.cart, col = colors[sSMRWithoutT.cut], sub = paste("Period",
            p))
        text(-0.5, 37.5, paste("Period", p))
        if (p == 3) {
            title(paste(diseases[dis], "-", sexes[sex]))
        }
        if (p == 5) {
            legend(x = "bottomright", fill = colors[7:1], c(">150", "125-150",
                "110-125", "91-110", "80-91", "66-80", "<66"), cex = 0.75, inset = 0.03,
                bty = "n")
        }
    }
}
```

Oral cancer – Men

Lung cancer – Men


```
# Choropleth maps figure for women
#-------------------------------
sex <- 2
par(mfrow = c(2, 3))
par(mar = c(0, 0, 1, 0) + 0.1)
for (dis in 1:2) {
```
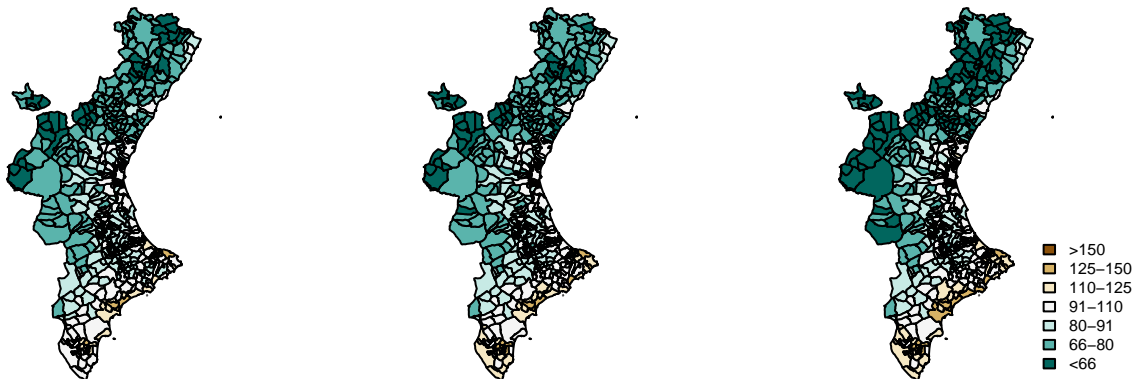
```r
for (p in c(1, 3, 5)) {
    sSMRWithoutT.cut <- as.numeric(cut(sSMRWithoutT[, p, dis, sex], cuts))
    plot(VR.cart, col = colors[sSMRWithoutT.cut], sub = paste("Period",
        p))
    if (p == 3) {
        title(paste(diseases[dis], "-", sexes[sex]))
    }
    if (p == 5) {
        legend(x = "bottomright", fill = colors[7:1], c(">150", "125-150",
            "110-125", "91-110", "80-91", "66-80", "<66"), cex = 0.75, inset = 0.03,
            bty = "n")
    }
}
}
```

Oral cancer – Women

Lung cancer – Women