

Used code in the simulation study

1. Simulation of data for each setting and city

Load libraries and data

```
# Working directory
DirMain = " " # Set an appropriate directory
setwd(DirMain)
# Load library and data
library(R2WinBUGS)
library(knitr)
library(pbugs) # For running the models in parallel calls to WinBUGS
load("datos.Rdata")
# Function to generate values of a CAR
# distribution
Genera_CAR <- function(desv, nvec, adj, rho = 1) {
  n <- length(nvec)
  D.W <- matrix(0, n, n)
  diag(D.W) <- nvec
  indice_veci <- cbind(rep(1:n, nvec),
    adj)
  D.W[indice_veci] <- -rho
  UDUt <- eigen(D.W)
  rango <- sum(UDUt$values > 1e-10)
  Spat <- as.vector(UDUt$vectors[, 1:rango] %*%
    matrix(rnorm(rango, 0, UDUt$values[1:rango])^{
      -1/2
    }, ncol = 1)) * desv
  return(Spat)
}
# Seeds for each replica (1:5) and city
# (1: Alicante, 2:Castellón, 3:Valencia)
seeds <- list()
seeds[[1]] <- c(20, 54, 86, 92, 6)
seeds[[2]] <- c(89, 94, 102, 92, 6)
seeds[[3]] <- c(20, 54, 67, 92, 6)
```

Setting 1

```
for (City in 1:3) {
  # 1: Alicante, 2:Castellón, 3:Valencia
  for (Ndiseases in c(5, 10)) {
    # Expected cases
    E <- t(apply(Esp[[City]][[1]][1,
      , ], c(1, 2), sum))[, 1:Ndiseases]
    for (Replica in 1:5) {
```

```

# Matrix with spatial random effects for
# each disease
Y <- matrix(NA, nrow = dim(Carto[[City]])[1],
            ncol = Ndiseases)
# Matrix with simulated observed cases
# for each disease
Obs_simu <- matrix(NA, nrow = dim(Carto[[City]])[1],
                  ncol = Ndiseases)
# Common spatial pattern to all diseases
set.seed(79 * seeds[[City]][Replica])
patron_comun <- Genera_CAR(desv = 0,
                          nvec = sapply(nb[[City]],
                                         length), adj = unlist(nb[[City]]),
                          rho = 0.9)
# Specific spatial pattern for each
# disease First disease
i <- 1
set.seed(i * seeds[[City]][Replica])
Y[, i] <- patron_comun + Genera_CAR(desv = 1,
                                   nvec = sapply(nb[[City]],
                                                  length), adj = unlist(nb[[City]]),
                                   rho = 0.9)
# Other diseases
for (i in 2:Ndiseases) {
  set.seed(i * seeds[[City]][Replica])
  Y[, i] <- patron_comun +
    Genera_CAR(desv = 0.2,
              nvec = sapply(nb[[City]],
                           length), adj = unlist(nb[[City]]),
              rho = 0.9)
}
# Simulation of the observed cases for
# each disease
for (i in 1:Ndiseases) {
  mu_Obs <- exp(Y[, i]) * E[,
    i]
  set.seed(i)
  Obs_simu[, i] <- rpois(dim(Carto[[City]])[1],
                        mu_Obs)
}
save(Obs_simu, Y, E, file = paste0(City,
                                   "/", Ndiseases, " enfermedades/Escenario 1/
                                   datos_simulados",
                                   Replica, ".RData"))
}
}

# Next, adjust the BYM model with
# independent diseases, NVA M-model, RVA
# M-model and CVA M-Model to the
# simulated observed cases for each data
# set (following the code specified in
# the document RCode.pdf).

```

Setting 2

```
for (City in 1:3) {  
  # 1: Alicante, 2:Castellón, 3:Valencia  
  for (Ndiseases in c(5, 10)) {  
    # Expected cases  
    E <- t(apply(Esp[[City]][[1]][1,  
      , ], c(1, 2), sum))[, 1:Ndiseases]  
    for (Replica in 1:5) {  
      #  
      trix with spatial random effects for  
      # each disease  
      Y <- matrix(NA, nrow = dim(Carto[[City]])[1],  
        ncol = Ndiseases)  
      #  
      trix with simulated observed cases  
      # for each disease  
      Obs_simu <- matrix(NA, nrow = dim(Carto[[City]])[1],  
        ncol = Ndiseases)  
      # Common spatial pattern to all diseases  
      set.seed(79 * seeds[[City]][Replica])  
      patron_comun <- Genera_CAR(desv = 0.5,  
        nvec = sapply(nb[[City]],  
          length), adj = unlist(nb[[City]]),  
          rho = 0.9)  
      # Specific spatial pattern for each  
      # disease First disease  
      i <- 1  
      set.seed(i * seeds[[City]][Replica])  
      Y[, i] <- patron_comun + Genera_CAR(desv = 1,  
        nvec = sapply(nb[[City]],  
          length), adj = unlist(nb[[City]]),  
          rho = 0.9)  
      # Other diseases  
      for (i in 2:Ndiseases) {  
        set.seed(i * seeds[[City]][Replica])  
        Y[, i] <- patron_comun +  
          Genera_CAR(desv = 0.2,  
            nvec = sapply(nb[[City]],  
              length), adj = unlist(nb[[City]]),  
              rho = 0.9)  
      }  
      # Simulation of the observed cases for  
      # each disease  
      for (i in 1:Ndiseases) {  
        mu_Obs <- exp(Y[, i]) * E[,  
          i]  
        set.seed(i)  
        Obs_simu[, i] <- rpois(dim(Carto[[City]])[1],  
          mu_Obs)  
      }  
      save(Obs_simu, Y, E, file = paste0(City,  
        "/", Ndiseases, " enfermedades/Escenario 2/  
          datos_simulados",
```

```

        Replica, ".RData"))
    }
}

# Next, adjust the BYM model with
# independent diseases, NVA M-model, RVA
# M-model and CVA M-Model to the
# simulated observed cases for each data
# set (following the code specified in
# the document RCode.pdf).

```

Setting 3

```

for (City in 1:3) {
  # 1: Alicante, 2:Castellón, 3:Valencia
  for (Ndiseases in c(5, 10)) {
    # Expected cases
    E <- t(apply(Esp[[City]][[1]][1,
      , ], c(1, 2), sum))[1:Ndiseases]
    for (Replica in 1:5) {
      # Matrix with spatial random effects for
      # each disease
      Y <- matrix(NA, nrow = dim(Carto[[City]])[1],
        ncol = Ndiseases)
      # Matrix with simulated observed cases
      # for each disease
      Obs_simu <- matrix(NA, nrow = dim(Carto[[City]])[1],
        ncol = Ndiseases)
      # Common spatial pattern to all diseases
      set.seed(79 * seeds[[City]][Replica])
      patron_comun <- Genera_CAR(desv = 1,
        nvec = sapply(nb[[City]],
          length), adj = unlist(nb[[City]]),
          rho = 0.9)
      # Specific spatial pattern for each
      # disease First disease
      i <- 1
      set.seed(i * seeds[[City]][Replica])
      Y[, i] <- patron_comun + Genera_CAR(desv = 1,
        nvec = sapply(nb[[City]],
          length), adj = unlist(nb[[City]]),
          rho = 0.9)
      # Other diseases
      for (i in 2:Ndiseases) {
        set.seed(i * seeds[[City]][Replica])
        Y[, i] <- patron_comun +
          Genera_CAR(desv = 0.2,
            nvec = sapply(nb[[City]],
              length), adj = unlist(nb[[City]]),
              rho = 0.9)
      }
      # Simulation of the observed cases for
      # each disease
    }
  }
}

```

```

    for (i in 1:Ndiseases) {
      mu_Obs <- exp(Y[, i]) * E[,
        i]
      set.seed(i)
      Obs_simu[, i] <- rpois(dim(Carto[[City]])[1],
        mu_Obs)
    }
    save(Obs_simu, Y, E, file = paste0(City,
      "/", Ndiseases, " enfermedades/Escenario 3/
        datos_simulados",
        Replica, ".RData"))
  }
}

# Next, adjust the BYM model with
# independent diseases, NVA M-model, RVA
# M-model and CVA M-Model to the
# simulated observed cases for each data
# set (following the code specified in
# the document RCode.pdf).

```

2. Mean standard deviation of the risks for the first disease and for the rest of diseases in each setting, city and model used in the adjustment of the data

```

# Specify number of diseases (in our
# study 5 and 10 diseases)
Ndiseases <- 5
# Object in which we save the results
Resul <- list()
for (City in 1:3) {
  Resul[[City]] <- list()
}
names(Resul) <- c("Alicante", "Castellon",
  "Valencia")
n_geographicalunits <- c(215, 95, 553)
names(n_geographicalunits) <- c("Alicante",
  "Castellon", "Valencia")
for (City in 1:3) {
  for (Setting in 1:3) {
    # Object in which we save the simulated
    # spatial patterns for each disease in
    # each replica
    Sim_data <- array(NA, dim = c(5,
      n_geographicalunits[City], Ndiseases))
    # Object in which we save the estimated
    # risks with the BYM model with
    # independent diseases for each replica
    BYM_indep <- array(NA, dim = c(5,
      n_geographicalunits[City], Ndiseases))
    # Object in which we save the estimated

```

```

# risks with the NVA M-model for each
# replica
NVA <- array(NA, dim = c(5, n_geographicalunits[City],
  Ndiseases))
# Object in which we save the estimated
# risks with the CVA M-model for each
# replica
CVA <- array(NA, dim = c(5, n_geographicalunits[City],
  Ndiseases))
# Object in which we save the estimated
# risks with the RVA M-model for each
# replica
RVA <- array(NA, dim = c(5, n_geographicalunits[City],
  Ndiseases))
for (Replica in 1:5) {
  # Simulated observed cases
  load(paste0(City, "/", Ndiseases,
    " enfermedades/Escenario ",
    Setting, "/datos_simulados",
    Replica, ".RData"))
  Sim_data[Replica, , ] <- Y
  # Estimated risks with the BYM model with
  # independent diseases
  load(paste0(City, "/", Ndiseases,
    " enfermedades/Escenario ",
    Setting, "/Resultados/Replica ",
    Replica, "/resul.BYMIndep.Rdata"))
  BYM_indep[Replica, , ] <- result$mean$SMR
  # Estimated risks with NVA M-model
  load(paste0(City, "/", Ndiseases,
    " enfermedades/Escenario ",
    Setting, "/Resultados/Replica ",
    Replica, "/resul.MmodelRE.Rdata"))
  NVA[Replica, , ] <- result$mean$SMR
  # Estimated risks with CVA M-model
  load(paste0(City, "/", Ndiseases,
    " enfermedades/Escenario ",
    Setting, "/Resultados/Replica ",
    Replica, "/resul.MmodelCVA.Rdata"))
  CVA[Replica, , ] <- result$mean$SMR
  # Estimated risks with RVA M-model
  load(paste0(City, "/", Ndiseases,
    " enfermedades/Escenario ",
    Setting, "/Resultados/Replica ",
    Replica, "/resul.MmodelRVA.Rdata"))
  RVA[Replica, , ] <- result$mean$SMR
}
# Original standard deviation of the
# simulated spatial patterns and standard
# deviation of the estimated risks with
# each model
Resul[[City]][[Setting]] <- list()
Resul[[City]][[Setting]]$sds <- cbind(apply(apply(exp(Sim_data),

```

```

      c(1, 3), sd), 2, mean), apply(apply(BYM_indep,
      c(1, 3), sd), 2, mean), apply(apply(NVA,
      c(1, 3), sd), 2, mean), apply(apply(CVA,
      c(1, 3), sd), 2, mean), apply(apply(RVA,
      c(1, 3), sd), 2, mean))
    dimnames(Resul[[City]][[Setting]]$sds)[[2]] <- c("Original",
      "BYM", "NVA", "CVA", "RVA")
  }
}
# Mean standard deviation of the first
# spatial pattern and the rest of spatial
# patterns
for (City in 1:3) {
  for (Setting in 1:3) {
    print(paste0("# ", names(Resul)[City],
      ", Escenario ", Setting, ", ",
      Ndiseases, " enfermedades"))
    print(round(rbind(Resul[[City]][[Setting]]$sds[1,
      ], apply(Resul[[City]][[Setting]]$sds[2:Ndiseases,
      ], 2, mean)), 2))
  }
}

```