Results of the original spatial BYM model

Implementation of the model

```
data {
  int<lower=1> N; // Número total de municipios
  int<lower=0> Obs[N]; // Casos observados en cada municipio
  vector[N] Exp; // Casos esperados de cada municipio

  int<lower=N> LengthNeigh;     // Número de bordes en el gráfico
//Sparse coding of the Adjacency matrix:
//(Edges are coded as pairs (Vertex_i,Vertex_j) with Vertex_i<Vertex_j)
  int NeighLow[LengthNeigh];    // Vertex_i
  int NeighHigh[LengthNeigh];   // Vertex_j
}

parameters {
  real m; // intercept
  vector[N-1] sp_raw; // Efecto aleatorio espacial (CAR)
  vector[N] het; // Efecto aleatorio heterogéneo (Normal)

  real<lower=0> sd_sp; // SD efecto CAR
  real<lower=0> sd_het; // SD efecto Normal
}

transformed parameters {
  vector[N] sp;
  for (i in 1:(N-1)) sp[i] = sp_raw[i];
  sp[N] = -sum(sp_raw);
}

model {
  vector[N] log_mu;

  real auxSp;
  real auxHet;

  // sp modeled as a car.normal process
  //sp[NeighHigh]~normal(sp[NeighLow],sd_sp);
  auxSp=-0.5*dot_self(sp[NeighHigh]-sp[NeighLow]);
  //het~normal(0.0,sd_het);
  auxHet=-0.5*dot_self(het);
  //target += 0.5*sum(log(EigenMap))+auxSp+auxHet;
  target += auxSp+auxHet;

  // Verosimilitud
  log_mu = log(Exp)+m+sd_sp*sp+sd_het*het;
  Obs ~ poisson_log(log_mu);
}

generated quantities {
```

```
  vector[N] SMR;
  SMR=exp(m+sd_sp*sp+sd_het*het);
}
```

Fitting the model to Spain's mortality data

```
### Preámbulo ###
library(rstan)
library(spdep)
library(R2WinBUGS)
library(RColorBrewer)
load("/home/corpas_fra/Trabajo/Mortalidad nacional/DatosSinTemporal.Rdata")
Paleta.RR <- brewer.pal(9, "BrBG")[9:1]
Paleta.P.RR <- brewer.pal(9, "RdYlBu")[9:1]

#Precálculos con la matriz de vecindad
aux <- list()
for(i in 1:length(CartoMuniSinIslas.nb)) {
  aux[[i]] <- CartoMuniSinIslas.nb[[i]][CartoMuniSinIslas.nb[[i]] > i]
  }
NeighLow <- rep(1:length(CartoMuniSinIslas.nb), sapply(aux, length))
NeighHigh <- unlist(aux)
#D.W <- matrix(0, ncol = length(CartoMuniSinIslas.nb), nrow = length(CartoMuniSinIslas.nb))
#D.W[cbind(NeighLow, NeighHigh)] <- -1
#D.W[cbind(NeighHigh, NeighLow)] <- -1
#diag(D.W) <- -apply(D.W, 1, sum)
#EigenMap <- eigen(D.W, symmetric = TRUE, nly.values = TRUE)$values
#save(EigenMap, NeighLow, NeighHigh, file="BYM.Veci.Stan.Rdata")
#load("/home/migue/Trabajo/EstudiosSeattle/1.-Espacial/BYM/Stan/BYM.Veci.Stan.Rdata")

#Modelo de BYM en Stan
tcomp02 <- system.time(mod.BYM <- stan_model("BYM.stan"))
#Compilación 56 segundos
save(mod.BYM, file = "mod.Stan.BYM.Rdata")
#load("/home/migue/Trabajo/EstudiosSeattle/1.-Espacial/BYM/Stan/mod.Stan.BYM.Rdata")

#Función que ejecuta BYM en Stan
Ejecuta.BYM.Stan <- function(Sexo, Causa){
  Obs <- MorTabu[Sexo, Causa, ]
  Esp <- Esperados[Sexo, Causa, ]

  datos <- list(NeighLow = NeighLow, NeighHigh = NeighHigh,
                LengthNeigh = length(NeighHigh), N = length(Obs), Obs = Obs, Exp = Esp)
  param <- c("SMR","m","sd_sp","sd_het")
  Res.t <- system.time(Res <- sampling(object = mod.BYM, data = datos, chains = 3, iter = 4400,
                                       warmup = 400, thin = max(1, floor(3 * (4400 - 400) / 1000)),
                                       cores = 3, pars=c("SMR", "m", "sd_sp", "sd_het")))

  Res.BYM[[Sexo]][[Causa]] <<- list()
  Res.BYM[[Sexo]][[Causa]]$tiempo <<- Res.t
  Res.BYM[[Sexo]][[Causa]]$summary <<- Res
  Res.BYM[[Sexo]][[Causa]]$RR <<- summary(Res)$summary[1:7907, 1]
```

```
  Res.BYM[[Sexo]][[Causa]]$P.RR <<- apply(extract(Res,pars="SMR")$SMR, 2, function(x){mean(x > 1)})
}


Res.BYM <- list(Hombres = list(), Mujeres = list())

indice <- as.numeric(dimnames(MorTabu[1, , ])[[1]][apply(MorTabu[1, , ], 1, sum) >= 10000])

for(i in indice){
    Ejecuta.BYM.Stan(1, i)
    save(Res.BYM, file="Res.BYM-Stan.Rdata")

  }

save(Res.BYM, file="Res.BYM-Stan.Rdata")
```

Descriptive principals

Cause	Time	sigma_phi	sigma_theta	max.Rhat	min.n_eff
(9) Mouth and pharynx	7613.0	0.3346 [0.2982,0.3719]	0.0899 [0.0377,0.1267]	1.02	285.91
(10) Esophagus	6407.6	0.2982 [0.2621,0.3373]	0.0434 [0.0026,0.0922]	1.02	223.29
(11) Stomach	7774.4	0.3248 [0.2988,0.3515]	0.0263 [9e-04,0.0633]	1.01	355.09
(12) Colon	11761.9	0.2398 [0.2121,0.2689]	0.101 [0.0827,0.1172]	1.02	453.19
(13) Rectum	7501.6	0.2069 [0.171,0.249]	0.1201 [0.0938,0.1451]	1.02	186.89
(14) Liver	6568.7	1.7507 [0.2821,4.6257]	0.3138 [0.1248,0.649]	149.11	1.50
(15) Pancreas	12059.5	0.4569 [0.1826,0.9516]	0.318 [0.0167,0.8331]	120.10	1.50
(16) Other digestives	12821.8	0.2051 [0.1597,0.2688]	0.0466 [0.0021,0.0985]	1.12	8.12
(17) Larynx	7661.3	0.3471 [0.3065,0.3956]	0.0809 [0.01,0.1242]	1.02	164.38
(18) Lung	6646.1	1.6606 [0.3405,4.2768]	0.1427 [0.065,0.2618]	277.89	1.50
(22) Other skin	6954.5	0.2393 [0.1841,0.2942]	0.0449 [0.0019,0.1163]	1.02	254.59
(28) Prostate	5792.2	0.1974 [0.169,0.2268]	0.0604 [0.0249,0.0844]	1.01	390.71
(30) Kidney	10112.4	0.2934 [0.2498,0.3352]	0.041 [0.0024,0.0924]	1.02	255.22
(31) Bladder	9551.9	0.3056 [0.2738,0.344]	0.0799 [0.0375,0.1077]	1.04	38.28
(33) Brain	5264.9	0.1504 [0.1094,0.1903]	0.0864 [0.0519,0.1169]	1.03	147.23
(35) Poorly defined	5426.8	0.5003 [0.1986,1.0638]	0.1929 [0.0791,0.3826]	133.26	1.50
(36) Other lymphatics	5413.0	0.8716 [0.1466,2.2637]	0.174 [0.0481,0.3742]	158.20	1.50
(37) Leukemias	5202.6	0.1454 [0.1082,0.1846]	0.0686 [0.0259,0.1024]	1.02	237.51
(41) Other tumors	5342.5	0.3012 [0.2631,0.3425]	0.0501 [0.006,0.0947]	1.02	233.44
Median	6954.5	0.3	0.08	1.02	186.89