## Results of the spatial BYM model in Stan

## 1 Implementation of the BYM 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)
                                // Vertex_i
  int NeighLow[LengthNeigh];
  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);
```

## 2 Fitting the model to Spain's mortality data.

```
### Preámbulo ###
library(rstan)
library(rstan)
library(spdep)
library(R2WinBUGS)
library(RColorBrewer)
load("/home/migue/Trabajo/EstudiosSeattle/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()</pre>
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))</pre>
NeighHigh <- unlist(aux)</pre>
D.W <- matrix(0, ncol = length(CartoMuniSinIslas.nb)), nrow = length(CartoMuniSinIslas.nb))</pre>
D.W[cbind(NeighLow, NeighHigh)] <- -1</pre>
D.W[cbind(NeighHigh, NeighLow)] <- -1</pre>
diag(D.W) <- -apply(D.W, 1, sum)</pre>
EigenMap <- eigen(D.W, symmetric = TRUE, nly.values = TRUE)$values
save(EigenMap, NeighLow, NeighHigh, file = "BYM.Veci.Stan.Rdata")
# load('/home/mique/Trabajo/EstudiosSeattle/1.-Espacial/BYM/Stan/BYM.Veci.Stan.Rdata')
# Modelo de BYM en Stan
tcomp02 <- system.time(mod.BYM <- stan_model("BYM.stan"))</pre>
# Compilación 56 segundos
save(mod.BYM, file = "mod.Stan.BYM.Rdata")
# load('/home/mique/Trabajo/EstudiosSeattle/1.-Espacial/BYM/Stan/mod.Stan.BYM.Rdata')
# Función que ejecuta BYM en Stan
Ejecuta.BYM.Stan <- function(Sexo, Causa) {</pre>
    Obs <- MorTabu[Sexo, Causa, ]</pre>
    Esp <- Esperados[Sexo, Causa, ]</pre>
    datos <- list(NeighLow = NeighLow, NeighHigh = NeighHigh, LengthNeigh = length(NeighHigh),
        N = length(Obs), EigenMap = EigenMap, Obs = Obs, Exp = Esp)
    param <- c("SMR", "m", "sd_sp", "sd_het")</pre>
    Res.t <- system.time(Res <- sampling(object = mod.BYM, data = datos, chains = 3,
        iter = 4400, warmup = 400, thin = max(1, floor(3 * (4400 - 400)/1000)),
        cores = 3, pars = c("SMR", "m", "sd_sp", "sd_het")))
    Res.BYM[[Sexo]][[Causa]] <<- list()</pre>
    Res.BYM[[Sexo]][[Causa]]$tiempo <<- Res.t</pre>
    Res.BYM[[Sexo]][[Causa]]$summary <<- Res</pre>
```

## 3 Descriptive principals.

Cause	Time	sigma_phi	sigma_theta	max.Rhat	${\rm min.n\_eff}$
(9) Mouth and pharynx	12771.5	$0.3324 \ [0.2937, 0.3738]$	0.0888 [0.0357,0.1288]	1.01	206.32
(10) Esophagus	18398.2	$0.2975 \ [0.2655, 0.3317]$	0.0418 [0.0021,0.0893]	1.01	418.72
(11) Stomach	9940.8	0.6501 [0.3024, 1.2971]	1.1499 [0.0018,3.3961]	11492.20	1.50
(12) Colon	21527.7	0.2411 [0.2116, 0.2712]	$0.1 \ [0.0798, 0.1175]$	1.02	189.49
(13) Rectum	12967.5	0.2021 [0.1633, 0.2451]	0.1207 [0.0939, 0.1461]	1.02	116.42
(14) Liver	17310.4	0.3112 [0.2738, 0.3476]	0.1455 [0.1225, 0.1687]	1.01	449.19
(15) Pancreas	15805.9	$0.211 \ [0.158, 0.2532]$	$0.063 \ [0.0225, 0.1205]$	1.19	5.31
(16) Other digestives	9252.6	0.1995 [0.1489, 0.2486]	$0.0506 \ [0.0026, 0.1082]$	1.01	205.27
(17) Larynx	7458.8	1.8507 [0.3094, 4.8495]	$0.2298 \ [0.0196, 0.5317]$	137.98	1.50
(18) Lung	9648.9	0.3099 [0.1668,0.3821]	0.4069 [0.0626, 1.0564]	122.30	1.50
(22) Other skin	14664.7	$0.279 \ [0.2005, 0.3505]$	0.3528 [0.004, 0.9742]	113.94	1.50
(28) Prostate	12660.3	0.1992 [0.1722, 0.2263]	$0.0591 \ [0.0255, 0.0834]$	1.01	482.81
(30) Kidney	16245.7	0.2908 [0.2437, 0.338]	0.0438 [0.0024, 0.0973]	1.01	300.24
(31) Bladder	22685.0	$0.3053 \ [0.2735, 0.3405]$	0.079 [0.041, 0.108]	1.02	402.43
(33) Brain	14553.7	0.1478 [0.1089, 0.1891]	0.0876 [0.0522, 0.1184]	1.02	141.77
(35) Poorly defined	14773.3	$0.2246 \ [0.1966, 0.2548]$	$0.0975 \ [0.0753, 0.1181]$	1.01	491.53
(36) Other lymphatics	23796.1	0.4418 [0.1429, 0.9853]	$0.6513 \ [0.0506, 1.8031]$	263.69	1.50
(37) Leukemias	13819.2	0.1452 [0.1072, 0.1887]	0.0681 [0.0244,0.1009]	1.03	126.68
(41) Other tumors	13115.9	0.3008 [0.2598,0.3423]	0.0477 [0.0037, 0.0977]	1.02	440.12
Median	14553.7	0.29	0.09	1.02	189.49