## Results of the spatial BYM model with stochastic restriction (2)

## 1 Implementation of the BYM model with stochastic restriction (2)

```
data {
  int<lower=0> N;
  int<lower=0> N edges;
  int<lower=1, upper=N> node1[N_edges]; // node1[i] adjacent to node2[i]
  int<lower=1, upper=N> node2[N_edges]; // and node1[i] < node2[i]</pre>
  int<lower=0> y[N];
                                 // count outcomes
// vector[N] x;
                                   // predictor
 int<lower=0, upper=0> cero;
  vector<lower=0>[N] E;
                                 // exposure
transformed data {
  vector[N] log_E = log(E);
parameters {
 real beta0;
                            // intercept
// real beta1;
                              // slope
 real<lower=0> sigma_theta; // sd of heterogeneous effects
 real<lower=0> sigma_phi;  // sd of spatial effects
 vector[N] theta_std; // standardized heterogeneous effects
  vector[N] phi_std; // raw, standardized spatial effects
transformed parameters {
                                                    // non-centered parameterization
  vector[N] theta = theta_std * sigma_theta;
   vector[N] phi = phi_std * sigma_phi;
 real mean_phi_std = mean(phi_std);
// y ~ poisson_log(log_E + beta0 + beta1 * x + theta + phi);
 y ~ poisson_log(log_E + beta0 + theta + phi);
 target += -0.5 * dot_self(phi_std[node1] - phi_std[node2]);
 theta std ~ normal(0, 1);
  cero ~ normal(mean_phi_std, 0.001);
}
generated quantities {
// vector[N] mu = exp(log_E + beta0 + beta1 * x + phi + theta);
 vector[N] mu = exp(log_E + beta0 + phi + theta);
  vector[N] SMR = exp(beta0 + phi + theta);
```

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

```
library(rstan)
library(spdep)
# options(mc.cores = parallel::detectCores())
options(mc.cores = 3)
source("mungeCARdata4stan.R")
load("../../Mortalidad nacional/DatosSinTemporal.Rdata")
Veci<-nb2WB(CartoMuniSinIslas.nb)</pre>
nbs = mungeCARdata4stan(Veci$adj, Veci$num);
N = nbs$N;
node1 = nbs$node1;
node2 = nbs$node2;
N_edges = nbs$N_edges;
tcomp02 <- system.time(mod.BYM <- stan_model("BYM_StanFast_0.stan"))</pre>
# Compilation in 66 seconds
save(mod.BYM, file = "mod.Stan.BYM.Fast.Rdata")
# load("mod.Stan.BYM.NoPriors3.Rdata")
Ejecuta.BYM.Stan<-function(Sexo, Causa){</pre>
  y <- MorTabu[Sexo,Causa, ]</pre>
 E <- Esperados[Sexo,Causa, ]</pre>
  datos <- list(N ,N_edges, node1, node2, y, E, cero=0)</pre>
  param <- c("SMR", "mu", "sigma_phi", "sigma_theta", "beta0")</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 = param))
  Res.BYM[[Sexo]][[Causa]] <<- list()</pre>
  Res.BYM[[Sexo]][[Causa]]$tiempo <<- Res.t</pre>
  Res.BYM[[Sexo]][[Causa]]$summary <<- Res</pre>
  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())</pre>
for(i in c(9:18, 22, 28, 30, 31, 33, 35:37, 41)){
  Ejecuta.BYM.Stan(1, i)
  save(Res.BYM, file = "Res.BYM-StanFast_0.Rdata")
```

## 3 Descriptive principals

Cause	Time	sigma_phi	sigma_theta	max.Rhat	min.n_eff
(9) Mouth and pharynx	818.4	0.3326 [0.2946,0.3706]	0.089 [0.0424,0.1261]	1.02	367.81
(10) Esophagus	520.1	0.3009 [0.268, 0.3405]	0.0417 [0.0029,0.086]	1.02	127.67

Cause	Time	sigma_phi	sigma_theta	max.Rhat	min.n_eff
(11) Stomach	944.6	0.325 [0.2994,0.3503]	0.0266 [0.0011,0.0662]	1.01	342.85
(12) Colon	1322.6	0.2393 [0.2112, 0.2667]	0.1014 [0.0837,0.1185]	1.01	525.60
(13) Rectum	538.9	0.2017 [0.1645, 0.2397]	$0.1219 \ [0.0942, 0.1476]$	1.02	97.51
(14) Liver	825.6	0.3125 [0.2743, 0.3485]	0.1462 [0.1193, 0.1708]	1.01	410.19
(15) Pancreas	623.7	0.2123 [0.1783, 0.2471]	$0.0603 \ [0.0185, 0.0895]$	1.02	194.65
(16) Other digestives	778.3	$0.2005 \ [0.1487, 0.2502]$	$0.0493 \ [0.0027, 0.1053]$	1.03	111.81
(17) Larynx	830.7	0.3452 [0.3035, 0.3888]	$0.0839 \ [0.0227, 0.1258]$	1.02	164.23
(18) Lung	966.4	0.3603 [0.3389, 0.383]	0.0832 [0.0626, 0.1001]	1.01	290.21
(22) Other skin	873.7	0.2394 [0.1818,0.2973]	0.0477 [0.0027,0.1115]	1.02	276.70
(28) Prostate	564.3	0.1989 [0.17, 0.226]	0.0608 [0.032, 0.0828]	1.02	217.35
(30) Kidney	869.5	0.2908 [0.2453,0.3375]	0.0434 [0.0017,0.0968]	1.02	368.60
(31) Bladder	609.0	0.3051 [0.2701,0.3396]	0.0792 [0.042, 0.1068]	1.01	206.85
(33) Brain	706.1	0.1518 [0.1114,0.1942]	0.0854 [0.0511,0.1154]	1.02	189.27
(35) Poorly defined	538.0	0.2239 [0.1959, 0.2525]	0.0982 [0.0773,0.1173]	1.02	319.99
(36) Other lymphatics	500.6	0.1755 [0.1413, 0.2101]	0.0756 [0.0492, 0.0998]	1.02	227.97
(37) Leukemias	795.1	0.1471 [0.1116,0.1833]	$0.067 \ [0.0213, 0.0986]$	1.02	243.87
(41) Other tumors	1162.2	0.3 [0.2589,0.3384]	0.0502 [0.0046, 0.0967]	1.02	449.18
Median	795.1	0.24	0.08	1.02	243.87