Results of the unrestricted spatial BYM model

1 Implementation of the unrestricted BYM model

```
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]

  int<lower=0> y[N];              // count outcomes
//  vector[N] x;                    // predictor
  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 {
  vector[N] theta = theta_std * sigma_theta;         // non-centered parameterization
  vector[N] phi = phi_std * sigma_phi;
}
model {
//  y ~ poisson_log(log_E + beta0 + beta1 * x + theta + phi);

  y ~ poisson_log(log_E + theta + phi);

  target += -0.5 * dot_self(phi_std[node1] - phi_std[node2]);

  theta_std ~ normal(0, 1);
}
generated quantities {
//  vector[N] mu = exp(log_E + beta0 + beta1 * x + phi + theta);
  vector[N] mu = exp(log_E + phi + theta);
  vector[N] SMR = exp(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)
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_NoMu.stan"))
# Compilation in 66 seconds

save(mod.BYM, file = "mod.Stan.BYM.NoMu.Rdata")

Ejecuta.BYM.Stan<-function(Sexo, Causa){
  y <- MorTabu[Sexo,Causa, ]
  E <- Esperados[Sexo,Causa, ]

  datos <- list(N ,N_edges, node1, node2, y, E)
  param <- c("SMR", "mu", "sigma_phi", "sigma_theta")
  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()
  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())

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-NoMu.Rdata")
}
```

3 Descriptive principals

Cause	Time	sigma_phi	sigma_theta	max.Rhat	min.n_eff
(9) Mouth and pharynx	365.1	0.3324 [0.2911,0.3753]	0.0863 [0.0038,0.1269]	1.03	84.90
(10) Esophagus	617.8	0.2974 [0.2608,0.335]	0.043 [0.0017,0.0919]	1.02	172.21
(11) Stomach	708.8	0.3251 [0.2999,0.3524]	0.0254 [0.0014,0.0616]	1.01	380.23
(12) Colon	944.1	0.2393 [0.2118,0.2693]	0.101 [0.081,0.1194]	1.01	179.63
(13) Rectum	340.4	0.2012 [0.1602,0.2409]	0.1212 [0.0959,0.1463]	1.03	101.27
(14) Liver	1068.7	0.3117 [0.2745,0.348]	0.1461 [0.1212,0.172]	1.01	232.26
(15) Pancreas	626.3	0.2121 [0.1798,0.245]	0.0619 [0.0228,0.091]	1.02	254.78

Cause	Time	sigma_phi	sigma_theta	max.Rhat	min.n_eff
(16) Other digestives	631.7	0.2021 [0.1593,0.2437]	0.0478 [0.0039,0.1011]	1.02	241.52
(17) Larynx	614.0	0.3476 [0.3044,0.3949]	0.0815 [0.0177,0.1283]	1.01	113.01
(18) Lung	736.9	0.3603 [0.3394,0.3822]	0.0839 [0.0624,0.1025]	1.01	283.44
(22) Other skin	583.6	0.2336 [0.1784,0.2897]	0.0471 [0.0022,0.1169]	1.02	192.69
(28) Prostate	356.4	0.197 [0.1686,0.2284]	0.0605 [0.0228,0.0839]	1.03	116.69
(30) Kidney	584.1	0.2917 [0.2464,0.3381]	0.0432 [0.0026,0.1019]	1.02	162.88
(31) Bladder	452.7	0.3021 [0.2691,0.3357]	0.081 [0.0462,0.1103]	1.01	193.65
(33) Brain	574.6	0.1519 [0.1121,0.1982]	0.0842 [0.0446,0.1152]	1.03	77.06
(35) Poorly defined	611.3	0.2244 [0.1981,0.2537]	0.0981 [0.0761,0.1182]	1.01	176.21
(36) Other lymphatics	412.1	0.1715 [0.1401,0.2046]	0.0779 [0.052,0.0998]	1.03	106.08
(37) Leukemias	391.4	0.1475 [0.11,0.1869]	0.0663 [0.0113,0.0982]	1.04	91.18
(41) Other tumors	639.5	0.2996 [0.2604,0.3373]	0.0486 [0.0034,0.0973]	1.01	328.65
Median	611.3	0.24	0.08	1.02	176.21