Results of the spatial BYM model with our implementation and with the previous distributions used in the model proposed by Mitzi

1 Implementation of the 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> tau_theta;   // sd of heterogeneous effects
  real<lower=0> tau_phi;     // sd of spatial effects

  vector[N] theta_std;       // standardized heterogeneous effects
  vector[N - 1] phi_std_raw; // raw, standardized spatial effects
}
transformed parameters {
  real<lower=0> sigma_theta = inv(sqrt(tau_theta));  // convert precision to sigma
  vector[N] theta = theta_std * sigma_theta;         // non-centered parameterization

  real<lower=0> sigma_phi = inv(sqrt(tau_phi));      // convert precision to sigma
//  vector[N] phi_std;
  vector[N] phi;
  phi[1:(N - 1)] = phi_std_raw;
  phi[N] = -sum(phi_std_raw);

  // vector[N] phi;
  // phi = phi * sigma_phi;    // non-centered parameterization
}
model {
//  y ~ poisson_log(log_E + beta0 + beta1 * x + theta + phi);

  y ~ poisson_log(log_E + beta0 + theta + sigma_phi * phi);

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

```
  beta0 ~ normal(0, 5);
//  beta1 ~ normal(0, 5);
  theta_std ~ normal(0, 1);
  tau_theta ~ gamma(3.2761, 1.81);  // Carlin WinBUGS priors
  tau_phi ~ gamma(1, 1);            // Carlin WinBUGS priors
}
generated quantities {
//  vector[N] mu = exp(log_E + beta0 + beta1 * x + phi + theta);
  vector[N] mu = exp(log_E + beta0 + sigma_phi * phi + theta);
  vector[N] SMR = exp(beta0 + sigma_phi * phi + theta);
//  real psi = sd(phi) / (sd(theta) + sd(phi));  // proportion spatial variation
}
```

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_Mitzi_Priors3.stan"))
# Compilation in 61 seconds

save(mod.BYM, file = "mod.Stan.BYM.Priors3.Rdata")
# load('mod.Stan.BYM.Priors3.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", "beta0", "sigma_phi", "tau_phi", "sigma_theta",
        "tau_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-StanMitzi.Priors3.Rdata")
}
```

3 Descriptive principals.

Cause	Time	sigma_phi	sigma_theta	max.Rhat	min.n_eff
(9) Mouth and pharynx	8552.9	0.5184 [0.2759,0.953]	0.8433 [0.1801,2.1384]	706.89	1.50
(10) Esophagus	4701.8	0.3013 [0.2586,0.3422]	0.5737 [0.172,1.3462]	88.21	1.50
(11) Stomach	4544.7	0.2856 [0.2611,0.309]	0.1607 [0.149,0.1733]	1.01	436.67
(12) Colon	4527.5	0.2302 [0.2099,0.2537]	0.1578 [0.1472,0.1688]	1.01	498.56
(13) Rectum	4582.8	0.227 [0.1999,0.2592]	0.1888 [0.1734,0.2054]	1.01	462.96
(14) Liver	4489.4	0.2975 [0.2694,0.3279]	0.1985 [0.1837,0.2142]	1.01	338.06
(15) Pancreas	4674.0	0.4495 [0.1966,0.9092]	0.2388 [0.1553,0.383]	92.11	1.50
(16) Other digestives	4464.5	0.2316 [0.2,0.2667]	0.2004 [0.181,0.2201]	1.01	292.06
(17) Larynx	4497.9	0.3125 [0.2786,0.3469]	0.1985 [0.1808,0.217]	1.01	350.67
(18) Lung	8260.6	0.3244 [0.3055,0.343]	0.1464 [0.1377,0.1551]	1.02	132.29
(22) Other skin	4526.0	0.2683 [0.2265,0.3162]	0.2303 [0.2055,0.2587]	1.02	260.59
(28) Prostate	4487.0	0.1895 [0.1705,0.209]	0.1431 [0.1339,0.153]	1.02	522.51
(30) Kidney	4572.0	0.2749 [0.2402,0.3139]	0.1994 [0.1808,0.2191]	1.01	330.08
(31) Bladder	4745.7	0.2739 [0.2468,0.3011]	0.1678 [0.1554,0.1805]	1.01	580.06
(33) Brain	8875.9	0.2108 [0.1826,0.2399]	0.1861 [0.1698,0.2031]	1.02	481.39
(35) Poorly defined	4832.4	0.2217 [0.1998,0.244]	0.1646 [0.1526,0.1768]	1.01	444.41
(36) Other lymphatics	4871.8	0.2046 [0.1792,0.2309]	0.1673 [0.1547,0.1826]	1.01	471.12
(37) Leukemias	4884.5	0.1998 [0.1756,0.2272]	0.176 [0.1605,0.1913]	1.02	436.37
(41) Other tumors	4840.7	0.2811 [0.2465,0.3158]	0.1922 [0.1742,0.2098]	1.01	344.39
Median	4674.0	0.27	0.19	1.01	350.67