Results of the 'bym_exposure_only' model

Implementation of the 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<lower=0>[N] E;           // exposure
}
transformed data {
  vector[N] log_E = log(E);
}
parameters {
  real beta0;                // intercept

  real<lower=0> tau_theta;   // precision of heterogeneous effects
  real<lower=0> tau_phi;     // precision of spatial effects

  vector[N] theta;       // 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
  real<lower=0> sigma_phi = inv(sqrt(tau_phi));      // convert precision to sigma
  vector[N] phi;
  phi[1:(N - 1)] = phi_std_raw;
  phi[N] = -sum(phi_std_raw);
}
model {
  y ~ poisson_log(log_E + beta0 + phi * sigma_phi + theta * sigma_theta);

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

  beta0 ~ normal(0, 5);
  theta ~ 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 + phi * sigma_phi + theta * sigma_theta);
  vector[N] SMR = exp(beta0 + phi * sigma_phi + theta * sigma_theta);
}
```

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_exposure_only.stan"))
# Compilation in 59 seconds

save(mod.BYM, file = "mod.bym_exposure_only.Rdata")
# load("bym_exposure_only.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_exposure_only.Rdata")
}
```

Descriptive principals

Cause	Time	sigma_phi	sigma_theta	max.Rhat	min.n_eff
(9) Mouth and pharynx	9114.0	0.3058 [0.2729,0.3412]	0.1959 [0.1782,0.2139]	1.01	440.91
(10) Esophagus	4989.3	0.2878 [0.2567,0.3205]	0.1885 [0.1727,0.2065]	1.01	371.81
(11) Stomach	5390.3	0.2847 [0.2617,0.311]	0.161 [0.1497,0.1729]	1.01	434.41
(12) Colon	6790.3	0.2304 [0.208,0.252]	0.1575 [0.146,0.1691]	1.01	505.98
(13) Rectum	11156.4	0.2264 [0.1976,0.2557]	0.1889 [0.1731,0.2068]	1.01	486.39

Cause	Time	sigma_phi	sigma_theta	max.Rhat	min.n_eff
(14) Liver	10734.0	0.2334 [0.1002,0.3273]	0.1668 [0.0996,0.2135]	36.68	1.51
(15) Pancreas	5548.5	0.2194 [0.1946,0.2474]	0.1669 [0.1545,0.1801]	1.01	343.59
(16) Other digestives	6427.1	0.2303 [0.1965,0.2654]	0.2005 [0.1821,0.2191]	1.02	403.09
(17) Larynx	6106.1	0.5428 [0.2774,1.018]	0.3407 [0.1818,0.6253]	128.35	1.50
(18) Lung	5636.5	0.3235 [0.3064,0.341]	0.1467 [0.1378,0.1565]	1.01	426.97
(22) Other skin	5753.4	0.2714 [0.2301,0.3186]	0.2301 [0.2046,0.2571]	1.01	376.17
(28) Prostate	6295.1	0.1891 [0.1701,0.2094]	0.1432 [0.1336,0.1528]	1.01	509.68
(30) Kidney	5818.6	0.2753 [0.2392,0.314]	0.1994 [0.1801,0.2207]	1.02	438.21
(31) Bladder	6126.6	0.2749 [0.2497,0.3024]	0.1674 [0.1548,0.181]	1.01	554.39
(33) Brain	6672.4	0.2104 [0.184,0.2401]	0.1866 [0.1683,0.2048]	1.01	382.78
(35) Poorly defined	5970.2	0.2222 [0.2003,0.2444]	0.164 [0.1512,0.1757]	1.01	386.60
(36) Other lymphatics	6060.5	0.2059 [0.1823,0.2319]	0.1677 [0.1537,0.1821]	1.02	485.64
(37) Leukemias	5106.0	0.2007 [0.1746,0.2274]	0.1765 [0.1616,0.1911]	1.01	428.56
(41) Other tumors	5087.5	0.2805 [0.2468,0.3164]	0.1915 [0.1738,0.2099]	1.01	490.96
Median	6060.5	0.23	0.18	1.01	428.56