

BYM models

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```
require('diseasemapping')

## Loading required package: diseasemapping

data('kentucky')
kentucky = terra::unwrap(kentucky)
```

Incidence rates

```
if (FALSE) {
  # must have an internet connection to do the following
  larynxRates = cancerRates("USA", year = 1998:2002, site = "Larynx")
  dput(larynxRates)
} else {
  larynxRates = structure(c(0, 0, 0, 0, 1e-06, 6e-06, 2.3e-05, 4.5e-05, 9.9e-05,
    0.000163, 0.000243, 0.000299, 0.000343, 0.000308, 0.000291, 0.000217, 0,
    0, 0, 1e-06, 1e-06, 3e-06, 8e-06, 1.3e-05, 2.3e-05, 3.5e-05, 5.8e-05, 6.8e-05,
    7.5e-05, 5.5e-05, 4.1e-05, 3e-05), .Names = c("M_10", "M_15", "M_20", "M_25",
    "M_30", "M_35", "M_40", "M_45", "M_50", "M_55", "M_60", "M_65", "M_70", "M_75",
    "M_80", "M_85", "F_10", "F_15", "F_20", "F_25", "F_30", "F_35", "F_40", "F_45",
    "F_50", "F_55", "F_60", "F_65", "F_70", "F_75", "F_80", "F_85"))
}
```

```
# get rid of under 10's
larynxRates = larynxRates[grep("_(0|5)$",names(larynxRates), invert=TRUE)]
# compute Sexpected
kentucky = diseasemapping::getSMR(
  popdata=kentucky,
  model = larynxRates,
```

```
casedata=larynx,  
regionCode="County")
```

The BYM model

The Besag, York and Mollie model for Poisson distributed case counts is:

$$\begin{aligned} Y_i &\sim \text{Poisson}(O_i \lambda_i) \\ \log(\mu_i) &= X_i \beta + U_i \\ U_i &\sim \text{BYM}(\sigma_1^2, \sigma_2^2) \end{aligned}$$

- Y_i is the response variable for region i
- O_i is the 'baseline' expected count, which is specified
- X_i are covariates
- U_i is a spatial random effect with a spatially structured variance parameter σ_1^2 and a spatially independent variance σ_2^2

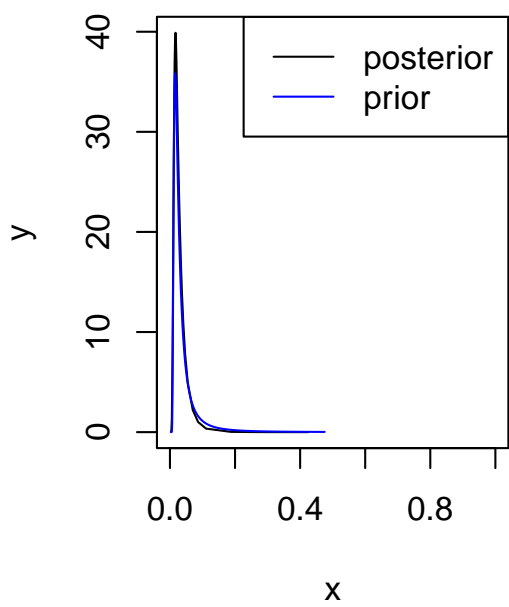
Gamma priors on precision

```
kBYM = try(bym(formula = observed ~ offset(logExpected) + poverty, data = kentucky,  
prior = list(sdSpatial = c(0.01, 0.2), sdIndep = c(0.01, 0.2)), region.id = "County"
```

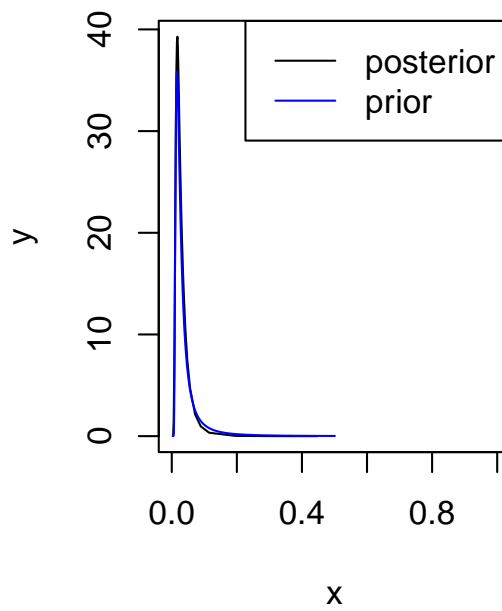
Above, Gamma priors are assigned to $1/\sigma_1^2$ and $1/\sigma_2^2$, with the shape and scale parameters set to produce 2.5% to 97.5% prior intervals of (0.1, 5) for each standard deviation parameter.

```
if(!is.null(kBYM$parameters))  
  knitr::kable(kBYM$parameters$summary[,c(1,3,5)], digits=3)
```

	mean	0.025quant	0.975quant
(Intercept)	0.066	-0.349	0.482
poverty	0.010	-0.010	0.030
sdSpatial	0.029	0.009	0.086
sdIndep	0.029	0.009	0.089



(a) spatial



(b) indep

Figure 1: gamma priors sd parameters

BYM with penalised complexity prior

'propSpatial = c(u=0.5, alpha=0.8)' means $pr(\phi < 0.5) = 0.8$, which is different from the specification of 'pc.prec'

```
kBYMpc = try(bym(formula = observed ~ offset(logExpected) + poverty, kentucky, prior = 1,
  alpha = 0.05), propSpatial = c(u = 0.5, alpha = 0.8)), verbose = TRUE), silent = TRUE)

## Warning in inla.model.properties.generic(inla.trim.family(model), mm[names(mm)]
== : Model 'bym2' in section 'latent' is marked as 'experimental'; changes may
appear at any time.
## Use this model with extra care!!! Further warnings are disabled.
```

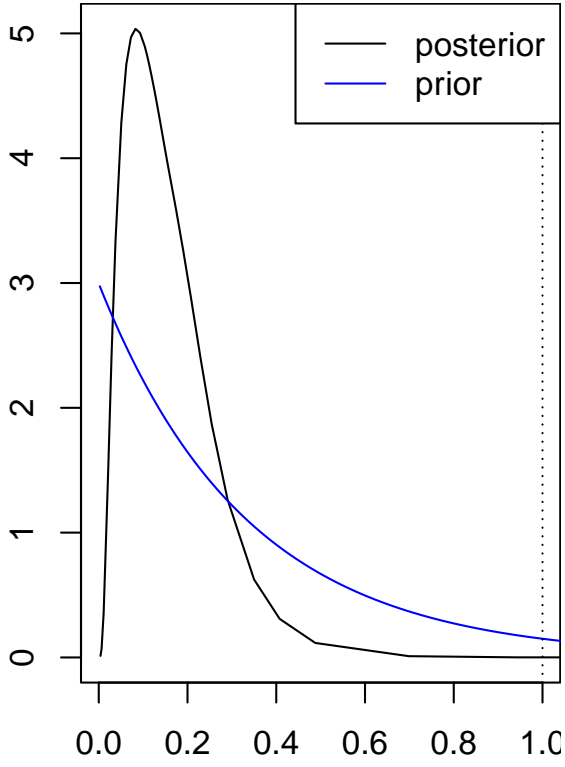
Here penalized complexity priors are used with $pr(\sqrt{\sigma_1^2 + \sigma_2^2} > 1) = 0.05$ and

$$pr(\sigma_1 / \sqrt{\sigma_1^2 + \sigma_2^2} < 0.5) = 0.8.$$

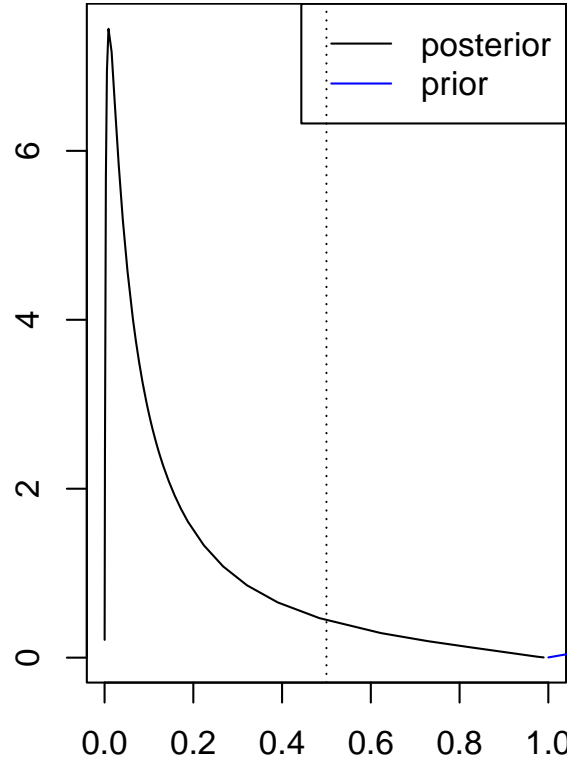
```
if(!is.null(kBYMpc$parameters))
  knitr::kable(kBYMpc$parameters$summary[,c(1,3,5)], digits=3)
```

	mean	0.025quant	0.975quant
(Intercept)	0.088	-0.360	0.545
poverty	0.009	-0.012	0.030
sd	0.154	0.029	0.408
propSpatial	0.186	0.005	0.728

```
## terra 1.7.41
##
## Attaching package: 'terra'
## The following object is masked from 'package:knitr':
##
## spin
## map images will be cached in /var/folders/1s/zkmc02qn4k18r6jdtbb459hc0000gn/T//Rtm
## Warning in RColorBrewer::brewer.pal(n, colName): minimal value for n is 3,
returning requested palette with 3 different levels
```

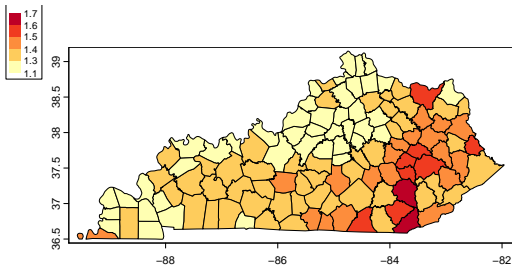


(a) sd

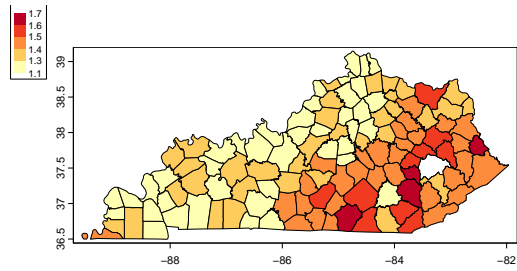


(b) prop spatial

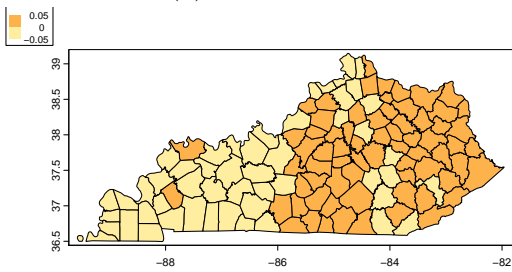
Figure 2: PC priors variance parameters



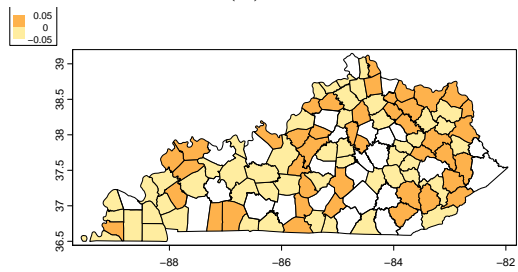
(a) gamma, fitted



(b) pc fitted



(c) gamma random



(d) pc random

Figure 3: Random effects and fitted values