BYM with PC priors

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```
require('diseasemapping')
## Loading required package: diseasemapping
data('kentucky')
```

Incidence rates

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

The BYM model

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

$$Y_i \sim \text{Poisson}(O_i \lambda_i)$$

 $\log(\mu_i) = X_i \beta + U_i$
 $U_i \sim \text{BYM}(\sigma_1^2, \sigma_2^2)$

- Y_i is the response variable for region i
- \bullet 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 = bym(formula = observed ~ offset(logExpected) + poverty, data = kentucky, priorCI = list(sdSpatial = c(0.1, 5), sdIndep = c(0.1, 5)), 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)	0.112	-0.381	0.613
poverty	0.007	-0.017	0.030
sdSpatial	0.193	0.083	0.426
sdIndep	0.198	0.085	0.411

BYM with penalised complexity prior

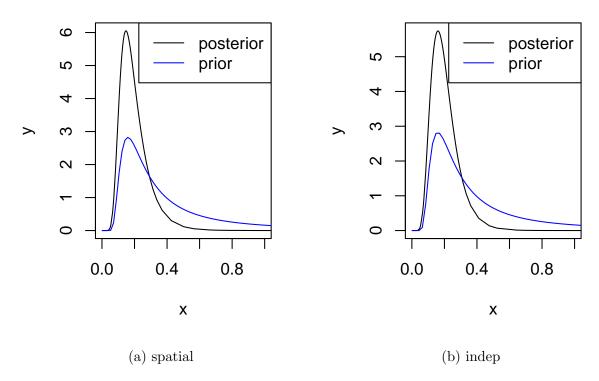


Figure 1: gamma priors sd parameters

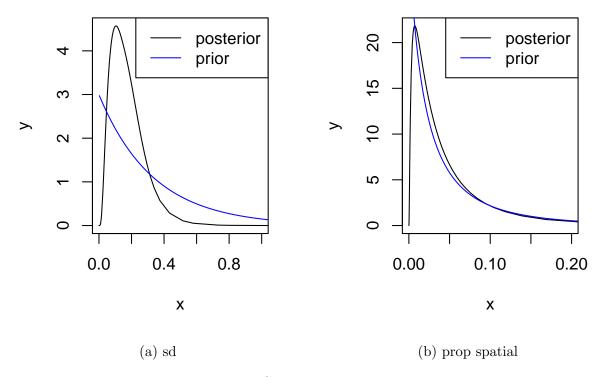


Figure 2: PC priors variance parameters

Here penalized complexity priors are used with $pr(\sqrt{\sigma_1^2 + \sigma_2^2} > 1) = 0.05$ and $pr(\sigma_1/\sigma_0 < 0.2) = 0.95$.

	mean	0.025quant	0.975quant
(Intercept)	0.078	-0.356	0.516
poverty	0.009	-0.012	0.030
sd	0.170	0.039	0.434
propSpatial	0.051	0.003	0.224

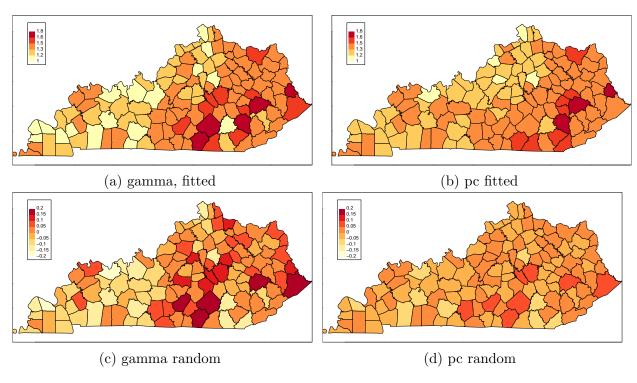


Figure 3: Random effects and fitted values