Proper/Non-intrinsic Besag model for spatial effects

Parametrization

The proper version of the Besag model for random vector $\mathbf{x} = (x_1, \dots, x_n)$ is defined as

$$x_i|x_{-i}, \tau, d \sim \mathcal{N}\left(\frac{1}{d+n_i} \sum_{i \sim j} x_j, \frac{1}{\tau(d+n_i)}\right)$$
 (1)

where n_i is the number of neighbours of node i, $i \sim j$ indicates that the two nodes i and j are neighbours, d > 0 is an extra term added on the diagonal controlling the "properness" and $\tau > 0$ is a "precision-like" (or scaling) parameter.

This parameterisation corresponds to this precision matrix $Q = (Q_{ij})$, where for $j \neq i$

$$Q_{ii} = \tau(n_i + d)$$
 and $Q_{ij} = -\tau$.

Hyperparameters

The precision parameter τ is represented as

$$\theta_1 = \log \tau$$

and the prior is defined on θ_1 . The diagonal parameter d is represented as

$$\theta_2 = \log d$$

and the prior is defined on θ_2 .

Specification

The besag model is specified inside the f() function as

```
f(<whatever>, model="besagproper", graph=<graph>,
  hyper=<hyper>)
```

The neighbourhood structure of \mathbf{x} is passed to the program through the graph argument. The structure of this file is described below.

Hyperparameter spesification and default values

 doc A proper version of the Besag model

hyper

theta1

hyperid 12001
name log precision
short.name prec
prior loggamma
param 1 5e-04
initial 2
fixed FALSE
to.theta function(x) log(x)
from.theta function(x) exp(x)

```
theta2
         hyperid 12002
         name log diagonal
         short.name diag
         prior loggamma
         param 1 1
         initial 1
         fixed FALSE
         to.theta function(x) log(x)
         from.theta function(x) exp(x)
constr FALSE
nrow.ncol FALSE
augmented FALSE
aug.factor 1
aug.constr
n.div.by
n.required TRUE
set.default.values TRUE
pdf besagproper
Example
## pick a graph
graph = system.file("demodata/germany.graph", package="INLA")
g = inla.read.graph(graph.file)
## we will use replicated samples in our testing
nrep = 5
## make life easy; use dense matrix algebra
d = 1.0
tau = 1.0
Q = matrix(0, g$n, g$n)
diag(Q) = tau * (d + g$nnbs)
for(i in 1:g$n) {
    if (g$nnbs[i] > 0) {
        Q[i, g$nbs[[i]]] = -tau
        Q[g$nbs[[i]], i] = -tau
    }
R = chol(Q) ## 'chol' returns the upper triangular
## simulate data with replications
y = c()
```

```
for(i in 1:nrep) {
    y = c(y, backsolve(R, rnorm(g$n)))
i = rep(1:g$n, nrep)
replicate = rep(1:nrep, each = g$n)
formula = y ~ f(i, model="besagproper", graph = graph,
        replicate=replicate,
        hyper = list(diag = list(param = c(1, 1)))) -1
## use 'exact' observations, so we fix the noise precisin to a high
## value
r = inla(formula,
        data = data.frame(y, i, replicate),
        family = "gaussian",
        control.family = list(
                hyper = list(
                        prec = list(
                                initial = 10,
                                fixed=TRUE))))
```

Notes

If d=0 and the parameter rankdef=1 is set, then this model corresponds to the besag model. constr=FALSE is default for this model.