Besag2 model for weighted spatial effects

Parametrization

The besag2 model is an extention to the besag model. Let the random vector $\mathbf{z} = (x_1, \ldots, x_n)$ be the besag model, then the besag2 is the following extentions

$$\mathbf{x} = (a\mathbf{z}, \mathbf{z}/a)$$

where $a > 0$ is an additional hyperparameter and $\dim(\mathbf{x}) = 2n$, and $\mathbf{z}$ is the *same* (up to tiny additive noise) random vector.

Hyperparameters

This model has two hyperparameters $\theta = (\theta_1, \theta_2)$.

The precision parameter τ is represented as

$$\theta_1 = \log \tau$$

and the prior is defined on θ_1.

The weight-parameter a is represented as

$$\theta_2 = \log a$$

and the prior is defined on θ_2.

Specification

The besag2 model is specified inside the `f()` function as

```
f(<whatever>,model="besag2",graph.file=<graph file name>
              precision=<precision>, hyper = <hyper>,
              adjust.for.con.comp = TRUE)
```

The precision is the precision defining how equal the two copies of $\mathbf{z}$ is. The neighbourhood structure of $\mathbf{x}$ is passed to the program through the `graph.file` argument. The structure of this file is described below.

Note that the besag2 model has dimension $2n$, where n is the size of the graph.

The option `adjust.for.con.comp` adjust the model if the graph has more than one connected compoment, and this adjustment can be disabled setting this option to `FALSE`. This means that `constr=TRUE` is interpreted as a sum-to-zero constraint on *each* connected component and the `rankdef` parameter is set accordingly.

Hyperparameter spesification and default values

hyper

theta1

name log precision
short.name prec
prior loggamma
param 1 5e-05
initial 4
fixed FALSE

to.theta

from.theta

theta2

name scaling parameter

short.name a

prior loggamma

param 10 10

initial 0

fixed FALSE

to.theta

from.theta

constr FALSE

nrow.ncol FALSE

augmented FALSE

aug.factor 1

aug.constr 1 2

n.div.by 2

n.required TRUE

set.default.values TRUE

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Structure of the graph file

We describe the required format for the graph file using a small example. Let the file `gra.dat`, relative to a small graph of only 5 elements, be

```
5
1  1  2
2  2  1  3
3  3  2  4  5
4  1  3
5  1  3
```

Line 1 declares the total number of nodes in the graph (5), then, in lines 2-6 each node is described. For example, line 4 states that node 3 has 4 neighbours and these are nodes 2, 4 and 5.

The graph file can either have nodes indexed from 1 to n, or from 0 to $n-1$. Note that in the latter case, node i seen from R corresponds to node $i-1$ in the 0-indexed graph.

Example

This is a simulated example.

```
data(Oral)
g = system.file("demodata/germany.graph", package="INLA")

## use data Oral to estimate a spatial field in order to simulate a
## 'realistic' dataset.
```

```
formula = Y ~ f(region, model="bym", graph.file=g)
result = inla(formula, data = Oral, family = "poisson", E = E)

x = result$summary.random$region$mean
n = length(x)/2

## simulate two new datasets. 'a' is the weighting between the
## log.rel.risk:
a = 2
xx = x[1:n]+1
x = c(a*xx, xx/a)
E = c(Oral$E, Oral$E)
N = 2*n
y = rpois(N, lambda = E*exp(x))

## model='besag2' defines a model with length N = 2*graph->n, the
## first half is weighted with 'a' the other half is weighted with
## 1/a. here there is no unstructed terms.
i = 1:N
formula = y ~ f(i, model="besag2", graph.file=g) -1
r = inla(formula, family = "poisson", data = data.frame(E,y,i), E=E, verbose=TRUE)
```

Notes

The besag2 model has default `constr=FALSE`, and `constr=TRUE` does not make sense.