

Proper/Non-intrinsic Besag model for spatial effects (variant 2)

Parametrization

The (2nd) proper version of the Besag model for random vector $\mathbf{x} = (x_1, \dots, x_n)$ is defined with precision matrix¹

$$\tau((1 - \lambda)I + \lambda R) \quad (1)$$

where R is the (unit precision) precision matrix for the Besag model, τ is a precision parameter and $0 < \lambda < 1$.

Hyperparameters

The precision parameter τ is represented as

$$\theta_1 = \log \tau$$

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

$$\theta_2 = \log (\lambda/(1 - \lambda))$$

and the prior is defined on θ_2 .

Specification

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

```
f(<whatever>, model="besagproper2", 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 specification and default values

doc An alternative proper version of the Besag model

hyper

theta1

hyperid 13001

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 13002

¹Brian G Leroux, Xingye Lei, and Norman Breslow. Estimation of disease rates in small areas: A new mixed model for spatial dependence. In Statistical Models in Epidemiology, the Environment, and Clinical Trials, Springer, 2000

```

    name logit lambda
    short.name lambda
    prior gaussian
    param 0 0.45
    initial 3
    fixed FALSE
    to.theta function(x) log(x / (1 - x))
    from.theta function(x) exp(x) / (1 + exp(x))

constr FALSE

nrow.ncol FALSE

augmented FALSE

aug.factor 1

aug.constr

n.div.by

n.required TRUE

set.default.values TRUE

status experimental

pdf besagproper2

```

Example

```

graph.file = system.file("demodata/germany.graph", package="INLA")
g = inla.read.graph(graph.file)

## we will use replicated samples in our testing
nrep = 5

tau = 10.0
lambda = 0.3
R = -inla.graph2matrix(g)
diag(R) = g$nnbs
n = g$n
Q = tau * ( (1-lambda) * diag(n) + lambda * R)
y = c(inla.qsample(nrep, Q))

i = rep(1:g$n, nrep)
replicate = rep(1:nrep, each = g$n)
formula = y ~ f(i, model="besagproper2", graph = g,
               replicate=replicate) - 1

r = inla(formula,
         data = data.frame(y, i, replicate),
         family = "gaussian",
         control.family = list(

```

```
hyper = list(  
    prec = list(  
        initial = 10,  
        fixed=TRUE)))
```

Notes

None