

# 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 matrix<sup>1</sup>

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

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

## Hyperparameters

The precision parameter  $\tau$  is represented as

$$\theta_1 = \log \tau$$

and the prior is defined on  $\theta_1$ . The  $\lambda$  parameter is represented as

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

and the prior is defined on  $\theta_2$ .

## 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

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<sup>1</sup>Brian 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