

Bayesian Statistics with R-INLA

University of Zurich, March, 2022

Instructor: Sara Martino

Department of Mathematical Science (NTNU)



NTNU

Norwegian University of
Science and Technology

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| oooo | oooooooo | ooooooooo | ooooooooooooo | oooooo | oooo |

What have we learned in the morning...

- What is a LGM
- Which kind of models are amenable to INLA
- How does INLA work....

What have we learned in the morning...

- What is a LGM
- Which kind of models are amenable to INLA
- How does INLA work....
- ..you have even implemented it yourself! :-)

Good News!

All the theory we have seen is wrapped up in the R-package
INLA which is easy to use.

Getting INLA

Getting INLA

- The web page www.r-inla.org contains source-code, worked-through examples, reports and instructions for installing the package.

Getting INLA

- The R-package INLA works on Linux, Windows and Mac and can be installed within R by

```
# stable version
install.packages("INLA",
  repos=c(getOption("repos"),
    INLA="https://inla.r-inla-download.org/R/stable"),
  dep=TRUE)

# devel version
install.packages("INLA",
  repos=c(getOption("repos"),
    INLA="https://inla.r-inla-download.org/R/testing"),
  dep=TRUE)
```

and then upgraded in R as:

```
inla.upgrade(testing = TRUE)
```

****NB** You need R version 4.1 or newer!!**

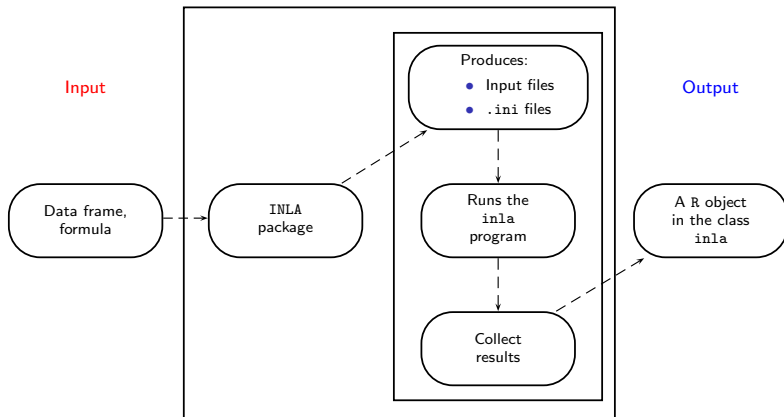
Which INLA version do I have?

```
inla.version()
```

```
## R-INLA version .....: 22.02.16-2
## Date .....: Wed Feb 16 02:22:38 PM +03 2022
## Maintainers .....: Havard Rue <hrue@r-inla.org>
##                  : Finn Lindgren <finn.lindgren@r-inla.org>
##                  : Elias Teixeira Krainski <elias.krainski@r-inla.org>
## Main web-page .....: www.r-inla.org
## Download-page .....: inla.r-inla-download.org
## Repository .....: github.com/hrue/r-inla
## Email support .....: help@r-inla.org
##                  : r-inla-discussion-group@googlegroups.com
```

Implementing the INLA algorithm

The INLA package for R



What happens in the black box?

The implementation of the INLA method consists of three parts:

- **GMRFLib-Library:** A library for GMRFs written in C
- **inla-program:** The implementation of INLA written in C
- **INLA package for R:** An R-interface to the inla-program

The first two are *not* particularly user-friendly. They are used in the background by the INLA package.

Implementing INLA

All procedures required to perform INLA need to be carefully implemented to achieve a good speed; easier to implement a slow version of INLA.

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All procedures required to perform INLA need to be carefully implemented to achieve a good speed; easier to implement a slow version of INLA.

- **The GMRFLib-library**
 - Basic library written in C, user friendly for programmers

Implementing INLA

All procedures required to perform INLA need to be carefully implemented to achieve a good speed; easier to implement a slow version of INLA.

- **The GMRFLib-library**
- **The inla-program**
 - Define *latent Gaussian models* and interface with the GMRFLib-library
 - Avoids the need for C-programming
 - Models are defined using `.ini`-files
 - Requires to write input files in a special format
 - `inla-program` write all the results (E/Var/marginals) to files

Implementing INLA

All procedures required to perform INLA need to be carefully implemented to achieve a good speed; easier to implement a slow version of INLA.

- **The GMRFLib-library**
- **The inla-program**
- **The INLA package for R**
 - R-interface to the inla-program. (That's why its not on CRAN.)
 - Convert **formula**-statements into **.ini**-files definitions
 - It also does much more (for example for survival models or when using **inlabru**)

How to use INLA

How to use INLA

There are essentially four parts to an INLA-program:

1. **Data organisation**: Make an object to store response, covariates,

```
data = data.frame(y = y, x = x)
```

2. **Use the 'formula'-notation** to specify the model (similar to lm and glm functions)

```
formula = y~x
```

3. **Call the 'inla'-program**

```
res = inla(formula, data=data, family="gaussian")
```

4. **Extract posterior information**, e.g. for a first overview use

```
summary(res)
```

Data organization

The responses and covariates are collected in a **list or data frame**. Assume response y , covariates x_1 and x_2 , and time index t . Then they can be organized with:

Option 1

```
data = list(y = y, x1 = x1, x2 = x2, t = t)
```

Option 2

```
data = data.frame(y = y, x1 = x1, x2 = x2, t = t)
```

formula: specifying the linear predictor

The model is specified through a ‘formula’ similar to `glm`:

```
formula = y ~ x1 + x2 + f(t, ...)
```

- `y` is the name of the response in the `data` object
- The fixed effects are given i.i.d. Gaussian priors
- The `f()` function specifies random effects (e.g. temporal, spatial, smooth effect of covariates and Besag model)
- Use `-1` in the formula if you don't want an automatic intercept

The inla() function

```
result = inla(
  # Description of linear predictor
  formula,
  # Likelihood
  family = "gaussian",
  # List or data frame with response,
  # covariates, etc.
  data = data,
  ## This is all that is needed for a basic call

  ## # check what happens
  verbose = TRUE,
  # ,..., there are also some "control statements"
  # to customize things
  # This you need if you later want to sample from the
  # fitted model
  control.compute=list(config = TRUE)
)
```

Likelihood functions

- gaussian
- T
- poisson
- nbinomial
- binomial
- exponential
- weibull
- gev
- coxph

For a complete list type

```
names(inla.models())$likelihood)
```

Posterior inference

Main functions:

```
# look at a first summary
summary(result)
# plot the main results
# (does not use ggplot...)
plot(result)
# rerun the model to get better
# estimate of the hyperparameters
result2 = inla.hyperpar(result)
# sample from the fitted model
# this can be very useful sometimes!
sample = inla.posterior.sample(results)
```


Simple example

Example: Simple linear regression

- **Stage 1:** Gaussian likelihood

$$y_i | \eta_i \sim \mathcal{N}(\eta_i, \sigma^2)$$

- **Stage 2:** Covariates are connected to likelihood by

$$\eta_i = \beta_0 + \beta_1 x_i$$

- **Stage 3:** σ^2 : variance of observation noise

Example: Simple linear regression

```
# Generate data
```

```
x = runif(10)
```

```
y = 1 + 2*x + rnorm(n = 100, sd = 0.1)
```

```
# Run inla
```

```
formula = y ~ 1 + x
```

```
result = inla(formula,  
              data = data.frame(x = x, y = y),  
              family = "gaussian")
```

Organization of the inla-object

```
names(result)
```

```
## [1] "names.fixed"           "summary.fixed"
## [3] "marginals.fixed"       "summary.lincomb"
## [5] "marginals.lincomb"     "size.lincomb"
## [7] "summary.lincomb.derived" "marginals.lincomb.derived"
## [9] "size.lincomb.derived"  "mlik"
## [11] "cpo"                   "po"
## [13] "waic"                  "model.random"
## [15] "summary.random"        "marginals.random"
## [17] "size.random"           "summary.linear.predictor"
## [19] "marginals.linear.predictor" "summary.fitted.values"
## [21] "marginals.fitted.values" "size.linear.predictor"
## [23] "summary.hyperpar"      "marginals.hyperpar"
## [25] "internal.summary.hyperpar" "internal.marginals.hyperpar"
## [27] "offset.linear.predictor" "model.spde2.blc"
## [29] "summary.spde2.blc"     "marginals.spde2.blc"
## [31] "size.spde2.blc"        "model.spde3.blc"
## [33] "summary.spde3.blc"     "marginals.spde3.blc"
## [35] "size.spde3.blc"        "logfile"
## [37] "misc"                  "dic"
## [39] "mode"                  "joint.hyper"
## [41] "nhyper"                "version"
## [43] "Q"                     "graph"
## [45] "ok"                    "cpu.used"
## [47] "all.hyper"             ".args"
## [49] "call"                  "model.matrix"
```

Organization of the inla-object

You can find summary information in

```
## [1] "summary.fixed"           "summary.lincomb"
## [3] "summary.lincomb.derived" "summary.random"
## [5] "summary.linear.predictor" "summary.fitted.values"
## [7] "summary.hyperpar"       "internal.summary.hyperpar"
## [9] "summary.spde2.blc"      "summary.spde3.blc"
```

for example

```
result$summary.fixed
```

```
##              mean          sd 0.025quant  0.5quant 0.975quant      mode
## (Intercept) 0.9792256 0.02529260  0.9294668 0.9792248  1.028942 0.9792255
## x           2.0208929 0.03944581  1.9432900 2.0208917  2.098429 2.0208929
##              kld
## (Intercept) 3.089110e-06
## x           3.089167e-06
```

Organization of the `inla`-object

You can find estimated posterior marginals in

```
## [1] "marginals.fixed"           "marginals.lincomb"
## [3] "marginals.lincomb.derived" "marginals.random"
## [5] "marginals.linear.predictor" "marginals.fitted.values"
## [7] "marginals.hyperpar"       "internal.marginals.hyperpar"
## [9] "marginals.spde2.blc"      "marginals.spde3.blc"
```

Each object is thereby a list. Get the marginal for intercept:

```
head(result$marginals.fixed[[1]])
```

```
##           x           y
## [1,] 0.7258546 1.680766e-17
## [2,] 0.7765288 2.702053e-11
## [3,] 0.8272030 1.522818e-06
## [4,] 0.8405167 1.794336e-05
## [5,] 0.8525401 1.441510e-04
## [6,] 0.8535878 1.717194e-04
```

Organization of the inla-object

Further general information

formula used

```
result$.args$formula
```

```
## y ~ 1 + x
```

```
## NULL
```

data used

```
result$.args$data[1:3,]
```

```
##           x           y
```

```
## 1 0.4444978 1.944043
```

```
## 2 0.8966812 2.845822
```

```
## 3 0.5178038 1.929968
```

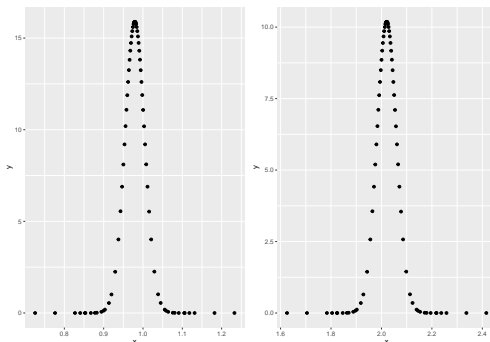
log-file including information of INLA approximations

```
result$logfile
```

Marginal posterior densities

The marginal posterior densities are stored as a matrices with x - and y -values

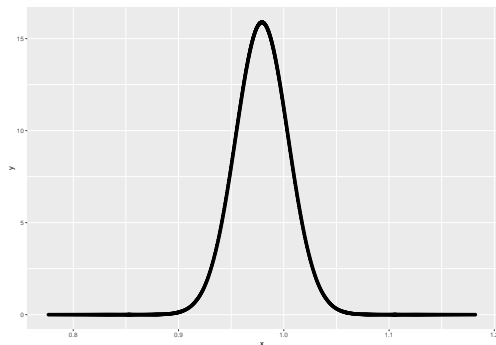
```
intercept = data.frame(result$marginals.fixed$`Intercept`)
x = data.frame(result$marginals.fixed$x)
p1 = ggplot(data = intercept) + geom_point(aes(x,y))
p2 = ggplot(data = x) + geom_point(aes(x,y))
p1+p2
```



Marginal posterior densities

The rough shape can be interpolated to higher resolution using the `inla.smarginal()` function:

```
smoother_dens = data.frame(inla.smarginal(intercept))
ggplot(data = smoother_dens) + geom_point(aes(x,y))
```



Marginal posterior densities

Manipulation of the computed posterior marginals is possible through the `inla.*marginal()` functions:

```
# compute the 0.05 quantile
inla.qmarginal(0.05, intercept)
```

```
## [1] 0.9375583
```

```
# Distribution function
inla.pmarginal(0.975, intercept)
```

```
## [1] 0.4347315
```

```
# Density function
inla.dmarginal(1, intercept)
```

```
## [1] 11.24
```

```
# Generate realizations
inla.rmarginal(4, intercept)
```

```
## [1] 0.9571780 0.9465501 0.9755172 0.9990279
```

Other `inla.*marginal()` functions.

| Function Name | Usage |
|---|--|
| <code>inla.dmarginal(x, marginal, ...)</code> | Density at a vector of evaluation points x |
| <code>inla.pmarginal(q, marginal, ...)</code> | Distribution function at a vector of quantiles q |
| <code>inla.qmarginal(p, marginal, ...)</code> | Quantile function at a vector of probabilities p . |
| <code>inla.rmarginal(n, marginal)</code> | Generate n random deviates |
| <code>inla.hpdmarginal(p, marginal, ...)</code> | Compute the highest posterior density interval at level p |
| <code>inla.emarginal(fun, marginal, ...)</code> | Compute the expected value of the marginal assuming the transformation given by <code>fun</code> |
| <code>inla.mmarginal(marginal)</code> | Compute the mode |
| <code>inla.smarginal(marginal, ...)</code> | Smoothed density in form of a list of length two. The first entry contains the x-values, the second entry includes the interpolated y-values |
| <code>inla.tmarginal(fun, marginal, ...)</code> | Transform the marginal using the function <code>fun</code> . |
| <code>inla.zmarginal(marginal)</code> | Summary statistics for the marginal |

Add random effects

Add random effects

```
f(name, model="...", hyper=...,
    constr=FALSE, cyclic=FALSE, ...)
```

- `name` – the index of the effect (each f-function needs its own!)
- `model` – the type of latent model. E.g. iid, rw2, ar1, besag, and so on
- `hyper` – specify the prior on the hyperparameters
- `constr` – sum-to-zero constraint?
- `cyclic` – are you cyclic?
- ...

Example: Add random effect

Add an AR(1) random effect to the linear predictor.

- **Stage 1:**

$$y_i | \eta_i \sim \mathcal{N}(\eta_i, \sigma^2)$$

- **Stage 2:** Covariates and AR(1) component connected to likelihood by

$$\eta_i = \beta_0 + \beta_1 x_i + a_i$$

- **Stage 3:**

- σ^2 : variance of observation noise
- ρ : dependence in AR(1) process
- σ^2 : variance of the innovations in AR(1) process

Example: Add random effect

```
# Generate AR(1) sequence
set.seed(580258)
t = 1:100
rho = 0.8
sd_ar1 = 0.1
ar = rep(0,100)
for(i in 2:100)
  ar[i] = rho * ar[i-1] + rnorm(n = 1, sd = sd_ar1)
# Generate data with AR(1) component
x = runif(100)
y = 1 + 2*x + ar + rnorm(n = 100, sd = 0.2)

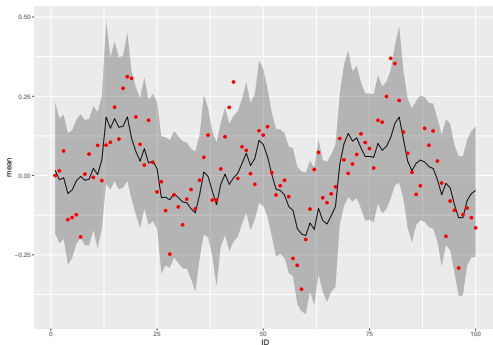
# Run inla
formula = y ~ 1 + x + f(t, model="ar1")

result = inla(formula,
  data = data.frame(x = x, y = y, t = t),
  family = "gaussian")
```

Example

Estimates of the random effect

```
result$summary.random$t %>% ggplot() +  
  geom_line(aes(ID, mean)) +  
  geom_ribbon(aes(ID, ymin = `0.025quant`, ymax = `0.975quant`),  
  geom_point(data = data.frame(t = t , ar = ar), aes(t,ar), color = "red"))
```



Example

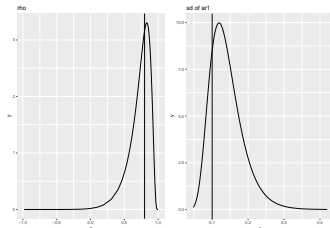
Estimates of the hyperparameters

rho

```
p1 = ggplot() + geom_line(data = data.frame(result$marginals.hyperpar$`
                                aes(x,y)) +
  geom_vline(xintercept = rho) + ggtitle("rho")
```

sd of the ar1 effect

```
prec = result$marginals.hyperpar$`Precision for t`
sd = inla.tmarginal(function(x) 1/sqrt(x), prec)
p2 = ggplot() + geom_line(data = data.frame(sd), aes(x,y)) +
  geom_vline(xintercept = sd_ar1 ) + ggtitle("sd of ar1")
p1+p2
```



Prediction

The interpretation of NA

R-INLA uses NA differently than other packages

- NA in the **response** means no likelihood contribution, i.e. response is unobserved
- NA in a **fixed effect** means no contribution to the linear predictor, i.e. the covariate is set equal to zero
- NA in a **random effect** $f(\dots)$ means no contribution to the linear predictor

Prediction

The distribution of the linear predictor at an unobserved location can be computed by specifying the value of the covariate x and the desired time index t and set y to NA.

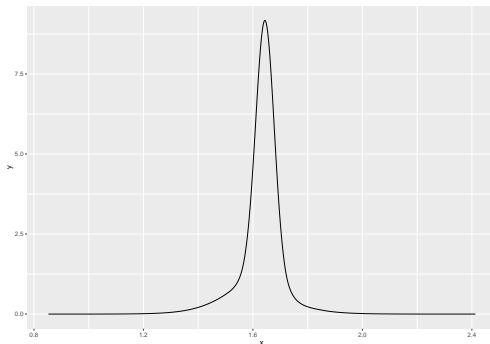
```
# Add one new location
n = 1
x = c(x, runif(n))
t = c(t, 101:(100+n))
y = c(y, rep(NA,n))

# Re-compute
result.pred = inla(formula,
  data = data.frame(x = x, t = t, y = y),
  family="gaussian",
  control.inla = list(int.strategy = "grid"),
  control.compute = list(config = TRUE,
    return.marginals.predictor=TRUE),
  # tell inla to return the marginals for eta!
  control.predictor = list(compute = TRUE))
```

Prediction

Predicted marginal of the linear predictor η_{101}

```
pred = result.pred$marginals.linear.predictor[[100+n]]
pred = inla.smarginal(pred)
ggplot() +
  geom_line(data = data.frame(pred), aes(x, y))
```



Prediction

Caution: This is **not** yet the predictive distribution, as the observation noise is missing.

The predictive distribution is

$$\pi(y_{101}|\mathbf{y})$$

what we got is

$$\pi(\eta_{101}|\mathbf{y})$$

Prediction

One way to add the observation noise to the linear predictor is by sampling from the posterior distribution.

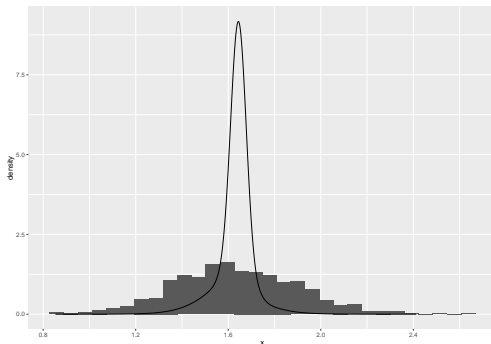
```
n = 1000
x = inla.posterior.sample(n, result.pred)

func = function(...)
{
  eta = Predictor
  eta = eta[101]
  sd = 1/sqrt(theta[1])
  out = rnorm(1, mean = eta, sd =sd)
  return(out)
}

samples = inla.posterior.sample.eval(func, x)[1,]
```

Prediction

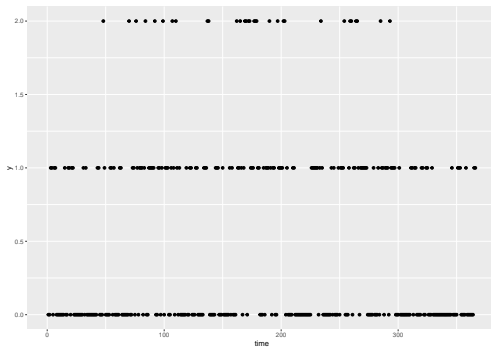
Comparing $\pi(y_{101}|\mathbf{y})$ and $\pi(\eta_{101}|\mathbf{y})$



Smoothing binary time series

Example: Smoothing binary time series

The data set **Tokyo** is available in the **INLA** package and consists of the number of days in Tokyo with rainfall above 1 mm in 1983–1984.



Observations

Each observation consists of

- t : Day of year; $t \in \{1, 2, \dots, 366\}$
- n_t : Number of observations for day t in 1983–1984;
 $n_t \in \{1, 2\}$
- y_t : Number of days with rain out of n_t days for day t ;
 $y_t \in \{0, 1, 2\}$

```
data(Tokyo)
head(Tokyo, 3)
```

```
##    y n time
## 1 0 2    1
## 2 0 2    2
## 3 1 2    3
```

```
Tokyo[60,]
```

```
##      y n time
## 60 0 1   60
```

Hierarchical model

- **Stage 1:** We have binomial responses with known n_t , but unknown probabilities

$$y_t \sim \text{Binomial}(n_t, p_t)$$

- **Stage 2:** A cyclic second order random walk (CRW2) is connected to the likelihood by

$$p_t = \frac{\exp(\eta_t)}{1 + \exp(\eta_t)} \text{ with linear predictor } \eta_t = \text{CRW2}_t$$

- **Stage 3:**
 - τ : Scale parameter in CRW2 with prior

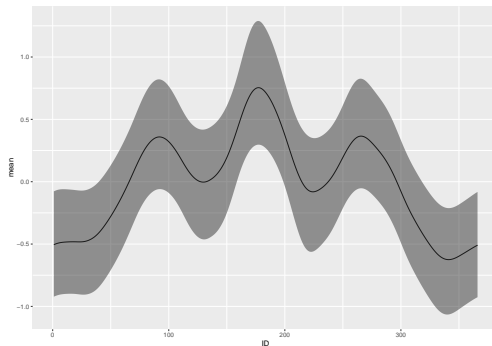
$$\pi(\tau) \sim \text{Gamma}(1, 5 \cdot 10^{-5})$$

INLA implementation

```
# Read data
data(Tokyo)
# Specify linear predictor
formula = y ~ -1 + f(time, model="rw2", cyclic=TRUE)
# Run model
result = inla(formula,
               family = "binomial",
               Ntrials = n,
               data = Tokyo)
```

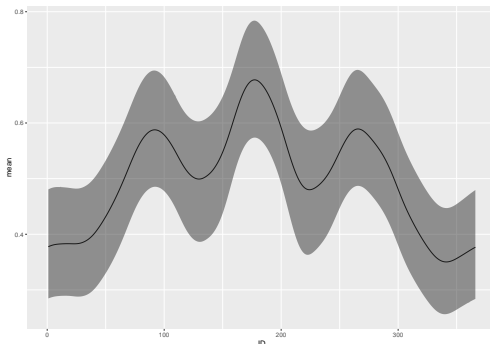
Marginal posterior of CRW2

```
ggplot(data = result$summary.random$t) +  
  geom_line(aes(ID, mean)) +  
  geom_ribbon(aes(ID, ymin = `0.025quant`, ymax = `0.975quant`,  
                  alpha = 0.5))
```



Transform to probability

```
pred = result$summary.fitted.values
pred$ID = 1:dim(Tokyo)[1]
ggplot(data = pred) +
  geom_line(aes(ID, mean)) +
  geom_ribbon(aes(ID, ymin = `0.025quant`, ymax = `0.975quant` )
            alpha = 0.5)
```

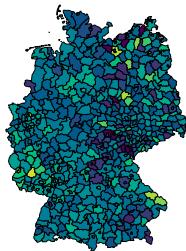


Disease Mapping

Example: disease mapping

We observed larynx cancer mortality counts for males in 544 district of Germany from 1986 to 1990 and want to make a model.

- y_i : The count at location i .
- E_i : An offset; expected number of cases in district i .
- c_i : A covariate (level of smoking consumption) at i
- s_i : spatial location i .



Disease mapping

Assume

$$Y_i \mid \eta_i \sim \text{Poisson}(E_i \exp(\eta_i))$$

where the log relative risk is decomposed into

$$\eta_i = \mu + u_i + v_i$$

- μ is the overall level (intercept).
- $v_i \sim \mathcal{N}(0, \tau_v^{-1})$ represents non-spatial overdispersion.
- u_i are random effects with spatial structure.

A spatially structured effect

To incorporate a spatial structure into a model, the so called **Besag model** is often used.

$$\begin{aligned} p(\mathbf{u} \mid \kappa_{\mathbf{u}}) &\propto \kappa_u^{(n-1)/2} \exp \left(-\frac{\kappa_u}{2} \sum_{i \sim j} (u_i - u_j)^2 \right) \\ &= \kappa_u^{(n-1)/2} \exp \left(-\frac{\kappa_u}{2} \mathbf{u}^T \mathbf{R} \mathbf{u} \right). \end{aligned}$$

where R is called structure matrix and defined as

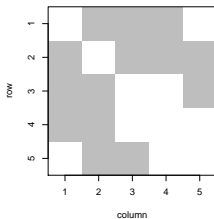
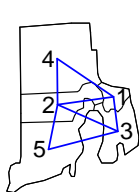
$$R_{ij} = \begin{cases} n_i & i = j \\ -1 & i \sim j \\ 0 & \text{otherwise.} \end{cases}$$

Here, $i \sim j$ denotes that i and j are neighbouring regions.

What does this mean?

Example: Five counties of the US state Rhode Island

The structure matrix \mathbf{R} defines the neighborhood structure.



| | | | | |
|----------|----------|----------|----------|----------|
| 3 | -1 | -1 | -1 | 0 |
| -1 | 4 | -1 | -1 | -1 |
| -1 | -1 | 3 | 0 | -1 |
| -1 | -1 | 0 | 2 | 0 |
| 0 | -1 | -1 | 0 | 2 |

Table 1: Structure matrix \mathbf{R}

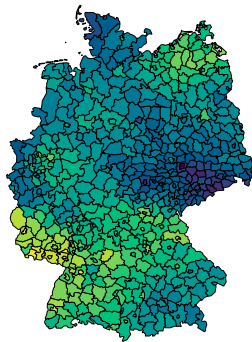
Figure 1: Adjacency matrix

With increasing number of regions \mathbf{R} will be sparse, which allows to do many computations very efficient.

INLA code

```
library(spam)
# load the dataset
data(Oral)
# load the file including neighbourhood information
g = system.file("demodata/germany.graph", package="INLA")
# add one column
Oral = cbind(Oral, region = 1:544, region.unstruc= 1:544)
# define formula
formula = Y ~ f(region, model="besag", graph=g) +
           f(region.unstruc, model="iid")
# run the model
result = inla(formula, family="poisson", E=E, data=Oral)
```

Median of u on exp-scale



Other choices for f-terms

| | | | | | |
|----|------|----------------|------------|------------|-----------|
| ## | [1] | "linear" | "iid" | "mec" | "meb" |
| ## | [6] | "cgeneric" | "rw1" | "rw2" | "crw2" |
| ## | [11] | "besag" | "besag2" | "bym" | "bym2" |
| ## | [16] | "besagproper2" | "fgn" | "fgn2" | "ar1" |
| ## | [21] | "ar" | "ou" | "intslope" | "generic" |
| ## | [26] | "generic1" | "generic2" | "generic3" | "spde" |
| ## | [31] | "spde3" | "iid1d" | "iid2d" | "iid3d" |
| ## | [36] | "iid5d" | "iidkd" | "2diid" | "z" |
| ## | [41] | "rw2diid" | "slm" | "matern2d" | "dmatern" |
| ## | [46] | "clinear" | "sigm" | "revsigm" | "log1exp" |

Changing the prior

Changing the prior: Internal scale

- Hyperparameters are represented internally with more well-behaved transformations, e.g. correlation ρ and precision τ are internally

$$\theta_1 = \log(\tau)$$

$$\theta_2 = \log\left(\frac{1+\rho}{1-\rho}\right)$$

- The prior must be set on the parameter in **internal scale**
- Initial values for the mode-search must be set in **internal scale**
- The functions `to.theta()` and `from.theta()` can be used to map back and forth.

Changing the prior: Code

```
hyper = list(prec = list(prior = "loggamma",
                        param = c(1, 0.1),
                        initial = 4,
                        fixed = FALSE))

formula = y ~ f(idx, model = "iid", hyper = hyper) + ...

# For the iid model, default options can be seen with
inla.doc("iid")
```

Repeated Poisson counts

EPIL example

Seizure counts in a randomised trial of anti-convulsant therapy in epilepsy. From WinBUGS manual.

```
## # A tibble: 6 x 8
##      Ind Repl1 Repl2 Repl3 Repl4   Trt   Base   Age
##    <int> <dbl> <dbl> <dbl> <dbl> <int> <int> <int>
## 1      1      5      3      3      3      0     11     31
## 2      2      3      5      3      3      0     11     30
## 3      3      2      4      0      5      0      6     25
## 4      4      4      4      1      4      0      8     36
## 5      5      7     18      9     21      0     66     22
## 6      6      5      2      8      7      0     27     29
```

Covariates are treatment (0,1), 8-week baseline seizure counts, and age in years.

Repeated Poisson counts

$$\begin{aligned}
 y_{jk} &\sim \text{Poisson}(\mu_{jk}); \quad j = 1, \dots, 59; \quad k = 1, \dots, 4 \\
 \log(\mu_{jk}) &= \alpha_0 + \alpha_1 \log(\text{Base}_j/4) + \alpha_2 \text{Trt}_j \\
 &\quad + \alpha_3 \text{Trt}_j \log(\text{Base}_j/4) + \alpha_4 \log(\text{Age}_j) \\
 &\quad + \alpha_5 V4 + \text{Ind}_j + \beta_{jk} \\
 \alpha_i &\sim \mathcal{N}(0, \tau_\alpha) \quad \tau_\alpha \text{ known (0.001)} \\
 \text{Ind}_j &\sim \mathcal{N}(0, \tau_{\text{Ind}}) \quad \tau_{\text{Ind}} \sim \text{Gamma}(1, 0.01) \\
 \beta_{jk} &\sim \mathcal{N}(0, \tau_\beta) \quad \tau_\beta \sim \text{Gamma}(1, 0.01)
 \end{aligned}$$

Here, V4 is an indicator variable for the 4th visit.

Model specification in INLA

The data:

```
##   y Trt Base Age V4 rand Ind
## 1 5   0  11  31  0   1   1
## 2 3   0  11  31  0   2   1
## 3 3   0  11  31  0   3   1
## 4 3   0  11  31  1   4   1
## 5 3   0  11  30  0   5   2
## 6 5   0  11  30  0   6   2
```

The formula:

```
formula = y ~ ClBase4*CTrt + ClAge + CV4 +
  f(Ind, model="iid",
    hyper = list(prec = list(prior = "loggamma",
                             param = c(1,0.01)))) +
  f(rand, model="iid",
    hyper = list(prec = list(prior = "loggamma",
                             param = c(1,0.01))))
```

Run the model:

```
result = inla(formula, family="poisson", data = Epil,
  control.fixed = list(prec.intercept = 0.001,
    prec = 0.001))
```

Comparing results with MCMC

- When comparing the results of R-INLA with MCMC, it is important to use the **same model**.

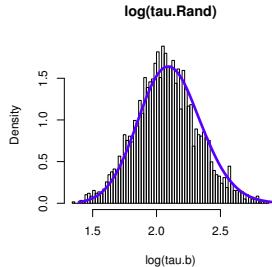
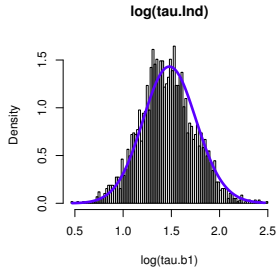
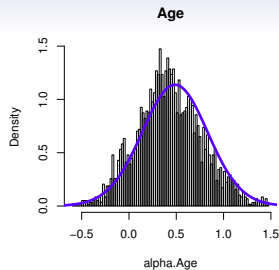
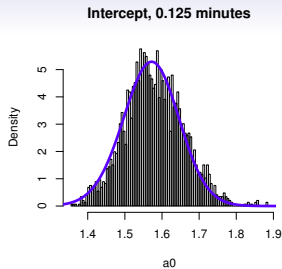
That means, same data, same priors, same constraints on parameters, intercept included or not,

Comparing results with MCMC

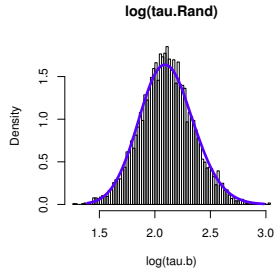
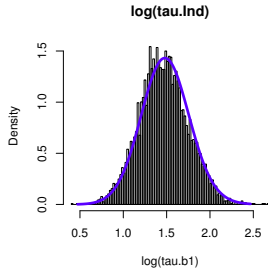
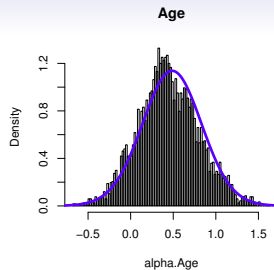
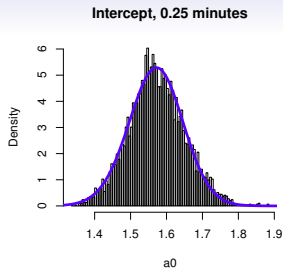
- When comparing the results of R-INLA with MCMC, it is important to use the **same model**.

That means, same data, same priors, same constraints on parameters, intercept included or not,

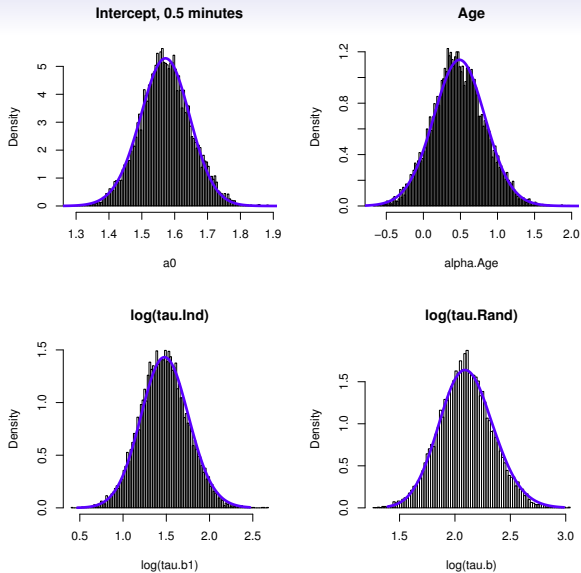
- Here we have compared the results with those obtained using ‘JAGS via the `rjags` package



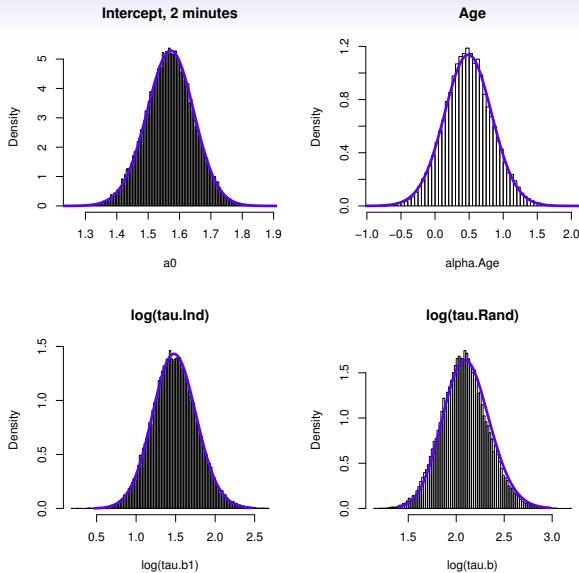
Running time of INLA < 0.5 seconds



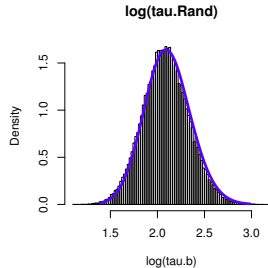
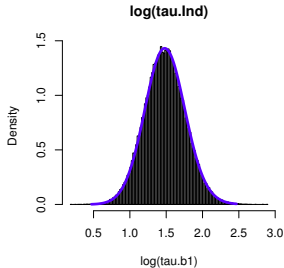
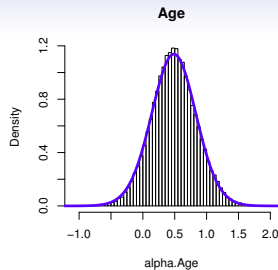
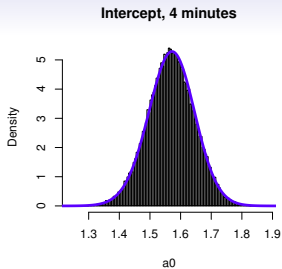
Running time of INLA < 0.5 seconds



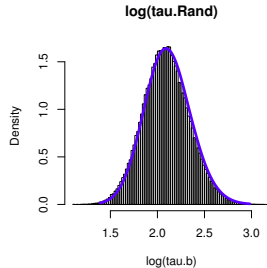
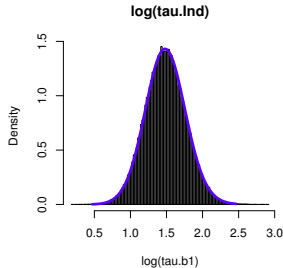
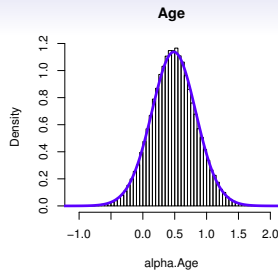
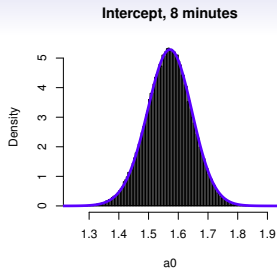
Running time of INLA < 0.5 seconds



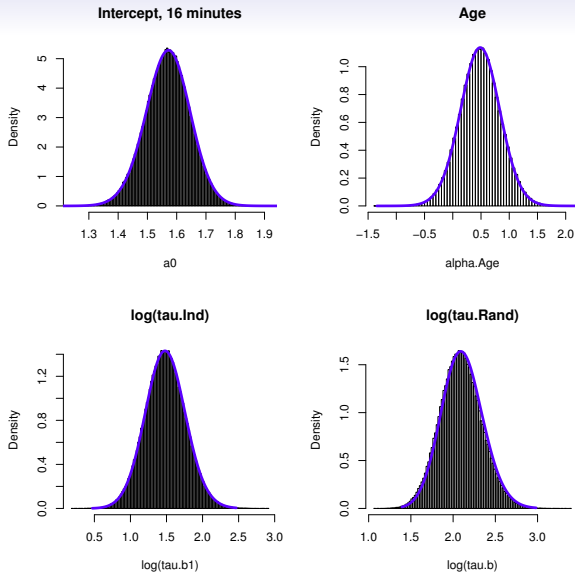
Running time of INLA < 0.5 seconds



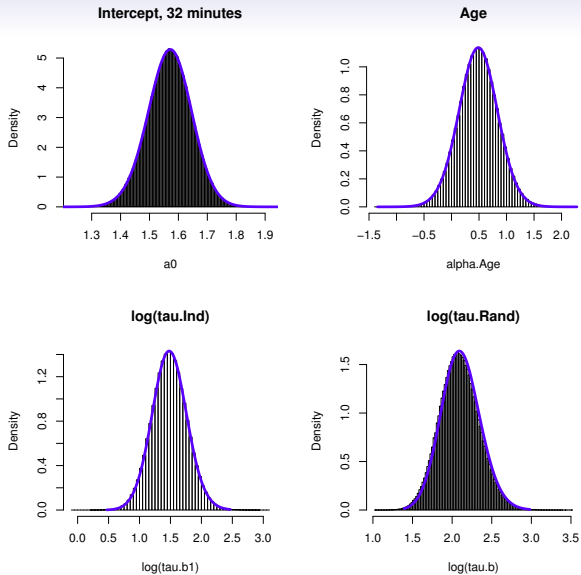
Running time of INLA < 0.5 seconds



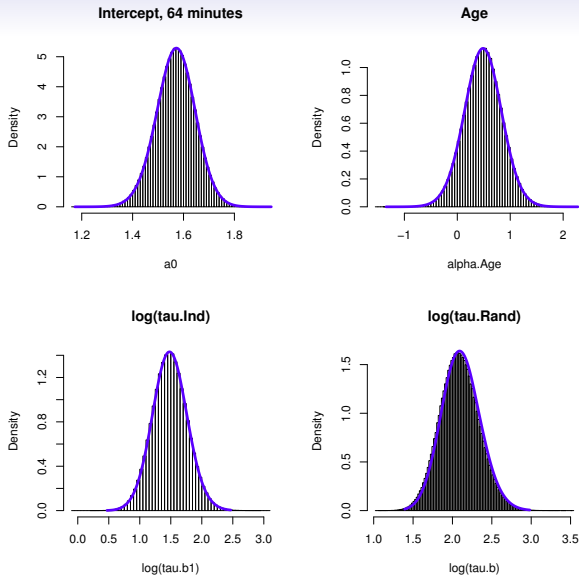
Running time of INLA < 0.5 seconds



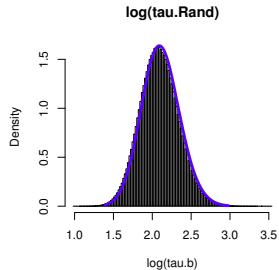
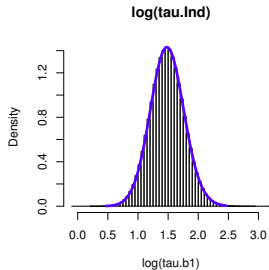
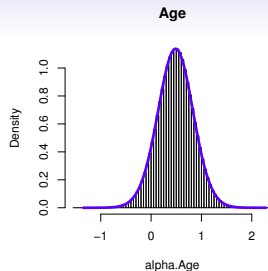
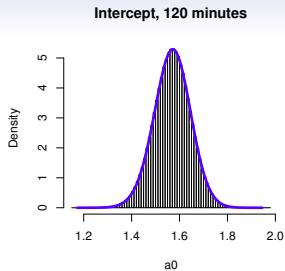
Running time of INLA < 0.5 seconds



Running time of INLA < 0.5 seconds



Running time of INLA < 0.5 seconds



Running time of INLA < 0.5 seconds

Control statements

Control statements

`control.xxx` statements control computations

- `control.fixed`
 - `prec`: Default precision for all fixed effects except the intercept.
 - `prec.intercept`: Precision for intercept (Default: 0.0)
- `control.predictor`
 - `compute`: Compute posterior marginals of linear predictors
- `control.compute`
 - `dic`, `mlik`, `cpo`: Compute measures of fit?
 - `config`: Save internal GMRF approximations? (needed to use `inla.posterior.sample()`)
- `control.inla`

`strategy` and `int.strategy` contain useful advanced features
- There are various others as well; see help.

Thank you for your attention!

If you have any doubts or questions, please write :
sara.martino@math.ntnu.no

