Bayesian Statistics with R-INLA

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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

```r
# 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:

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

NB You need R version 4.1 or newer!!

INLA runs in parallel!

INLA can run in parallel for faster computations with large models.

It uses the PARDISO 7.2 Solver Project and you need to get a license to use it!

```
library(INLA)
inla.pardiso()
```

..and follow the instruction there!

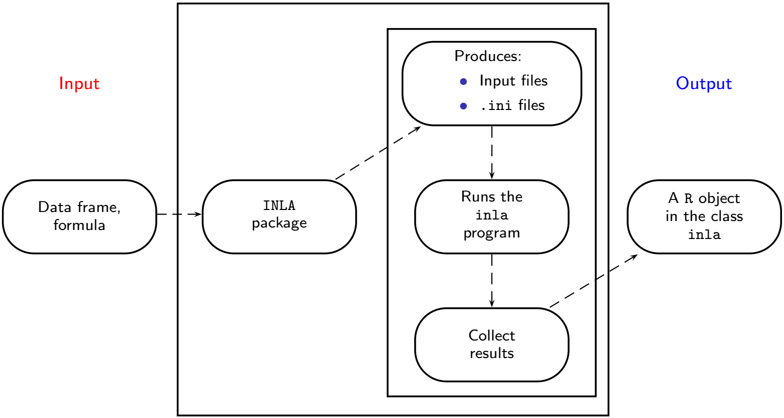
Which INLA version do I have?

```
inla.version()
```

```
## R-INLA version ..........: 22.01.25
## Date ....................: Tue Jan 25 08:26:03 PM +03 2
## Maintainers .............: Havard Rue <hrue@r-inla.org>
##                           : Finn Lindgren <finn.lindgren
##                           : Elias Teixeira Krainski <eli
## 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@goog
```

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.

- **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.fame(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 `x1` and `x2`, 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 hyperparemeters
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

```r
# 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) 0.998189 0.02724618   0.944587 0.9981882   1.051745 0.998189
## x           2.011824 0.04765814   1.918065 2.0118226   2.105502 2.011824
##                      kld
## (Intercept) 3.087429e-06
## x           3.087245e-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.hyperp
##  [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,] 0.7252481 1.560719e-17
## [2,] 0.7798363 2.508686e-11
## [3,] 0.8344244 1.413692e-06
## [4,] 0.8487663 1.665664e-05
## [5,] 0.8617185 1.338179e-04
## [6,] 0.8628470 1.594073e-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,]
```

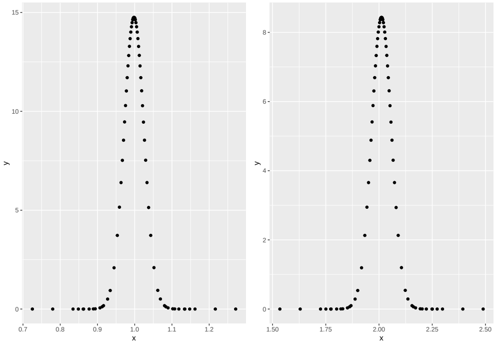
```
##           x        y
## 1 0.4979424 1.859431
## 2 0.1780295 1.324177
## 3 0.7881542 2.700296
```

```
# 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

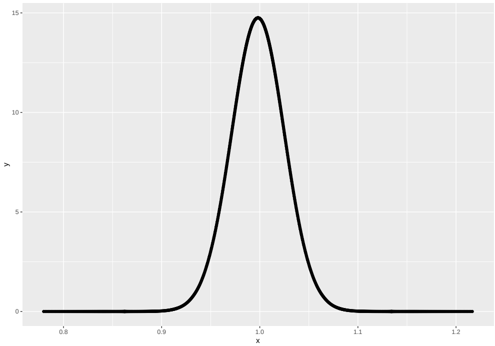
```
intercept = data.frame(result$marginals.fixed$`(Intercept)`)
x = data.frame(result$marginals.fixed$x)
p1 = ggplot(data = intercept) + geom_point(aes(x,y))
p2 = ggplot(data = x) + geom_point(aes(x,y))
p1+p2
```



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] 0.9533034
```

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

```
## [1] 0.1971282
```

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

```
## [1] 14.716
```

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

```
## [1] 1.0200040 1.0019901 0.9926437 0.9555379
```

Other `inla.*marginal()` functions.

Function Name	Usage
`inla.dmarginal(x, marginal, ...)`	Density at a vector of evaluation points x
`inla.pmarginal(q, marginal, ...)`	Distribution function at a vector of quantiles q
`inla.qmarginal(p, marginal, ...)`	Quantile function at a vector of probabilities p.
`inla.rmarginal(n, marginal)`	Generate n random deviates
`inla.hpdmarginal(p, marginal, ...)`	Compute the highest posterior density interval at level p
`inla.emarginal(fun, marginal, ...)`	Compute the expected value of the marginal assuming the transformation given by fun
`inla.mmarginal(marginal)`	Compute the mode
`inla.smarginal(marginal, ...)`	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
`inla.tmarginal(fun, marginal, ...)`	Transform the marginal using the function fun.
`inla.zmarginal(marginal)`	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

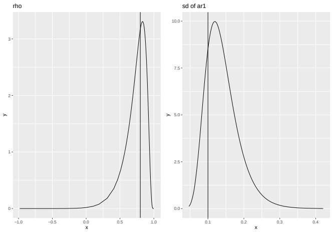
Estimates of the random effect

```
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
```

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(...)` means no contribution to the linear predictor

Prediction

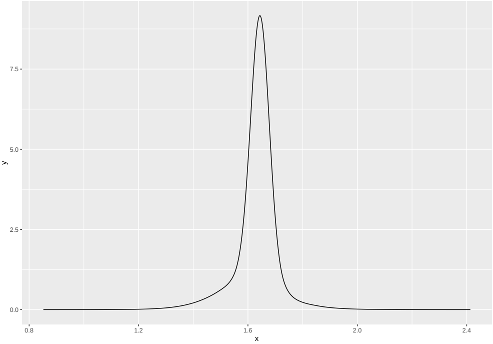
The distribution of the linear predictor at an unobserved location can be computed by specifying the value of the covariate x and the desired time index t and set y to `NA`.

```
# 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)
```

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

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

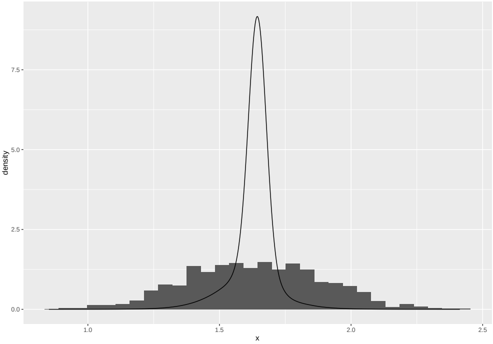
Prediction

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

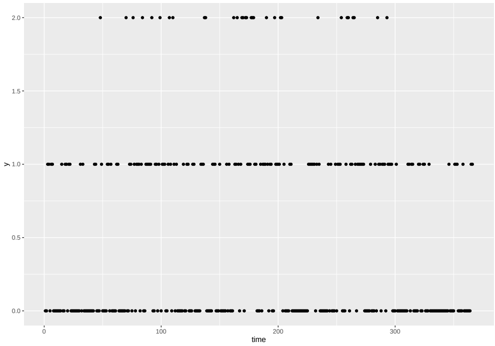
Comparing $\pi(y_{101}|\mathbf{y})$ and $\pi(\eta_{101}|\mathbf{y})$



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; $t \in \{1, 2, \ldots, 366\}$
- 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

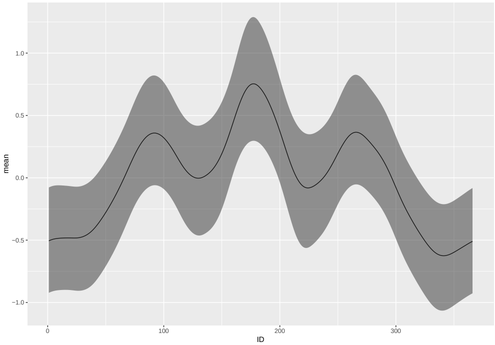
$$\pi(\tau) \sim \text{Gamma}(1, 5 \cdot 10^{-5})$$

INLA implementation

```r
# 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)
```

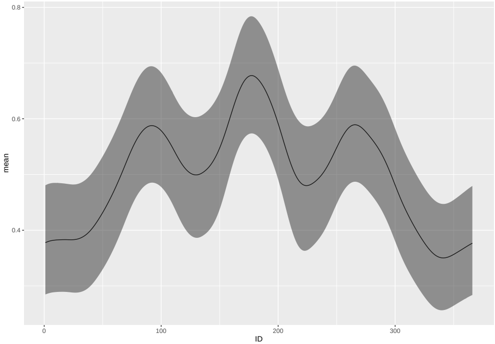
Marginal posterior of CRW2

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

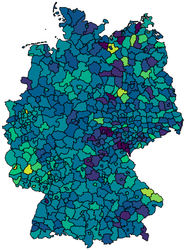


Disease Mapping

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
- $\boldsymbol{s}_i$: 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.

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

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.

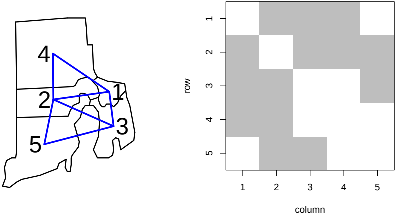


Figure 1: Adjacency matrix

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

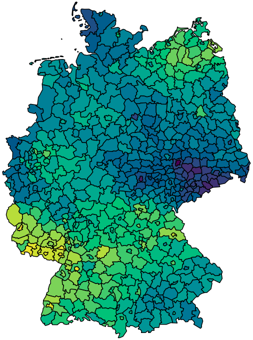
Table 1: Structure matrix $\mathbf{R}$

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

INLA code

```r
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

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

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

```r
# 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

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

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:

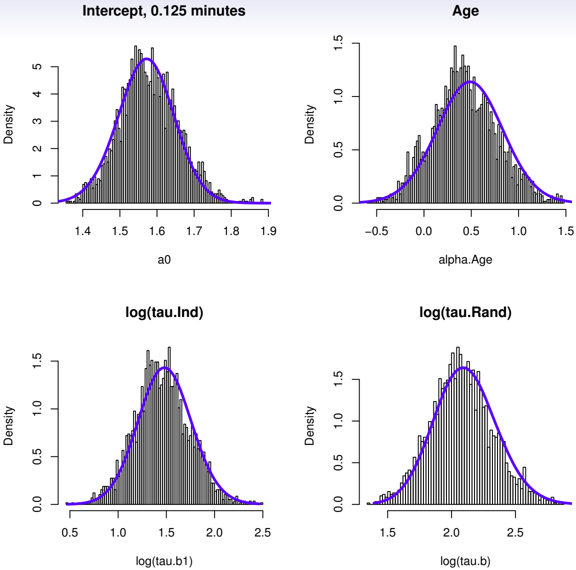
```
result = inla(formula, family="poisson", data = Epil,
              control.fixed = list(prec.intercept = 0.001,
                                   prec = 0.001))
```

Comparing results with MCMC

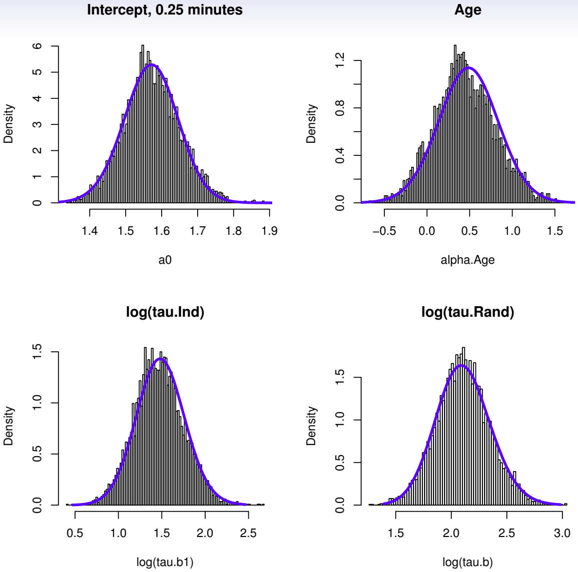
- When comparing the results of `R-INLA` with MCMC, it is important to use the same model.

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

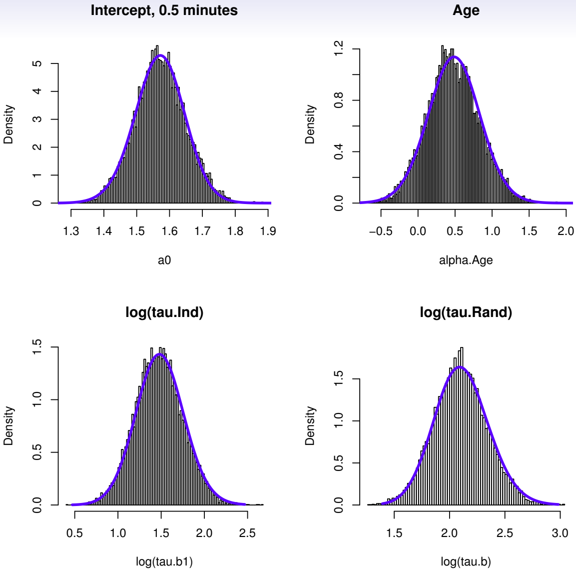
- Here we have compared the results with those obtained using ‘`JAGS` via the `rjags` package



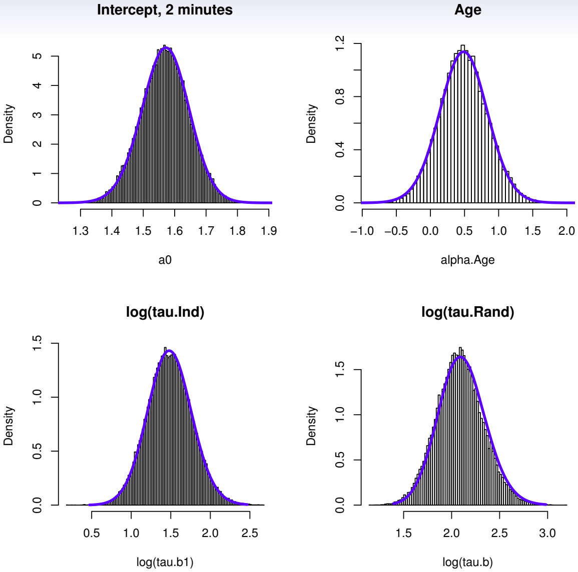
Running time of INLA < 0.5 seconds



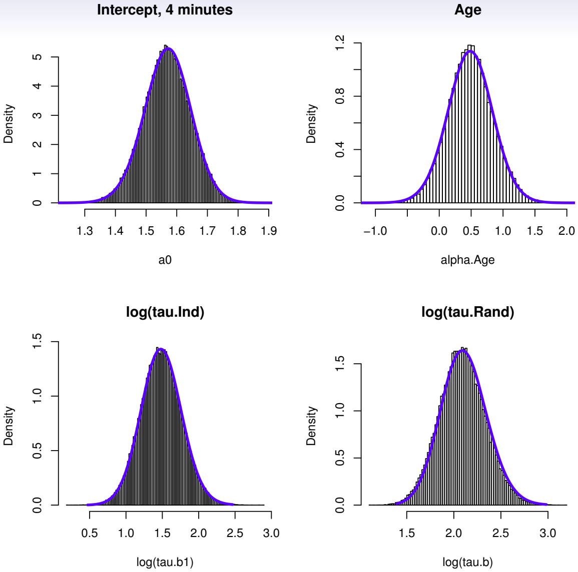
Running time of INLA < 0.5 seconds



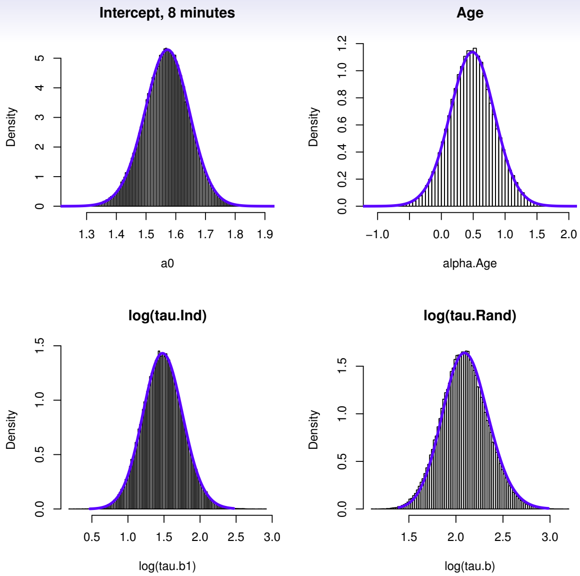
Running time of INLA < 0.5 seconds



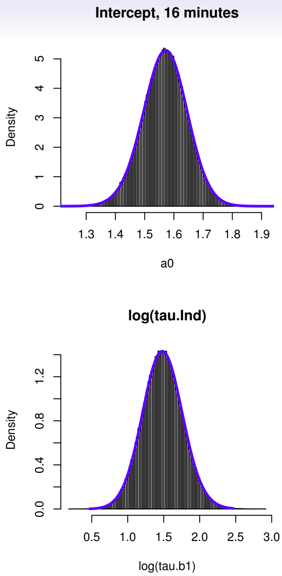
Running time of INLA < 0.5 seconds



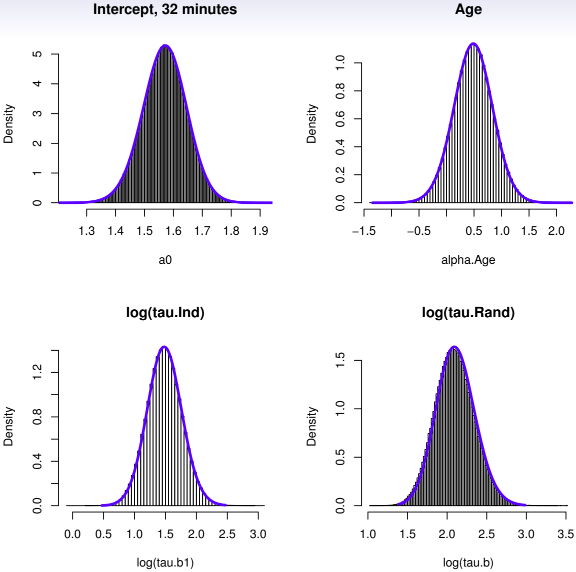
Running time of INLA < 0.5 seconds



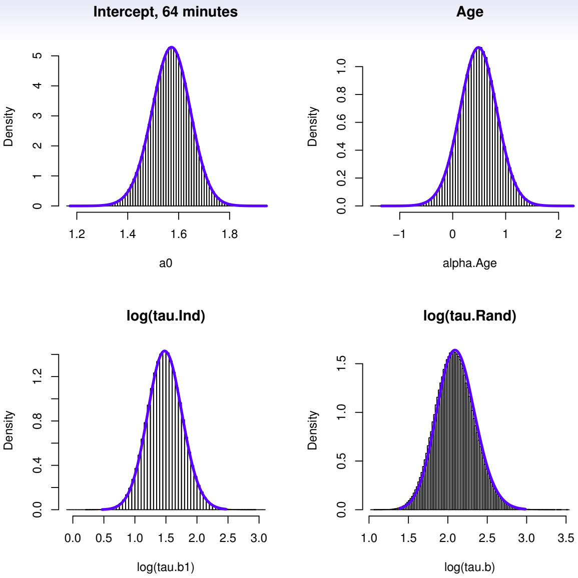
Running time of INLA < 0.5 seconds



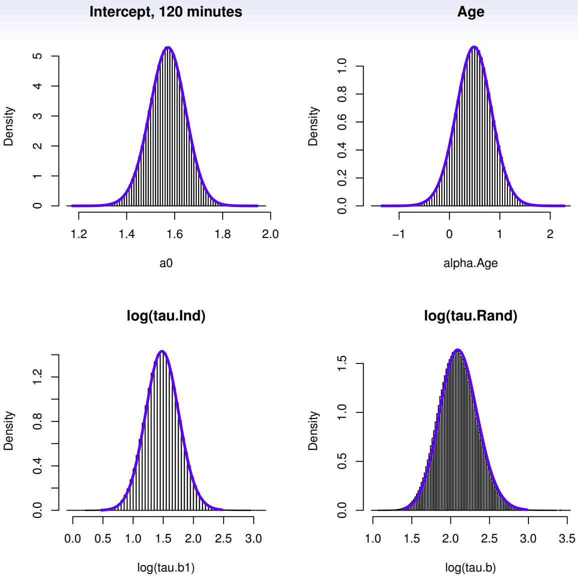
Running time of INLA < 0.5 seconds



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

Thank you for your attention!

If you have any doubts or questions, please write :
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