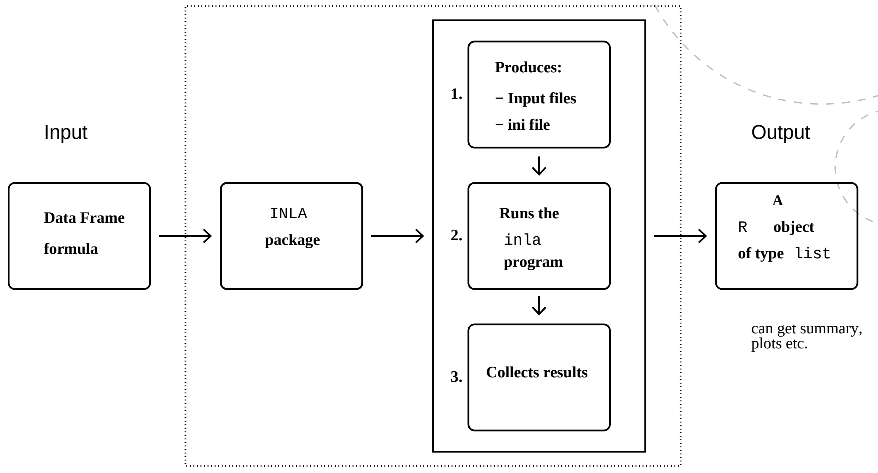
NTNU
Norwegian University of
Science and Technology

R-INLA: An R-package for INLA

Andrea Riebler <andrea.riebler@math.ntnu.no>

March 1, 2016

The INLA package for R



Getting R-INLA

— The web page www.r-inla.org contains source-code, worked-through examples, reports and instructions for installing the package. INLA tutorial is in preparation.

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

```
install.packages("INLA",
    repos="http://www.math.ntnu.no/inla/R/testing")
```

Later, it can be upgraded with

```
update.packages(oldPkgs="INLA",
   repos="http://www.math.ntnu.no/inla/R/testing")
```

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 `formula` similar to `glm`:

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

- y is the name of the response in the `data`
- 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` 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,
    # keep working files
    keep = TRUE,

    # there are also some "control statements"
    # to customize things)
```

Likelihood functions

- "gaussian"
- "poisson"
- "nbinomial"
- "binomial"
- See list at `http://www.r-inla.org/models/likelihoods` or

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

Example: Simple linear regression

...such as our ski flying example.

Stage 1: Gaussian likelihood

$$y_i \mid \eta_i \sim \mathcal{N}(\eta_i, \sigma_o^2)$$

Stage 2: Covariates are connected to likelihood by

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

Stage 3: σ_o^2: variance of observation noise

Example: Simple linear regression

```r
# Generate data
x = sort(runif(100))
y = 1 + 2*x + rnorm(n = 100, sd = 0.1)

# Run inla
formula = y ~ 1 + x
result = inla(formula,
              data = list(x = x, y = y),
              family = "gaussian")

# Get summary
summary(result)
```

summary(result)

```
Call:
c("inla(formula = formula, family = \"gaussian\", data = list(x = x, ",  "    y = y))")

Time used:
 Pre-processing    Running inla Post-processing           Total
         0.0571          0.0188          0.0166          0.0925

Fixed effects:
              mean     sd 0.025quant 0.5quant 0.975quant   mode kld
(Intercept) 1.0204 0.0201     0.9808   1.0204     1.0599 1.0204   0
x           1.9818 0.0328     1.9173   1.9818     2.0462 1.9818   0

The model has no random effects

Model hyperparameters:
                                          mean    sd 0.025quant 0.5quant
Precision for the Gaussian observations 111.15 15.75      82.88   110.29
                                        0.975quant   mode
Precision for the Gaussian observations     144.53 108.78

Expected number of effective parameters(std dev): 2.183(0.0206)
Number of equivalent replicates : 45.82

Marginal log-Likelihood:  76.74
```

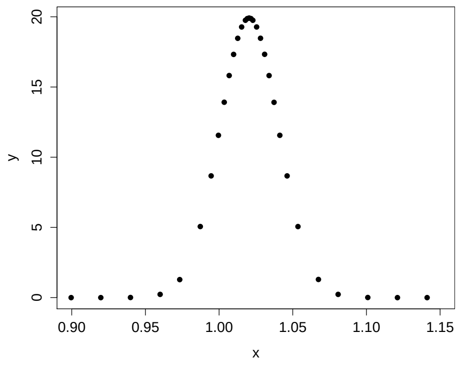
result$summary.fixed

```
                mean          sd 0.025quant 0.5quant 0.975quant     mode
(Intercept) 1.020390 0.02013356  0.9808057 1.020389   1.059935 1.020390
x           1.981786 0.03277825  1.9173423 1.981786   2.046167 1.981787
                     kld
(Intercept) 1.095541e-12
x           9.299953e-13
```

Marginal posterior densities

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

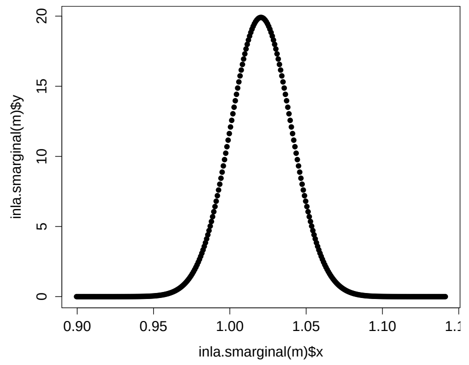
```r
m = result$marginals.fixed[[1]]
plot(m)
```



Marginal posterior densities

The rough shape can be interpolated to higher resolution

```
plot(inla.smarginal(m))
```



Marginal posterior densities

```
# Extract quantiles
> inla.qmarginal(0.05, m)
[1] 0.9818604

# Distribution function
> inla.pmarginal(0.975, m)
[1] 0.02314047

# Density function
> inla.dmarginal(1, m)
[1] 15.80794

# Generate realizations
> inla.rmarginal(4, m)
[1] 1.009122 1.013116 1.032004 1.007458
```

Organisation of the returned `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"
...
```

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:

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

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

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

Stage 3:
- σ_o^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
t = 1:100
ar = rep(0,100)
for(i in 2:100)
    ar[i] = 0.8*ar[i-1]+rnorm(n = 1, sd = 0.1)

# Generate data with AR(1) component
x = runif(100)
y = 1 + 2*x + ar + rnorm(n = 100, sd = 0.1)

# Run inla
formula = y ~ 1 + x + f(t, model="ar1")
result = inla(formula,
              data = list(x = x, y = y, t = t),
              family = "gaussian")

# Get summary
summary(result)
```

summary(result)

```
Fixed effects:
              mean     sd 0.025quant 0.5quant 0.975quant   mode kld
(Intercept) 1.0354 0.0624      0.913   1.0344     1.1635 1.0328   0
x           2.0173 0.0459      1.927   2.0173     2.1077 2.0173   0

Random effects:
Name      Model
 t    AR1 model

Model hyperparameters:
                                        mean     sd       0.025quant 0.5quant
Precision for the Gaussian observations 129.8753  49.6529  60.8214   120.5645
Precision for t                          38.3033  13.9965  16.8866    36.4192
Rho for t                                 0.8031   0.0817   0.6028     0.8181
                                        0.975quant mode
Precision for the Gaussian observations 251.9389   104.1904
Precision for t                          70.9695    32.7097
Rho for t                                 0.9185     0.8463
```

Other choices for `f`-terms

For example:
- `rw1`, `rw2`
- `besag`
- `iid`

For a complete list see:|| `names(inla.models()$latent)`

Changing the prior: Internal scale

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

$$\theta_1 = \log(\tau)$$
$$\theta_2 = \log\left(\frac{1+\rho}{1-\rho}\right)$$

— The prior must be set on the parameter in **internal scale**

Changing the prior: Code

```
hyper = list(prec = list(prior = "loggamma",
                         param = c(1, 0.1))

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

EPIL example

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

Patient	y1	y2	y3	y4	Trt	Base	Age
1	5	3	3	3	0	11	31
2	3	5	3	3	0	11	30
3	2	4	0	5	0	6	25
....							
59	1	4	3	2	1	12	37

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

Repeated Poisson counts

$$y_{jk} \sim \text{Poisson}(\mu_{jk});\ j = 1,\dots,59;\ k = 1,\dots,4$$

$$\begin{aligned}\log(\mu_{jk}) = {} & \alpha_0 + \alpha_1 \log(\text{Base}_j/4) + \alpha_2 \text{Trt}_j \\ & + \alpha_3 \text{Trt}_j \log(\text{Base}_j/4) + \alpha_4 \log(\text{Age}_j) \\ & + \alpha_5 V4 + \text{Ind}_j + \beta_{jk}\end{aligned}$$

$$\begin{aligned}\alpha_i &\sim \mathcal{N}(0,\tau_\alpha) && \tau_\alpha \text{ known } (0.001) \\ \text{Ind}_j &\sim \mathcal{N}(0,\tau_{\text{Ind}}) && \tau_{\text{Ind}} \sim \text{Gamma}(1, 0.01) \\ \beta_{jk} &\sim \mathcal{N}(0,\tau_\beta) && \tau_\beta \sim \text{Gamma}(1, 0.01)\end{aligned}$$

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

Model specification in INLA

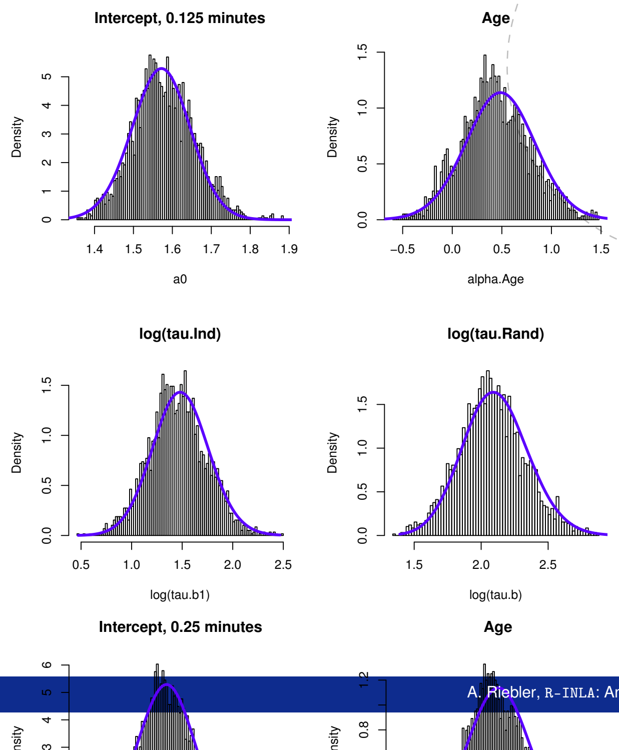
```
> data(Epil)
> head(Epil,n=3)
  y Trt Base Age V4 rand Ind       CTrt     ClBase4   CV4      ClAge
1 5   0   11  31  0    1   1 -0.5254237 -0.75635379 -0.25 0.11420370
2 3   0   11  31  0    2   1 -0.5254237 -0.75635379 -0.25 0.11420370
3 3   0   11  31  0    3   1 -0.5254237 -0.75635379 -0.25 0.11420370
4 3   0   11  31  1    4   1 -0.5254237 -0.75635379  0.75 0.11420370
```

```
> 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)))
```

```
> 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



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: Compute measures of fit, here DIC, to do model comparison?
- There are various others as well; see help.

Model choice

There is a need to compare and choose between various models, i.e. with covariates versus without, smoothed effects versus linear, etc.

One option to this in R-INLA is the deviance information criterion (DIC):

```
result = inla(formula,
              data = data,
              control.compute=list(dic=TRUE))

# See result
result$dic$dic
```

Deviance information criterion

DIC is a measure of complexity and fit. It is used to compare complex hierarchical models and is defined as:

$$\text{DIC} = \overline{D} + p_D$$

where $\overline{D}$ is the posterior mean of the deviance (measures model fit) and p_D is the effective number of parameters (measures model complexity).

$\Rightarrow$ Smaller values of the DIC indicate a better trade-off between complexity and fit of the model to the data.

Useful features

There are several features that can be used to extend the standard models in R-INLA.
However, we do not have time to cover those in this course.

Discussion

INLA is a promising alternative to MCMC for the class of latent Gaussian models. It avoids time-conusming sampling and approximates the quantities of interest directly.