

Bayesian animal model using Integrated Nested Laplace Approximations

-A wild house sparrow population case study

Anna M. Holand
Ingelin Steinsland

Animal model workshop with application to ecology at Oulu
November 2014

- Lecture
 - Motivating cases
 - Animal models
 - Bayesian inference
 - INLA
 - Animal model and INLA
- Computer exercise 1: `AnimalINLA` R package
- Computer exercise 2: R – INLA package

AnimalINLA R package

- Can be downloaded from `www.r – inla.org`
- Available from Unix, Windows and Mac
- Requires the R – INLA package

Package 'AnimalINLA'

October 31, 2013

Type Package

Title Bayesian Animal Models

Version 1.3

Date 2013-10-31

Author Anna Marie Hildén and Sara Martin

Maintainer Anna Marie Hildén <anna.h@lin.lth.se>, 00.000.0007

Description Package to perform Bayesian inference for Animal models using Inco-
porated Nested Laplace Approximations.

Depends INLA, quad, gls4

License GPL

LazyLoad yes

R topics documented:

AnimalINLA-package	1
animal.inla	2
compile_Animal	9
compile_Zinvar	10
intraid_functions	12
plot_AnimalInla	12
Simulation	13
SimulationOut	14
spatresidual	16
spatresidualmean	17
spatresidualprior	18
spatresidualvar	18
summary_AnimalInla	19
Zinvarpedigree	21

The R-INLA project

 Search this site

The home of the R-INLA project
Contact us, stay updated, get help or report an error
Discussion forum
Download

Examples and tutorials

Case studies and code from papers
Tutorials
Volume I
Volume II

FAQ

Getting started

Help

Internal use

Models

Latent models
Likelihoods
Priors
Tools to manipulate models and likelihoods

News

1.5 day INLA course in Oslo, 5-6 November 2014
10th Applied Statistics 2013 International conference, Slovenia
3-day INLA course in St Andrews, June 2nd-4th
Bayes 2013: An

[Related R-packages](#) >

R-package: AnimalINLA

AnimalINLA is a R-package built on INLA that provides functionality for analyzing 'animal models' / additive genetic models / pedigree based models using INLA. The theory is described in Holand et al. 2013, G3: Genes, Genome, Genetics 3: 1241-1251 (case study data files available [here](#)). Please refer to this paper if you use AnimalINLA.

Download

Version 1.3: [AnimalINLA 1.3](#) (use `.tar.gz` for linux and `.zip` for Windows)

You need to install INLA before installing AnimalINLA. If you experience problems, upgrading R might help. Please contact us ([email](#)) if you have any problems using AnimalINLA, or questions about extensions.

Installation for Linux / Mac

-Start R

```
>install.packages("/directory/AnimalINLA_1.3.tar.gz", repos=NULL)
where /directory/ is the directory where you downloaded/saved the package.
```

Installation for Windows

Alternative 1:

-Start R

-Select the Packages menu

-Install package from local zip file by find and highlight the location of the zip file

- Click on to open

- Load package:

```
>library(AnimalINLA)
```

Alternative 2:

-Start R

```
>install.packages("/directory/AnimalINLA_1.3.zip", repos=NULL)
```

where /directory/ is the directory where you downloaded/saved the package.

```
> library(AnimalINLA)
```

Old versions

AnimalINLA R package

R-package for animal model using R-INLA as inference:

Created as a help for starting using INLA as inference method for animal models

- Provide functionality needed for animal models:
Precision matrices A^{-1} and Z^{-1}
- A simplified interface to R-INLA for these models
 - Good default settings for finding $\pi(h^2|y)$
 - Calculate σ_a^2 , σ_β^2 and σ_e^2
 - Calculate $\sum_{i \in a_i}$
 - Summary and plot
- INLA model formulations
- Provide functionality for simulation studies

animal.inla()

```
animal.inla(response, fixed, random, genetic,  
  Ainverse, type.data,  
data, standardize=FALSE, E=NULL, lambda=NULL,  
sigma.e=FALSE, Ntrials=NULL,  
  linear.comb=FALSE, linear.comb.name=NULL,  
  verbose=FALSE, dic=FALSE, only.hyperparam=FALSE)
```

Input arguments - `animal.inla()`

`response`: response variable, distribution specified in `type.data`

`fixed`: fixed effects, \sim i.i.d.

`random`: random effects, \sim i.i.d

`genetic`: random genetic effect, `c(.)...`

`Ainverse`: precision matrix, inverse relationship matrix

Input arguments - `animal.inla()`

Likelihood functions

`type.data =:`

- "gaussian"-identity link
- "binomial"-logit link
- "poisson"-log link
- "zeroinflatedpoisson1"-log link
- "zeroinflatedpoisson0"-log link

Input arguments - `animal.inla()`

`data`: a dataframe containing the parameters in the model. The genetic numbering should match the one used in `compute.Ainverse` if using `Ainverse`. Each effect in `fixed`, `random` and `genetic` should correspond to a column in `data`. NA values are allowed.

`standardize = FALSE`: if `type.data = "gaussian"` and `standardize = TRUE` response variable is standardized

`E = NULL`: number of trials in `Poisson` likelihoods, `type.data = poisson`, `zeroinflatedpoisson1` and `zeroinflatedpoisson0`. A numeric vector of the same length of the data vector (Default 1).

`lambda = NULL`: the intensity in `poisson` likelihoods, included if heritability of `type.data = poisson`, `zeroinflatedpoisson1` and `zeroinflatedpoisson0` is wanted (default `NULL`).

Input arguments - `animal.inla()`

`sigma.e = TRUE`: environmental effect (individual effects) on the heritability are given, only obtainable for `type.data="gaussian"` (default FALSE).

`Ntrials`: a vector containing the number of trials for each individual, added as a column in data if `type.data = "binomial"`, (default 1).

`linear.comb = TRUE`: linear combination of the posterior mean of the individual breeding values and a covariate, specified in `linear.comb.name` (default=FALSE).

`linear.comb.name`: If `linear.comb = TRUE` `linear.comb.name` specifies the covariate (in data) to which linear combinations of the posterior mean of the individual breeding values are to be estimated (default=NULL).

Input arguments - `animal.inla()`

`verbose = TRUE`: inla-program runs in a verbose mode (default FALSE).

`dic = TRUE`: calculating the deviance information criteria (DIC) (default FALSE).

Output - `animal.inla()`

`animal.inla` returns an object of class "Animalinla".

- Marginals of σ_a^2 and σ_e^2
- Marginals of heritability
- Individual breeding values and summary
- Linear combinations, mean and sd
- DIC

Also information on

- Mapping, model info, time used, dataset, messages, warnings
- Priors: parameter values for the hyperparameters used in `animal.inla`, `hyper` defined in `inla`.

AND

Output - animal.inla()

-a starting point for further use of INLA:

- inla formula
- the call to inla
- prior definitions

Additional functions-plot and summary of `animal.inla()`

- `summary.Animalinla()`
- `plot.Animalinla()`
- datasets and pedigrees

A^{-1} - compute.Ainverse

compute.Ainverse(): computes the non-zero elements and the inverse of the additive relationship matrix, A^{-1} .

- Checks for errors and sorts the pedigree chronologically
- For programming reasons gives individual new id numbers.

Input arguments:

pedigree: a data frame or matrix with 3 columns

- Not contain characters/letters.
- Parents should be denoted with 0 when unknown.
 - 1. column: vector of id number of the individuals in the pedigree
 - 2. and 3. column are vectors of id numbers, indicating the parents of the individuals in column 1.

Output: A map is provided for mapping the individual numbers back to the original one.

Z^{-1} - compute.Zinverse

compute.Zinverse(): computes the non-zero elements and the inverse of the additive relationship matrix, Z^{-1} .

- Checks for errors and sorts the pedigree chronologically
- For programming reasons gives individual new id numbers.

Input arguments:

pedigree: a data frame or matrix with 4 columns

- Not contain characters/letters.
- Parents should be denoted with 0 when unknown.
 - 1. column: id of the individuals in the pedigree
 - 2. column: id of the heterozygote parent for the sex-chromosome
 - 3. column: id of the homozygote parent for the sex-chromosome
 - 4. column: the sex of the individuals in 1. column, numbered homozygote parent=1 and heterozygote parent=2

SimulateBreeding()

- Simulates breeding values by drawing from a multivariate normal using the sparse precision matrix \mathbf{A}^{-1} computed from `compute.Ainverse`.

Input arguments:

`Ainverse`: a precision matrix (\mathbf{A}^{-1}) of class="ped" (computed from `compute.Ainverse`).

`sigma2.u`: a numeric value or vector of additive genetic variances values.

Value:

list containing a vector of breeding values for each value of `sigma2.u`. The length of the vector of breeding values is the length of the number of individual in the pedigree argument in `compute.Ainverse`.

SimulateData()

- Simulates Gaussian, binomial and Poisson data from \mathbf{A}^{-1} , for different additive genetic variances. Uses `SimulateBreeding` to simulate breeding values internal

Input arguments:

Ainverse: a precision matrix (\mathbf{A}^{-1}) of class="ped" (computed from `compute.Ainverse`).

Sigma2.u: a numeric value or vector of additive genetic variances values.

type.data: the distribution of data to be computed (gaussian, binomial and `poisson(zeroinflatedpoisson1, zeroinflatedpoisson0)`).

Sigma2.e = NULL: a numeric value or vector of residual variances, corresponding to the values of `Sigma2.u`. Only when `type.data = "gaussian"`. Default value is `(1-Sigma2.u)`.

SimulateData()

- Simulates Gaussian, binomial and Poisson data from \mathbf{A}^{-1} , for different additive genetic variances.

Input arguments:

`n = 1`: the number of datasets to be computed for each value of `Sigma2.u`.

`individual.data = NULL`: a vector of individuals (id number corresponding to the id numbering in pedigree/`Ainverse`) that have data values in an real dataset. To create the same missing structure.

`Ntrials = NULL`: a vector of the number of trials when `type.data = "binomial"`.

`E = NULL`: a vector of the number of trials when `type.data = "poisson/"zero..."`.

- No NA are permitted, 0 are though of as missing, and are 0 in the resulting dataset.

SimulateData()

Output arguments:

SimulateData: list containing an element for each value of `sigma2.u`.

-For each `sigma2.u` there is a list with elements for each number of `n`.

-Each element contains a data.frame containing columns:

- `y`: simulated data
- `u`: new individual numbering (matching the map in `Ainverse`)
- `Ntrials/E`: number of trials for the binomiallikelihood/number of trials in Poisson likelihoods
- `animal`: old/original individual numbering (matching the map in `Ainverse`)

Computer exercises 1

Exercises:

- Run `animal.inla()` with different likelihoods
 - Look at the summary (plot)
 - Take out variables and compare DIC values
 - Find the list of individual breeding values and summary of breeding values
 - Find the marginal distributions for the additive genetic variance and heritability
 - Run with linear combinations for year
 - Find the `inla` call, `inla` formula and prior definitions
 - Simulate breeding values and data