Package ‘AnimalINLA’

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Type Package

Title Bayesian Animal Models

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Description Package to perform Bayesian inference for Animal models using Integrated Nested Laplace Approximations.

Depends INLA, spam, gtools

License GPL

LazyLoad yes

R topics documented:

`AnimalINLA-package` *Bayesian Animal Models*

Description

Package to perform Bayesian inference for Animal models using Integrated Nested Laplace Approximations.

Details

Package:	AnimalINLA
Type:	Package
Version:	1.0
Date:	2010-08-26
License:	GPL
LazyLoad:	yes

Package to perform Bayesian inference for Animal models using Integrated Nested Laplace Approximations, for Gaussian, binomial and Poisson likelihoods. In addition, functions to compute the non-zero elements and the inverse of the additive relationship matrix, A^{-1}, and sex-linked additive relationship matrix, Z^{-1}, and simulate breeding values and data.

Author(s)

Anna Marie Holand and Sara Martino

Maintainer: Anna Marie Holand <anna.holand@bio.ntnu.no>

References

Rue, H.; Martino, S. & Chopin, N. *Approximate Bayesian Inference for Latent Gaussian Models using integrated nested Laplace approximations*, Journal of the Royal Statistical Society, Series B, 2009, 71, 319-392. Steinsland, I. & Jensen, H. *Utilizing Gaussian Markov Random Field Properties of Bayesian Animal Models*, Biometrics, 2010, 66, 763-771. Holand, A. M.;Steinsland, I. ; Martino, S. & Jensen, H. *Animal model and Integrated Nested Laplace Approximations* (Submitted). Holand, A. M.;Steinsland, I. ; Martino, S. & Jensen, H. *Animal model and Integrated Nested Laplace Approximations.* Preprint Statistics No. 4/2011. Norwegian University of Science and Technology, Trondheim, Norway.

See Also

`INLA`

`animal.inla` *Bayesian analyses of Animal Model using Integrated Nested Laplace Approximation*

Description

`animal.inla` performs inference on animal models using the Bayesian approximation methology `INLA`.

Usage

```
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)
```

Arguments

`response`	The response variable `y` with an exponential family distribution (e.g. Normal, Poisson, binomial), modelled by a linear predictor specified by the link function (see `type.data`)
`fixed`	Fixed effects, given the latent model are "iid".
`random`	Random effects, given the latent model are "iid".
`genetic`	The random genetic effect, the individuals in the dataset (must be in the pedigree (Ainverse)), must be written as a vector: c("."), given the latent model `generic 0` if `type.data`="binomial","poisson" or for `DIC=TRUE` and `sigma.e=TRUE` for type.data="gaussian", `generic 2` if type.data="gaussian".
`Ainverse`	The precision matrix (inverse relationship matrix, A^-1). See `details`.
`type.data`	A string indicating the likelihood family, the distribtuion of the response variable. The distribution specify the link function. The different distributions are `gaussian` with identity link, `binomial` with a logit link, `poisson`, `zeroinflatedpoisson1` and `zeroinflatedpoisson0` with a log link.

`data`	A dataframe containing the parameters in the model. The `genetic` numbering should match the one used in `compute.Ainverse` if itis used to find `Ainverse`, see `Details`. Each effect in `fixed`, `random` and `genetic` should correspond to a column in `data`. NA values are allowed, see `INLA` for documentation on how it handles NA values.
`standardize`	If `type.data="gaussian"` and standarize=TRUE response variable is standardized.
`E`	Number of trials in Poisson liklihoods (known component in the mean), `type.data`=`poisson`, `zeroinflatedpoisson1` and `zeroinflatedpoisson0`. A numeric vector of the same length of the data vector (Default 1).
`lambda`	The intensity in poisson likelihoods, included if heritability of `type.data`=`poisson`, `zeroinflatedpoisson1` and `zeroinflatedpoisson0` is wanted (default NULL). See `Details`.
`sigma.e`	If TRUE, the 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`	If TRUE, a 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` is 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).
`verbose`	Indicating if the `inla`-program should run in a verbose mode (default FALSE).
`dic`	Calculating the deviance information criteria (DIC) value should be computed (default FALSE).
`only.hyperparam`	Indicating if only the hyperparameters are to be computed (default FALSE).

Details

`animal.inla` creates a formula from the arguments `response`, `fixed`, `random` and `genetic` to fit the `INLA` formulations (see `INLA` formulae and `inla.models`) A `inla` formula, can be written as y ~ 1 + z + f(ind, model="iid"), where y is the response variable, z a fixed variable and ind a random variable.

If the precision matrix from `compute.Ainverse` is used, with class="ped", `animal.inla` automaticly maps the numbering in `genetic` variable (pedigree numbering) with the new index for individuals in the pedigree used in `compute.Ainverse`, so that the `genetic` has the new index number corresponding to the one from `compute.Ainverse`. If not using `compute.Ainverse` to calculate the precision matrix, the precision matrix has to be on the form sparseMatrix(i = ,j = , x =), the two first (i ,j) are the individuals compared in the relationship matrix (remember the individual numbers must match in the relationship matrix and the individual number in data (`genetic`)), third list element (values) are the precision values (the corresponding element of the precision matrix).

`lambda` is often calculated as sum over all observations in the response variable divided by the sum of n_i, the known exposure, (given in `E`).

Priors value are not a argument in the function and are in fixed effects fixed to `initial`=-10 with model `iid`, random effects set to `param`=c(1,0.001)) with model `iid`. In addition, the priors for genetic effect is set to `param`=0.5 and the residual effect to `param`=0.5, and fixed to `initial`=10 in the latent field. See `prec.A` and so forth in the output so see how it is defined in `INLA`.

If wanted to use different priors, it is possible to compute it from `inla`, using the `inla.call` and formula output from `animal.inla`.

See ?`plot.Animalinla` and ?`summary.Animalinla` for plot and summary in `animal.inla`.

Value

animal.inla returns an object of class "Animalinla". This is a list containing the following arguments:

`Ainversemapping`	The map from `compute.Ainverse` used in Animalinla, mapping the numbering given in `genetic` to new numbering.
`binary.h`	The marginal distribution of the Binomial heritability.
`breedingvalues`	The marginal distribution for the random genetic variable, a list of individual breeding values.
`Cmatrix`	The (sparse) precision matrix used in inla defined from the `Ainverse`.
`dataset`	The dataset given in `data`. The numbering in `genetic` has been given new mapping name, corresponding the map in `Ainversemapping` .
`dic`	The deviance information criteria, DIC.
`family`	The `type.data` used.
`fixed.names`	The names of the fixed effects.
`formula`	The matched formula for `inla`.
`formula.gaussianDIC`	The matched formula for `type.data="gaussian"` and/or `dic=TRUE`, `sigma.e=TRUE` and/or `linear.comb=TRUE` (`model.covariatesDIC`) for `inla`.
`genetic.names`	The random name given in `genetic`.
`gaussian.h`	The marginal distribution of the Gaussian heritability.
`inla.call`	The matched call for `inla` .
`inla.call.gaussianDIC`	The matched call for `inla` for `type.data="gaussian"` and/or `dic=TRUE`, `sigma.e=TRUE` and `linear.comb=TRUE`.
`intercept`	The intercept mean and standard deviation (sd) with (0.025,0.5,0.975)
`linear.combinations`	Posterior mean and standard deviation (sd) with (0.025,0.5,0.975)
`model.covariates`	List of models for the latent Gaussian field for random variables.
`model.covariatesDIC`	Model for the latent Gaussian field for random variables when `type.data="gaussian"` and/or `dic=TRUE`, `sigma.e=TRUE` and `linear.comb=TRUE`.

`Message`	A message is given if data are standardized, only in if `type.data="gaussian"`.
`name.covariates`	The name of the random covariates.
`poisson.h`	The marginal distribution of the Poisson (zero-inflated Poisson) heritability if `lambda` is given.
`prec.A`	Parameter values for the hyperparameters used in `animal.inla`, `hyper` defined in `inla`.
`prec.e.generic0`	Parameter values for the hyperparameters used in `animal.inla`, `hyper` defined in `inla`.
`prec.Fixed`	Parameter values for the hyperparameters used in `animal.inla`, `hyper` defined in `inla`.
`prec.fixed.generic2`	Parameter values for the hyperparameters used in `animal.inla`, `hyper` defined in `inla`.
`prec.Random`	Parameter values for the hyperparameters used in `animal.inla`, `hyper` defined in `inla`.
`random.names`	The names of the random effects.
`sigma.u`	The marginal distribution for the genetic hyperparameter (additive genetic variance).
`sigma.e`	The marginal distribution for the individual effet hyperparameter (environmental variance), only for Gaussian likelihoods.
`summary.breedingvalues`	Summary for individual breedingvalues, mean and standard deviation (sd) with (0.025,0.5,0.975)
`summary.hyperparam`	Summary for the posterior marginals for the hyperparameters, mean and standard deviation with (0.025, 0.5,0.975)
`Time.used`	Time used for computation.

Warning

Caution!! Choice of priors may effect results.

Author(s)

Anna Marie Holand and Sara Martino

References

Rue, H.; Martino, S. & Chopin, N. *Approximate Bayesian Inference for Latent Gaussian Models using integrated nested Laplace approximations*, Journal of the Royal Statistical Society, Series B, 2009, 71, 319-392. Steinsland, I. & Jensen, H. *Utilizing Gaussian Markov Random Field Properties of Bayesian Animal Models*, Biometrics, 2010, 66, 763-771. Holand, A. M.;Steinsland, I. ; Martino, S. & Jensen, H. *Animal model and Integrated Nested Laplace Approximations* (Submitted). Holand, A. M.;Steinsland, I. ; Martino, S. & Jensen, H. *Animal model and Integrated Nested Laplace Approximations.* Preprint Statistics No. 4/2011. Norwegian University of Science and Technology, Trondheim, Norway.

See Also

`compute.Ainverse`,`inla`

Examples

```
#compute the inverse of the relationship matrix A
data(sparrowpedigree)
xx=compute.Ainverse(sparrowpedigree)

##Gaussian example
#data are standardized
data(sparrowGaussian)

#run animal.inla
gauss = animal.inla(response=y,
    genetic=c("Individual"),
    Ainverse =xx,
    type.data="gaussian",
    data=sparrowGaussian,
    sigma.e=TRUE,
    dic=TRUE)

#example results: summary and summary over hyperparameters
summary(gauss)
gauss$summary.hyperparam


#In inla these can be written as:
#Cmatrix
Cmatrix=gauss$Cmatrix

#formula in inla
 gauss$formula

#call to inla for DIC=FALSE,
 gauss$inla.call

#inla call when, dic==TRUE ,sigma.e==TRUE , linear.comb==TRUE
 gauss$inla.call.gaussianDIC
 gauss$formula.gaussianDIC

#examples of parameter values for hyperparameters
gauss$prec.fixed.generic2
gauss$prec.A
gauss$prec.e.generic0
gauss$prec.Fixed
gauss$prec.Random

##Binomial example
data(sparrowBinomial)

#run animal.inla
```

```
binom = animal.inla(response=y,
    genetic=c("Individual"),
    Ainverse =xx,
    type.data="binomial",
                    data=sparrowBinomial,
    Ntrials=Ntrial,
                    dic=TRUE)


##example results: summary and summary over hyperparameters
summary(binom)
binom$summary.hyperparam


#In inla these can be written as:
#Cmatrix
Cmatrix=binom$Cmatrix

#inla formula
binom$formula

#call to inla
binom$inla.call


##Poisson example
data(sparrowPoisson)

#run animal.inla
pois = animal.inla(response="y",
   genetic=c("Individual"),
   Ainverse =xx,
   type.data="poisson",
   data=sparrowPoisson,
   E=n,
                   dic=TRUE)


##example results: summary and summary over hyperparameters
summary(binom)
pois$summary.hyperparam


#In inla these can be written as:
#Cmatrix
Cmatrix=pois$Cmatrix

#inla formula
pois$formula

#call to inla
pois$inla.call
```

`compute.Ainverse` *Computing the non-zero elements and the inverse of the additive relationship matrix, $A\hat{}-1$*

Description

`compute.Ainverse` computes the non-zero elements and the inverse of the additive relationship matrix, A^{-1}, from a pedigree. `compute.Ainverse` can be used in defining the precison matrix used in `animal.inla`. In addition, the function checks the pedigree for errors and sorts the pedigree chronologically.

Usage

```
compute.Ainverse(pedigree, debug=FALSE)
```

Arguments

`pedigree`	A data frame or matrix containing the pedigree. The data frame or matrix should contain 3 columns, where 1. column is a vector of id number of the individuals in the pedigree and the 2. and 3. column are vectors of id numbers,indicating the parents of the individuals in column 1. Parents should be denoted with 0 when unknown.
`debug`	debugging the code, default FALSE.

Details

The id numbers of the individuals in the pedigree can not contain characters / letters. If sorted=FALSE, the function sorts the pedigree chronologically, for programming reasons giving the individual new id numbers. A map is provided for mapping the individual numbers back to the original one. Before starting, `compute.Ainverse` checks the pedigree for errors, if errors are detected a warning/error message will be generated.

Value

compute.Ainverse returns an object of class "ped". This is a list containing the following arguments:

`Ainverse`	The inverse relationship matrix, A^{-1}, computed as in Quaas, R. (1976) and Zhang, Z. et al. (2009)
`map`	A map, mapping the original id numbers (given in the 'pedigree' argument) to the new one.

Author(s)

Anna Marie Holand <`anna.holand@bio.ntnu.no`> and Sara Martino

References

Quaas, R. (1976) *Computing the diagonal elements and inverse of a large numerator relationship matrix*, Biometrics, vol 32, pp 949-953.

Zhang, Z.; Li, C.; Todhunter, R. J.; Lust, G.; Goonewardene, L. and Wang, Z. (2009) *An algorithm to sort complex pedigrees chronologically without birthdates*, Journal of Animal and Veterinary Advances, vol 8, pp 177-182.

See Also

`animal.inla`

Examples

```
require(AnimalINLA)

data(sparrowpedigree)

compute.Ainverse = function(sparrowpedigree)
```

`compute.Zinverse` *Computing the non-zero elements and the inverse of the sex-linked additive relationship matrix $Z\hat{}-1$*

Description

`compute.Zinverse` computes the non-zero elements and the inverse of the sex-linked additive relationship matrix Z^{-1} from a pedigree. `compute.Zinverse` can be used in defining the precison matrix for linked dependencies used in `inla`. In addition, the function checks the pedigree for errors and sorts the pedigree chronologically.

Usage

```
compute.Zinverse(pedigree, debug=FALSE)
```

Arguments

`pedigree`	A data frame or matrix containing the pedigree. The data frame or matrix should contain 4 columns, where 1. column is a vector of id number of the individuals in the pedigree, 2. column is a vector of id number of the heterozygote parent for the sex-chromosome (i.e. for birds the mother, for mammals the father), 3. column is a vector of id number of the homozygote parent for the sex-chromosome (i.e. for birds the father, for mammals the mother), indicating the parents of the individuals in column 1. 4. column is a vector of the sex of the individuals in pedigree, corresponding to individuals in 1. column, numbered 1 and 2, where the homozygote parent=1 and heterozygote parent=2. Parents should be denoted with 0 when unknown.
`debug`	debugging the code, default FALSE.

Details

The id numbers of the individuals in the pedigree can not contain characters / letters. The function sorts the pedigree chronologically, for programming reasons giving the individual new id numbers. A map is provided for mapping the individual numbers back to the original one. Before starting, `compute.Zinverse` checks the pedigree for errors, if errors are detected a warning/error message will be generated.

Value

compute.Zinverse returns an object of class "pedZ". This is a list containing the following arguments:

`Zinverse`	The inverse sex-chromosomal relationship matrix, Z^{-1}, computed as in Fernando, R. L. and Grossman, M. (1990) and Zhang, Z et al. (2009).
`map`	A map, mapping the original id numbers (given in the 'pedigree' argument) to the new one.

Author(s)

Camilla Thorrud Larsen `<camilla.t.larsen@ntnu.no>`,
Anna Marie Holand `<anna.holand@bio.ntnu.no>` and Sara Martino

References

Fernando, R. L. and Grossman, M. (1990) *Genetic evaluation with autosomal and X-chromosomal inheritance*, Theoretical and applied genetics, vol 80, pp 75-80.

Quaas, R. (1976) *Computing the diagonal elements and inverse of a large numerator relationship matrix*, Biometrics, vol 32, pp 949-953.

Zhang, Z.; Li, C.; Todhunter, R. J.; Lust, G.; Goonewardene, L. and Wang, Z. (2009) *An algorithm to sort complex pedigrees chronologically without birthdates*, Journal of Animal and Veterinary Advances, vol 8, pp 177-182.

See Also

`compute.Ainverse`

Examples

```
require(AnimalINLA)

data(Zsparrowpedigree)

Z.inverse=compute.Zinverse(Zsparrowpedigree)
```

`Internal functions` *Internal functions*

Description

Internal functions

`plot.Animalinla` *Default AnimalINLA plotting.*

Description

Takes a fitted ‘Animalinla’ object produced by ‘AnimalINLA’ and plots

Usage

```
## S3 method for class 'Animalinla'
plot(x,...)
```

Arguments

`x`	A fitted ‘Animalinla’ object produced by ‘AnimalINLA’.
`...`	Additional arguments to plot().

Details

Plots posterior marginal distribution depending on the options in the fitted ‘Animalinla’ object.

Author(s)

Anna Marie Holand `<anna.holand@bio.ntnu.no>` and Sara Martino

See Also

`animal.inla`

Examples

```

## --- Continuing the Gaussian example from  ?animla.inla:
## Not run:
plot(gauss)

## End(Not run)
```

`simulate.breeding` *Simulating breeding values from the inverse of the additive relationship matrix,* $A\hat{}-1$

Description

Simulates breeding values by drawing from a multivariate normal using the sparse precision matrix A^{-1} (inverse additive relationship matrix) computed from `compute.Ainverse`.

Usage

```
simulate.breeding(Ainverse,
sigma2.u)
```

Arguments

`Ainverse`	A precision matrix (inverse relationship matrix, A^{-1}) of class="ped". See `details`.
`sigma2.u`	A numeric value or vector of additive genetic variances.

Details

The precision matrix 'Ainverse' has to be of class="ped", computed from `compute.Ainverse`.

Value

`simulate.breeding` returns an object of class "sim.breeding". This is a 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`.

Author(s)

Anna Marie Holand `<anna.holand@bio.ntnu.no>` and Sara Martino

References

Holand, A. M.;Steinsland, I. ; Martino, S. & Jensen, H. *Animal model and Integrated Nested Laplace Approximations* (Submitted). Holand, A. M.;Steinsland, I. ; Martino, S. & Jensen, H. *Animal model and Integrated Nested Laplace Approximations.* Preprint Statistics No. 4/2011. Norwegian University of Science and Technology, Trondheim, Norway.

See Also

`animal.inla`, `simulate.data`, `compute.Ainverse`

Examples

```
require(AnimalINLA)

data(sparrowpedigree)

A.inverse = compute.Ainverse(sparrowpedigree)

breeding.values = simulate.breeding(Ainverse = A.inverse, sigma2.u = c(0,0.5))

head(breeding.values$"0")
```

`simulate.data` *Simulating Gaussian, binomial or Poisson data*

Description

Simulates Gaussian, binomial and Poisson data from the inverse of the additive relationship matrix, A^{-1}, for different additive genetic variances.

Usage

```
simulate.data(Ainverse,
     Sigma2.u,
     type.data,
     Sigma2.e=NULL,
     n=1,
     individual.data=NULL,
     Ntrials=NULL,
     E=NULL)
```

Arguments

`Ainverse`	A precision matrix (inverse relationship matrix, A^{-1}) of class="ped". See `Details`.
`Sigma2.u`	A numeric value or vector of additive genetic variances.
`type.data`	A string indicating the likelihood family, the distribtuion of data to be computated. The different distributions are `gaussian`, `binomial` and `poisson` (`zeroinflatedpoisson1`, `zeroinflatedpoisson0`).
`Sigma2.e`	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).
`n`	The number of datasets to be computed for each value od 'Sigma2.u'. Default value is 1.
`individual.data`	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. See `Details`.

`Ntrials`	A vector containing the number of trials for the 'binomial'likelihood (`type.data`="binomial"). If `individual.data`=NULL `Ntrials` is a numeric vector of the same length as the number of individual in the 'pedigree' argument in `compute.Ainverse`. If `individual.data` is defined, `Ntrials` is a numeric vector of the same length as the vector given in `individual.data`, with number of trials for each individual given in 'individual.data'. No NA are permitted, 0 are though of as missing, and are 0 in the resulting dataset.
`E`	Number of trials in 'poisson' liklihoods (known component in the mean) (`type.data`="poisson"/"zeroinflatedpoisson1"/"zeroinflatedpoisson0"). If `individual.data=` `E` is a numeric vector of the same length as the number of individual in the 'pedigree' argument in `compute.Ainverse`. If `individual.data` is defined `E` is a numeric vector of the same length as the vector given in `individual.data`, with number of trials for each individual given in 'individual.data'. No NA are permitted, 0 are though of as missing, and are 0 in the resulting dataset.

Details

The precision matrix 'Ainverse' has to be of class="ped", computed from `compute.Ainverse`. Uses `simulate.breeding` to simulate breeding values internal. If 'individual.data' is not defined, a data.frame is computed with column length same as the length of the 'pedigree' argument in `compute.Ainverse`. If 'individual.data' is defined, a data frame is computed with a missing structure (if length of 'individual.data' is shorter than length of the number of individual in the 'pedigree' argument in `compute.Ainverse`) corresponding to the individuals given in the simulated data.

Value

`simulate.data` returns an object of class "compute.sim". This is a 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 (trait) data
`u`	New individual numbering, matching the 'map' in 'Ainverse'
`Ntrials/E`	Number of trials for the 'binomial'likelihood/number of trials in Poisson liklihoods
`animal`	Old/original individual numbering, matching the 'map' in 'Ainverse'

See Details for the dimention of the data.frame.

Author(s)

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References

Holand, A. M.;Steinsland, I. ; Martino, S. & Jensen, H. *Animal model and Integrated Nested Laplace Approximations* (Submitted). Holand, A. M.;Steinsland, I. ; Martino, S. & Jensen, H. *Animal model and Integrated Nested Laplace Approximations.* Preprint Statistics No. 4/2011. Norwegian University of Science and Technology, Trondheim, Norway.

See Also

`animal.inla`

Examples

```
require(AnimalINLA)

data(sparrowpedigree)
data(sparrowGaussian)

A.inverse = compute.Ainverse(sparrowpedigree)

sim.data = simulate.data(Ainverse = A.inverse,
                Sigma2.u=c(0,0.5),
             type.data="gaussian",
             n=2,
             individual.data=sparrowGaussian$Individual)
```

`sparrowBinomial` *Synthetic Binomial data*

Description

This example considers simulated Binomial distributed data based on the a wild house sparrow population pedigree.

Usage

```
data(sparrowBinomial)
```

Format

A data frame with 3574 synthetic individual data on the following 3 variables.

‘y’ individual data for a Binomial trait

‘Ntrial’ number of trials for a individual

‘Individual’ index for individuals corresponding to the index in `sparrowpedigree`

Details

`sparrowBinomial` are simulated data based on the `sparrowpedigree`. `Ntrial` the number of trials are simulated with a range between 1 and 9.

References

Holand, A. M.;Steinsland, I. ; Martino, S. & Jensen, H. *Animal model and Integrated Nested Laplace Approximations* (Submitted).

Examples

```
data(sparrowBinomial)
```

`sparrowGaussian` *Synthetic Gaussian data*

Description

This example considers simulated Gaussian distributed data based on the a wild house sparrow population pedigree.

Usage

```
data(sparrowGaussian)
```

Format

A data frame with 3574 synthetic individual data on the following 2 variables.

‘y’ individual data for a Gaussian trait

‘Individual’ index for individuals corresponding to the index in `sparrowpedigree`

Details

`sparrowGaussian` are simulated data based on the `sparrowpedigree`. Simulated with additive genetic variance 0.4 and environmental (random effect) variance 0.6.

References

Holand, A. M.;Steinsland, I. ; Martino, S. & Jensen, H. *Animal model and Integrated Nested Laplace Approximations* (Submitted).

Examples

```
data(sparrowGaussian)
```

`sparrowpedigree` *Wild House Sparrow Pedigree*

Description

Pedigree with 3574 individuals from a wild house sparrow population.

Usage

```
data(sparrowpedigree)
```

Format

A data frame with 3574 individual data on the following 3 variables.

‘Individual’	index for individuals in pedigree
‘Parent1’	First parent of the ’Individual’
‘Parent2’	Second parent of the ’Individual’

Details

The pedigree in `sparrowpedigree` are taken from a wild house sparrow population in northern Norway. Missing parent is defined by 0.

References

Holand, A. M.;Steinsland, I. ; Martino, S. & Jensen, H. *Animal model and Integrated Nested Laplace Approximations* (Submitted).

Examples

```
data(sparrowpedigree)
```

`sparrowPoisson` *Synthetic Poisson data*

Description

This example considers simulated Poisson distributed data based on the a wild house sparrow population pedigree.

Usage

```
data(sparrowPoisson)
```

Format

A data frame with 3574 synthetic individual data on the following 3 variables.

‘y’ individual data for a Poisson trait

‘n’ number of trials for a individual

‘Individual’ index for individuals corresponding to the index in `sparrowpedigree`

Details

`sparrowPoisson` are simulated data based on the `sparrowpedigree`.

References

Holand, A. M.;Steinsland, I. ; Martino, S. & Jensen, H. *Animal model and Integrated Nested Laplace Approximations* (Submitted).

Examples

```
data(sparrowPoisson)
```

`summary.Animalinla` *Summary for a AnimalINLA fit*

Description

Takes a fitted ‘Animalinla’ object produced by ‘AnimalINLA’ and produces a summary from it.

Usage

```
## S3 method for class 'Animalinla'
summary(object, ...)
```

Arguments

`object`	a fitted ‘Animalinla’ object produced by ‘AnimalINLA’.
`...`	other arguments.

Details

Posterior mean and standard deviation (together with quantiles or cdf) are printed for the hyperparameters.

Value

‘summary.Animalinla’ returns an object of call ‘summary.Animalinla’, a list with components:

`dic`	the component from ‘object’.
`family`	the component from ‘object’.
`fixed.names`	the component from ‘object’.
`formula`	the component from ‘object’.
`formula.gaussianDIC`	the component from ‘object’.
`genetic.names`	the component from ‘object’.
`inla.call`	the component from ‘object’.
`inla.call.gaussianDIC`	the component from ‘object’.
`Message`	the component from ‘object’.
`Model.summary`	Containing component from ‘object’.
`random.names`	the component from ‘object’.
`summary.hyparparam`	the component from ‘object’.
`Time used`	the component from ‘object’.

Author(s)

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References

Rue, H.; Martino, S. & Chopin, N. *Approximate Bayesian Inference for Latent Gaussian Models using integrated nested Laplace approximations*, Journal of the Royal Statistical Society, Series B, 2009, 71, 319-392. Steinsland, I. & Jensen, H. *Utilizing Gaussian Markov Random Field Properties of Bayesian Animal Models*, Biometrics, 2010, 66, 763-771. Holand, A. M.;Steinsland, I. ; Martino, S. & Jensen, H. *Animal model and Integrated Nested Laplace Approximations* (Submitted).

See Also

`animal.inla`

`Zsparrowpedigree` *Wild House Sparrow Pedigree with sex*

Description

Pedigree with 3574 individuals with sex from a wild house sparrow population.

Usage

```
data(sparrowpedigree)
```

Format

A data frame with 3574 individual data on the following 4 variables.

'Individual' index for individuals in pedigree

'mother' Mother of the 'Individual'

'father' Father of the 'Individual'

'sex' Sex of the 'Individual'

Details

The pedigree in `Zsparrowpedigree` are taken from a wild house sparrow population in northern Norway (we have assumed a sex for some individuals original missing sex). No NA is allowed in 'sex'. Missing parent is defined by 0.

References

Holand, A. M.;Steinsland, I. ; Martino, S. & Jensen, H. *Animal model and Integrated Nested Laplace Approximations* (Submitted).

Examples

```
data(Zsparrowpedigree)
```