Package ‘pedigreemm’

July 23, 2025

Version 0.3-5

Date 2024-10-10

Title Pedigree-Based Mixed-Effects Models

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Description Fit pedigree-based mixed-effects models.

Depends R(>= 3.0.0), lme4 (>= 1.0), Matrix (>= 1.0), methods

LazyLoad yes

LazyData yes

License GPL (>= 2)

URL `https://github.com/anainesvs/pedigreemm/`

NeedsCompilation yes

Repository CRAN

Date/Publication 2024-10-14 14:40:02 UTC

Contents

`Dmat` *vector of the diagonal for the D matrix from the decomposition A= TDT'*

Description

numeric vector that should be the diagonal elements of the diagonal matrix D

Usage

```
Dmat(ped)
```

Arguments

`ped`	an object that inherits from class pedigree

Details

Determine the diagonal factor in the decomposition of the relationship matrix from a pedigree equal to TDT'. Where T is unit lower triangular and D is a diagonal matrix. This function returns a numeric vector with the entries of D

Value

a numeric vector

Examples

```
ped <- pedigree(sire = c(NA,NA,1, 1,4,5),
                dam  = c(NA,NA,2,NA,3,2), label= 1:6)
Dmat(ped)
```

`editPed` *Complete and Order a Pedigree*

Description

This function helps to prepare a pedigree to generate a pedigree object

Usage

```
editPed(sire, dam, label, verbose)
```

Arguments

`sire`	a vector (with some `NA` entries) with the father IDs
`dam`	similarly as `sire` for the "mother" of each entry. The vector must be of the same length than the one for the sire
`label`	a vector with the subjects id. Giving a unique ID for the corresponding entry. The length as `sire` and `dam` should be the same
`verbose`	logical entry inquiring whether to print line that the program is evaluating. The default is FALSE.

Details

The function takes a vector of sires, another for dams and a final one for subjects all of the same length, convert them to character. If there are dams or sires not declared as subjects the function generates them. Finally, it orders the pedigree. The output can be used to build a pedigree object `ped`

Value

A data frame with strings as characters. All subjects are in the label column, and all subjects will appear in this column before appering as sires or dams.

Examples

```
  #(1)
  pede<-data.frame(sire=as.character(c(NA,NA,NA,NA,NA,1,3,5,6,4,8,1,10,8)),
             dam= as.character(c(NA,NA,NA,NA,NA,2,2,NA,7,7,NA,9,9,13)),
             label=as.character(1:14))
   #scrambled original pedigree:
   (pede<- pede[sample(replace=FALSE, 1:14),]  )
   (pede<- editPed(sire=pede$sire, dam= pede$dam, label=pede$label))
   ped<- with(pede, pedigree(label=label, sire=sire, dam=dam))
#################################################################################################
   #(2) With missing labels
   pede<-data.frame(sire=as.character(c(NA,1,3,5,6,4,8,1,10,8)),
             dam= as.character(c(NA,2,2,NA,7,7,NA,9,9,13)),
             label=as.character(5:14))
```

```
   #scrambled original pedigree:
   (pede<- pede[sample(replace=FALSE, 1:10),]  )
   (pede<- editPed(sire=pede$sire, dam= pede$dam, label=pede$label))
   ped<- with(pede, pedigree(label=label, sire=sire, dam=dam))

################################################################################################
   #(2) A larger pedigree
 #Useing pedCows pedigree
# str(pedCows)
# pede<-data.frame(id=pedCows@label, sire=pedCows@sire, dam=pedCows@dam)
# pede<-pede[sample(1:nrow(pede),replace=FALSE),]
# pede<- editPed(sire=pede$sire, dam=pede$dam, label=pede$id)
# ped<- with(pede, pedigree(label=label, sire=sire, dam=dam))
```

`getA` *Additive Relationship Matrix*

Description

Additive relationship matrix from a pedigree

Usage

```
getA(ped)
```

Arguments

`ped`	a pedigree that includes the individuals who occur in `labs`

Details

Returns the additive relationship matrix for the pedigree `ped` .

Value

Sparse matrix

Examples

```
## Example from chapter 2 of Mrode (2005)

ped <- pedigree(sire = c(NA,NA,1, 1,4,5),
                dam  = c(NA,NA,2,NA,3,2), label= 1:6)
(getA(ped))
```

`getAInv` *Inverse of the relationship matrix*

Description

Inverse of the Relationship matrix from a pedigree

Usage

```
getAInv(ped)
```

Arguments

`ped`	a pedigree that includes the individuals who occur in `labs`

Details

Determine the inverse of the relationship matrix from a pedigree `ped`.

Value

sparse matrix, inverse of the relationship matrix

References

2010. A.I. Vazquez, D.M. Bates, G.J.M. Rosa, D. Gianola and K.A. Weigel. Technical Note: An R package for fitting generalized linear mixed models in animal breeding. Journal of Animal Science, 88:497-504.

Examples

```
## Example from chapter 2 of Mrode (2005)

ped <- pedigree(sire = c(NA,NA,1, 1,4,5),
                dam  = c(NA,NA,2,NA,3,2), label= 1:6)
getAInv(ped)
```

`inbreeding` *Inbreeding coefficients from a pedigree...*

Description

Inbreeding coefficients from a pedigree

Usage

```
inbreeding(ped)
```

Arguments

`ped`	an object that inherits from class pedigree

Details

Determine the inbreeding coefficients for all the individuals of a pedigree. This function a numeric vector.

Value

a numeric vector

Source

Sargolzaei, M. and H. Iwaisaki, 2005. Comparison of four direct algorithms for computing the inbreeding coefficients. J. Anim. Sci, 76: 401-406.

References

2010. A.I. Vazquez, D.M. Bates, G.J.M. Rosa, D. Gianola and K.A. Weigel. Technical Note: An R package for fitting generalized linear mixed models in animal breeding. Journal of Animal Science, 88:497-504.

Examples

```
ped <- pedigree(sire = c(NA,NA,1, 1,4,5),
                dam  = c(NA,NA,2,NA,3,2), label= 1:6)
inbreeding(ped)
```

`mastitis` *Mastitis cases in dairy cattle*

Description

Records of the number of cases of clinical mastitis during the first lactation of 1,675 cows, primarily Holsteins. Cows belonged to 41 herds and were daughters of 38 sires. There were 1,491 healthy cows, 134 had only one case of mastitis, 36 had 2 cases, and 14 had between 4 and cases. Overall, mastitis incidence was 0.11. Calving years for these records were from 2000 through 2005. The sire, herd and days in milk are also recorded for each cow.

Format

A data frame with 1675 observations on the following 8 variables.

`id` Identifier of the animal.

`sire` Identifier of the animal's sire.

`birth` year of birth of the animal (as a factor).

`herd` herd id number (as a factor).

`calvingYear` year of calving for this lactation.

`DIM` total number of days in milk for the lactation.

`mastitis` a factor indicating if the cow had any incidents of clinical mastitis during the lactation.

`NCM` An ordered factor giving the number of clinical mastitis cases for the cow during this lactation.

Details

The pedigree of the sires is given in the companion `pedSires` data set.

Source

Vazquez, A.I. 2007. Analysis of number of episodes of clinical mastitis in Norwegian Red and Holstein cows with Poisson and categorical data mixed models. Master of Science Thesis. University of Wisconsin - Madison. 162 pp.

2010. A.I. Vazquez, D.M. Bates, G.J.M. Rosa, D. Gianola and K.A. Weigel. Technical Note: An R package for fitting generalized linear mixed models in animal breeding. Journal of Animal Science, 88:497-504.

References

2010. A.I. Vazquez, D.M. Bates, G.J.M. Rosa, D. Gianola and K.A. Weigel. Technical Note: An R package for fitting generalized linear mixed models in animal breeding. Journal of Animal Science, 88:497-504.

See Also

`pedSires`, `pedigree`

Examples

```
str(mastitis)
summary(mastitis, maxsum = 10)
```

`milk` *Milk production*

Description

Records of the milk production of 3397 lactations from first through fifty parity Holsteins. These were 1,359 cows, daughters of 38 sires in 57 herds. The data was downloaded from the USDA internet site. All lactation records represent cows with at least 100 days in milk, with an average of 347 days. Milk yield ranged from 4,065 to 19,345 kg estimated for 305 days, averaging 11,636 kg. There were 1,314, 1,006, 640, 334 and 103 records were from first thorough fifth lactation animals.

Format

A data frame with 3397 observations on the following 9 variables.

`id`	numeric identifier of cow
`lact`	number of lactation for which production is measured
`herd`	a factor indicating the herd
`sire`	a factor indicating the sire
`dim`	number of days in milk for that lactation
`milk`	milk production estimated at 305 days
`fat`	fat production estimated at 305 days
`prot`	protein production estimated at 305 days
`scs`	the somatic cell score

Source

USDA web site. http://www.aipl.arsusda.gov/

References

2010. A.I. Vazquez, D.M. Bates, G.J.M. Rosa, D. Gianola and K.A. Weigel. Technical Note: An R package for fitting generalized linear mixed models in animal breeding. Journal of Animal Science, 88:497-504.

Examples

```
str(milk)
```

`pedCows` *Pedigree of the cows in milk*

Description

A `pedigree` object giving (part of) the pedigree of the cows in the `milk` data frame.

Format

The format is: Formal class 'pedigree' [package "pedigreemm"] with 3 slots ..@ sire : int [1:6547] NA NA NA NA NA NA NA NA NA NA ... ..@ dam : int [1:6547] NA NA NA NA NA NA NA NA NA NA ... ..@ label: chr [1:6547] "1" "2" "3" "4" ...

References

2010. A.I. Vazquez, D.M. Bates, G.J.M. Rosa, D. Gianola and K.A. Weigel. Technical Note: An R package for fitting generalized linear mixed models in animal breeding. Journal of Animal Science, 88:497-504.

See Also

`milk`

Examples

```
str(pedCows)
```

`pedCowsR` *Pedigree of the cows in milk with 0.70 of the information in pedCows*

Description

A `pedigree` object giving (part of) the pedigree of the cows in the `milk` data frame. This pedigree allows the example with 'milk' to run faster.

Format

The format is: Formal class 'pedigree' [package "pedigreemm"] with 3 slots ..@ sire : int [1:6547] NA NA NA NA NA NA NA NA NA NA ... ..@ dam : int [1:6547] NA NA NA NA NA NA NA NA NA NA ... ..@ label: chr [1:6547] "1" "2" "3" "4" ...

References

2010. A.I. Vazquez, D.M. Bates, G.J.M. Rosa, D. Gianola and K.A. Weigel. Technical Note: An R package for fitting generalized linear mixed models in animal breeding. Journal of Animal Science, 88:497-504.

See Also

`milk`

Examples

```
str(pedCowsR)
```

`pedigree` *Pedigree Constructor*

Description

Construct an object of class `"pedigree"`, more conveniently than by `new("pedigree", ....)`.

Usage

```
pedigree(sire, dam, label)
```

Arguments

`sire`	numeric vector (with some `NA` entries) of integer IDs, denoting a *previous* entry in the pedigree corresponding to the current entry's “father”.
`dam`	similarly as `sire` for the “mother” of each entry.
`label`	a vector coercable to `"character"` of the same length as `sire` and `dam` giving a unique ID for the corresponding entry.

Value

an object of formal class `"pedigree"`.

References

2010. A.I. Vazquez, D.M. Bates, G.J.M. Rosa, D. Gianola and K.A. Weigel. Technical Note: An R package for fitting generalized linear mixed models in animal breeding. Journal of Animal Science, 88:497-504.

See Also

the `pedigree` class.

Examples

```
example("pedigree-class") ## 'p1' pedigree object `the hard way'

ped <- pedigree(sire = c(NA,NA,1, 1,4,5),
                dam  = c(NA,NA,2,NA,3,2), label= 1:6)
## note that 'label' is coerced to character automatically
ped
stopifnot(identical(ped, p1))
```

`pedigree-class` *Class "pedigree"*

Description

Objects of class `"pedigree"` represent a set of individuals that can have two parents including their parent-child relations. The terminology has been taken from cattle breeding. The `"pedinbred"` class is an extension of the pedigree class with an additional slot of the inbreeding coefficients.

Objects from the Class

Objects in the `"pedigree"` class can be created by calls of the form `new("pedigree", ...)`, or more conveniently, `pedigree(sire= ., dam = ., label =.)`.

Objects of the `"pedinbred"` class are created by coercing a pedigree to class `"pedinbred"`.

Slots

`sire`**:** integer vector (with some `NA` entries), denoting a *previous* entry in the pedigree corresponding to the current entry's "father".

`dam`**:** similarly as `sire` for the "mother" of each entry.

`label`**:** a `"character"` vector of the same length as `sire` and `dam` giving a unique ID for the corresponding entry.

`F`**:** (class `"pedinbred"` only) a numeric vector of inbreeding coefficients.

Methods

coerce `signature(from = "pedigree", to = "sparseMatrix")`: returns a sparse, unit lower-triangular matrix which is the inverse of the "L" part of the "LDL'" form of the Cholesky factorization of the relationship matrix. All non-zero elements below the diagonal are -0.5.

coerce `signature(from = "pedigree", to = "data.frame")`: ...

head `signature(x = "pedigree")`: ...

show `signature(object = "pedigree")`: ...

tail `signature(x = "pedigree")`: ...

References

R. A. Mrode, *Linear Models for the Prediction of Animal Breeding Values, 2nd ed*, CABI Publishing, 2005.

2010. A.I. Vazquez, D.M. Bates, G.J.M. Rosa, D. Gianola and K.A. Weigel. Technical Note: An R package for fitting generalized linear mixed models in animal breeding. Journal of Animal Science, 88:497-504.

See Also

`pedigree`, `inbreeding`

Examples

```
## Rather use, pedigree()!   The following is "raw code":
## Example from chapter 2 of Mrode (2005)
p1 <- new("pedigree",
          sire = as.integer(c(NA,NA,1, 1,4,5)),
          dam  = as.integer(c(NA,NA,2,NA,3,2)),
          label = as.character(1:6))
p1
(dtc <- as(p1, "sparseMatrix"))   # T-inverse in Mrode's notation
solve(dtc)
inbreeding(p1)
```

`pedigreemm` *Fit mixed-effects models incorporating pedigrees*

Description

Fit linear or generalized linear mixed models incorporating the effects of a pedigree.

Usage

```
pedigreemm(formula, data, family = NULL, REML = TRUE,
            pedigree = list(), control = list(),
            start = NULL, verbose = FALSE, subset, weights,
            na.action, offset, contrasts = NULL, model = TRUE,
            x = TRUE, ...)
```

Arguments

`pedigree`	a named list of `pedigree` objects. The names must correspond to the names of grouping factors for random-effects terms in the `formula` argument.
`formula`	as in `lmer`
`data`	as in `lmer`
`family`	as in `glmer`
`REML`	as in `lmer`
`control`	as in `lmer`
`start`	as in `lmer`
`verbose`	as in `lmer`
`subset`	as in `lmer`
`weights`	as in `lmer`
`na.action`	as in `lmer`
`offset`	as in `lmer`
`contrasts`	as in `lmer`
`model`	as in `lmer`
`x`	as in `lmer`
`...`	as in `lmer`

Details

All arguments to this function are the same as those to the function `lmer` except `pedigree` which must be a named list of `pedigree` objects. Each name (frequently there is only one) must correspond to the name of a grouping factor in a random-effects term in the `formula`. The observed levels of that factor must be contained in the pedigree. For each pedigree the (left) Cholesky factor of the relationship matrix restricted to the observed levels is calculated using `relfactor` and applied to the model matrix for that term.

Value

a `pedigreemm` object.

References

2010. A.I. Vazquez, D.M. Bates, G.J.M. Rosa, D. Gianola and K.A. Weigel. Technical Note: An R package for fitting generalized linear mixed models in animal breeding. Journal of Animal Science, 88:497-504.

See Also

`pedigreemm`, `pedigree`, `relfactor`.

Examples

```
p1 <- new("pedigree",
         sire = as.integer(c(NA,NA,1, 1,4,5)),
         dam  = as.integer(c(NA,NA,2,NA,3,2)),
         label = as.character(1:6))
A<-getA(p1)
cholA<-chol(A)
varU<-0.4; varE<-0.6; rep<-20
n<-rep*6
set.seed(108)
bStar<- rnorm(6, sd=sqrt(varU))
b<-crossprod(as.matrix(cholA),bStar)
ID <- rep(1:6, each=rep)
e0<-rnorm(n, sd=sqrt(varE))
y<-b[ID]+e0
fm1 <- pedigreemm(y ~ (1|ID) , pedigree = list(ID = p1))
table(y01<-ifelse(y<1.3,0,1))
fm2 <- pedigreemm(y01 ~ (1|ID) , pedigree = list(ID = p1), family = 'binomial')
```

`pedigreemm-class` *Pedigree-based mixed-effects model fits*

Description

A mixed-effects model fit by `pedigreemm`. This class extends class `"merMod"` class and includes one additional slot, `relfac`, which is a list of (left) Cholesky factors of the relationship matrices derived from `"pedigree"` objects.

Objects from the Class

Objects are created by calls to the `pedigreemm` function.

Slots

`relfac`**:** A list of relationship matrix factors. All other slots are inherited from class `"merMod"`.

Extends

Class `"merMod"`, directly.

Methods

fitted `signature(object = "pedigreemm")`: actually a non-method in that `fitted` doesn't apply to such objects because of the pre-whitening.

ranef `signature(object = "pedigreemm")`: incorporates the pedigree into the random effects as returned for the object viewed as a `"merMod)"` object.

residuals `signature(object = "pedigreemm")`: also a non-method for the same reason as `fitted`

See Also

`pedigreemm`

Examples

```
showClass("pedigreemm")
```

`pedSires` *Pedigree of the sires from mastitis*

Description

A `pedigree` object giving (part of) the pedigree of the sires from the `mastitis` data frame. The pedigree is traced back on sires only.

Format

The format is: Formal class 'pedigree' [package "pedigreemm"] with 3 slots ..@ sire : int [1:352] NA NA NA NA NA NA NA NA NA NA ... ..@ dam : int [1:352] NA NA NA NA NA NA NA NA NA NA ... ..@ label: chr [1:352] "1" "2" "3" "4" ...

References

2010. A.I. Vazquez, D.M. Bates, G.J.M. Rosa, D. Gianola and K.A. Weigel. Technical Note: An R package for fitting generalized linear mixed models in animal breeding. Journal of Animal Science, 88:497-504.

See Also

mastitis

Examples

```
str(pedSires)
```

`relfactor` *Relationship factor from a pedigree...*

Description

Relationship factor from a pedigree

Usage

```
relfactor(ped, labs)
```

Arguments

`ped`	a pedigree that includes the individuals who occur in `labs`
`labs`	a character vector or a factor giving the labels to which to restrict the relationship matrix. If `labs` is a factor then the levels of the factor are used as the labels. Default is the complete set of labels in the pedigree.

Details

Determine the right Cholesky factor of the relationship matrix for the pedigree ped, possibly restricted to the specific labels that occur in `labs`.

Value

an upper triangular, sparse (right) Cholesky factor of the relationship matrix

References

2010. A.I. Vazquez, D.M. Bates, G.J.M. Rosa, D. Gianola and K.A. Weigel. Technical Note: An R package for fitting generalized linear mixed models in animal breeding. Journal of Animal Science, 88:497-504.

Examples

```
## Example from chapter 2 of Mrode (2005)

ped <- pedigree(sire = c(NA,NA,1, 1,4,5),
                dam  = c(NA,NA,2,NA,3,2), label= 1:6)
(fac <- relfactor(ped))
crossprod(fac)    # the relationship matrix
getA(ped)         # the relationship matrix
```

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