Package 'nadiv'

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Type Package

Title Constructs non-additive genetic relatedness matrices.

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Depends Matrix, kinship

Description Constructs non-additive genetic relationship matrices from
a pedigree. These and their inverses can be passed to a linear
mixed effect model, known as the 'animal model'.

License GPL (>=2)

LazyLoad yes

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nadiv-package *Creates non-additive relationship matrices and their inverses*

Description

From a supplied pedigree, creates the matrices of dominance and epistatic relatedness. Also, the inverses of these matrices are produced, which is what is needed to estimate these non-additive variance components in a linear mixed effects model (i.e., the 'animal model').

Details

Package:	nadiv
Type:	Package
Version:	2.2
Date:	2011-11-03
License:	GPL (>=2)
LazyLoad:	yes

Author(s)

Matthew Wolak <matthewwolak@gmail.com>

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aiFun *Sampling (co)variances and correlations of random terms*

Description

This function returns the sampling covariances, variances, and correlations of the random effects fitted in an ASReml-R model

Usage

```
aiFun(model, Dimnames = NULL)
```

Arguments

`model`	A model object returned by a call to the `asreml` function.
`Dimnames`	A vector of characters if names are desired for the (co)variance/correlation matrix.

Details

The inverse of the average information provides the sampling (co)variance of each random term in the mixed model. This function extracts the AI matrix from an ASReml-R model and organizes it so that the sampling covariances between random terms are located below the diagonal, the sampling variances of random terms are located along the diagonal, and the sampling correlations between random terms are located above the diagonal. The order of the variances along the diagonal is the same as the order entered in the random section of the `asreml` function. This is the same order as the rows of a call to the summary function, `summary(model)$varcomp`.

Value

A matrix of k x k dimensions is returned, if k is the number of random effects estimated in the model. If `Dimnames` is specified, the row and column names are assigned according the vector of names in the argument.

Note

The vector of `Dimnames` should match the same order of variance components specified in the model (the row order in the `summary(model)$varcomp` object).

Author(s)

`<matthewwolak@gmail.com>`

References

Gilmour, A.R., Gogel, B.J., Cullis, B.R., & Thompson, R. 2009. ASReml User Guide Release 3.0. VSN International Ltd., Hemel Hempstead, UK.

Examples

```
## Not run:
  data(warcolak)
  library(asreml)
  ginvA <- asreml.Ainverse(warcolak)$ginv
  ginvD <- makeD(warcolak[,1:3])$listDinv
  warcolak$IDD <- warcolak$ID
  warcolak.mod <- asreml(phenotype ~ 1, random = ~ped(ID) + giv(IDD), ginverse = list(ID =
  summary(warcolak.mod)$varcomp
  aiFun(warcolak.mod, Dimnames = c("Va", "Vd", "Ve"))

## End(Not run)
```

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choose   *Internal function for* makeDsim

Description

Selects items, given an index and list of choices

Author(s)

<matthewwolak@gmail.com>

IBD   *Identical by descent*

Description

determines if two individuals are IBD, given their genotypes

Usage

```
IBD(pair, genotypes, n)
```

Arguments

pair	which two individuals
genotypes	each individuals' genotype
n	number of individuals in the population to index the second haploid complement of genes

Author(s)

<matthewwolak@gmail.com>

IBD2 *Identity by descent helper function*

Description

applies IBD over a set of pairs

Usage

```
IBD2(pairs, genos, n)
```

Arguments

pairs	see IBD
genos	see IBD
n	see IBD

Author(s)

```
<matthewwolak@gmail.com>
```

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makeA *Creates the additive genetic relationship matrix*

Description

Using a pedigree, this returns the kinship matrix. Note, elements are the coefficient of coancestry, not two times this value. The latter being what is typically used when conducting genetic analysis using the 'animal model'.

Usage

```
makeA(pedigree)
```

Arguments

pedigree	A pedigree where the columns are ordered ID, Dam, Sire

Details

Used as a support function to makeD. Uses the algorithm of Meuwissen and Luo (1992)

Value

Returns A, or the numerator relationship matrix, in sparse matrix form.

Author(s)

<matthewwolak@gmail.com>

References

Meuwissen, T.H.E. & Luo, Z. 1992. Computing inbreeding coefficients in large populations. Genetics, Selection, Evolution 24, 305-313.

See Also

makeD

Examples

```
data(Mrode2)
Mrode2<-Mrode2
makeA(Mrode2)
```

| makeAA | *Creates the additive by additive epistatic genetic relationship matrix* |

Description

Given a pedigree, the matrix of additive by additive genetic relatedness (AA) among all individuals in the pedigree is returned.

Usage

```
makeAA(pedigree)
```

Arguments

pedigree   A pedigree where the columns are ordered ID, Dam, Sire

Details

The function first estimates the A matrix using makeA, then it calculates the Hadamard (element-wise) product of the A matrix with itself (A # A).

Value

AA	the AA matrix in sparse matrix form
logDet	the log determinant of the AA matrix
AAinv	the inverse of the AA matrix in sparse matrix form
listAAinv	the three column form of the non-zero elements for the inverse of the AA matrix

Author(s)

```
<matthewwolak@gmail.com>
```

See Also

makeA

Examples

```
data(Mrode2)
Mrode2 <- Mrode2
AAoutput <- makeAA(Mrode2)
```

| makeD | *Creates the dominance genetic realationship matrix* |

Description

Given a pedigree, the matrix of coefficients of fraternity are returned - the D matrix. Note, no inbreeding must be assumed. Will return the inverse of the D matrix by default, otherwise this operation can be skipped if desired.

Usage

```
makeD(pedigree, invertD = TRUE)
```

Arguments

pedigree	A pedigree with columns organized: ID, Dam, Sire
invertD	A logical indicating whether or not to invert the D matrix

Details

There exists no convenient method of obtaining the inverse of the dominance genetic relatedness matrix (or the D matrix itself) directly from a pedigree (such as for the inverse of A, i.e., Quaas (1995)). Therefore, this function computes the coefficient of fraternity (Lynch and Walsh, 1998) for every individual in the pedigree with a non-zero additive genetic relatedness. Note, the construction of the D matrix is more computationally demanding (in time and space) than is the construction of A.

Value

A	the A matrix in sparse matrix form
D	the D matrix in sparse matrix form
logDet	the log determinant of the D matrix
Dinv	the inverse of the D matrix in sparse matrix form
listDinv	the three column form of the non-zero elements for the inverse of the D matrix

Author(s)

<matthewwolak@gmail.com>

References

Quaas, R.L. 1995. Fx algorithms. An unpublished note.

Lynch M., & Walsh, B. 1998. Genetics and Analysis of Quantitative Traits. Sinauer, Sunderland, Massachusetts.

See Also

makeDsim

Examples

```
data(Mrode9)
Mrode9 <- Mrode9
DinvMat <- makeD(Mrode9)$Dinv
```

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makeDomEpi	*Creates the additive by dominance and dominance by dominance epistatic genetic relationship matrices*

Description

Given a pedigree, the matrix of additive by dominance (AD) genetic relatedness, dominance by dominance (DD) genetic relatedness, or both are returned.

Usage

```
makeDomEpi(pedigree, output = c("AD", "DD", "both"), Dinverse=FALSE)
```

Arguments

pedigree	A pedigree where the columns are ordered ID, Dam, Sire
output	Character(s) denoting which matrix and its inverse is to be constructed.
Dinverse	A logical indicating whether or not to invert the D matrix

Details

Because of the computational demands of constructing the D matrix (see makeD), this function allows for the inverses that are derived from the D matrix (i.e., D-inverse, AD-inverse, and DD-inverse)to be constructed at the same time. This way, the D matrix will only have to be constructed once for use in the three seperate genetic relatedness inverse matrices that depend upon it. However, using the output and Dinverse options in different combinations will ensure that only the desired matrix inverses are constructed.

Both the AD and DD matrix are computed from the Hadamard product of the respective matrices (see also, makeAA).

Value

All of the following will be returned. However, the values of the `output` and `Dinverse` options passed to the function will determine which of the following are not NULL objects within the list:

`D`	the D matrix in sparse matrix form
`logDetD`	the log determinant of the D matrix
`AD`	the AD matrix in sparse matrix form
`logDetAD`	the log determinant of the AD matrix
`DD`	the DD matrix in sparse matrix form
`logDetDD`	the log determinant of the DD matrix
`Dinv`	the inverse of the D matrix in sparse matrix form
`ADinv`	the inverse of the AD matrix in sparse matrix form
`DDinv`	the inverse of the DD matrix in sparse matrix form
`listDinv`	the three column form of the non-zero elements for the inverse of the D matrix
`listADinv`	the three column form of the non-zero elements for the inverse of the AD matrix
`listDDinv`	the three column form of the non-zero elements for the inverse of the DD matrix

Author(s)

`<matthewwolak@gmail.com>`

See Also

makeA, makeD, makeAA

Examples

```
data(Mrode9)
Mrode9 <- Mrode9
Boutput <- makeDomEpi(Mrode9, output = "b", Dinverse = FALSE)
str(Boutput)

DADoutput <- makeDomEpi(Mrode9, output = "AD", Dinverse = TRUE)
str(DADoutput)
```

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makeDsim	*Creates the dominance genetic relationship matrix through simulation*

Description

Given a pedigree, the matrix of coefficients of fraternity are returned - the D matrix - as well as a simulated set of coefficients of fraternity (Ovaskainen et al. 2008).

Usage

```
makeDsim(pedigree, N, invertD = FALSE, calcSE = FALSE)
```

Arguments

pedigree	A pedigree with columns organized: ID, Dam, Sire
N	The number of times to simulate genotypes for the pedigree
invertD	A logical indicating whether or not to invert the D matrix
calcSE	A logical indicating whether or not the standard errors for each coefficient of fraternity should be calculated

Details

Ovaskainen et al. (2008) indicated that the method of calculating the D matrix (see makeD) is only an approximation. They proposed a simulation method that is implemented here. This should be more appropriate when inbreeding occurs in the pedigree.

The value, listDsim will list both the approximate values (returned from makeD) as well as the simulated values. If calcSE is TRUE, these values will be listed in listDsim.

Value

A	the A matrix in sparse matrix form
D	the approximate D matrix in sparse matrix form
logDetD	the log determinant of the approximate D matrix
Dinv	the inverse of the approximate D matrix in sparse matrix form
listDinv	the three column form of the non-zero elements for the inverse of the approximate D matrix
Dsim	the simulated D matrix in sparse matrix form
logDetDsim	the log determinant of the simulated D matrix
Dsiminv	the inverse of the simulated D matrix in sparse matrix form
listDsim	the three column form of the non-zero and non-self elements for the simulated D matrix
listDsiminv	the three column form of the non-zero elements for the inverse of the simulated D matrix

Note

This simulation can take a long time for large values of N. If unsure, it is advisable to start with a lower N and gradually increase to gain a sense of the time required to execute a desired N.

Author(s)

```
<matthewwolak@gmail.com>
```

References

Ovaskainen, O., Cano, J.M., & Merila, J. 2008. A Bayesian framework for comparative quantitative genetics. Proceedings of the Royal Society B 275, 669-678.

See Also

makeD

Examples

```
data(Mrode9)
Mrode9 <- Mrode9
simDinvMat <- makeDsim(Mrode9, N = 1000, invertD = FALSE, calcSE = TRUE)$listDsim
```

Mrode2   *Pedigree from Table 2.1 of Mrode (2005)*

Description

An example pedigree

Usage

```
data(Mrode2)
```

Format

A data frame with 6 observations on the following 3 variables.

id a numeric vector

dam a numeric vector

sire a numeric vector

Source

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

Mrode9   *Pedigree, adapted from example 9.1 of Mrode (2005)*

Description

An example pedigree

Usage

```
data(Mrode9)
```

Format

A data frame with 12 observations on the following 3 variables.

pig a numeric vector

dam a numeric vector

sire a numeric vector

Source

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

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numPed   *Creates a numeric form of a pedigree*

Description

This function takes a pedigree and converts it into a standard integer form used by many functions in the 'nadiv' package.

Usage

```
numPed(pedigree)
```

Arguments

pedigree   A three column pedigree object, where the columns correspond to: ID, Dam, &
             Sire

Details

individuals must appear in the ID column in rows preceeding where they appear in either the Dam or Sire column.

Value

The pedigree, where individuals are now numbered from 1 to n and unknown parents are assigned at value of '-998'.

Author(s)

<matthewwolak@gmail.com>

| SEfun | *Estimate of the standard error for a simulated coefficient of fraternity* |

Description

The standard error for coefficients of fraternity that are derived from simulation ([makeDsim](#)) as described in the appendix to Ovaskainen et al. (2008).

Usage

```
SEfun(coef.frat, N)
```

Arguments

coef.frat	the simulated coefficient of fraternity
N	the number of times the simulation was conducted

Author(s)

<matthewwolak@gmail.com>

References

Ovaskainen, O., Cano, J.M., & Merila, J. 2008. A Bayesian framework for comparative quantitative genetics. Proceedings of the Royal Society B 275, 669-678.

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sm2list   *Converts a sparse matrix into a three column format.*

Description

From a sparse matrix object, the three column, row ordered lower triangle of non-zero elemetns is created. Mostly used within other functions (i.e., `makeD`)

Usage

```
sm2list(A = NULL, rownames = NULL, colnames = c("row", "column", "A"))
```

Arguments

A   a sparse matrix

rownames   a list of rownames from the 'A' matrix.

colnames   the columns will be labelled however they are entered in this character vector

Details

The sparse matrix and three column format must fit CERTAIN assumptions about row/column sorting and lower/upper triangle matrix.

Value

returns the list form of the sparse matrix as a `data.frame`

Author(s)

`<matthewwolak@gmail.com>`

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vchoose   *Helper function for another internal function in* `makeDsim`

Description

Selects items, given indices and a list of choices

Author(s)

`<matthewwolak@gmail.com>`

warcolak	*Pedigree and phenotypic values for a mythical half-sib population of Warcolaks*

Description

An example pedigree with phenotypic data constructed from simulated additive, dominance, and environmental effects.

Usage

```
data(warcolak)
```

Format

A data frame with 480 observations on the following 4 variables.

ID a factor specifying 480 unique individual IDs

Dam a factor specifying the unique ID for each of 3 dams per sire

Sire a factor specifying the unique ID for all 30 sires

phenotype a numeric vector of phenotypic values

Details

The dataset was simulated to have a population mean of 50 (with no other fixed effects) and additive, dominance, and environmental variances of 40, 30, & 30, respectively. The random effects were drawn from a multivariate random normal distribution [e.g., additive effects: $N \sim (0, A * Va)$] with means of zero and variances equal to the product of the desired additive genetic variance and the additive genetic relatedness matrix. Because of this, the actual variance in random effects will vary slightly from the amount specified in the simulation (i.e., 40, 30, & 30)

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