

Package ‘AGHmatrix’

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Title Relationship Matrices for Diploid and Autopolyploid Species

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Description Computation of A (pedigree), G (genomic-base), and H (A corrected by G) relationship matrices for diploid and autopolyploid species. Several methods are implemented considering additive and non-additive models.

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Suggests knitr, MASS, rmarkdown

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License GPL-3

URL <http://github.com/prmunoz/AGHmatrix>

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Amatrix

Construction of Relationship Matrix A

Description

Creates a additive relationship matrix *A* from a pedigree data in a 3-column way format based on ploidy level (an even number) and, if ploidy equals 4, based on proportion of parental gametes that are IBD (Identical by Descent) due to double reduction. Returns a dominance relationship matrix if dominance true (ploidy 2 only). Autopolyploid matrices based on Kerr (2012). Construction is based on the Henderson's recursive method described in Mrode (2005).

Usage

```
Amatrix(data = NULL, ploidy = 2, w = 0, verify = TRUE,
        dominance = FALSE, slater = FALSE, ...)
```

Arguments

<code>data</code>	pedigree data name (3-column way format). Unknown value should be equal 0.
<code>ploidy</code>	an even number (default=2).
<code>w</code>	proportion of parental gametas IBD due to double reduction (default=0), only if ploidy=4.
<code>verify</code>	verifies pedigree file for conflictuos entries (default=TRUE).
<code>dominance</code>	if true, returns the dominance relationship matrix
<code>slater</code>	if true, returns the additive autotetraploid relationship matrix as Slater (2013)
<code>...</code>	arguments to be passed to <code>datatreat()</code>

Value

Matrix with the Relationship between the individuals.

Author(s)

Rodrigo R Amadeu, <rramadeu@gmail.com>

References

Chapter 2: Genetic Covariance Between Relatives and Chapter 9: Non-additive Animal Models in Mrode, R. A., and Thompson, R. Linear models for the prediction of animal breeding values. Cabi, 2005.

Slater, A. T., Wilson, G. M., Cogan, N. O., Forster, J. W., & Hayes, B. J. (2013). Improving the analysis of low heritability complex traits for enhanced genetic gain in potato. Theoretical and Applied Genetics, 1-12.

Kerr, Richard J., et al. "Use of the numerator relationship matrix in genetic analysis of autopolyploid species." Theoretical and Applied Genetics 124.7 (2012): 1271-1282.

Examples

```
data(ped.mrode)
#Computing additive relationship matrix considering diploidy
Amatrix(ped.mrode, ploidy=2)
#Computing non-additive relationship matrix considering diploidy:
Amatrix(ped.mrode, ploidy=2, dominance=TRUE)
#Computing additive relationship matrix considering autotetraploidy:
Amatrix(ped.mrode, ploidy=4)
#Computing additive relationship matrix considering autooctaploidy:
Amatrix(ped.mrode, ploidy=8)
#Computing additive relationship matrix considering autotetraploidy and double-reduction of
Amatrix(ped.mrode, ploidy=4, w=0.1)
#Computing additive relationship matrix considering
#autotetraploidy and double-reduction of 10% as Slater et al. (2014):
Amatrix(ped.mrode, ploidy=4, w=0.1, slater = TRUE)
#Computing additive relationship matrix considering autohexaploidy and double-reduction of 1
Amatrix(ped.mrode, ploidy=6, w=0.1)
```

datatreat

Organizes pedigree data in a chronological way

Description

This function organizes pedigree data in a chronological way and return 3 lists: i) parental 1 values (numeric); ii) parental 2 values (numeric); iii) real names of the individuals. Also save a .txt file with new pedigree file.

Usage

```
datatreat(data = NULL, n.max = 50, unk = 0, save = FALSE)
```

Arguments

data	name of the pedigree data frame. Default=NULL.
n.max	max number of iterations to get the chronological order. Default = 50
unk	the code of the data missing. Default=0.
save	if TRUE, save the genealogy in a .txt file

Value

list with parental 1, parental 2, and real names of the individuals (key) also saves a txt file with the new chronological pedigree.

Author(s)

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Examples

```
data(ped.mrode)
datatreat(ped.mrode)
```

formatmatrix	<i>Transform a matrix in 3 columns</i>
--------------	--

Description

Given any square matrix transform it in a 3 columns way (row, column, value) mainly to be used in outsourcing data processing (as ASREML-standalone)

Usage

```
formatmatrix(data = NULL, save = TRUE, return = FALSE,
             name = deparse(substitute(data)), round.by = 12, exclude.0 = TRUE)
```

Arguments

data	matrix (nxn).
save	if TRUE save the output in a file. Default=TRUE.
return	if TRUE return the output in a object. Default=FALSE.
name	name of the csv file to be saved. Default=data name.
round.by	select the number of digits after 0 you want in your data. Default = 12
exclude.0	if TRUE, remove all lines equal to zero (ASREML option). Default = TRUE

Value

a object or a csv file with a table with 3 columns representing the matrix.

Author(s)

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Examples

```

#Example with random matrix
data<-matrix(c(1,0.1,0,0.1,1,0,0,0,1.1),3)
formatmatrix(data=data,save=FALSE,return=TRUE,exclude.0=TRUE)

#Example with pedigree matrix
#Reading the example data
data(ped.mrode)
#Making Relationship Matrix
Amrode<-Amatrix(ped.mrode)
#Inverting the Matrix
Amrode.inv<-solve(Amrode)
#Making the 3 columns format
Amrode.inv.ASREML<-formatmatrix(Amrode,save=FALSE,return=TRUE,exclude.0=TRUE)
#Printing it
Amrode.inv.ASREML

```

Gmatrix

*Construction of Relationship Matrix G***Description**

Given a matrix (individual x markers), a method, a missing value, and a maf threshold, return a additive or non-additive relationship matrix. For diploids, the methods "Yang" and "VanRaden" for additive relationship matrices, and "Su" and "Vitezica" for non-additive relationship matrices are implemented. For autopolyploids, the method "VanRaden" for additive relationship, method "Slater" for full-autopolyploid model including non-additive effects, and pseudo-diploid parametrization are implemented.

Usage

```

Gmatrix(SNPmatrix = NULL, method = "VanRaden", missingValue = -9,
  maf = 0, thresh.missing = 1, verify.posdef = FALSE, ploidy = 2,
  pseudo.diploid = FALSE, integer = TRUE, ratio = FALSE,
  impute.method = FALSE, ratio.check = TRUE)

```

Arguments

SNPmatrix	matrix (n x m), where n is individual names and m is marker names (coded inside the matrix as 0, 1, 2, ..., ploidy, and, missingValue).
method	"Yang" or "VanRaden" for marker-based additive relationship matrix. "Su" or "Vitezica" for marker-based dominance relationship matrix. "Slater" for full-autopolyploid model including non-additive effects. "Endelman" for autotetraploid dominant (digentic) relationship matrix. "MarkersMatrix" for a matrix with the amount of shared markers between individuals (3). Default is "VanRaden", for autopolyploids will be computed a scaled product (similar to Covarrubias-Pazaran, 2006).

missingValue missing value in data. Default=-9.

maf max of missing data accepted to each marker. Default=0.05.

thresh.missing threshold on missing data, SNPs below of this frequency value will be maintained, if equal to 1, no threshold and imputation is considered. Default = 1.

verify.posdef verify if the resulting matrix is positive-definite. Default=FALSE.

ploidy data ploidy (an even number between 2 and 20). Default=2.

pseudo.diploid if TRUE, uses pseudodiploid parametrization of Slater (2016).

integer if FALSE, not check for integer numbers. Default=TRUE.

ratio if TRUE, molecular data are considered ratios and its computed the scaled product of the matrix (as in "VanRaden" method).

impute.method FALSE to not impute missing data, "mean" to impute the missing data by the mean, "mode" to impute the missing data by the mode. Default = FALSE.

ratio.check if TRUE, run snp.check with ratio data.

Value

Matrix with the marker-bases relationships between the individuals

Author(s)

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References

- Covarrubias-Pazarán G., 2016. *Genome assisted prediction of quantitative traits using the R package sommer*. *PLoS ONE* 11(6):1-15.
- Slater, A.T., et al., 2016. *Improving genetic gain with genomic selection in autotetraploid potato*. *The Plant Genome* 9(3), pp.1-15.
- Su, G., et al., 2012. *Estimating additive and non-additive genetic variances and predicting genetic merits using genome-wide dense single nucleotide polymorphism markers*. *PloS one*, 7(9), p.e45293.
- VanRaden, P.M., 2008. *Efficient methods to compute genomic predictions*. *Journal of dairy science*, 91(11), pp.4414-4423.
- Vitezica, Z.G., Varona, L. and Legarra, A., 2013. *On the additive and dominant variance and covariance of individuals within the genomic selection scope*. *Genetics*, 195(4), pp.1223-1230.
- Yang, J., et al., 2010. *Common SNPs explain a large proportion of the heritability for human height*. *Nature genetics*, 42(7), pp.565-569.
- Endelman, J. B., et al., 2018. *Genetic variance partitioning and genome-wide prediction with allele dosage information in autotetraploid potato*. *Genetics*, 209(1) pp. 77-87.

Examples

```
## Not run:
## Diploid Example
data(snp.pine)
#Verifying if data is coded as 0,1,2 and missing value.
str(snp.pine)
#Build G matrices
Gmatrix.Yang <- Gmatrix(snp.pine, method="Yang", missingValue=-9, maf=0.05)
Gmatrix.VanRaden <- Gmatrix(snp.pine, method="VanRaden", missingValue=-9, maf=0.05)
Gmatrix.Su <- Gmatrix(snp.pine, method="Su", missingValue=-9, maf=0.05)
Gmatrix.Vitezica <- Gmatrix(snp.pine, method="Vitezica", missingValue=-9, maf=0.05)

## Autetraploid example
#Generating fake data
data(snp.sol)
#Build G matrices
Gmatrix.VanRaden <- Gmatrix(snp.sol, method="VanRaden", ploidy=4)
Gmatrix.Endelman <- Gmatrix(snp.sol, method="Endelman", ploidy=4)
Gmatrix.Slater <- Gmatrix(snp.sol, method="Slater", ploidy=4)
Gmatrix.Pseudodiploid <- Gmatrix(snp.sol, method="VanRaden", ploidy=4, pseudo.diploid=TRUE)

## End(Not run)
```

Hmatrix

Construction of Combined Relationship Matrix H

Description

Given a matrix A and a matrix G returns a H matrix.

Usage

```
Hmatrix(A = NULL, G = NULL, markers = NULL, c = 0,
        method = "Martini", tau = 1, omega = 1, missingValue = -9,
        maf = 0, ploidy = 2, roundVar = 3)
```

Arguments

A	A matrix from function Amatrix
G	G matrix from function Gmatrix
markers	matrix marker which generated the Gmatrix
c	constant value of H computation, default: c=0
method	"Martini" or "Munoz", default="Martini"
tau	to be used for Martini's method, default=1.
omega	to be used of Martini's method, default=1.

missingValue missing value in data, default=-9.
 maf max of missing data accepted to each marker default=0.05.
 ploidy data ploidy (an even number between 2 and 20), default=2.
 roundVar Munoz's method, how many digits to consider the relationship be of same class, default=2.

Value

H Matrix with the relationship between the individuals based on pedigree and corrected by molecular information

Author(s)

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References

Munoz, P. R., Resende, M. F. R., Gezan, S. A., Resende, M. D. V., de los Campos, G., Kirst, M., Huber, D., Peter, G. F. (2014). *Unraveling additive from nonadditive effects using genomic relationship matrices. Genetics*, 198.4: 1759-1768.

Martini, J. W., Schrauf, M. F., Garcia-Baccino, C. A., Pimentel, E. C., Munilla, S., Rogberg-Munoz, A., ... & Simianer, H. (2018). *The effect of the H-1 scaling factors tau and omega on the structure of H in the single-step procedure. Genetics Selection Evolution*, 50(1), 16.

Examples

```
## Not run:
data(ped.sol)
data(snp.sol)
#Computing the numerator relationship matrix 10% of double-reduction
Amat <- Amatrix(ped.sol, ploidy=4, w = 0.1)
#Computing the additive relationship matrix based on VanRaden (modified)
Gmat <- Gmatrix(snp.sol, ploidy=4, missingValue=-9,
               maf=0.05, method="VanRaden")
#Computing H matrix (Martini)
Hmat_Martini <- Hmatrix(A=Amat, G=Gmat, method="Martini",
                      ploidy=4, missingValue=-9, maf=0.05)
#Computing H matrix (Munoz)
Hmat_Munoz <- Hmatrix(A=Amat, G=Gmat, markers = snp.sol,
                    ploidy=4, method="Munoz",
                    roundVar=2,
                    missingValue=-9, maf=0.05)

## End(Not run)
```

missingdata	<i>Surviving on missing data</i>
-------------	----------------------------------

Description

This function verify which rows in a pedigree data has missing parental or conflictuos data

Usage

```
missingdata(data, unk = 0)
```

Arguments

data	data name from a pedigree list
unk	unknown value of your data

Value

list with \$conflict: rows of the data which are at least one parental name equal to the individual. \$missing.sire: rows of the data which arie missing data sire (Parental 1) information. \$missing.dire: same as above for dire (Parental 2). \$summary.missing: summary of the missing data. 2 columns, 1st for the name of the parental listed, 2nd for the how many times appeared in the data.

Author(s)

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Examples

```
data(ped.mrode)
missingdata(ped.mrode)
```

ped.mrode	<i>Pedigree Data</i>
-----------	----------------------

Description

Data from pedigree example proposed by Mrode 2005

Usage

```
data(ped.mrode)
```

Format

table

References

R. A. Mrode, R. Thompson. Linear Models for the Prediction of Animal Breeding Values. CABI, 2005.

Examples

```
data(ped.mrode)
```

```
ped.sol
```

Pedigree data for autopolyploid examples

Description

Dataset extract from supplementary material from Endelman et al. (2018). Pedigree data frame of Potato population, missing data as 0.

Usage

```
data(ped.sol)
```

Format

```
data.frame
```

References

Endelman, JB, et al., 2018 Genetic variance partitioning and genome-wide prediction with allele dosage information in autotetraploid potato. *Genetics*, 209(1) pp. 77-87.

Examples

```
data(ped.sol)
```

`snp.pine`*Molecular data for diploid examples*

Description

Dataset extract from supplementary material from Resende et al. (2012). SNP marker matrix from Pine tree coded as 0,1, and 2, and missing value as -9.

Usage

```
data(snp.pine)
```

Format

```
matrix
```

References

Resende, MF, et al., 2012 Accuracy of genomic selection methods in a standard data set of loblolly pine (*Pinus taeda* L.). *Genetics* 190: 1503–1510.

Examples

```
data(snp.pine)
```

`snp.sol`*Molecular data for autopolyploid examples*

Description

Dataset extract from supplementary material from Endelman et al. (2018). SNP marker matrix from Pine tree coded as 0,1,2,3,4 and missing value as -9.

Usage

```
data(snp.sol)
```

Format

```
data.frame
```

References

Endelman, JB, et al., 2018 Genetic variance partitioning and genome-wide prediction with allele dosage information in autotetraploid potato. *Genetics*, 209(1) pp. 77-87.

Examples

```
data(snp.sol)
```