Package 'GeneticsPed'

May 29, 2024

Title Pedigree and genetic relationship functions

Description Classes and methods for handling pedigree data. It also includes functions to calculate genetic relationship measures as relationship and inbreeding coefficients and other utilities. Note that package is not yet stable. Use it with care!

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biocViews Genetics

Version 1.66.0

Depends R (>= 2.4.0), MASS

Imports gdata, genetics

Date 2007-09-20

Suggests RUnit, gtools

git_url https://git.bioconductor.org/packages/GeneticsPed

git_branch RELEASE_3_19

git_last_commit 59c71e1

git_last_commit_date 2024-04-30

Repository Bioconductor 3.19

Date/Publication 2024-05-29

Contents

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check *Check consistency of data in pedigree*

Description

check performs a series of checks on pedigree object to ensure consistency of data.

Usage

```
check(x, ...)
checkId(x)
```

Arguments

x	pedigree, object to be checked
...	arguments to other methods, none for now

Details

checkId performs various checks on individuals and their ascendants. These checks are:

- idClass: all ids must have the same class
- idIsNA: individual can not be NA
- idNotUnique: individual must be unique
- idEqualAscendant: individual can not be equal to its ascendant
- ascendantEqualAscendant: ascendant can not be equal to another ascendant

- ascendantInAscendant: ascendant can not appear again as asescendant of other sex i.e. father can not be a mother to someone else
- unusedLevels: in case factors are used for id presentation, there might be unused levels for some ids - some functions rely on number of levels and a check is provided for this

`checkAttributes` is intended primarly for internal use and performs a series of checks on attribute values needed in various functions. It causes stop with error messages for all given attribute checks.

Value

List of more or less self-explanatory errors and "pointers" to these errors for ease of further work i.e. removing errors.

Author(s)

Gregor Gorjanc

See Also

Pedigree

Examples

```
## EXAMPLES BELLOW ARE ONLY FOR TESTING PURPOSES AND ARE NOT INTENDED
## FOR USERS, BUT IT CAN NOT DO ANY HARM.

## --- checkAttributes ---
tmp <- generatePedigree(5)
attr(tmp, "sorted") <- FALSE
attr(tmp, "coded") <- FALSE
GeneticsPed:::checkAttributes(tmp)
try(GeneticsPed:::checkAttributes(tmp, sorted=TRUE, coded=TRUE))

## --- idClass ---
tmp <- generatePedigree(5)
tmp$id <- factor(tmp$id)
class(tmp$id)
class(tmp$father)
try(GeneticsPed:::idClass(tmp))

## --- idIsNA ---
tmp <- generatePedigree(2)
tmp[1, 1] <- NA
GeneticsPed:::idIsNA(tmp)

## --- idNotUnique ---
tmp <- generatePedigree(2)
tmp[2, 1] <- 1
GeneticsPed:::idNotUnique(tmp)

## --- idEqualAscendant ---
tmp <- generatePedigree(2)
```

```
tmp[3, 2] <- tmp[3, 1]
GeneticsPed:::idEqualAscendant(tmp)

## --- ascendantEqualAscendant ---
tmp <- generatePedigree(2)
tmp[3, 2] <- tmp[3, 3]
GeneticsPed:::ascendantEqualAscendant(tmp)

## --- ascendantInAscendant ---
tmp <- generatePedigree(2)
tmp[3, 2] <- tmp[5, 3]
GeneticsPed:::ascendantInAscendant(tmp)
## Example with multiple parents
tmp <- data.frame(id=c("A", "B", "C", "D"),
                  father1=c("E", NA, "F", "H"),
                  father2=c("F", "E", "E", "I"),
                  mother=c("G", NA, "H", "E"))
tmp <- Pedigree(tmp, ascendant=c("father1", "father2", "mother"),
                ascendantSex=c(1, 1, 2),
                ascendantLevel=c(1, 1, 1))
GeneticsPed:::ascendantInAscendant(tmp)

## --- unusedLevels ---
tmp <- generatePedigree(2, colClass="factor")
tmp[3:4, 2] <- NA
GeneticsPed:::unusedLevels(tmp)
```

`extend` *Extend pedigree*

Description

`extend` finds ascendants, which do not appear as individuals in pedigree and assigns them as individuals with unknown ascendants in extended pedigree.

Usage

```
extend(x, ascendant=NULL, col=NULL, top=TRUE)
```

Arguments

`x`	pedigree object
`ascendant`	character, column names of ascendant(s), see details
`col`	character, column name(s) of attribute(s), see details
`top`	logical, add ascendants as individuals on the top or bottom of the pedigree

Details

Argument `ascendant` can be used to define, which ascendants will be extended. If `ascendant=NULL`, which is the default, all ascendant columns in the pedigree are used. The same approach is used with other pedigree attributes such as sex, generation, etc. with argument `col`. Use `col=NA`, if none of the pedigree attributes should be extended.

Sex of "new" individuals is infered from attribute `ascendantSex` as used in `Pedigree` function. Generation of "new" individuals is infered as minimal (`generationOrder="increasing"`) or maximal (`generationOrder="decreasing"`) generation value in descendants - 1. See `Pedigree` on this issue. Family values are extended with means of `family`.

Value

Extended pedigree, where all ascendants also appear as individuals with unknown ascendants and infered other attributes such as sex, generation, etc. if this attributes are in the pedigree.

Author(s)

Gregor Gorjanc

See Also

`Pedigree`, `family`, geneticGroups???

Examples

```
# --- Toy example ---
ped <- generatePedigree(nId=5, nGeneration=4, nFather=1, nMother=2)
ped <- ped[10:20,]
ped[5, "father"] <- NA # to test robustnes of extend on NA
extend(ped)
extend(ped, top=FALSE)

## Extend only ascendant and their generation
extend(ped, col="generation")
extend(ped, col=c("generation", "sex"))

# --- Bigger example ---
ped <- generatePedigree(nId=1000, nGeneration=10, nFather=100,
                        nMother=500)
nrow(ped)
# Now keep some random individuals
ped <- ped[unique(sort(round(runif(n=nrow(ped)/2, min=1,
                                   max=nrow(ped))))), ]
nrow(ped)
nrow(extend(ped))
```

`family` *Find families (lines) in the pedigree*

Description

`family` classifies individuals in the pedigree to distinct families or lines. Two individuals are members of one family if they have at least one common ascendant. `family<-` provides mean to properly add family information into the pedigree.

Usage

```
family(x)
family(x, col=NULL) <- value
```

Arguments

`x`	pedigree object
`col`	character, column name in `x` for family
`value`	family values for individuals in the pedigree

Details

`col` provides a mean to name or possibly also rename family column with user specified value, say "familia" in Spanish. When `col=NULL`, which is default, "family" is used.

Value

A vector of family values (integers)

Author(s)

Gregor Gorjanc

See Also

`Pedigree`

Examples

```
## Two families examples
ped <- data.frame(    id=c(1, 2, 3, 4, 5, 6, 7, 8, 9, 10, 11),
                  father=c(0, 0, 0, 0, 0, 0, 5, 1, 3,  8,  7),
                  mother=c(0, 0, 0, 0, 0, 0, 6, 2, 4,  9, 10),
              generation=c(1, 1, 1, 1, 1, 1, 2, 2, 2,  3,  4))
ped <- Pedigree(ped, unknown=0, generation="generation")
family(ped)

## After break we get two families
```

```
ped1 <- removeIndividual(ped, individual=11)
family(ped1)

## Subsetting can also be used
family(ped[1:10,])
family(ped[7:10,])

## Pedigree need not be sorted in advance
ped2 <- ped[sample(1:10), ]
family(ped2)

## Assign family values to pedigree
family(ped) <- family(ped)
ped
family(ped, col="familia") <- family(ped)
ped
```

`geneContribution` *Gene contribution or proportion of genes in pedigree by individual*

Description

`geneContribution` calculates gene contribution as proportion of genes in pedigree by individual with higher number of descendants will have higher values.

Usage

```
geneContribution(x, relative=TRUE)
```

Arguments

`x`	pedigree
`relative`	logical, should results be presented relative to number of individuals in the pedigree

Value

Gene contribution values i.e. higher the values higher the contribution of genes by particular individual in the pedigree. When `relative=FALSE`, values represent number of individuals (in conceptually additive manner i.e. 0.5 + 0.75 = 1.25 individual) in the pedigree that carry genes of a particular individual. With `relative=TRUE`, values represent the same result as ratios to all individuals in the pedigree. Value 0 indicates that individual did not pass its genes to next generations.

Author(s)

Gregor Gorjanc

See Also

Pedigree

Examples

```
ped <- generatePedigree(nId=5, nGeneration=4, nFather=1, nMother=2)
geneContribution(ped)
geneContribution(ped, relative=FALSE)
## geneContribution(ped[5:15, ]) ## needs [ method

## More than one father example
ped <- data.frame(     id=c(1, 2, 3, 4, 5, 6, 7),
                  father1=c(0, 0, 0, 2, 1, 1, 2),
                  father2=c(0, 0, 0, 0, 0, 2, 0),
                   mother=c(0, 0, 0, 0, 3, 3, 3),
                  generat=c(1, 1, 1, 2, 2, 2, 2))
ped <- Pedigree(ped, ascendant=c("father1", "father2", "mother"),
                ascendantSex=c(1, 1, 2), ascendantLevel=c(1, 1, 1),
                unknown=0, generation="generat")
geneContribution(ped)
```

---

geneFlowT *Gene and gamete flow matrices*

Description

geneFlowT and geneFlowTinv creates gene flow matrix (T) and its inverse (Tinv), while gameteFlowM creates gamete flow matrix (M). mendelianSamplingD creates a mendelian sampling covariance matrix (D).

Usage

```
geneFlowT(x, sort=TRUE, names=TRUE, ...)
geneFlowTinv(x, sort=TRUE, names=TRUE, ...)
gameteFlowM(x, sort=TRUE, names=TRUE, ...)
mendelianSamplingD(x, matrix=TRUE, names=TRUE, ...)
```

Arguments

x	Pedigree
sort	logical, for the computation the pedigree needs to be sorted, but results are sorted back to original sorting (sort=TRUE) or not (sort=FALSE)
names	logical, should returned matrix have row/colnames; this can be used to get leaner matrix
matrix	logical, should returned value be a diagonal matrix or a vector
...	arguments for other methods

Details

geneFlowT returns a matrix with coefficients that show the flow of genes from one generation to the next one etc. geneFlowTinv is simply the inverse of geneFlowT, but calculated as $I - M$, where M is gamete flow matrix with coefficients that represent parent gamete contribution to their offspring. mendelianSamplingD is another matrix (D) for construction of relationship additive matrix via decomposition i.e. $A = TDT'$ (Henderson, 1976). Mrode (2005) has a very nice introduction to these concepts.

Take care with sort=FALSE, names=FALSE. It is your own responsibility to assure proper handling in this case.

Value

Matrices of $n * n$ dimension, with coeficients as described in the details, where n is number of subjects in x

Author(s)

Gregor Gorjanc

References

Henderson, C. R. (1976) A simple method for computing the inverse of a numerator relationship matrix used in prediction of breeding values. *Biometrics* **32**(1):69-83

Mrode, R. A. (2005) Linear models for the prediction of animal breeding values. 2nd edition. CAB International. ISBN 0-85199-000-2 http://www.amazon.com/gp/product/0851990002

See Also

Pedigree, relationshipAdditive, kinship and inbreeding

Examples

```
if(require(gdata))
  data(Mrode2.1)
  Mrode2.1$dtB <- as.Date(Mrode2.1$dtB)
  x2.1 <- Pedigree(x=Mrode2.1, subject="sub", ascendant=c("fat", "mot"),
                   ascendantSex=c("M", "F"), family="fam", sex="sex",
                   generation="gen", dtBirth="dtB")

  fractions(geneFlowT(x2.1))
  fractions(geneFlowTinv(x2.1))
  fractions(gameteFlowM(x2.1))
  mendelianSamplingD(x2.1)
```

`generatePedigree` *Generate Pedigree example*

Description

`generatePedigree` creates nonoverlapping pedigree example, which can be used for demos and code testing.

Usage

```
generatePedigree(nId, nGeneration=3, nFather=round(nId/3),
  nMother=nId - nFather, start=1, generationOrder="increasing",
  colClass="integer")
```

Arguments

`nId`	integer, number of individuals per generation, at least 2
`nGeneration`	integer, number of generations
`nFather`	integer, number of fathers per generation
`nMother`	integer, number of mothers per generation
`start`	first generation value
`generationOrder`	character, generation value is "increasing" or "decreasing" through generations
`colClass`	character, class for columns: "integer" or "factor"

Value

An extended, sorted and possibly coded pedigree object with following columns: id, father, mother, generation and sex.

Author(s)

Marcos Rico Gutierrez (author of MATLAB code) and Gregor Gorjanc (R implementation)

References

Rico Gutierrez, M. (1999) Los modelos lineales en la mejora genetica animal. Ediciones Peninsular. ISBN 84-605-9910-8.

See Also

`Pedigree`

Examples

```
generatePedigree(5)
generatePedigree(nId=5, nGeneration=4, nFather=1, nMother=2)
generatePedigree(nId=5, nGeneration=4, nFather=1, nMother=2,
                 start=0, generationOrder="decreasing")
generatePedigree(nId=100, nGeneration=20, nFather=10, nMother=50)
```

`generation` *Calculate generation value*

Description

`generation` calculates generation value of individuals in given pedigree. `generation<-` provides a way to properly add generation information into the pedigree.

Usage

```
generation(x, start=1, generationOrder=NULL)
generation(x, generationOrder=NULL, col=NULL) <- value
```

Arguments

`x`	pedigree object
`start`	first generation value
`generationOrder`	character, should be generation values "increasing" or "decreasing" through generations, see details
`col`	character, column name in `x` for generation
`value`	generation values for individuals in the pedigree

Details

Generation value for founders is set to value `start`, which is by default 1, while other individuals get it according to:

$$G_s = max(G_{1a} + G_{2a} + ...G_{na}) + 1$$

where G represents generation value for s - individual, a - ascendant e.g. father and mother, where n=2. N might be higher if there are multiple ascendants i.e. this function can also handle pedigrees with higher order ascendants e.g. grandfather.

`generationOrder` can be used to define "increasing" or "decreasing" order of generation values. If this argument is `NULL`, which is default, then this information is taken from the pedigree - see `Pedigree` for more on this issue.

`col` provides a way to name or possibly also rename generation column with user specified value, say "generazione" in Italian. When `col=NULL`, which is default, "generation" is used.

Value

A vector of generation values (integers)

Author(s)

Gregor Gorjanc

See Also

Pedigree

Examples

```
# Nonoverlapping pedigree
ped <- generatePedigree(nId=5, nGeneration=4, nFather=1, nMother=2)
ped$generation1 <- generation(ped)
ped

# Overlapping Pedigree
ped <- data.frame(     id=c(1, 2, 3, 4, 5, 6, 7),
                   father=c(0, 0, 2, 2, 2, 4, 4),
                   mother=c(0, 0, 1, 0, 3, 3, 5),
                  dtBirth=c(2, 1, 3, 4, 5, 6, 7))
ped <- Pedigree(ped, unknown=0, dtBirth="dtBirth")
generation(ped) <- generation(ped)

# Overlapping pedigree + one individual (4) comes late in pedigree and
# has no ascendants
ped <- data.frame(     id=c(1, 2, 3, 4, 5, 6, 7),
                   father=c(0, 0, 2, 0, 2, 4, 4),
                   mother=c(0, 0, 1, 0, 3, 3, 5),
                  dtBirth=c(2, 1, 3, 2, 5, 6, 7))
ped <- Pedigree(ped, unknown=0, dtBirth="dtBirth")
generation(ped)
generation(ped, generationOrder="decreasing",
           col="generazione") <- generation(ped, generationOrder="decreasing")
```

---

gpi *Genotype probability index*

Description

gpi calculates Genotype Probability Index (GPI), which indicates the information content of genotype probabilities derived from segregation analysis.

Usage

```
gpi(gp, hwp)
```

Arguments

gp	numeric vector or matrix, individual genotype probabilities
hwp	numeric vector or matrix, Hard-Weinberg genotype probabilities

Details

Genotype Probability Index (GPI; Kinghorn, 1997; Percy and Kinghorn, 2005) indicates information that is contained in multi-allele genotype probabilities for diploids derived from segregation analysis, say Thallman et. al (2001a, 2001b). GPI can be used as one of the criteria to help identify which ungenotyped individuals or loci should be genotyped in order to maximise the benefit of genotyping in the population (e.g. Kinghorn, 1999).

gp and hwp arguments accept genotype probabilities for multi-allele loci. If there are two alleles (1 and 2), you should pass vector of probabilities for genotypes (11 and 12) i.e. one value for heterozygotes (12 and 21) and always skipping last homozygote. With three alleles this vector should hold probabilities for genotypes (11, 12, 13, 22, 23) as also shown bellow and in examples. hwp and gpLong2Wide functions can be used to ease the setup for gp and hwp arguments.

```
2 alleles: 1 and 2
11 12
--> no. dimensions = 2

3 alleles: 1, 2, and 3
11 12 13
   22 23
--> no. dimensions = 5

...

5 alleles: 1, 2, 3, 4, and 5
11 12 13 14 15
   22 23 24 25
      33 34 35
         44 45
--> no. dimensions = 14
```

In general, number of dimensions (k) for n alleles is equal to:

$$k = (n * (n + 1)/2) - 1.$$

If you have genotype probabilities for more than one individual, you can pass them to gp in a matrix form, where each row represents genotype probabilities of an individual. In case of passing matrix to gp, hwp can still accept a vector of Hardy-Weinberg genotype probabilities, which will be used for all individuals due to recycling. If hwp also gets a matrix, then it must be of the same dimension as that one passed to gp.

Value

Vector of N genotype probability indices, where N is number of individuals

Author(s)

Gregor Gorjanc R code, documentation, wrapping into a package; Andrew Percy and Brian P. Kinghorn Fortran code

References

Kinghorn, B. P. (1997) An index of information content for genotype probabilities derived from segregation analysis. *Genetics* **145**(2):479-483 http://www.genetics.org/cgi/content/abstract/145/2/479

Kinghorn, B. P. (1999) Use of segregation analysis to reduce genotyping costs. *Journal of Animal Breeding and Genetics* **116**(3):175-180 http://dx.doi.org/10.1046/j.1439-0388.1999.00192.x

Percy, A. and Kinghorn, B. P. (2005) A genotype probability index for multiple alleles and haplotypes. *Journal of Animal Breeding and Genetics* **122**(6):387-392 http://dx.doi.org/10.1111/j.1439-0388.2005.00553.x

Thallman, R. M. and Bennet, G. L. and Keele, J. W. and Kappes, S. M. (2001a) Efficient computation of genotype probabilities for loci with many alleles: I. Allelic peeling. *Journal of Animal Science* **79**(1):26-33 http://jas.fass.org/cgi/reprint/79/1/34

Thallman, R. M. and Bennet, G. L. and Keele, J. W. and Kappes, S. M. (2001b) Efficient computation of genotype probabilities for loci with many alleles: II. Iterative method for large, complex pedigrees. *Journal of Animal Science* **79**(1):34-44 http://jas.fass.org/cgi/reprint/79/1/34

See Also

hwp and gpLong2Wide

Examples

```
## --- Example 1 from Percy and Kinghorn (2005) ---
## No. alleles: 2
## No. individuals: 1
## Individual genotype probabilities:
##   Pr(11, 12, 22) = (.1, .5, .4)
##
## Hardy-Weinberg probabilities:
##   Pr(1, 2)   = (.75, .25)
##   Pr(11, 12,   (.75^2, 2*.75*.25,
##           22) =             .25^2)
##               = (.5625, .3750,
##                         .0625)

gp <- c(.1, .5)
hwp <- c(.5625, .3750)
gpi(gp=gp, hwp=hwp)

## --- Example 1 from Percy and Kinghorn (2005) extended ---
## No. alleles: 2
## No. individuals: 2
## Individual genotype probabilities:
```

```
##   Pr_1(11, 12, 22) = (.1, .5, .4)
##   Pr_2(11, 12, 22) = (.2, .5, .3)

(gp <- matrix(c(.1, .5, .2, .5), nrow=2, ncol=2, byrow=TRUE))
gpi(gp=gp, hwp=hwp)

## --- Example 2 from Percy and Kinghorn (2005) ---
## No. alleles: 3
## No. individuals: 1
## Individual genotype probabilities:
##   Pr(11, 12, 13,   (.1, .5, .0,
##          22, 23  =      .4, .0,
##              33)            .0)
##
## Hardy-Weinberg probabilities:
##   Pr(1, 2, 3)    = (.75, .25, .0)
##   Pr(11, 12, 13,   (.75^2, 2*.75*.25, .0,
##          22, 23, =            0.25^2, .0,
##              33)                     .0)
##                  = (.5625, .3750, .0
##                            .0625, .0,
##                                   .0)

gp <- c(.1, .5, .0, .4, .0)
hwp <- c(.5625, .3750, .0, .0625, .0)
gpi(gp=gp, hwp=hwp)

## --- Example 3 from Percy and Kinghorn (2005) ---
## No. alleles: 5
## No. individuals: 1
## Hardy-Weinberg probabilities:
##   Pr(1, 2, 3, 4, 5)   = (.2, .2, .2, .2, .2)
##   Pr(11, 12, 13, ...) = (Pr(1)^2, 2*Pr(1)+Pr(2), 2*Pr(1)*Pr(3), ...)
##
## Individual genotype probabilities:
##   Pr(11, 12, 13, ...) = gp / 2
##   Pr(12) = Pr(12) + .5

(hwp <- rep(.2, times=5) %*% t(rep(.2, times=5)))
hwp <- c(hwp[upper.tri(hwp, diag=TRUE)])
(hwp <- hwp[1:(length(hwp) - 1)])
gp <- hwp / 2
gp[2] <- gp[2] + .5
gp

gpi(gp=gp, hwp=hwp)

## --- Simulate gp for n alleles and i individuals ---
n <- 3
i <- 10

kAll <- (n*(n+1)/2) # without -1 here!
k <- kAll - 1
```

```
if(require("gtools")) {
  gp <- rdirichlet(n=i, alpha=rep(x=1, times=kAll))[, 1:k]
  hwp <- as.vector(rdirichlet(n=1, alpha=rep(x=1, times=kAll)))[1:k]
  gpi(gp=gp, hwp=hwp)
}
```

---

hwp *Utility functions for gpi()*

Description

gpLong2Wide changes data.frame with genotype probabilities in long form (one genotype per row) to wide form (one individual per row) for use in gpi.

hwp calculates genotype probabilities according to Hardy-Weinberg law for use in gpi.

Usage

```
gpLong2Wide(x, id, genotype, prob, trim=TRUE)
hwp(x, trim=TRUE)
```

Arguments

x	data.frame for gpLong2Wide, genotype for hwp
id	character, column name in x holding individual identifications
genotype	character, column name in x holding genotypes
prob	character, column name in x holding genotype probabilities
trim	logical, remove last column (for gpLong2Wide) or value (for hwp) of a result

Details

Hardy-Weinberg probabilities for a gene with two alleles A and B, with probabilities $Pr(A)$ and $Pr(B)$ are:

- $Pr(AA) = Pr(A)^2$
- $Pr(AB) = 2 * Pr(A) * Pr(A)$
- $Pr(BB) = Pr(B)^2$

Value

gpLong2Wide returns a matrix with number of rows equal to number of individuals and number of columns equal to number of possible genotypes.

hwp returns a vector with Hardy-Weinberg genotype probabilities.

Author(s)

Gregor Gorjanc

See Also

gpi, genotype, expectedGenotypes

Examples

```
if(require(genetics)) {
  gen <- genotype(c("A/A", "A/B"))
  hwp(x=gen)
  hwp(x=gen, trim=FALSE)
}
```

---

inbreeding *Inbreeding coefficient*

Description

inbreeding calculates inbreeding coefficients of individuals in the pedigree

Usage

```
inbreeding(x, method="meuwissen", sort=TRUE, names=TRUE, ...)
```

Arguments

x	pedigree object
method	character, method of calculation "tabular", "meuwissen" or "sargolzaei", see details
sort	logical, for the computation the pedigree needs to be sorted, but results are sorted back to original sorting (sort=TRUE) or not (sort=FALSE)
names	logical, should returned vector have names; this can be used to get leaner returned object
...	arguments for other methods

Details

Coefficient of inbreeding (F) represents probability that two alleles on a loci are identical by descent (Wright, 1922; Falconer and Mackay, 1996). Wright (1922) showed how F can be calculated but his method of paths is not easy to wrap in a program. Calculation of F can also be performed using tabular method for setting the additive relationship matrix (Henderson, 1976), where $F_i = A_{ii} - 1$. Meuwissen and Luo (1992) and VanRaden (1992) developed faster algorithms for F calculation. Wiggans et al. (1995) additionally explains method in VanRaden (1992). Sargolzaei et al. (2005) presented yet another fast method.

Take care with sort=FALSE, names=FALSE. It is your own responsibility to assure proper handling in this case.

Value

A vector of length n with inbreeding coefficients, where n is number of subjects in x

Author(s)

Gregor Gorjanc and Dave A. Henderson

References

Falconer, D. S. and Mackay, T. F. C. (1996) Introduction to Quantitative Genetics. 4th edition. Longman, Essex, U.K. http://www.amazon.com/gp/product/0582243025

Henderson, C. R. (1976) A simple method for computing the inverse of a numerator relationship matrix used in prediction of breeding values. *Biometrics* **32**(1):69-83

Meuwissen, T. H. E. and Luo, Z. (1992) Computing inbreeding coefficients in large populations. *Genetics Selection and Evolution* **24**:305-313

Sargolzaei, M. and Iwaisaki, H. and Colleau, J.-J. (2005) A fast algorithm for computing inbreeding coefficients in large populations. *Journal of Animal Breeding and Genetics* **122**(5):325–331 http://dx.doi.org/10.1111/j.1439-0388.2005.00538.x

VanRaden, P. M. (1992) Accounting for inbreeding and crossbreeding in genetic evaluation for large populations. *Journal of Dairy Science* 75(11):3136-3144 http://jds.fass.org/cgi/content/abstract/75/11/3136

Wiggans, G. R. and VanRaden, P. M. and Zuurbier, J. (1995) Calculation and use of inbreeding coefficients for genetic evaluation of United States dairy cattle. *Journal of Dairy Science* **78**(7):1584-1590 http://jds.fass.org/cgi/content/abstract/75/11/3136

Wright, S. (1922) Coefficients of inbreeding and relationship. *American Naturalist* 56:330-338

See Also

Pedigree, relationshipAdditive, kinship and geneFlowT

Examples

```
data(Mrode2.1)
Mrode2.1$dtB <- as.Date(Mrode2.1$dtB)
x2.1 <- Pedigree(x=Mrode2.1, subject="sub", ascendant=c("fat", "mot"),
                 ascendantSex=c("M", "F"), family="fam", sex="sex",
                 generation="gen", dtBirth="dtB")
fractions(inbreeding(x=x2.1))

## Compare the speed
ped <- generatePedigree(nId=25)
system.time(inbreeding(x=ped))
# system.time(inbreeding(x=ped, method="sargolzaei")) # not yet implemented
system.time(inbreeding(x=ped, method="tabular"))
```

isFounder *Founder and non-founder individuals in the pedigree*

Description

isFounder classifies individuals in the pedigree as founders (base) or non-founders (non-base individuals).

Usage

```
isFounder(x, col=attr(x, ".ascendant"))
```

Arguments

x	pedigree object
col	character, which columns should be checked, see examples

Details

By definition founders do not have any known ascendants, while the opossite is the case for non-founders i.e. they have at least one known ascendant.

FIXME: any relation with founderGeneSet in GeneticsBase

Value

Boolean vector.

Author(s)

Gregor Gorjanc

See Also

Pedigree

Examples

```
ped <- generatePedigree(nId=5)
isFounder(ped)
## Based only on fathers
isFounder(ped, col=c("father"))
## Works also only on a part of a pedigree
isFounder(ped[1:5, ])
```

`model.matrix.Pedigree` *Model matrix for individuals with and without records*

Description

`model.matrix` for pedigree creates design matrix (Z) for individuals with and without records. Used mainly for educational purposes.

Usage

```
## S3 method for class 'Pedigree'
model.matrix(object, y, id, left=TRUE, names=TRUE,
                                    ...)
```

Arguments

`object`	Pedigree
`names`	logical, should returned matrix have row/colnames; this can be used to get leaner matrix
`y`	numeric, vector of (phenotypic) records
`id`	vector of subjects for `y`
`left`	logical, bind columns of individuals without records to left (`left=TRUE`) or right (`left=FALSE`) side of Z
`...`	arguments passed to `model.matrix`

Value

A model matrix of $n * q$ dimension, where n is number of records in `y` and q is number of subjects in the pedigree

Author(s)

Gregor Gorjanc

See Also

`Pedigree`, `relationshipAdditive`, `inverseAdditive` and `model.matrix`

Examples

```
data(Mrode3.1)
(x <- Pedigree(x=Mrode3.1, subject="calf", ascendant=c("sire", "dam"),
               ascendantSex=c("Male", "Female"), sex="sex"))
model.matrix(object=x, y=x$pwg, id=x$calf)
```

Mrode *Pedigree and data examples*

Description

Various pedigree and data examples

Usage

```
data(Falconer5.1)
data(Mrode2.1)
data(Mrode3.1)
```

Format

`Falconer5.1` is a rather complex (inbreed) pedigree example from book by Falconer and Mackay (1996) - page 84 with 18 individuals and following columns:

sub individual

fat father

mot mother

`Mrode2.1` is an extended pedigree example from book by Mrode (2005) - page 27 with 6 individuals and following columns:

sub individual

fat father

mot mother

fam family

sex sex

gen generation

dtB date of birth

`Mrode3.1` is a pedigree and data example from book by Mrode (2005) - page 43: it shows a beef breeding scenario with 8 individuals (animals), where 5 of them have phenotypic records (pre-weaning gain) and 3 three of them are without records and link others through the pedigree:

calf calf

sex sex of a calf

sire father of a calf

dam mother of a calf

pwg pre-weaning gain of a calf in kg

References

Falconer, D. S. and Mackay, T. F. C. (1996) Introduction to Quantitative Genetics. 4th edition. Longman, Essex, U.K. http://www.amazon.com/gp/product/0582243025

Mrode, R. A. (2005) Linear models for the prediction of animal breeding values. 2nd edition. CAB International. ISBN 0-85199-000-2 http://www.amazon.com/gp/product/0851990002

Examples

```
data(Falconer5.1)
Pedigree(x=Falconer5.1, subject="sub", ascendant=c("fat", "mot"))

data(Mrode2.1)
Mrode2.1$dtB <- as.Date(Mrode2.1$dtB)
Pedigree(x=Mrode2.1, subject="sub", ascendant=c("fat", "mot"),
         ascendantSex=c("M", "F"), family="fam", sex="sex",
         generation="gen", dtBirth="dtB")

data(Mrode3.1)
Pedigree(x=Mrode3.1, subject="calf", ascendant=c("sire", "dam"),
         ascendantSex=c("Male", "Female"), sex="sex")
```

---

nIndividual *Number of individuals in a pedigree*

Description

nIndividual returns number of individuals (individuals and/or ascendants) in a pedigree object.

Usage

```
nIndividual(x, col=NULL, extend=TRUE, drop=TRUE)
```

Arguments

x	pedigree
col	character, which id column should be the source: "id" (default) or particular ascendant i.e. "father" and "mother"
extend	logical, extend pedigree
drop	logical, drop unused levels in case factors are used

Details

FIXME - this will change a lot!!!! There is always one additional level in levels in case factors are used to represent individuals in a pedigree as described in Pedigree. However, nlevels.Pedigree prints out the number of levels actually used to represent individuals i.e. level unknown is not included into the result.

Author(s)

Gregor Gorjanc

See Also

summary.Pedigree, extend

Examples

```
# Deafult example
ped <- generatePedigree(5)
nIndividual(ped)

# Other id columns
nIndividual(ped, col="father")
nIndividual(ped, col="mother")

# Remove individuals with unknown fathers - FIXME
# ped <- ped[!is.na(ped, col="father"), ]
# nIndividual(ped)
# nIndividual(ped, extend=FALSE)
```

Pedigree *Pedigree*

Description

Pedigree function creates a pedigree object

Usage

```
Pedigree(x, subject="id", ascendant=c("father", "mother"),
  ascendantSex=c(1, 2), ascendantLevel=c(1, 1), unknown=NA, sex=NA,
  dtBirth=NA, generation=NA, family=NA, generationOrder="increasing",
  check=TRUE, sort=FALSE, extend=FALSE, drop=TRUE, codes=FALSE)
```

Arguments

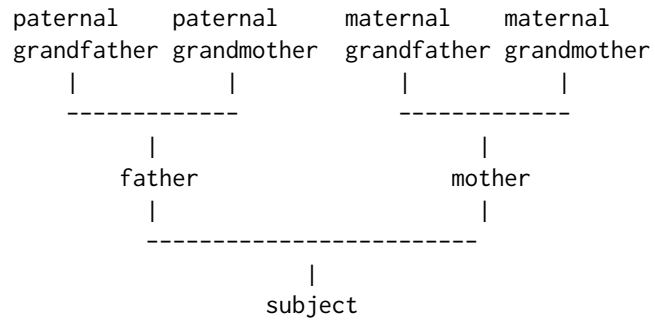
x	data.frame or matrix
subject	character, column name in x for subjects
ascendant	character, column name(s) in x for ascendants
family	character, column name in x for family
ascendantSex	integer orcharacter, sex of ascendant(s); see details
ascendantLevel	integer, generation level of ascendant(s); see details

unknown	vector or list, uknown representation of identification and other data in the pedigree; see details
sex	character, column name in x for sex
dtBirth	character, column name in x for date of birth
generation	character, column name in x for generation
generationOrder	character, generation value is "increasing" or "decreasing" through generations; see details
check	logical, check for common errors
sort	logical, sort pedigree
extend	logical, extend pedigree
drop	logical, drop unused levels if factors are used
codes	logical, code individuals into integers

Details

FIXME: study geneSet class

Pedigree can be one source of information on genetic relationship between relatives. Take for example the following pedigree:



This information can be stored in a data.frame as

mother	maternal grandfather	maternal grandmother
father	paternal grandfather	paternal grandmother
subject	father	mother

There is considerable variability in terminology between as well as within various fields of genetics. We use the following terms throughout the help and code: individual (any individual in a pedigree), subject (individual whose pedigree is given i.e. individuals in the first column in upper data.frame), ascendant and descendant. Additionally, family, sex, dtBirth and generation are used for additional data in the pedigree. Their meaning should be clear. For these, argument col is usually used in function calls.

family TODO

`ascendantSex` can be used to define sex of ascendant(s); for example c("Male", "Female") or c("M", "F") or even c(1, 2) for father and mother or c(2, 1, 1) for mother and two possible fathers or c(1, 1) for father and maternal father etc. This data is needed only for the structure of the class and defaults should be ok for the majority. But you need to make sure that data defined here must be in accordance with values in `sex` column.

`ascendantLevel` can be used to define generation level of ascendant(s) in relation to a subject; for example c(1, 1) for father and mother or c(1, 1, 1) for mother and two possible fathers or c(1, 2) for father and maternal father etc. This data is needed only for the structure of the class and defaults should be ok for the majority.

There is no need for `as.integer` TODO in arguments `ascendantLevel` as this is done internally.

unknown TODO

Sex TODO

Date of birth TODO

`generationOrder` defines in which order are `generation` values: "increasing" if values increase from ascendants to descendants and "decreasing" if values decrease from ascendants to descendants.

`check`, `sort`, `extend`, and `codes` are actions on the pedigree and have their own help pages.

Individuals can be stored as either integer, numeric or factor TODO. In any case all id columns must have the same class and this is automatically checked. Argument `drop` can be used to drop unused levels, if factors are used.

`as.Pedigree.*` FIXME `as.*.Pedigree` FIXME

Object of Pedigree class is a data.frame with columns that can be divided into core columns (subject, ascendant(s), sex, dtBirth and generationTODO) and possibly other columns such as data on phenotype and genotype and other subject attributes, for example factors and covariates TODO.

Additionally, the following attributes are set on pedigree:

- .subjectcharacter, column name of subject identification in pedigree
- .ascendantcharacter, column name(s) of ascendant(s) identification in pedigree
- .familycharacter, column name of family identification in pedigree
- .ascendantSexinteger, sex of ascendant(s)
- .ascendantLevelinteger, generation level of ascendant(s)
- .sexcharacter, column name of subject's sex
- .dtBirthcharacter, column name of subject's date of birth
- .generationcharacter, column name of subject's generation
- .generationOrdercharacter, generation value is "increasing" or "decreasing" through generations
- .colClasscharacter, storage class for id columns: "integer", "numeric" or "factor"
- .checkedlogical, is pedigree checked for common errors
- .sortedlogical, is pedigree sorted; by TODO
- .extendedlogical, is pedigree extended
- .codedlogical, is pedigree coded
- .unknownlist, uknown representation for individual identification and other data in the pedigree; names of the list are c(".id", ".family", ".sex", ".dtBirth", ".generation")

Value

Pedigree object as described in the details

Author(s)

Gregor Gorjanc

See Also

check, sort, and extend provide help on pedigree utility functions.

Examples

```
data(Mrode2.1)
Mrode2.1$dtB <- as.Date(Mrode2.1$dtB)
x2.1 <- Pedigree(x=Mrode2.1, subject="sub", ascendant=c("fat", "mot"),
                 ascendantSex=c("M", "F"), family="fam", sex="sex",
                 generation="gen", dtBirth="dtB")


if (FALSE) {
  ## How to handle different pedigree types
  ## * multiple parents
  ped2 <- ped
  ped2$father1 <- ped$father
  ped2$father2 <- ped$father
  ped2$father <- NULL
  ped2 <- as.data.frame(ped2)
  str(Pedigree(ped2, ascendant=c("father1", "father2", "mother"),
               ascendantSex=c(1, 1, 2), ascendantLevel=c(1, 1, 1)))

  ## * different level of parents
  ped3 <- as.data.frame(ped)
  ped3$m.grandfather <- ped3$mother
  ped3$mother <- NULL
  str(Pedigree(ped3, ascendant=c("father", "m.grandfather"),
               ascendantSex=c(1, 1), ascendantLevel=c(1, 2)))
}
```

---

prune *Prune pedigree*

Description

prune removes noninformative individuals from a pedigree. This process is usually called trimming or pruning. Individuals are removed if they do not provide any ancestral ties between other individuals. It is possible to add some additional criteria. See details.

Usage

```
prune(x, id, father, mother, unknown=NA, testAdd=NULL, verbose=FALSE)
```

Arguments

x	data.frame, pedigree data
id	character, individuals's identification column name
father	character, father's identification column name
mother	character, mother's identification column name
unknown	value(s) used for representing unknown parent in x
testAdd	logical, additional criteria; see details
verbose	logical, print some more info

Details

NOTE: this function does not yet work with Pedigree class.

There are always some individuals in the pedigree that jut out. Usually this are older individuals without known ancestors, founders. If such individuals have only one (first) descendant and no phenotype/genotype data, then they do not give us any additional information and can be safely removed from the pedigree. This process resembles cutting/pruning the branches of a tree.

By default prune iteratively removes individuals from the pedigree (from top to bottom) if:

- they are founders, have both ancestors i.e. father and mother unknown and
- have only one or no (first) descendants i.e. children

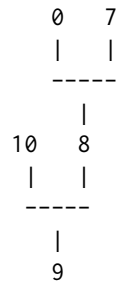
If there is a need to take into account availability of say phenotype/genotype data or any other information, argument testAdd can be used. Value of this argument must be logical and with length equal to number of rows in the pedigree. The easiest way to achieve this is to merge any data to the pedigree and then to perform a test, which will return logical values. Note that value of TRUE in testAdd means to remove an individual - this function is removing individuals! To keep an individual without known parents and one or no children, value of testAdd must be FALSE for that particular individual. Take a look at the examples.

There are various conventions on representing unknown/missing ancestors, say 0. R's default is to use NA. If other values than NA are present, argument unknown can be used to convert unknown/missing values to NA.

It is assumed that pedigree is in extended form i.e. that each father and mother has each own record as an individual. Otherwise error is returned with information on which parents do not appear as individuals.

prune does not only remove lines for pruned individuals but also removes them from father and mother columns.

Pruning is done from top to bottom of the pedigree i.e. from oldest individuals towards younger ones. Take for example the following part of the pedigree in example section:



Individual 7 is not removed since it has two (first) descendants i.e. 8 and 5 (not shown here). Consecutively, individuals 8 and 9 are also not removed from the pedigree. Individual 10 is removed, since it has only one descendant. Why should individuals 8 and 9 and therefore also 7 stay in the pedigree? Current behaviour is reasonable if pedigree is built in such a way that first individuals with some phenotype or genotype data are gathered and then their pedigree is being built. Say, individual 9 has pehnotype/genotype data and its pedigree is build and there is therefore no need to remove such an individual. However, if pedigree is not built in such a way, then `prunPedigree` function can not prune all noninformative individuals. Argument `testAdd` can not help with this issue, since basic tests (founder and one or no first descendants) and `testAdd` are combined with `&`.

Value

`prune` returns a data.frame with possibly fewer individuals. Read also the details.

Author(s)

Gregor Gorjanc

See Also

`Pedigree`

Examples

```
## Pedigree example
x <- data.frame(oseba=c(1,  9, 11, 2, 3, 10, 8, 12, 13,  4, 5, 6, 7, 14, 15, 16, 17),
                 oce=c(2, 10, 12, 5, 5,  0, 7,  0,  0,  0, 7, 0, 0,  0,  0,  0,  0),
                mama=c(3,  8, 13, 0, 4,  0, 0,  0,  0, 14, 6, 0, 0, 15, 16, 17,  0),
                spol=c(2,  2,  2, 1, 2,  1, 2,  1,  2,  2, 1, 2, 1,  1,  1,  1,  1),
          generacija=c(1,  1,  1, 2, 2,  2, 2,  2,  2,  3, 3, 4, 4,  5,  6,  7,  8),
                last=c(2, NA,  8, 4, 1,  6,NA, NA, NA, NA,NA,NA,NA, NA, NA, NA, NA))

## Default case
prune(x=x, id="oseba", father="oce", mother="mama", unknown=0)

## Use of additional test i.e. do not remove individual if it has
## known value for "last"
prune(x=x, id="oseba", father="oce", mother="mama", unknown=0,
              testAdd=is.na(x$last))

## Use of other data
```

```
y <- data.frame(oseba=c( 11,  15, 16),
                last2=c(8.5, 7.5, NA))

x <- merge(x=x, y=y, all.x=TRUE)
prune(x=x, id="oseba", father="oce", mother="mama", unknown=0,
              testAdd=is.na(x$last2))
```

`relationshipAdditive` *Additive relationship matrix and its inverse*

Description

`relationshipAdditive` creates additive relationship matrix, while `inverseAdditive` creates its inverse directly from a pedigree. `kinship` is another definition of relationship and is equal to half of additive relationship.

Usage

```
relationshipAdditive(x, sort=TRUE, names=TRUE, ...)
inverseAdditive(x, sort=TRUE, names=TRUE, ...)
kinship(x, sort=TRUE, names=TRUE, ...)
```

Arguments

`x`	Pedigree
`sort`	logical, for the computation the pedigree needs to be sorted, but results are sorted back to original sorting (sort=TRUE) or not (sort=FALSE)
`names`	logical, should returned matrix have row/colnames; this can be used to get leaner matrix
`...`	arguments for other methods

Details

Additive or numerator relationship matrix is symetric and contains $1 + F_i$ on diagonal, where F_i is an inbreeding coefficients (see `inbreeding`) for subject i. Off-diagonal elements represent numerator or relationship coefficient bewteen subjects i and j as defined by Wright (1922). Henderson (1976) showed a way to setup inverse of relationship matrix directly. Mrode (2005) has a very nice introduction to these concepts.

Take care with `sort=FALSE, names=FALSE`. It is your own responsibility to assure proper handling in this case.

Value

A matrix of $n * n$ dimension, where n is number of subjects in `x`

Author(s)

Gregor Gorjanc and Dave A. Henderson

References

Henderson, C. R. (1976) A simple method for computing the inverse of a numerator relationship matrix used in prediction of breeding values. *Biometrics* **32**(1):69-83

Mrode, R. A. (2005) Linear models for the prediction of animal breeding values. 2nd edition. CAB International. ISBN 0-85199-000-2 http://www.amazon.com/gp/product/0851990002

Wright, S. (1922) Coefficients of inbreeding and relationship. *American Naturalist* 56:330-338

See Also

Pedigree, inbreeding and geneFlowT

Examples

```
data(Mrode2.1)
Mrode2.1$dtB <- as.Date(Mrode2.1$dtB)
x2.1 <- Pedigree(x=Mrode2.1, subject="sub", ascendant=c("fat", "mot"),
                 ascendantSex=c("M", "F"), family="fam", sex="sex",
                 generation="gen", dtBirth="dtB")

(A <- relationshipAdditive(x2.1))
fractions(A)
solve(A)
inverseAdditive(x2.1)
relationshipAdditive(x2.1[3:6, ])

## Compare the speed
ped <- generatePedigree(nId=10, nGeneration=3, nFather=1, nMother=2)
system.time(solve(relationshipAdditive(ped)))
system.time(inverseAdditive(ped))
```

---

removeIndividual *Remove individual from pedigree*

Description

removeIndividual provides utility for removing individuals from a pedigree.

Usage

```
removeIndividual(x, individual, remove="all")
```

Arguments

x	pedigree
individual	vector of individuals
remove	character, column names of id columns and/or "all", see details

Details

Individuals passed to argument individual will be removed from the pedigree. If there is a pedigree with individual "id" and two ascendants, say "father" and "mother", then one can pass any combination of these three id columns or "all" for all of them in short to argument remove. In case only "id" is passed to remove, individuals will be removed from the pedigree, but not from ascendant id columns, which might be a matter of interest only if specified individuals show up as ascendants for some other individuals. In case you want to remove an individual completely from the pedigree "all" must be used.

Individuals in id column are removed via removal of the whole record from the pedigree. Individuals in ascendant id columns are only replaced by attr(x, "unknown").

If founder is removed, attribute extended status is changed to FALSE.

Author(s)

Gregor Gorjanc

See Also

Pedigree

Examples

```
ped <- generatePedigree(3)
summary(ped)
removeIndividual(ped, individual=c(1, 3, 4), remove="father")
removeIndividual(ped, individual=c(1, 3, 4), remove=c("mother", "father"))
(ped <- removeIndividual(ped, individual=c(1, 3, 4), remove=c("all")))
summary(ped)
```

---

sort.Pedigree *Sort pedigree*

Description

Pedigree sort

Usage

```
## S3 method for class 'Pedigree'
sort(x, decreasing=FALSE, na.last=TRUE, ..., by="default")
```

Arguments

x	pedigree, object to be sorted
decreasing	logical, sort order
na.last	logical, control treatment of NAs; check order
...	arguments passed to order, see details
by	character, sort by "default", "pedigree", "generation", or "dtBirth" information, see details

Details

Sorting of the pedigree can be performed in different ways. Since pedigree can contain date of birth, sorting by this would be the most obvious way and it would be the most detailed sort. However, there might be the case that date of birth is not available for some or all individuals. Therefore, this function by default (when by="default") tries to figure out what would be the best way to perform the sort. If date of birth is available for all individuals then date of birth is used for sorting. If not, generation information is used, but only if it is known for all individuals (it should be more or less easy to figure out the generation for all individuals in the pedigree CHECK). Again if not, sorting is done via information in pedigree i.e. ascendants will precede descendants or vice versa. User can always define it's own preference by argument by. When by="dtBirth" or by="generation" sorting is performed via order and its arguments na.last and decreasing can be used. With by="pedigree" argument decreasing has an effect.

Generation values can have different meaning i.e. values might either increase or decrease from ascendants to descendant with the same meaning. This information is stored in attribute generationOrder (at the time of creating the pedigree object via Pedigree) and used for determining the order of sorting if sorting is by generation. The output of the result might therefore be opposite of what user might expect. If that is the case, use argument decreasing as defined in order. Look also into examples bellow.

Value

Sorted pedigree

Author(s)

Gregor Gorjanc

See Also

Pedigree and order

Examples

```
ped <- generatePedigree(nId=5)
ped <- ped[sample(1:nrow(ped)), ]
sort(ped)
## sort(ped, by="dtBirth")       ## TODO
sort(ped, by="generation")
## try(sort(ped, by="pedigree")) ## TODO
```

```
## Sorting with decreasing generation values from ascendants to descendants
ped1 <- generatePedigree(nId=5, generationOrder="decreasing")
sort(ped1, by="generation")
sort(ped1, decreasing=TRUE, by="generation")
sort(ped1, decreasing=FALSE, by="generation")

## Sorting with unknown values
ped[1, "generation"] <- NA
sort(ped, na.last=TRUE, by="generation")
sort(ped, na.last=FALSE, by="generation")
sort(ped, na.last=NA, by="generation")
```

---

summary.Pedigree *Pedigree summary*

Description

summary.Pedigree reports TODO.

Usage

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

Arguments

object	pedigree object
...	additional arguments for other methods (not used)

Details

TODO.

Value

TODO.

Author(s)

Gregor Gorjanc

See Also

Pedigree

Examples

```
ped <- generatePedigree(nId=5)
summary(ped)
```

undocumented *Undocumented functions*

Description

These functions are undocumented. Some are internal and not intended for direct use. Some are not yet ready for end users. Others simply haven't been documented yet.

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