Package ‘ggroups’
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Title Pedigree and Genetic Groups
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Description Calculates additive and dominance genetic relationship matrices and their inverses, in matrix and tabular-sparse formats. It includes functions for checking and processing pedigree, as well as functions to calculate the matrix of genetic group contributions (Q), and adding those contributions to the genetic merit of animals (Quaas (1988) doi:10.3168/jds.S0022-0302(88)79691-5). Calculation of Q is computationally extensive. There are computationally optimized functions to calculate Q.
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R topics documented:
groups-package .................................................. 2
buildA .......................................................... 3
buildD .......................................................... 3
gghead .......................................................... 4
inb .............................................................. 5
mat2tab ......................................................... 6
Pedigree and genetic groups

Description

This package contains pedigree processing and analyzing functions, including functions for checking and renumbering the pedigree, making the additive and dominance pedigree relationship matrices and their inverses, in matrix and tabular formats, as well as functions related to genetic groups.

Details

First, it is recommended to check the pedigree data.frame with the pedcheck function. Pedigree relationship matrix and its inverse are fundamentals in the conventional and modern animal breeding. The concept of genetic groups stems from the fact that not all the unknown parents are of the same genetic level. The genetic group contribution matrix ($Q$) is required to weight and add genetic group effects ($\hat{g}$) to the genetic merit of animals ($\hat{u}$), which is equal to $Q\hat{g} + \hat{u}$ (Quaas, 1988). Calculating $Q$ is computationally challenging, and for large pedigree, large RAM and long computational time is required. Therefore, the functions qmatL and its parallel version, qmatXL are introduced. Overlap between sire and dam genetic groups is supported.

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References

buildA

Description
Builds the pedigree-based additive genetic relationship matrix.

Usage
buildA(ped)

Arguments
ped : data.frame with integer columns corresponding to ID, SIRE, DAM. Missing value is 0.

Value
Relationship matrix A

Examples
ped = data.frame(ID=1:6, SIRE=c(0,0,1,3,1,4), DAM=c(0,0,2,2,2,5))
buildA(ped)

buildD

Description
Builds the pedigree-based dominance relationship matrix.

Usage
buildD(ped, A)
Arguments

ped : data.frame with integer columns corresponding to ID, SIRE, DAM. Missing value is 0.
A : Relationship matrix A created by function buildA.

Value

Relationship matrix D

Examples

```r
ped = data.frame(ID=1:6, SIRE=c(0,0,1,3,1,4), DAM=c(0,0,2,2,2,5))
buildD(ped, buildA(ped))
```

Description

This function appends parents that are not available in the first column of the pedigree, to the head of the pedigree, and sorts it. Given a pedigree with all missing parents replaced with the corresponding genetic groups, this functions appends genetic groups to the head of the pedigree.

Usage

```r
gghead(ped)
```

Arguments

ped : data.frame with integer columns corresponding to ID, SIRE, DAM. Missing value is 0.

Details

Consider this simple pedigree:

```
3 0 0
4 3 0
6 4 5
5 0 0
```

First, unknown parents are replaced with the corresponding genetic groups. Please note that unknown parent IDs should be smaller than progeny IDs.

```
3 1 2
4 3 2
```
Then, `gghead` is applied to this pedigree (see the example).

**Value**

Processed pedigree data.frame

**Examples**

```r
ped = data.frame(ID=c(3,4,6,5), SIRE=c(1,3,4,1), DAM=c(2,2,5,2))
gghead(ped)
```

---

### inb

**Inbreeding coefficient**

**Description**

Calculates inbreeding coefficient for an individual.

**Usage**

`inb(ped, id)`

**Arguments**

- `ped`: data.frame with integer columns corresponding to ID, SIRE, DAM. Missing value is 0.
- `id`: Numeric ID of an individual

**Value**

Inb: Inbreeding coefficient of the individual

**Examples**

```r
ped = data.frame(ID=1:7, SIRE=c(0,0,1,1,3,1,5), DAM=c(0,0,0,2,4,4,6))
inb(ped, 7)
```
### mat2tab  
*Matrix to tabular*

**Description**

Converts matrix data to tabular data.

**Usage**

```r
mat2tab(mat)
```

**Arguments**

- `mat` : matrix

**Value**

- `tab` : data.frame with 2 integer (IDs) and 1 numeric (values) columns.

**Examples**

```r
ped = data.frame(ID=1:6, SIRE=c(0,0,1,3,1,4), DAM=c(0,0,2,2,2,5))
mat2tab(buildA(ped))
```

### offspring  
*Descendants of an individual per generation*

**Description**

Counts and collects progeny and phenotyped progeny of an individual in successive generations.

**Usage**

```r
offspring(ped, id, pheno)
```

**Arguments**

- `ped` : data.frame with columns corresponding to ID, SIRE, DAM. Missing value is 0.
- `id` : The ID of the individual, for which the descendants to be extracted.
- `pheno` : Vector of phenotyped individuals.

**Value**

- `prgn` : list of progeny per generation.
- `prgn.ph` : list of phenotyped progeny per generation.
Examples

ped = data.frame(V1 = 1:19,
                 V2 = c(0,0,1,1,0,0,0,0,4,5,7,0,9,0,0,12),
                 V3 = c(0,0,2,0,2,0,3,3,3,0,6,8,8,8,10,11,11,0))
pheno = 10:18
# Find progeny and phenotyped progeny of individual 1.
offspring(ped, 1, pheno)
# Find phenotyped progeny of individual 1, in the 2nd generation.
offspring(ped, 1, 10:18)$prgn.ph[[2]]
# If only interested in finding the progeny of individual 1:
offspring(ped, 1, c())$prgn

Description

Performs basic pedigree checks.

Usage

pedcheck(ped)

Arguments

ped : data.frame with integer columns corresponding to ID, SIRE, DAM. Missing value is 0.

Examples

set.seed(127)
ped = data.frame(ID=c(1:50,NA,0,1:3),
                 SIRE=c(0, sample(c(0,10:25), 53, replace=TRUE), 51),
                 DAM=c(0, NA, 52, sample(c(0,20:35), 52, replace=TRUE)))
pedcheck(ped)
peddown  

**Description**

Extracts pedigree downward for one or a group of individuals to find their descendants.

**Usage**

`peddown(ped, parents, maxgen = c())`

**Arguments**

- `ped` : data.frame with integer columns corresponding to ID, SIRE, DAM. Missing value is 0.
- `parents` : Vector of individual ID(s), from which the new pedigree is being extracted.
- `maxgen` : (optional) a positive integer for the maximum number of generations to proceed. If no value is provided, there is no limitation on the maximum number of generations to proceed.

**Value**

`newped` : Extracted pedigree data.frame

**Examples**

```r
ped = data.frame(ID=1:6, SIRE=c(0,0,1,3,1,4), DAM=c(0,0,2,2,2,5))
peddown(ped, c(1,4))
peddown(ped, 1, maxgen=1)
```

pedup  

**Description**

Extracts pedigree upward for one or a group of individuals to find their ascendants.

**Usage**

`pedup(ped, progeny, maxgen = c())`

**Examples**

```r
ped = data.frame(ID=1:6, SIRE=c(0,0,1,3,1,4), DAM=c(0,0,2,2,2,5))
pedup(ped, c(1,4))
pedup(ped, 1, maxgen=1)
```
pruneped

Arguments

ped : data.frame with integer columns corresponding to ID, SIRE, DAM. Missing value is 0.
progeny : Vector of individual ID(s), from which the new pedigree is being extracted.
maxgen : (optional) a positive integer for the maximum number of generations (continuing from parents of progeny) to proceed. If no value is provided, there is no limitation on the maximum number of generations to proceed.

Value

newped : Extracted pedigree data.frame

Examples

ped = data.frame(ID=1:6, SIRE=c(0,0,1,3,1,4), DAM=c(0,0,2,2,2,5))
pedup(ped, c(1,4))
pedup(ped, 6, maxgen=1)

pruneped

Pedigree pruning

Description

Pruning pedigree in two different modes (strict, loose)

Usage

pruneped(ped, pheno, mode)

Arguments

ped : data.frame with integer columns corresponding to ID, SIRE, DAM. Missing value is 0.
pheno : Vector of phenotyped individuals
mode : strict or loose

Details

In strict pruning, individuals without progeny and phenotype are recursively deleted from the pedigree, and then individuals without known parent and without progeny (if any) are deleted. Therefore, all uninfluential individuals are deleted. The downside is that individuals without phenotype or phenotyped progeny cannot receive any genetic merit based on the information from their phenotyped relatives. In loose pruning, the pedigree is upward extracted for phenotyped individuals to their founders, and then the pedigree is downward extracted from the founders.
Value

newped : Pruned pedigree data.frame

Examples

```r
ped = data.frame(ID=1:7, SIRE=c(0,0,1,3,1,4,0), DAM=c(0,0,2,2,2,5,0))
pheno = c(1,4)
pruneped(ped, pheno, mode="strict")
pruneped(ped, pheno, mode="loose")
```

---

### Qgpu

**Vector Qg + u**

**Description**

Adds genetic group contributions to the genetic merit of individuals.

**Usage**

```r
Qgpu(Q, sol)
```

**Arguments**

- **Q** : The output matrix from qmatL (for more details: ?qmatL)
- **sol** : data.frame with 2 numeric columns corresponding to ID, EBV ([g, u]), where g and u are the genetic group and genetic merit solutions, respectively. The order of solutions must be the order of columns and the order of rows in matrix Q.

**Value**

Vector of Qg + u

**Examples**

```r
ped = data.frame(ID=c(3,4,6,5), SIRE=c(1,3,4,1), DAM=c(2,2,5,2))
Q = qmatL(gghead(ped))
ghat = c(0.1, -0.2)
what = seq(-1.5, 1.5, 1)
sol = data.frame(ID=1:6, EBV=c(ghat, what))
Qgpu(Q, sol)
```
**qmat**

*Matrix Q*

**Description**

Creates the genetic group contribution matrix.

**Usage**

```r
qmat(ped2)
```

**Arguments**

- `ped2`: The output data.frame from `gghead` (for more details: ?gghead)

**Value**

Q matrix

**Examples**

```r
ped = data.frame(ID=c(3,4,6,5), SIRE=c(1,3,4,1), DAM=c(2,2,5,2))
ped2 = gghead(ped)
qmat(ped2)
```

---

**qmatL**

*Matrix Q for large pedigrees*

**Description**

Creates the genetic group contribution matrix for large pedigrees.

**Usage**

```r
qmatL(ped2)
```

**Arguments**

- `ped2`: The output data.frame from `gghead` (for more details: ?gghead)

**Value**

Q matrix
Examples

```r
ped = data.frame(ID=c(3,4,6,5), SIRE=c(1,3,4,1), DAM=c(2,2,5,2))
ped2 = gghead(ped)
qmatL(ped2)
```

---

Matrix Q for large pedigrees (parallel processing)

Description

Creates the genetic group contribution matrix for large pedigrees, with parallel processing.

Usage

```r
qmatXL(ped2, ncl)
```

Arguments

- `ped2`: The output `data.frame` from `gghead` (for more details: `?gghead`)
- `ncl`: User defined number of nodes; if the number of user defined nodes is greater than the number of genetic groups, the number genetic groups is considered as the number of nodes.

Details

This function is the parallel version of `qmatL`. It requires `foreach` and `doParallel` packages.

Value

`Q` matrix

Examples

```r
ped = data.frame(ID=c(3,4,6,5), SIRE=c(1,3,4,1), DAM=c(2,2,5,2))
ped2 = gghead(ped)
qmatXL(ped2, 2)
```
renum  

**Pedigree renumbering**

**Description**
Renumbering pedigree to numerical IDs, so that progeny’s ID is smaller than parents’ IDs.

**Usage**
renum(ped)

**Arguments**
- `ped` : data.frame with columns corresponding to ID, SIRE, DAM. Missing value is 0.

**Value**
- `newped` : Pedigree data.frame with renumberred IDs.
- `xrf` : Cross-reference data.frame with 2 columns for original and renumberred IDs.

**Examples**
```r
ped = data.frame(ID=letters[1:6], SIRE=c(0,0,letters[c(1,3,1,4)]), DAM=c(0,0,letters[c(2,2,2,5)]))
renum(ped)$newped
renum(ped)$xrf
```

---

rg  

**Genetic relationship coefficient**

**Description**
Calculates genetic relationship coefficient between two individuals.

**Usage**
rg(ped, id1, id2)

**Arguments**
- `ped` : data.frame with integer columns corresponding to ID, SIRE, DAM. Missing value is 0.
- `id1` : Numeric ID of an individual
- `id2` : Numeric ID of an individual
smgsped

Value

rG : Genetic relationship coefficient between the two individuals

Examples

```r
ped = data.frame(ID=1:7, SIRE=c(0,0,1,1,3,1,5), DAM=c(0,0,0,2,4,4,6))
rg(ped, 5, 6)
```

smgsped

*Sire-maternal grandsire (S-MGS) pedigree*

Description

Extract sire-maternal grandsire (S-MGS) pedigree from a sire-dam pedigree. Sire and MGS information is extracted for sires of phenotyped individuals.

Usage

`smgsped(ped, pheno)`

Arguments

- `ped` : *data.frame* with integer columns corresponding to ID, SIRE, DAM. Missing value is 0.
- `pheno` : Vector of phenotyped individuals

Value

- `newped` : S-MGS pedigree *data.frame*

Examples

```r
ped = data.frame(ID=1:10, SIRE=c(0,0,1,2,0,5,4,4,0,8), DAM=c(0,0,0,3,0,6,6,6,6,0))
smgsped(ped, 7:10)
```
### tab2mat

**Tabular to matrix**

**Description**

Converts tabular data to matrix data.

**Usage**

```r
tab2mat(tab)
```

**Arguments**

- `tab`: data.frame with 2 integer (IDs) and 1 numeric (values) columns.

**Value**

- `mat`: matrix

**Examples**

```r
ped = data.frame(ID=1:6, SIRE=c(0,0,1,3,1,4), DAM=c(0,0,2,2,2,5))
tab2mat(tabA(ped))
```

### tabA

**Relationship matrix A in a tabular format**

**Description**

Creates the pedigree-based additive genetic relationship data.frame.

**Usage**

```r
tabA(ped)
```

**Arguments**

- `ped`: data.frame with integer columns corresponding to ID, SIRE, DAM. Missing value is 0.

**Value**

Genetic relationship data.frame
Examples

```r
tabAinv(ped, inbr)
```

Description

Creates the data.frame of the inverse of the pedigree-based genetic relationship matrix.

Usage

```r
tabAinv(ped, inbr)
```

Arguments

- `ped`: data.frame with integer columns corresponding to ID, SIRE, DAM. Missing value is 0.
- `inbr`: Vector of inbreeding coefficients in the order of individuals in the relationship matrix.

Value

data.frame of the inverse of the genetic relationship matrix

Examples

```r
tabAinv(ped, inbr)
```
**tabD**

*Dominance relationship matrix D in a tabular-sparse format*

---

**Description**

Creates the pedigree-based dominance relationship data.frame.

**Usage**

```r
tabD(ped, A)
```

**Arguments**

- `ped`: data.frame with integer columns corresponding to ID, SIRE, DAM. Missing value is 0.
- `A`: Relationship matrix A in a tabular format created by function `tabA`.

**Value**

Dominance relationship data.frame

**Examples**

```r
ped = data.frame(ID=1:6, SIRE=c(0,0,1,3,1,4), DAM=c(0,0,2,2,2,5))
tabD(ped, tabA(ped))
```

---

**tabDinv**

*Inverse of the dominance relationship matrix D in a tabular format*

---

**Description**

Creates the data.frame of the inverse of the pedigree-based dominance relationship matrix.

**Usage**

```r
tabDinv(ped, A)
```

**Arguments**

- `ped`: data.frame with integer columns corresponding to ID, SIRE, DAM. Missing value is 0.
- `A`: Relationship matrix A in a tabular format created by function `tabA`.
Value

data.frame of the inverse of the dominance relationship matrix

Examples

```r
ped = data.frame(ID=1:6, SIRE=c(0,0,1,3,1,4), DAM=c(0,0,2,2,2,5))
tabDinv(ped, tabA(ped))
```
Index

buildA, 3
buildD, 3

gghead, 4
groups-package, 2

inb, 5

mat2tab, 6

offspring, 6

pedcheck, 7
peddown, 8
pedup, 8
pruneped, 9

Qgpu, 10
qmat, 11
qmatL, 11
qmatXL, 12

renum, 13
rg, 13

smgsped, 14

tab2mat, 15
tabA, 15
tabAinv, 16
tabD, 17
tabDinv, 17