

# Package ‘gggroups’

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**Title** Pedigree and Genetic Groups

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**Description** Calculates additive genetic relationship matrix and its inverse, 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.

**License** GPL-3

**LazyData** true

**Suggests** doParallel (>= 1.0.14), foreach (>= 1.4.4)

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gggroups-package	<i>Pedigree and genetic groups</i>
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**Description**

This package contains pedigree processing and analyzing functions, including functions for checking and renumbering the pedigree, making the pedigree relationship matrix and its inverse, 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 (**g**) to the genetic merit of animals (**u**), which is equal to **Qg + 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.

**Author(s)**

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**References**

Quaas, R. L. 1988. Additive Genetic Model with Groups and Relationships. J. Dairy Sci., 71:1338-1345. <doi:10.3168/jds.S0022-0302(88)79691-5>

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buildA	<i>Relationship matrix A</i>
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**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)
```

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gghead

*Append genetic groups to the pedigree*


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**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**

```
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 animal IDs.

```
3 1 2
4 3 2
6 4 5
5 1 2
```

Then, gghead is applied to this pedigree (see the example).

**Value**

Processed pedigree data.frame

**Examples**

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

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pedcheck	<i>Basic pedigree checks</i>
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**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)
```

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peddown	<i>Downward pedigree extraction</i>
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**Description**

Extract pedigree downward for one or a group of animals to find their descendants

**Usage**

```
peddown(ped, parents)
```

**Arguments**

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

`parents` : Vector of animal(s), from which the new pedigree is being extracted.

**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))
peddown(ped, c(1,4))
```

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pedup	<i>Upward pedigree extraction</i>
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**Description**

Extract pedigree upward for one or a group of animals to find their ascendants

**Usage**

```
pedup(ped, progeny)
```

**Arguments**

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

`progeny` : Vector of animal(s), from which the new pedigree is being extracted.

**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))
```

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pruneped	<i>Pedigree pruning</i>
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## Description

Prunning 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 animals
mode	: strict or loose

## Details

In strict pruning, animals without progeny and phenotype are recursively deleted from the pedigree. Therefore, all uninfluent animals are deleted. The downside is that animals 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 animals to thier founders, and then the pedigree is downward extracted from the founders.

## Value

newped : Pruned pedigree data.frame

## Examples

```
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	<i>Vector <math>\mathbf{Qg} + \mathbf{u}</math></i>
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**Description**

Adds genetic group contributions to the genetic merit of animals.

**Usage**

Qgpu(Q, sol)

**Arguments**

- Q : The output matrix from qmat (for more details: ?qmat)
- sol : data.frame with 2 numeric columns corresponding to ID, EBV ( $[\mathbf{g}, \mathbf{u}]$ ), where  $\mathbf{g}$  and  $\mathbf{u}$  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  $\mathbf{Q}$ .

**Value**

Vector of  $\mathbf{Qg} + \mathbf{u}$

**Examples**

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

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qmat	<i>Matrix <math>\mathbf{Q}</math></i>
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**Description**

Creates the genetic group contribution matrix.

**Usage**

qmat(ped2)

**Arguments**

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

**Value**

Matrix **Q**

**Examples**

```
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)
```

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qmatL

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*Matrix **Q** for large pedigrees*


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**Description**

Creates the genetic group contribution matrix for large pedigrees.

**Usage**

```
qmatL(ped2)
```

**Arguments**

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

**Details**

Calculation of the genetic group contribution matrix for large pedigrees requires a lot of memory and time. This might not be possible on ordinary computers, using the function qmat. The function qmatL takes less RAM and time, making the calculation possible for ordinary computers.

**Value**

Matrix **Q**

**Examples**

```
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)
```



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qmatXL	<i>Matrix <b>Q</b> for large pedigrees (parallel processing)</i>
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**Description**

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

**Usage**

```
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**

Matrix **Q**

**Examples**

```
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)
```

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renum	<i>Pedigree renumbering</i>
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**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 renumbered IDs.  
Cross-reference data.frame with 2 columns for original and renumbered IDs.

**Examples**

```
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)
```

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tab2mat	<i>Tabular to matrix</i>
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**Description**

Converts tabular data to matrix data.

**Usage**

```
tab2mat(tab)
```

**Arguments**

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

**Value**

matrix

**Examples**

```
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))
```

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tabA	<i>Relationship matrix <b>A</b> in a tabular format</i>
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---

**Description**

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

**Usage**

```
tabA(ped)
```

**Arguments**

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

**Value**

Genetic relationship 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))
tabA(ped)
```

---

tabAinv	<i>Inverse of the relationship matrix <b>A</b> in a tabular format</i>
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**Description**

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

**Usage**

```
tabAinv(ped, inb)
```

**Arguments**

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

inb : Inbreeding coefficients in the order of animals in the relationship matrix.

**Value**

Inverse of the genetic relationship 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))
inb = c(0, 0, 0, 0.25, 0, 0.25)
# or
(inb = diag(buildA(ped)) - 1)
# or
inb = tabA(ped); (inb[inb[,1]==inb[,2],]$a - 1)
tabAinv(ped, inb)
```

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