

# Package ‘ggroups’

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**Title** Pedigree and Genetic Groups

**Version** 2.1.2

**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, calculating inbreeding coefficients (Meuwissen & Luo, 1992 <[doi:10.1186/1297-9686-24-4-305](https://doi.org/10.1186/1297-9686-24-4-305)>), 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](https://doi.org/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

**URL** <https://github.com/nilforooshan/ggroups>

**BugReports** <https://github.com/nilforooshan/ggroups/issues>

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ggroups-package

*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, calculating inbreeding coefficients, 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 ( $\mathbf{Q}$ ) is required to weight and add genetic group effects ( $\hat{\mathbf{g}}$ ) to the genetic merit of animals ( $\hat{\mathbf{u}}$ ), which is equal to  $\mathbf{Q}\hat{\mathbf{g}} + \hat{\mathbf{u}}$  (Quaas, 1988). Calculating  $\mathbf{Q}$  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**

- Meuwissen, T. and Luo, Z. 1992. Computing Inbreeding Coefficients in Large Populations. *Genet. Sel. Evol.*, 24:305. <doi:10.1186/1297-9686-24-4-305>
- Mrode, R. A. 2005. *Linear Models for the Prediction of Animal Breeding Values*, 2nd ed. Cambridge, MA: CABI Publishing.
- 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>

---

buildA	<i>Relationship matrix A</i>
--------	------------------------------

---

**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	<i>Relationship matrix D</i>
--------	------------------------------

---

**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**

```
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))
```

---

gghead

*Append genetic groups to the pedigree*

---

**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 progeny 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)
```

---

inb	<i>Individual's inbreeding coefficient</i>
-----	--

---

**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**

Inbreeding coefficient of the individual

**Examples**

```
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)
```

---

inbreed	<i>Inbreeding coefficients</i>
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---

**Description**

Calculates inbreeding coefficients for all animals in the pedigree.

**Usage**

```
inbreed(ped)
```

**Arguments**

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

**Value**

Vector of inbreeding coefficients

**Examples**

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

---

mat2tab	<i>Matrix to tabular</i>
---------	--------------------------

---

**Description**

Converts matrix data to tabular data.

**Usage**

```
mat2tab(mat)
```

**Arguments**

mat : matrix

**Value**

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

**Examples**

```
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	<i>Descendants of an individual per generation</i>
-----------	--

---

**Description**

Counts and collects progeny and phenotyped progeny of an individual in successive generations. In pedigrees with generation overlap, animals are reported in the 1st generation that they appear in, rather than in multiple generations.

**Usage**

```
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(0,0,1,1,0,0,0,0,0,4,5,5,7,0,0,9,0,0,12),
  V3 = c(0,0,0,2,0,2,0,3,3,3,0,6,8,8,8,10,11,11,0))
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
```

---

pedcheck                      *Basic pedigree checks*

---

### 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                      *Downward pedigree extraction*

---

### 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**

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))
peddown(ped, 1, maxgen=1)
```

---

pedup

*Upward pedigree extraction*

---

**Description**

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

**Usage**

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

**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**

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)
```

prunedped

*Pedigree pruning*

---

**Description**

Pruning pedigree in two different modes (strict, loose)

**Usage**

```
prunedped(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**

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)
prunedped(ped, pheno, mode="strict")
prunedped(ped, pheno, mode="loose")
```

---

Qgpu *Vector  $\mathbf{Qg} + \mathbf{u}$*

---

**Description**

Adds genetic group contributions to the genetic merit of individuals.

**Usage**

```
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 ( $[\hat{\mathbf{g}}, \hat{\mathbf{u}}]$ ), where  $\hat{\mathbf{g}}$  and  $\hat{\mathbf{u}}$  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 **Q**.

**Value**

Vector of  $\mathbf{Q}\hat{\mathbf{g}} + \hat{\mathbf{u}}$

**Examples**

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

---

qmat *Matrix  $\mathbf{Q}$*

---

**Description**

Creates the genetic group contribution matrix.

**Usage**

```
qmat(ped2)
```

**Arguments**

**ped2** : The output data.frame from [gghead](#) (for more details: [?gghead](#))

**Value**

**Q** matrix

**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)
```

---

qmatL

*Matrix **Q** for large pedigrees*

---

**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](#))

**Value**

**Q** matrix

**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)
```

---

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

---

**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**

**Q** matrix

**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)
```

---

renum	<i>Pedigree renumbering</i>
-------	-----------------------------

---

**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.

`xrf` : 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)$newped
renum(ped)$xrf
```

---

<code>rg</code>	<i>Genetic relationship coefficient</i>
-----------------	---

---

**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

**Value**

Genetic relationship coefficient between the two individuals

**Examples**

```
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	<i>Sire-maternal grandsire (S-MGS) pedigree</i>
---------	---

---

**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**

S-MGS pedigree data.frame

**Examples**

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

---

tab2mat	<i>Tabular to matrix</i>
---------	--------------------------

---

**Description**

Converts tabular data to matrix data.

**Usage**

```
tab2mat(tab)
```

**Arguments**

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

**Value**

Converted data.frame to 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))
```

---

tabA	<i>Relationship matrix <math>\mathbf{A}</math> in a tabular format</i>
------	--

---

**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 <math>\mathbf{A}</math> in a tabular format</i>
---------	---

---

**Description**

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

**Usage**

```
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**

```
ped = data.frame(ID=1:6, SIRE=c(0,0,1,3,1,4), DAM=c(0,0,2,2,2,5))
inbr = c(0, 0, 0, 0.25, 0, 0.25)
# or
(inbr = diag(buildA(ped)) - 1)
# or
inbr = tabA(ped); (inbr[inbr[,1]==inbr[,2],]$a - 1)
# or
# For individual inbreeding values, use function inb.
tabAinv(ped, inbr)
```

---

tabD

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


---

**Description**

Creates the pedigree-based dominance relationship data.frame.

**Usage**

```
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**

```
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**

```
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**

```
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))
```

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