# Package 'ggroups'

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**Type** Package

**Title** Genetic Group Contributions

**Version** 0.1.2

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**Description** Genetic group contributions to individuals in a pedigree.

**License** GPL-3

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

**Encoding** UTF-8

**LazyData** true

**RoxygenNote** 6.1.0

**Repository** GitHub

**Installation** devtools::install_github('nilforooshan/ggroups')
Alternatively:
installer = file.path(tempdir(), 'ggroups_0.1.2.tar.gz')
download.file('https://github.com/nilforooshan/Link-resources/raw/master/link_resources/ggroups_0.1.2.tar.gz', destfile=installer)
install.packages(installer, repos=NULL, type='source')

## R topics documented:

## ggroups-package *Genetic Group Contribution*

### Description

This package contains functions related to calculating the matrix of genetic group contributions to individuals in a pedigree, and adding genetic group contributions to genetic merit of animals in a pedigree. It also calculates the genetic relationship matrix **A** from the pedigree.

### Details

The concept of genetic groups or phantom parent groups is based on the fact that unknown parents do not belong to the same base population and they might come from different genetic levels. With **Q**, $\hat{\mathbf{g}}$, and $\hat{\mathbf{u}}$ being the matrix of genetic group contributions to individuals in the pedigree, the vector of predicted additive genetic merit of animals, and the vector of predicted genetic group effects, respectively, the contribution of genetic groups should be added to the predicted genetic merit of animals ($\mathbf{Q}\hat{\mathbf{g}} + \hat{\mathbf{u}}$).

Forming Mixed Model Equations corresponding to the model, $\hat{\mathbf{u}}$ and $\hat{\mathbf{g}}$ are predicted (Quaas, 1988: Eq. [3]). However, using Quaas and Pollak (1981) transformation, $\mathbf{Q}\hat{\mathbf{g}} + \hat{\mathbf{u}}$ can be obtained directly (Quaas, 1988: Eq. [4]).

Some solver packages obtain $\mathbf{Q}\hat{\mathbf{g}} + \hat{\mathbf{u}}$ directly, some not. The aim of this package is to find the genetic contribution of each genetic group on each individual in the pedigree (matrix **Q**), and also calculating $\mathbf{Q}\hat{\mathbf{g}} + \hat{\mathbf{u}}$, given the pedigree and a vector of [$\hat{\mathbf{g}}$, $\hat{\mathbf{u}}$].

### Author(s)

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### References

Quaas, R. L. 1988. Additive Genetic Model with Groups and Relationships. J. Dairy Sci., 71:1338-1345.

Quaas, R. L., and E. J. Pollak. 1981. Modified equations for sire models with groups. J. Dairy Sci., 64:1868-1872.

## buildA *Relationship matrix* **A**

### Description

Creates the pedigree-based additive genetic relationship matrix.

### Usage

```
buildA(ped)
```

### Arguments

ped : The pedigree `data.frame` with integer columns corresponding to ID, SIRE, DAM.

### Value

A : 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 *Pedigree processing*

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### Description

Does specific pedigree checks; adds genetic groups to the head of the pedigree and sorts it.

### Usage

```
gghead(ped)
```

### Arguments

ped : A `data.frame` with integer columns corresponding to ID, SIRE, DAM

### 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

This pedigree is used as an example.

## Value

ped2 : A 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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`Qgpu` *Vector* **Qg** + **u**

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## Description

Adds genetic group contributions to genetic merit of animals in a pedigree.

## Usage

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

## Arguments

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

## Value

uhatplus : 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 = qmat(gghead(ped))
ghat = c(0.1, -0.1)
uhat = seq(-0.15, 0.15, 0.1)
sol = data.frame(ID=1:6, EBV=c(ghat, uhat))
Qgpu(Q, sol)
```

qmat *Matrix* **Q**

## Description

Creates the genetic group contribution matrix.

## Usage

```
qmat(ped2)
```

## Arguments

| | |
|---|---|
| ped2 | : The output of gghead; for more details: ?gghead |

## Value

Q : 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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