

# Package ‘gggroups’

September 1, 2018

**Type** Package

**Title** Genetic group contributions

**Version** 0.1.0

**Author** Mohammad Ali Nilforooshan

**Maintainer** Mohammad Ali Nilforooshan <m.a.nilforooshan@gmail.com>

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

**License** GPL (>= 2)

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

**Encoding** UTF-8

**LazyData** true

**Imports** pedigreemm

**RoxygenNote** 6.1.0

**Repository** GitHub

**Date** 2018-09-01

**Installation** devtools::install\_github('nilforooshan/gggroups')

## R topics documented:

gggroups . . . . .	2
Qgpu . . . . .	2
qmat . . . . .	3
<b>Index</b>	<b>5</b>

---

ggroups

*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.

### 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  $\mathbf{Q}$ ,  $\hat{\mathbf{g}}$ , 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  $\mathbf{Q}$ ), 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)

Mohammad Ali Nilforooshan <m.a.nilforooshan@gmail.com>

### 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.

---

Qgpu

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


---

### Description

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

### Usage

Qgpu(Qmat, sol)

Arguments

Qmat

: The output matrix from function qmat

sol

: A data.frame with 2 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(1:2,4:7), SIRE=c(0,0,1,4,1,5), DAM=c(0,0,2,2,2,6))
Qmat = qmat(ped)
# For details about qmat and ped: ?qmat
sol = data.frame(ID=c(1:2,4:7), EBV=c(0.2,seq(-0.1,0.3,0.1)))
Qgpu(Qmat, sol)
```

qmat	Create matrix $\mathbf{Q}$
------	----------------------------

Description

Creates the genetic group contribution matrix.

Usage

```
qmat(ped)
```

Arguments

ped

: A data.frame with 3 integer columns corresponding to ID, SIRE, DAM

Details

Individuals are sorted numerically, with parent IDs smaller than progeny ID. Only genetic groups should have unknown parents, denoted as 0.

Consider this simple pedigree:

```
4 0 0
5 4 0
6 0 0
7 5 6
```

First, unknown parents are replaced with the corresponding genetic groups.

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

```
7 5 6
```

Then, rows corresponding to genetic groups are added to the head of the pedigree.

```
1 0 0
```

```
2 0 0
```

```
4 1 2
```

```
5 4 2
```

```
6 1 2
```

```
7 5 6
```

This pedigree is used as a `data.frame`. See the example.

**Value**

Qmat : Matrix **Q**

**Examples**

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

# Index

gggroups, [2](#)

gggroups-package (gggroups), [2](#)

Qgpu, [2](#)

qmat, [3](#)