Package 'gvcR'

October 13, 2022

Type Package

Title Genotypic Variance Components

Version 0.1.0

Maintainer Muhammad Yaseen <myaseen208@gmail.com>

Description Functionalities to compute model based genetic components i.e. genotypic variance, phenotypic variance and heritability for given traits of different genotypes from replicated data using methodology explained by Burton, G. W. & Devane, E. H. (1953) (<doi:10.2134/agronj1953.00021962004500100005x>) and Allard, R.W. (2010, ISBN:8126524154).

Depends R (>= 3.2.3)

Imports dplyr, eda4treeR, lme4, magrittr, stats

License GPL-3

URL https://github.com/MYaseen208/gvcR

LazyData TRUE

RoxygenNote 6.0.1

Suggests testthat

NeedsCompilation no

Author Muhammad Yaseen [aut, cre],
Sami Ullah [aut, ctb]

Repository CRAN

Date/Publication 2018-02-20 18:56:27 UTC

R topics documented:

gvcR	*Genotypic Variance Components*

Description

Functionalities to compute model based genetic components i.e genotypic, phenotypic variances and heritability for given traits of different genotypes from replicated data using methodology explained by Burton, G. W. & Devane, E. H. (1953) (<doi:10.2134/agronj1953.00021962004500100005x>) and Allard, R.W. (2010, ISBN:8126524154).

Author(s)

1. Sami Ullah (<samiullahuos@gmail.com>)
2. Muhammad Yaseen (<myaseen208@gmail.com>)

References

1. R.K. Singh and B.D.Chaudhary *Biometrical Methods in Quantitative Genetic Analysis.* Kalyani Publishers, New Delhi

1. Williams, E.R., Matheson, A.C. and Harwood, C.E. (2002).*Experimental Design and Analysis for Tree Improvement.* CSIRO Publishing.

gvc_gvar	*Genotypic Variance*

Description

gvc_gvar computes genotypic variances for given traits of different genotypes from replicated data using methodology explained by Burton, G. W. & Devane, E. H. (1953) (<doi:10.2134/agronj1953.00021962004500100005x and Allard, R.W. (2010, ISBN:8126524154).

Usage

```
gvc_gvar(y, x = NULL, rep, geno, env, data)
```

Arguments

y	Response
x	Covariate by default NULL
rep	Repliction
geno	Genotypic Factor
env	Environmental Factor
data	data.frame

Value

Genotypic Variance

Author(s)

1. Sami Ullah (<samiullahuos@gmail.com>)
2. Muhammad Yaseen (<myaseen208@gmail.com>)

References

1. R.K. Singh and B.D.Chaudhary *Biometrical Methods in Quantitative Genetic Analysis.* Kalyani Publishers, New Delhi

1. Williams, E.R., Matheson, A.C. and Harwood, C.E. (2002).*Experimental Design and Analysis for Tree Improvement.* CSIRO Publishing.

Examples

```
set.seed(12345)
Response <- c(
                rnorm(48, mean = 15000, sd = 500)
              , rnorm(48, mean =  5000, sd = 500)
              , rnorm(48, mean =  1000, sd = 500)
              )
Rep      <- as.factor(rep(1:3, each = 48))
Variety  <- gl(n = 4, k =  4, length = 144, labels = letters[1:4])
Env      <- gl(n = 3, k = 16, length = 144, labels = letters[1:3])
df1      <- data.frame(Response, Rep, Variety, Env)

# Genotypic Variance
gvar <-
 gvc_gvar(
          y    = Response
        , rep  = Rep
        , geno = Variety
        , env  = Env
        , data = df1
        )
gvar

library(eda4treeR)
data(DataExam6.2)
gvar <-
  gvc_gvar(
          y    = Dbh.mean
        , rep  = Replication
        , geno = Family
        , env  = Province
        , data = DataExam6.2
        )
gvar
```

---

gvc_herit   *Heritability*

Description

gvc_herit computes model based genetic heritability for given traits of different genotypes from replicated data using methodology explained by Burton, G. W. & Devane, E. H. (1953) (<doi:10.2134/agronj1953.000219620 and Allard, R.W. (2010, ISBN:8126524154).

Usage

```
gvc_herit(y, x = NULL, rep, geno, env, data)
```

Arguments

y	Response
x	Covariate by default NULL
rep	Repliction
geno	Genotypic Factor
env	Environmental Factor
data	data.frame

Value

Heritability

Author(s)

1. Sami Ullah (<samiullahuos@gmail.com>)

2. Muhammad Yaseen (<myaseen208@gmail.com>)

References

1. Williams, E.R., Matheson, A.C. and Harwood, C.E. (2002).*Experimental Design and Analysis for Tree Improvement*. CSIRO Publishing.

Examples

```
set.seed(12345)
Response <- c(
                rnorm(48, mean = 15000, sd = 500)
              , rnorm(48, mean =  5000, sd = 500)
              , rnorm(48, mean =  1000, sd = 500)
              )
Rep      <- as.factor(rep(1:3, each = 48))
Variety  <- gl(n = 4, k =  4, length = 144, labels = letters[1:4])
```

```
Env       <- gl(n = 3, k = 16, length = 144, labels = letters[1:3])
df1       <- data.frame(Response, Rep, Variety, Env)

# Heritability
herit <-
  gvc_herit(
          y    = Response
        , rep  = Rep
        , geno = Variety
        , env  = Env
        , data = df1
        )
herit

library(eda4treeR)
data(DataExam6.2)
herit <-
  gvc_herit(
          y    = Dbh.mean
        , rep  = Replication
        , geno = Family
        , env  = Province
        , data = DataExam6.2
        )
herit
```

---

gvc_pvar   *Phenotypic Variance*

Description

gvc_pvar computes phenotypic variances for given traits of different genotypes from replicated data
using methodology explained by Burton, G. W. & Devane, E. H. (1953) (<doi:10.2134/agronj1953.00021962004500100005x>)
and Allard, R.W. (2010, ISBN:8126524154).

Usage

```
gvc_pvar(y, x = NULL, rep, geno, env, data)
```

Arguments

y	Response
x	Covariate by default NULL
rep	Repliction
geno	Genotypic Factor
env	Environmental Factor
data	data.frame

Value

Phenotypic Variance

Author(s)

1. Sami Ullah (<samiullahuos@gmail.com>)
2. Muhammad Yaseen (<myaseen208@gmail.com>)

References

1. R.K. Singh and B.D.Chaudhary *Biometrical Methods in Quantitative Genetic Analysis*. Kalyani Publishers, New Delhi

1. Williams, E.R., Matheson, A.C. and Harwood, C.E. (2002).*Experimental Design and Analysis for Tree Improvement*. CSIRO Publishing.

Examples

```
set.seed(12345)
Response <- c(
               rnorm(48, mean = 15000, sd = 500)
            , rnorm(48, mean =  5000, sd = 500)
            , rnorm(48, mean =  1000, sd = 500)
            )
Rep      <- as.factor(rep(1:3, each = 48))
Variety  <- gl(n = 4, k =  4, length = 144, labels = letters[1:4])
Env      <- gl(n = 3, k = 16, length = 144, labels = letters[1:3])
df1      <- data.frame(Response, Rep, Variety, Env)

#' # Penotypic Variance
pvar <-
  gvc_pvar(
           y    = Response
         , rep  = Rep
         , geno = Variety
         , env  = Env
         , data = df1
         )
pvar

library(eda4treeR)
data(DataExam6.2)
pvar <-
  gvc_pvar(
           y    = Dbh.mean
         , rep  = Replication
         , geno = Family
         , env  = Province
         , data = DataExam6.2
         )
pvar
```

Index