

# Package ‘gvcR’

February 20, 2018

**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

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**Repository** CRAN

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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	Replication
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	Replication
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**

<code>y</code>	Response
<code>x</code>	Covariate by default NULL
<code>rep</code>	Replication
<code>geno</code>	Genotypic Factor
<code>env</code>	Environmental Factor
<code>data</code>	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
```

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