

# Package ‘gvcR’

October 1, 2024

**Type** Package

**Title** Genotypic Variance Components

**Version** 0.4.0

**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, rlang, stats, supernova, tibble, R6

**License** GPL-3

**URL** <https://myaseen208.com/gvcR/> <https://github.com/MYaseen208/gvcR>

**BugReports** <https://github.com/myaseen208/gvcR/issues>

**RoxygenNote** 7.3.2

**Encoding** UTF-8

**Suggests** testthat

**NeedsCompilation** no

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

**Repository** CRAN

**Date/Publication** 2024-10-01 06:50:02 UTC

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gvc

*Genotypic Variance*

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### Description

The 'gvc' class calculates genotypic variance, phenotypic variance, and broad-sense heritability from replicated data.

### Details

The 'gvc' class uses methods explained by Burton, G. W. & Devane, E. H. (1953) and Allard, R.W. (2010). It includes methods for calculating genetic variance, phenotypic variance, and heritability.

### Public fields

data A 'tibble' containing the data for analysis.

y The name of the response variable.

x The name of the covariate (optional).

rep The name of the replicate factor.

gen The name of the genotype factor.

env The name of the environmental factor.

### Methods

#### Public methods:

- [gvc\\$new\(\)](#)
- [gvc\\$calculate\\_gvar\(\)](#)
- [gvc\\$calculate\\_pvar\(\)](#)
- [gvc\\$calculate\\_herit\(\)](#)
- [gvc\\$clone\(\)](#)

**Method** `new()`: Initialize the 'gvc' class with the data and variable names.

*Usage:*

```
gvc$new(.data, .y, .x = NULL, .rep, .gen, .env)
```

*Arguments:*

.data A 'data.frame' containing the data for analysis.

.y The response variable.

.x The covariate (optional).

.rep The replicate factor.

.gen The genotype factor.

.env The environmental factor.

*Returns:* An instance of the 'gvc' class.

**Method** `calculate_gvar()`: Calculate genetic variance.

*Usage:*

```
gvc$calculate_gvar()
```

*Returns:* A list with the genetic variance ('gvar').

**Method** `calculate_pvar()`: Calculate phenotypic variance.

*Usage:*

```
gvc$calculate_pvar()
```

*Returns:* A list with the phenotypic variance ('pvar').

**Method** `calculate_herit()`: Calculate broad-sense heritability.

*Usage:*

```
gvc$calculate_herit()
```

*Returns:* A list with the heritability ('h2').

**Method** `clone()`: The objects of this class are cloneable with this method.

*Usage:*

```
gvc$clone(deep = FALSE)
```

*Arguments:*

`deep` Whether to make a deep clone.

## Examples

```
df1 <- data.frame(
  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])
)

# Create an instance of the class
gvc1 <- gvc$new(
  .data = df1
  , .y   = Response
  , .rep = Rep
  , .gen = Variety
  , .env = Env
)

# Calculate genetic variance (gvar)
gvc1$calculate_gvar()

# Calculate phenotypic variance (pvar)
gvc1$calculate_pvar()
```

```
# Calculate heritability (h2)
gvc1$calculate_herit()
```

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gvcR

*Genotypic Variance Components*

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### **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.

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