

Package ‘gvcR’

September 14, 2024

Type Package

Title Genotypic Variance Components

Version 0.3.0

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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

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Repository CRAN

Date/Publication 2024-09-14 14:30:13 UTC

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gvc

Genotypic Variance

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()
```

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).

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References

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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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