Package: vGWAS (via r-universe)

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Type Package

Title Variance Heterogeneity Genome-wide Association Study - Reimplementation

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Description The package reimplementation provides models and tests for variance heterogeneity genome-wide association study (vGWAS).

License GPL

Encoding UTF-8

LazyData true

Depends R (>= 4.4.0)

Imports methods, stats, doParallel (>= 1.0.17), foreach(>= 1.5.2), Matrix(>= 1.7-0), onewaytests (>= 3.0)

Suggests dglm (>= 1.8.3), genio (>= 1.1.2), hglm (>= 2.2-1), knitr, rmarkdown

VignetteBuilder knitr

NeedsCompilation yes

URL https://github.com/kullrich/vGWAS, https://kullrich.github.io/vGWAS/

BugReports https://github.com/kullrich/vGWAS/issues

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Repository https://kullrich.r-universe.dev

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RemoteUrl https://github.com/kullrich/vgwas

RemoteRef HEAD

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Contents

`bfmedian.test` *Brown-Forsythe's Test of Equality of Variances*

Description

The function performs the robust Brown-Forsythe test using the group medians.

Usage

```
bfmedian.test(formula, data, alpha = 0.05, na.rm = TRUE,
verbose = TRUE)
```

Arguments

`formula`	a formula of the form lhs ~ rhs where lhs gives the sample values and rhs the corresponding groups.
`data`	a tibble or data frame containing the variables in formula.
`alpha`	the level of significance to assess the statistical difference. Default is set to alpha = 0.05.
`na.rm`	a logical value indicating whether NA values should be stripped before the computation proceeds. Default us set to TRUE.
`verbose`	a logical for printing output to R console.

Details

Levene (1960) proposed a test for homogeneity of variances in k groups which is based on the ANOVA statistic applied to absolute deviations of observations from the corresponding group mean. The robust Brown-Forsythe version of the Levene-type test substitutes the group mean by the group median in the classical Levene statistic.

Value

A list with class "owt" containing the following components:

`statistic`	the Brown-Forsythe test statistic.
`parameter`	the parameter(s) of the approximate F distribution of the test statistic.
`p.value`	the p-value of the test.
`alpha`	the level of significance to assess the statistical difference.
`method`	the character string "Brown-Forsythe-Median Test".
`data`	a data frame containing the variables in which NA values (if exist) are removed.
`formula`	a formula of the form lhs ~ rhs where lhs gives the sample values and rhs the corresponding groups.

Note

Modified from the `onewaytests` package and `vGWAS`.

Author(s)

Kristian Ullrich

References

Brown, M. B. and Forsythe, A.B. (1974). **Robust tests for equality of variances.** *Journal of the American Statistical Association*, **69**, 364-367.

Levene, H. (1960). **Robust Tests for Equality of Variances**, *in Contributions to Probability and Statistics*, ed. I. Olkin, Palo Alto, CA: Stanford Univ. Press.

Examples

```
data(pheno)
data(geno)
df <- data.frame(phenotype = pheno, genotype = as.factor(geno[, 911]))
bfmedian.test(phenotype ~ genotype, data = df)
```

`brown.forsythe.test` *Brown-Forsythe's Test of Equality of Variances*

Description

The function performs the robust Brown-Forsythe test using the group medians. Instead of the ANOVA statistic, the Kruskal-Wallis ANOVA may also be applied using this function.

Usage

```
brown.forsythe.test(y, group, kruskal.test=FALSE)
```

Arguments

`y`	a numeric vector of data values.
`group`	factor of the data.
`kruskal.test`	a `logical` value specifying whether to use Kruskal-Wallis statistic. The default option is `FALSE`, i.e., the usual ANOVA statistic is used in place of Kruskal-Wallis statistic.

Details

Levene (1960) proposed a test for homogeneity of variances in k groups which is based on the ANOVA statistic applied to absolute deviations of observations from the corresponding group mean. The robust Brown-Forsythe version of the Levene-type test substites the group mean by the group median in the classical Levene statistic.

Value

A list with the following numeric components.

`statistic`	the value of the test statistic.
`p.value`	the p-value of the test.
`method`	type of test performed.
`data.name`	a character string giving the name of the data.

Note

Modified from the `lawstat` package.

Author(s)

Xia Shen

References

Brown, M. B. and Forsythe, A.B. (1974). **Robust tests for equality of variances.** *Journal of the American Statistical Association*, **69**, 364-367.

Levene, H. (1960). **Robust Tests for Equality of Variances**, *in Contributions to Probability and Statistics*, ed. I. Olkin, Palo Alto, CA: Stanford Univ. Press.

Examples

```
data(pheno)
data(geno)
brown.forsythe.test(pheno, geno[,911])
```

---

chr-data *Chromosome Indices for The Markers of The Simulated Data*

Description

Chromosome indices for the markers of the simulated data

Usage

```
data(chr)
```

Format

A numeric vector of chromosome indices for the 20K simulated markers.

Examples

```
data("chr", package="vGWAS")
table(chr)
```

---

geno-data *The Marker Genotypes of The Simulated Data*

Description

The marker genotypes of the simulated data

Usage

```
data(geno)
```

Format

A character matrix of size (number of individuals) times (number of markers in the genome).

Details

Note that there is only one column for each marker.

Examples

```
data("geno", package="vGWAS")
```

`geno.df-data` *The Marker Genotypes of The Simulated Data (as data.frame)*

Description

The marker genotypes of the simulated data

Usage

```
data(geno.df)
```

Format

A data.frame of size (number of markers in the genome) times (number of individuals).

Details

Note that there is only one column for each marker.

Examples

```
data("geno.df", package="vGWAS")
```

geno.num-data *The Marker Genotypes of The Simulated Data (as matrix)*

Description

The marker genotypes of the simulated data

Usage

```
data(geno.num)
```

Format

A matrix of size (number of individuals) times (number of markers in the genome).

Details

Note that there is only one column for each marker.

Examples

```
data("geno.num", package="vGWAS")
```

geno.sparse-data *The Marker Genotypes of The Simulated Data (as sparse matrix)*

Description

The marker genotypes of the simulated data

Usage

```
data(geno.sparse)
```

Format

A sparse matrix of size (number of markers in the genome) times (number of individuals).

Details

Note that there is only one column for each marker.

Examples

```
data("geno.sparse", package="vGWAS")
```

getMAF *Get minor-allele-frequency*

Description

Calculates minor-allele-frequency (MAF)

Usage

```
getMAF(geno.matrix, geno.snp = "row", include.het = FALSE)
```

Arguments

geno.matrix	a matrix or data.frame or sparseMatrix with individuals as columns and markers as rows (geno.snp = "row") or individuals as rows and markers as columns (geno.snp = "col").
geno.snp	if individuals at columns and markers at rows use "row" else if individuals at rows and markers at columns use "col"
include.het	specify if heterozygous calls should be split and added equally to homozygous ref and alt counts (default = FALSE)

Value

a vector containing minor-allele-frequency values

Author(s)

Kristian Ullrich

Examples

```
data(geno)
maf <- getMAF(geno.matrix = geno, geno.snp = "col")
data(geno.num)
maf.num <- getMAF(geno.matrix = geno.num, geno.snp = "col")
data(geno.df)
maf.df <- getMAF(geno.matrix = geno.df, geno.snp = "row")
data(geno.sparse)
maf.sparse <- getMAF(geno.matrix = geno.sparse, geno.snp = "row")
```

map-data *Map Positions for The Markers of The Simulated Data*

Description

Map positions for the markers of the simulated data

Usage

```
data(map)
```

Format

A numeric vector of chromosomal map positions of the 20K simulated markers.

Examples

```
data("map", package="vGWAS")
```

package-vGWAS *Variance Heterogeneity Genome-wide Association Study*

Description

The package provides models and tests for variance heterogeneity genome-wide association study (vGWAS). "_PACKAGE"

Author(s)

Xia Shen

References

Shen, X., Pettersson, M., Ronnegard, L. and Carlborg, O. (2011): **Inheritance beyond plain heritability: variance-controlling genes in *Arabidopsis thaliana***. *PLoS Genetics*, **8**, e1002839.

Ronnegard, L., Shen, X. and Alam, M. (2011): **hglm: A Package for Fitting Hierarchical Generalized Linear Models**. *The R Journal*, **2**(2), 20-28.

Brown, M. B. and Forsythe, A.B. (1974). **Robust tests for equality of variances.** *Journal of the American Statistical Association*, **69**, 364-367.

Levene, H. (1960). **Robust Tests for Equality of Variances**, *in Contributions to Probability and Statistics*, ed. I. Olkin, Palo Alto, CA: Stanford Univ. Press.

See Also

R package `lawstat` for other types of nonparametric variance tests and `onewaystats`.

`pheno-data` *Phenotypic Values for The Markers of The Simulated Data*

Description

Phenotypic values for the markers of the simulated data

Usage

```
data(pheno)
```

Format

A numeric vector of the phenotypic values of 93 simulated individuals.

Details

Note that there is only one column for each marker.

Examples

```
data("pheno", package="vGWAS")
hist(pheno, breaks = 30)
```

`plot.vGWAS` *Variance GWA Manhattan Plot*

Description

The function plots the variance GWA result for the given scan object.

Usage

```
## S3 method for class 'vGWAS'
plot(x, sig.threshold = NULL, low.log.p = 0,
pch = 16, cex = 0.6, col.manhattan = c("slateblue4", "olivedrab"),
col.sig.threshold = "darkgoldenrod", ...)
```

Arguments

x	a result object from vGWAS scan. It can be any list or data.frame that contains chromosome, marker.map, and p.value, with class = 'vGWAS'. See vGWAS.
sig.threshold	a numeric value giving the significance threshold for -log(pvalues, 10). If NULL, Bonferroni correction will be used.
low.log.p	a numeric value giving the lower limit of the -log(pvalues, 10) to plot.
pch	point character. See par.
cex	size of points. See par.
col.manhattan	two colors as a vector for the Manhattan plot.
col.sig.threshold	one color for the significance threshold
...	not in use

Value

a plot for viewing vGWAS result.

Author(s)

Xia Shen

References

Shen, X., Pettersson, M., Ronnegard, L. and Carlborg, O. (2011): **Inheritance beyond plain heritability: variance-controlling genes in *Arabidopsis thaliana***. *PLoS Genetics*, **8**, e1002839.

See Also

package-vGWAS, vGWAS

Examples

```
# ----- load data ----- #
data(pheno)
data(geno)
data(chr)
data(map)
# ----- variance GWA scan ----- #
vgwa <- vGWAS(phenotype = pheno, geno.matrix = geno,
marker.map = map, chr.index = chr, pB = FALSE)
# ----- visualize the scan ----- #
plot(vgwa)
summary(vgwa)
# ----- calculate the variance explained by the strongest marker ----- #
vGWAS.variance(phenotype = pheno,
marker.genotype = geno[, vgwa[["p.value"]] == min(vgwa[["p.value"]])])
# ----- genomic control ----- #
```

```
vgwa2 <- vGWAS.gc(vgwa)
plot(vgwa2)
summary(vgwa2)
```

`summary.vGWAS` *Variance GWA Summary*

Description

The function summarized the variance GWA result for the given scan object.

Usage

```
## S3 method for class 'vGWAS'
summary(object, nrMarkers = 10, ...)
```

Arguments

`object`	a result object from `vGWAS` scan. It can be any `list` or `data.frame` that contains `chromosome`, `marker.map`, and `p.value`, with `class = 'vGWAS'`. See `vGWAS`.
`nrMarkers`	a numeric value giving the number of top markers to be summarized.
`...`	not in use

Value

a summary for viewing vGWAS result.

Author(s)

Xia Shen

References

Shen, X., Pettersson, M., Ronnegard, L. and Carlborg, O. (2011): **Inheritance beyond plain heritability: variance-controlling genes in *Arabidopsis thaliana***. *PLoS Genetics*, **8**, e1002839.

Ronnegard, L., Shen, X. and Alam, M. (2010): **hglm: A Package for Fitting Hierarchical Generalized Linear Models**. *The R Journal*, **2**(2), 20-28.

See Also

`package-vGWAS`, `vGWAS`

Examples

```
# ----- load data ----- #
data(pheno)
data(geno)
data(chr)
data(map)
# ----- variance GWA scan ----- #
vgwa <- vGWAS(phenotype = pheno, geno.matrix = geno,
marker.map = map, chr.index = chr, pB = FALSE)
# ----- visualize the scan ----- #
plot(vgwa)
summary(vgwa)
# ----- calculate the variance explained by the strongest marker ----- #
vGWAS.variance(phenotype = pheno,
marker.genotype = geno[, vgwa[["p.value"]] == min(vgwa[["p.value"]])])
# ----- genomic control ----- #
vgwa2 <- vGWAS.gc(vgwa)
plot(vgwa2)
summary(vgwa2)
```

---

vGWAS *Variance Genome-wide Association*

Description

Variance Genome-wide association for using nonparametric variance test

Usage

```
vGWAS(phenotype, geno.matrix, kruskal.test = FALSE,
marker.map = NULL, chr.index = NULL, pB = TRUE)
```

Arguments

phenotype	a numeric or logical vector of the phenotyic values. See **Examples**.
geno.matrix	a matrix or data.frame with individuals as rows and markers as columns. The marker genotypes for each marker are coded as one column. See **Examples**.
kruskal.test	a logical value specifying whether to use Kruskal-Wallis statistic. The default option is FALSE, i.e., the usual ANOVA statistic is used in place of Kruskal-Wallis statistic.
marker.map	a numeric vector giving the marker map positions for each chromosome. See **Examples**.
chr.index	a numeric vector giving the chromosome index for each marker. See **Examples**.
pB	show progress bar

Value

a `data.frame` containing columns of `marker` names, `chromosome` indices, `marker.map` positions, test `statistic` values, and `p.value` for each position.

Author(s)

Xia Shen

References

Shen, X., Pettersson, M., Ronnegard, L. and Carlborg, O. (2011): **Inheritance beyond plain heritability: variance-controlling genes in *Arabidopsis thaliana***. *PLoS Genetics*, **8**, e1002839.

Ronnegard, L., Shen, X. and Alam, M. (2010): **hglm: A Package for Fitting Hierarchical Generalized Linear Models**. *The R Journal*, **2**(2), 20-28.

See Also

package-vGWAS

Examples

```
# ----- load data ----- #
data(pheno)
data(geno)
data(chr)
data(map)
# ----- variance GWA scan ----- #
vgwa <- vGWAS(phenotype = pheno, geno.matrix = geno,
marker.map = map, chr.index = chr, pB = FALSE)
# ----- visualize the scan ----- #
plot(vgwa)
summary(vgwa)
# ----- calculate the variance explained by the strongest marker ----- #
vGWAS.variance(phenotype = pheno,
marker.genotype = geno[, vgwa[["p.value"]] == min(vgwa[["p.value"]])])
# ----- genomic control ----- #
vgwa2 <- vGWAS.gc(vgwa)
plot(vgwa2)
summary(vgwa2)
```

vGWAS.gc *Genomic Control for vGWAS*

Description

The function does genomic control for the variance GWA result object.

Usage

```
vGWAS.gc(object, plot = TRUE, proportion = 1, ...)
```

Arguments

object	a result object from vGWAS scan. It can be any list or data.frame that contains chromosome, marker.map, and p.value, with class = 'vGWAS'. See vGWAS.
plot	a logical value turning on/off the QQ plot for genomic control.
proportion	a numeric value between 0 and 1 giving the proportion of obtained p-values to be used for genomic control.
...	not in use

Value

lambda	estimated inflation ratio.
lambda.se	standard error of the estimated inflation ratio.
gc.p.value	p-values after genomic control.

Author(s)

Xia Shen

References

Shen, X., Pettersson, M., Ronnegard, L. and Carlborg, O. (2011): **Inheritance beyond plain heritability: variance-controlling genes in *Arabidopsis thaliana***. *PLoS Genetics*, **8**, e1002839.

See Also

package-vGWAS, vGWAS

Examples

```
# ----- load data ----- #
data(pheno)
data(geno)
data(chr)
data(map)
# ----- variance GWA scan ----- #
vgwa <- vGWAS(phenotype = pheno, geno.matrix = geno,
marker.map = map, chr.index = chr, pB = FALSE)
# ----- visualize the scan ----- #
plot(vgwa)
summary(vgwa)
# ----- calculate the variance explained by the strongest marker ----- #
vGWAS.variance(phenotype = pheno,
marker.genotype = geno[, vgwa[["p.value"]] == min(vgwa[["p.value"]])])
# ----- genomic control ----- #
vgwa2 <- vGWAS.gc(vgwa)
plot(vgwa2)
summary(vgwa2)
```

`vGWAS.variance` *Calculating Variance Explained by A Single Marker*

Description

The function calculates and reports the variance explained for a single marker by fitting a double generalized linear model. It gives both the variance explained by the mean and variance parts of model.

Usage

```
vGWAS.variance(phenotype, marker.genotype, print = TRUE)
```

Arguments

`phenotype`	a `numeric` vector of the phenotyic values. See **Examples**.
`marker.genotype`	a `numeric` or `character` or `factor` vector of the genotypes of a single marker. See **Examples**.
`print`	a `logical` value. If `FALSE`, the heritability values will be returned for storage.

Details

The **Value** will only be available if `only.print = FALSE`.

Value

variance.mean	the variance explained by the mean part of model.
variance.disp	the variance explained by the variance part of model.

Author(s)

Xia Shen

References

Shen, X., Pettersson, M., Ronnegard, L. and Carlborg, O. (2011): **Inheritance beyond plain heritability: variance-controlling genes in *Arabidopsis thaliana***. *PLoS Genetics*, **8**, e1002839.

See Also

package-vGWAS, vGWAS, plot.vGWAS

Examples

```
# ----- load data ----- #
data(pheno)
data(geno)
data(chr)
data(map)
# ----- variance GWA scan ----- #
vgwa <- vGWAS(phenotype = pheno, geno.matrix = geno,
marker.map = map, chr.index = chr, pB = FALSE)
# ----- visualize the scan ----- #
plot(vgwa)
summary(vgwa)
# ----- calculate the variance explained by the strongest marker ----- #
vGWAS.variance(phenotype = pheno,
marker.genotype = geno[, vgwa[["p.value"]] == min(vgwa[["p.value"]])])
```

---

vGWASparallel *Variance Genome-wide Association (parallel)*

Description

Variance Genome-wide association for using nonparametric variance test and other

Usage

```
vGWASparallel(phenotype, geno.matrix, marker.map = NULL,
chr.index = NULL, geno.snp = "row", method = "bfmedian", test.alpha = 0.05,
test.na.rm = TRUE, p.adjust.method = "none", include.het = FALSE, pB = TRUE,
ncores = 1)
```

Arguments

phenotype	a numeric or logical vector of the phenotyic values.
geno.matrix	a matrix or data.frame or sparseMatrix with individuals as columns and markers as rows (geno.snp = "row") or individuals as rows and markers as columns (geno.snp = "col").
marker.map	a numeric vector giving the marker map positions for each chromosome.
chr.index	a numeric vector giving the chromosome index for each marker.
geno.snp	if individuals at columns and markers at rows use "row" else if individuals at rows and markers at columns use "col"
method	the test method to use (default = bfmedian). Default is set to the Brown-Forsythe's Test of Equality of Variances using group medians. There are 31 other tests available via the onewaytests package: Alvandi's F test ("af"), Alexander-Govern test ("ag"), Alvandi's generalized p-value ("agp"), One-way analysis of variance ("aov"), Approximate F test ("ap"), Adjusted Welch's heteroscedastic F test ("aw"), B square test ("b2"), Brown-Forsythe test ("bf"), Box F test ("box"), Cochran test ("cochran"), Generalized tests equivalent to Parametric Bootstrap ("gtb"), Generalized tests equivalent to Fiducial tests ("gtf"), Variance homogeneity tests ("homog"), James second order test ("james"), Johansen F test ("johansen"), Kruskal-Wallis test ("kw"), Modified Brown-Forsythe test ("mbf"), Mann-Whitney U test ("mw"), Anderson-Darling normility test ("nor_ad"), Cramer-vin Mises normility test ("nor_cvm"), Kolmogorov-Smirnov normility test ("nor_ks"), Pearson Chi-square normility test ("nor_pct"), Shapiro-Wilk normility test ("nor_sw"), Shapiro-Francia normility test ("nor_sf"), Permutation F test ("pf"), Scott-Smith test ("ss"), Student's t-test ("st"), Welch-Aspin test ("wa"), Welch's heteroscedastic F test with trimmed means and Winsorized variances ("welch"), Weerahandi's generalized F test ("wgf"), Welch's t-test ("wt").
test.alpha	the level of significance to assess the statistical difference. Default is set to alpha = 0.05.
test.na.rm	a logical value indicating whether NA values should be stripped before the computation proceeds. Default us set to TRUE.
p.adjust.method	correction method (default = "none"). There are 8 p-value correction methods available via the p.adjust function: "holm", "hochberg", "hommel", "bonferroni", "BH", "BY", "fdr", "none"
include.het	specify if heterozygous calls should be split and added equally to homozygous ref and alt counts (default = FALSE)
pB	show progress bar
ncores	number of cores to parallelize (default = 1)

Value

a data.frame containing columns of marker names, chromosome indices, marker.map positions, test statistic values, and p.value for each position.

Author(s)

Xia Shen

Kristian Ullrich

References

Shen, X., Pettersson, M., Ronnegard, L. and Carlborg, O. (2011): **Inheritance beyond plain heritability: variance-controlling genes in *Arabidopsis thaliana***. *PLoS Genetics*, **8**, e1002839.

Ronnegard, L., Shen, X. and Alam, M. (2010): **hglm: A Package for Fitting Hierarchical Generalized Linear Models**. *The R Journal*, **2**(2), 20-28.

See Also

package-vGWAS onewaytests

Examples

```
# ----- load data ----- #
data(pheno)
data(geno)
data(chr)
data(map)
# ----- variance GWA scan ----- #
vgwa <- vGWASparallel(phenotype = pheno, geno.matrix = geno,
marker.map = map, chr.index = chr,
geno.snp = "col", pB = FALSE)
# ----- other test GWA scan ----- #
vgwa.mw <- vGWASparallel(phenotype = pheno, geno.matrix = geno,
marker.map = map, chr.index = chr,
geno.snp = "col", method = "mw", pB = FALSE)
# ----- multiple cores ----- #
vgwa.st <- vGWASparallel(phenotype = pheno, geno.matrix = geno,
marker.map = map, chr.index = chr,
geno.snp = "col", method = "st", ncores = 2, pB = FALSE)
```

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