

# Package ‘rqt’

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**Type** Package

**Title** rqt: utilities for gene-level meta-analysis

**Version** 1.28.0

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**Description** Despite the recent advances of modern GWAS methods, it still remains an important problem of addressing calculation an effect size and corresponding p-value for the whole gene rather than for single variant. The R- package rqt offers gene-level GWAS meta-analysis. For more information, see: ``Gene-set association tests for next-generation sequencing data" by Lee et al (2016), Bioinformatics, 32(17), i611-i619, <doi:10.1093/bioinformatics/btw429>.

**URL** <https://github.com/izhbannikov/rqt>

**BugReports** <https://github.com/izhbannikov/rqt/issues>

**License** GPL

**RoxygenNote** 6.0.1

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**VignetteBuilder** knitr

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build.null.model	<i>Applies linear of logistic regression to the data.</i>
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Description

Applies linear of logistic regression to the data.

Usage

```
build.null.model(y, x, reg.family = "binomial", verbose = FALSE)
```

Arguments

- y                    A vector with values of dependent variable (outcome).
- x                    A data.frame of covariates.
- reg.family          A regression family. Can be either "binomial" or "gaussian."
- verbose             Indicates verbosing output. Default: FALSE.

Value

A list of two: "S" - a dataframe with predictors and "fit" - an object returned by "glm" function.

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covariates	<i>This function performs an access to covariates</i>
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---

**Description**

This function performs an access to covariates

An accessor to covariates

**Usage**

```
covariates(obj)

## S4 method for signature 'rqt'
covariates(obj)
```

**Arguments**

obj                    An object of rqt class.

**Value**

covariates returns the covariates

**Examples**

```
data <- data.matrix(read.table(system.file("extdata/test.bin1.dat",
package="rqt"), header=TRUE))
pheno <- data[,1]
geno <- data[, 2:dim(data)[2]]
colnames(geno) <- paste(seq(1, dim(geno)[2]))
geno.obj <- SummarizedExperiment(geno)
obj <- rqt(pheno=pheno, genotype=geno.obj)
covariates(obj)
```

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geneTest	<i>This function performs a gene-level test based on combined effect sizes.</i>
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**Description**

This function performs a gene-level test based on combined effect sizes.

geneTest This function performs a gene-level test based on combined effect sizes.

**Usage**

```
geneTest(obj, ...)

## S4 method for signature 'rqt'
geneTest(obj, perm = 0, STT = 0.2, weight = FALSE,
  cumvar.threshold = 75, out.type = "D", method = "pca",
  scaleData = FALSE, asym.pval = FALSE, penalty = 0.001,
  verbose = FALSE)
```

**Arguments**

obj	Object of class rqt
...	Additional parameters to pass to the function
perm	Integer indicating the number of permutations to compute p-values. Default: 0.
STT	Numeric indicating soft truncation threshold (STT) to convert to gamma parameter (must be $\leq 0.4$ ). Needed for an optimal parameter $a$ in Gamma-distribution. Default: 0.2. See, for example, Fridley, et al 2013: "Soft truncation thresholding for gene set analysis of RNA-seq data: Application to a vaccine study".
weight	Logical value. Indicates using weights (see Lee et al 2016). Default: FALSE.
cumvar.threshold	Numeric value indicating the explained variance threshold for PCA-like methods. Default: 75
out.type	Character, indicating a type of phenotype. Possible values: D (dichotomous or binary), C (continuous or quantitative).
method	Method used to reduce multicollinearity and account for LD. Default: pca. Another methods available: lasso, ridge, pls.
scaleData	A logic parameter (TRUE/FALSE) indicating scaling of the genotype dataset.
asym.pval	Indicates Monte Carlo approximation for p-values. Default: FALSE.
penalty	A value of penalty parameter for LASSO/ridge regression. Default: 0.001
verbose	Indicates verbosing output. Default: FALSE.

**Value**

Updated rqt object with result slot

**Examples**

```
data <- data.matrix(read.table(system.file("extdata/test.bin1.dat",
  package="rqt"), header=TRUE))
pheno <- data[,1]
geno <- data[, 2:dim(data)[2]]
colnames(geno) <- paste(seq(1, dim(geno)[2]))
geno.obj <- SummarizedExperiment(geno)
obj <- rqt(phenotype=pheno, genotype=geno.obj)
res <- geneTest(obj, method="pca", out.type = "D")
print(res)
```

---

geneTestMeta	<i>This function performs a gene-level meta-analysis based on combined effect sizes.</i>
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---

## Description

This function performs a gene-level meta-analysis based on combined effect sizes.

This function performs a gene-level meta-analysis based on combined effect sizes.

## Usage

```
geneTestMeta(objects, ...)

## S4 method for signature 'list'
geneTestMeta(objects, perm = 0, STT = 0.2,
  weight = FALSE, cumvar.threshold = 75, out.type = "D", method = "pca",
  scaleData = FALSE, asym.pval = FALSE, comb.test = "wilkinson",
  penalty = 0.001, verbose = FALSE)
```

## Arguments

objects	List of objects of class rqt
...	Additional parameters to pass to the function
perm	Integer indicating the number of permutations to compute p-values. Default: 0.
STT	Numeric indicating soft truncation threshold (STT) to convert to gamma parameter (must be $\leq 0.4$ ). Needed for an optimal parameter $a$ in Gamma-distribution. Default: 0.2. See, for example, Fridley, et al 2013: "Soft truncation thresholding for gene set analysis of RNA-seq data: Application to a vaccine study".
weight	Logical value. Indicates using weights (see Lee et al 2016). Default: FALSE.
cumvar.threshold	Numeric value indicating the explained variance threshold for PCA-like methods. Default: 75
out.type	Character, indicating a type of phenotype. Possible values: D (dichotomous or binary), C (continuous or quantitative).
method	Method used to reduce multicollinearity and account for LD. Default: pca. Other methods available: lasso, ridge, pls.
scaleData	A logic parameter (TRUE/FALSE) indicating scaling of the genotype dataset.
asym.pval	Indicates Monte Carlo approximation for p-values. Default: FALSE.
comb.test	Statistical test for combining p-values.
penalty	Value of penalty parameter for LASSO/ridge regression. Default: 0.001
verbose	Indicates verbosing output. Default: FALSE.

**Value**

A list of two: (i) final.pvalue - a final p-value across all studies; (ii) pvalueList - p-values for each study;

A list of two: (i) final.pvalue - a final p-value across all studies; (ii) pvalueList - p-values for each study;

**Examples**

```
data1 <- data.matrix(read.table(system.file("extdata/phengen2.dat",
                                           package="rqt"), skip=1))

pheno <- data1[,1]
geno <- data1[, 2:dim(data1)[2]]
colnames(geno) <- paste(seq(1, dim(geno)[2]))
geno.obj <- SummarizedExperiment(geno)
obj1 <- rqt(pheno=pheno, geno=geno.obj)

data2 <- data.matrix(read.table(system.file("extdata/phengen3.dat",
                                           package="rqt"), skip=1))

pheno <- data2[,1]
geno <- data2[, 2:dim(data2)[2]]
colnames(geno) <- paste(seq(1, dim(geno)[2]))
geno.obj <- SummarizedExperiment(geno)
obj2 <- rqt(pheno=pheno, geno=geno.obj)

data3 <- data.matrix(read.table(system.file("extdata/phengen.dat",
                                           package="rqt"), skip=1))

pheno <- data3[,1]
geno <- data3[, 2:dim(data3)[2]]
colnames(geno) <- paste(seq(1, dim(geno)[2]))
geno.obj <- SummarizedExperiment(geno)
obj3 <- rqt(pheno=pheno, geno=geno.obj)

res.meta <- geneTestMeta(list(obj1, obj2, obj3))
print(res.meta)
```

---

genotype

*This function performs an access to genotype.*


---

**Description**

This function performs an access to genotype.

A genotype accessor

**Usage**

```
genotype(obj)

## S4 method for signature 'rqt'
genotype(obj)
```

**Arguments**

obj                    An object of rqt class.

**Value**

genotype returns the genotype

**Examples**

```
data <- data.matrix(read.table(system.file("extdata/test.bin1.dat",
package="rqt"), header=TRUE))
pheno <- data[,1]
geno <- data[, 2:dim(data)[2]]
colnames(geno) <- paste(seq(1, dim(geno)[2]))
geno.obj <- SummarizedExperiment(geno)
obj <- rqt(pheno=pheno, genotype=geno.obj)
genotype(obj)
```

---

get.a	<i>Get a given STT</i>
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---

**Description**

Get a given STT

**Usage**

```
get.a(L, STT = 0.2)
```

**Arguments**

L	TODO
STT	Numeric indicating soft truncation threshold (STT) to convert to gamma parameter (must be $\leq 0.4$ ).

**Value**

a TODO

---

phenotype	<i>This function performs an access to phenotype</i>
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---

### Description

This function performs an access to phenotype

A phenotype accessor

### Usage

```
phenotype(obj)

## S4 method for signature 'rqt'
phenotype(obj)
```

### Arguments

obj                      An object of rqt class.

### Value

phenotype returns the phenotype

### Examples

```
data <- data.matrix(read.table(system.file("extdata/test.bin1.dat",
package="rqt"), header=TRUE))
pheno <- data[,1]
geno <- data[, 2:dim(data)[2]]
colnames(geno) <- paste(seq(1, dim(geno)[2]))
geno.obj <- SummarizedExperiment(geno)
obj <- rqt(phenotype=pheno, genotype=geno.obj)
phenotype(obj)
```

---

preprocess	<i>Preprocess input data with Principal Component Analysis method (PCA)</i>
------------	---

---

### Description

Preprocess input data with Principal Component Analysis method (PCA)

### Usage

```
preprocess(data, pheno = NULL, method = "pca", reg.family = "binomial",
scaleData = FALSE, cumvar.threshold = 75, out.type = "D",
penalty = 0.001, verbose = FALSE)
```



**Arguments**

<code>data</code>	An input matrix with values of independent variables (predictors).
<code>pheno</code>	A phenotype - column-vector, needed for LASSO/ridge and NULL by default.
<code>method</code>	A dimensionality reduction method. Default: <code>pca</code> .
<code>reg.family</code>	A regression family. Default: <code>"binomial"</code> .
<code>scaleData</code>	A logical variable, indicates wheither or not scaling should be performed. Default: <code>FALSE</code> .
<code>cumvar.threshold</code>	A threshold value for explained variance. Default: <code>75</code>
<code>out.type</code>	An output (phenotype) type. Default: <code>"D"</code>
<code>penalty</code>	Value of penalty parameter for LASSO/ridge regression. Default: <code>0.001</code>
<code>verbose</code>	Indicates verbosing output. Default: <code>FALSE</code> .

**Value**

A list of one: "S" - a data frame of predictor values.

---

<code>results</code>	<i>This function performs an access to covariates</i>
----------------------	---

---

**Description**

This function performs an access to covariates

An accessor to results

**Usage**

```
results(obj)
```

```
## S4 method for signature 'rqt'  
results(obj)
```

**Arguments**

<code>obj</code>	An object of <code>rqt</code> class.
------------------	--------------------------------------

**Value**

`results` returns the results

**Examples**

```
data <- data.matrix(read.table(system.file("extdata/test.bin1.dat",
package="rqt"), header=TRUE))
pheno <- data[,1]
geno <- data[, 2:dim(data)[2]]
colnames(geno) <- paste(seq(1, dim(geno)[2]))
geno.obj <- SummarizedExperiment(geno)
obj <- rqt(pheno=pheno, genotype=geno.obj)
res <- geneTest(obj, method="pca", out.type = "D")
results(res)
```

rqt

*The rqt class constructor***Description**

This function generates rqt class objects

**Usage**

```
rqt(pheno = NULL, genotype = NULL, covariates = NULL,
    results = NULL)
```

**Arguments**

pheno	Phenotype (a vector of length N, where N - number of individuals).
genotype	Genotype - an object of class SummarizedExperiment. Should contain one assay (matrix, N by M where N - number of individuals, M - number of genetic variants).
covariates	Covariates, a data frame N by K where N - number of individuals, K - number of covariates
results	A list of two: test statistics: (Q1, Q2, Q3), p-values: (p1.Q1, p2.Q2, p3.Q3)

**Value**

Object of class rqt

**Examples**

```
data <- data.matrix(read.table(system.file("extdata/test.bin1.dat",
package="rqt"), header=TRUE))
pheno <- data[,1]
geno <- data[, 2:dim(data)[2]]
colnames(geno) <- paste(seq(1, dim(geno)[2]))
geno.obj <- SummarizedExperiment(geno)
obj <- rqt(pheno=pheno, genotype=geno.obj)
print(obj)
```

---

rqt-class	<i>The rqt class</i>
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---

**Description**

This class stores parameters and results of the rtq algorithms

**Slots**

**phenotype:** Phenotype (a vector of length N, where N - number of individuals).  
**genotype:** Genotype - an object of class SummarizedExperiment. Should contain one assay (matrix, N by M where N - number of individuals, M - number of genetic variants).  
**covariates:** data frame N by K where N - number of individuals, K - number of covariates)  
**results:** A list of two: test statistics (Q1, Q2, Q3), p-values (p1.Q1, p2.Q2, p3.Q3)

---

rqt-general	<i>General functions of rqt such as accessors and printing.</i>
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**Description**

Common methods for class rqt. This document lists a series of basic methods for the class rqt

**Details**

Common methods for class rqt

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simple.multivar.reg	<i>Applies linear of logistic regression to the data.</i>
---------------------	---

---

**Description**

Applies linear of logistic regression to the data.

**Usage**

```
simple.multivar.reg(null.model, Z, verbose = FALSE)
```

**Arguments**

null.model	A fitted null model
Z	A genotype matrix
verbose	Indicates verbosing output. Default: FALSE.

**Value**

A list of two: "S" - a dataframe with predictors and "fit" - an object returned by "glm" function.

---

vcov_ridge	<i>vcov_ridge: returns variance-covariance matrix and standard deviation for ridge/LASSO regression object</i>
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---

**Description**

vcov\_ridge: returns variance-covariance matrix and standard deviation for ridge/LASSO regression object

**Usage**

```
vcov_ridge(x, y, rmod, verbose = FALSE)
```

**Arguments**

x	Genotype matrix
y	Phenotype
rmod	Ridge/LASSO regression object
verbose	Indicates verbosing output, Default: FALSE.

**Value**

list(vcov, se). vcov: variance-covariance matrix; se: standard deviation

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