

Package ‘loci2path’

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Type Package

Title Loci2path: regulatory annotation of genomic intervals based on tissue-specific expression QTLs

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Description loci2path performs statistics-rigorous enrichment analysis of eQTLs in genomic regions of interest.
Using eQTL collections provided by the Genotype-Tissue Expression (GTEx) project and pathway collections from MSigDB.

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Depends R (>= 3.4)

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URL <https://github.com/StanleyXu/loci2path>

BugReports <https://github.com/StanleyXu/loci2path/issues>

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'check.geneid.R' 'loci2path.demo-data.R'
'loci2pathResult-methods.R' 'query-methods.R' 'show-methods.R'

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R topics documented:

biocarta	2
check.geneid	3
eqlSet-class	3
eset.list	4
geneSet-class	5
getHeatmap	6
getMat	7
getPathDescription	8
getPval	9
getTissueDegree	10
getWordcloud	11
loci2pathResult-class	11
query	12
query.gr	14

Index	16
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biocarta	<i>eQTL geneset enrichment query demo data</i>
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Description

Demo Data to show how to perform eQTL-geneset enrichment query.

Usage

data(loci2path.demo)

Format

An object of class geneSet of length 1.

Details

eql.set.list A list of eQTLset objects; eQTL data are collected from GTeX.
biocarta A Geneset object; Geneset are from Broad Institute’s MSigDB: curated gene set, category ‘cp’: BIOCARTA
query.gr A Genomic Region object; Query regions are from immunoBase, crohn’s disease.

Examples

data(loci2path.demo)

check.geneid	<i>check compatibility of gene identifiers between eQTL set and gene set</i>
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Description

This function perform enrichment test between one eQTL set and one gene set

Usage

```
check.geneid(e.set, g.set)
```

Arguments

e.set	an eqtlSet object; the eQTL set to be queried against
g.set	an object of geneSet class; the gene set to be tested

Value

a data.frame shows the number of genes from (1) eqtl Set (2) gene Set (3) shared

Examples

```
check.geneid(eset.list$Skin, biocarta)
```

eqtlSet-class	<i>eqtlSet Class</i>
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Description

eqtlSet Class contains information for eqtl-gene association, gene identifier, position of SNPs, etc.

Usage

```
tissue(x)

eqtlId(x)

eqtlRange(x)

eqtlGene(x)

## S4 method for signature 'eqtlSet'
tissue(x)

## S4 method for signature 'eqtlSet'
eqtlId(x)
```

```
## S4 method for signature 'eqtlSet'
eqtlRange(x)

## S4 method for signature 'eqtlSet'
eqtlGene(x)
```

Arguments

x An eqtlSet object

Value

Object of class eqtlSet

Slots

tissue character; name of the cell/tissue of the eQTL study
 eqtlId character; name of the SNPs
 eqtlRange GenomicRanges; position of the SNPs
 gene character; gene identifier

Examples

```
require(GenomicRanges)
brain.file <- system.file("extdata", "eqtl/brain.gtex.txt",
  package="loci2path")
tab <- read.table(brain.file, stringsAsFactors=FALSE, header=TRUE)
eqtlRange <- GRanges(seqnames=Rle(tab$snp.chr),
  ranges=IRanges(start=tab$snp.pos,
  width=1))
brain.eset <- eqtlSet(tissue="brain",
  eqtlId=tab$snp.id,
  eqtlRange=eqtlRange,
  gene=as.character(tab$gene.entrez.id))
tissue(brain.eset)
head(eqtlId(brain.eset))
eqtlRange(brain.eset)
head(eqtlGene(brain.eset))
```

eset.list

eQTL geneset enrichment query demo data

Description

Demo Data to show how to perform eQTL-geneset enrichment query.

Usage

```
data(loci2path.demo)
```

Format

An object of class `list` of length 3.

Details

`eset.list` A list of `eQTLset` objects; eQTL data are collected from GTeX.

`biocarta` A `Geneset` object; Geneset are from Broad Institute's MSigDB: curated gene set, category 'cp': BIOCARTEA

`query.gr` A `Genomic Region` object; Query regions are from immunoBase, Psoriasis disease.

Examples

```
data(loci2path.demo)
```

geneSet-class

geneSet Class

Description

`geneSet Class` contains information for names of gene sets and a list of gene sets

Usage

```
numGene(x)
```

```
description(x)
```

```
geneSetList(x)
```

```
## S4 method for signature 'geneSet'
numGene(x)
```

```
## S4 method for signature 'geneSet'
description(x)
```

```
## S4 method for signature 'geneSet'
geneSetList(x)
```

Arguments

`x` An `geneSet` object

Value

Object of class `geneSet`

Slots

`numGene` numeric; the total number of all genes; This number is used in enrichment tests

`description` vector of character; additional information for gene sets, such as names, URLs, a short description, etc.

`geneSetList` list; a list of gene sets; each member is a vector containing a group of gene identifiers

Examples

```
biocarta.link.file <- system.file("extdata",
  "geneSet/biocarta.txt", package="loci2path")
biocarta.link <- read.delim(biocarta.link.file, header=FALSE,
  stringsAsFactors=FALSE)
biocarta.set.file <- system.file("extdata", "geneSet/biocarta.set.txt",
  package="loci2path")
set.geneid <- read.table(biocarta.set.file, stringsAsFactors=FALSE)
set.geneid <- strsplit(set.geneid[,1], split=",")
names(set.geneid) <- biocarta.link[,1]
biocarta <- geneSet(
  geneSetList=set.geneid,
  description=biocarta.link[,2],
  numGene=31847)
numGene(biocarta)
head(description(biocarta))
head(geneSetList(biocarta))
```

getHeatmap

Generate heatmap of enrichment matrix from query result

Description

This function generate the enrichment heatmap using pheatmap package.

Usage

```
getHeatmap(res, ...)

## S4 method for signature 'loci2pathResult'
getHeatmap(res, main = "",
  test.method = c("gene", "eqtl", "glm"), filter.quantile = 0.5,
  max.ptw.gene = 5000)
```

Arguments

<code>res</code>	query result from function <code>query.egset.list()</code>
<code>...</code>	additional params
<code>main</code>	title of the heatmap, default is ""
<code>test.method</code>	Choose which enrichment test should be used to retrieve p-values from. Options include: "gene" (default, gene-based fisher's exact test), "eqtl" (eqtl based fisher's exact test), "glm" (ordered query)
<code>filter.quantile</code>	Filter option; choose the max quantile of all p-values being kept in the matrix; default is 0.5, which means p-values larger than median p-values are discarded
<code>max.ptw.gene</code>	Filter option; minimum number of genes in a pathway; default is 5000 (pathway with >5000 genes are not included in the matrix)

Value

<code>pathways</code>	frequent pathways
<code>tissues</code>	frequent tissues

Examples

```
result <- query(query.gr=query.gr,
  loci=eset.list, path=biocarta)
getHeatmap(result)
```

getMat

*Extract tissue/geneset enrichment matrix from query result***Description**

This function extracts the enrichment matrix from eQTL list query result. The rows of the matrix are pathways; and the columns of the matrix are tissues/cell lines of the eQTL sets. P-Values from enrichment tests are summarized in this matrix

Usage

```
getMat(res, ...)

## S4 method for signature 'loci2pathResult'
getMat(res, test.method = c("gene", "eqtl",
  "glm"), filter.quantile = 0.5, max.ptw.gene = 5000)
```

Arguments

<code>res</code>	query result from function <code>query.egset.list()</code>
<code>...</code>	additional params
<code>test.method</code>	Choose which enrichment test should be used to retrieve p-values from. Options include: "gene" (default, gene-based fisher's exact test), "eqtl" (eqtl based fisher's exact test), "glm" (ordered query)
<code>filter.quantile</code>	Filter option; choose the max quantile of all p-values being kept in the matrix; default is 0.5, which means p-values larger than median p-values are discarded
<code>max.ptw.gene</code>	Filter option; minimum number of genes in a pathway; default is 5000 (pathway with >5000 genes are not included in the matrix)

Value

p-value matrix collected from enrichment result table

Examples

```
result <- query(query.gr=query.gr,
  loci=eset.list, path=biocarta)
mat <- getMat(result, test.method="gene")
```

<code>getPathDescription</code>	<i>Extract description for enriched pathways from query result and gene-Set object</i>
---------------------------------	--

Description

This function extracts the pathway description from geneSet object.

Usage

```
getPathDescription(res, ...)

## S4 method for signature 'loci2pathResult'
getPathDescription(res, geneset)
```

Arguments

<code>res</code>	query result from function <code>query.egset.list()</code>
<code>...</code>	additional params
<code>geneset</code>	A geneSet object

Value

a vector of gene set description from geneSet description slot

Examples

```
result <- query(query.gr=query.gr,
  loci=eset.list, path=biocarta)
path.des <- getPathDescription(result, biocarta)
```

getPval	<i>Extract tissue/geneset enrichment p-value distribution from query result</i>
---------	---

Description

This function extracts the enrichment p-value distribution from eQTL list query result. P-values from different tissues/cell types are organized, and QQ-plot is generated against uniform distribution

Usage

```
getPval(res, ...)

## S4 method for signature 'loci2pathResult'
getPval(res, test.method = c("gene", "eqtl",
  "glm"))
```

Arguments

res	query result from function query.egset.list()
...	additional params
test.method	Choose which enrichment test should be used to retrieve p-values from. Options include: "gene" (default, gene-based fisher's exact test), "eqtl" (eqtl based fisher's exact test), "glm" (ordered query)

Value

generate pval distribution plot

Examples

```
result <- query(query.gr=query.gr,
  loci=eset.list, path=biocarta)
getPval(result, test.method="gene")
```

getTissueDegree	<i>Extract tissue degree from query result</i>
-----------------	--

Description

This function extracts the tissue degree from eQTL list query result for each pathway.

Usage

```
getTissueDegree(res, ...)

## S4 method for signature 'loci2pathResult'
getTissueDegree(res, loci)
```

Arguments

res	query result from function query.egset.list()
...	additional params
loci	a list of eqtlSet; each member should be an eqtlSet object

Value

gene.tissue.map	shows mapping:gene<->tissue
gene.tissue.degree	shows tissue degree for each gene
mean.tissue.degree	shows the average tissue degree for each pathway in the result table

Examples

```
result <- query(query.gr=query.gr,
  loci=eset.list, path=biocarta)
tissue.degree=getTissueDegree(result, eset.list)
head(tissue.degree$gene.tissue.map)
head(tissue.degree$gene.tissue.degree)
head(tissue.degree$mean.tissue.degree)
```

`getWordcloud`*Plot word cloud using frequent terms of pathways and genes*

Description

This function draw the enrichment heatmap using wordcloud package.

Usage

```
getWordcloud(res, ...)

## S4 method for signature 'loci2pathResult'
getWordcloud(res, min.freq.tissue = 5,
  min.freq.gset = 5, max.words = 50)
```

Arguments

<code>res</code>	query result from function <code>query.egset.list()</code>
<code>...</code>	additional params
<code>min.freq.tissue</code>	minimum frequency of tissue/cell to be plotted in the word cloud
<code>min.freq.gset</code>	minimum frequency of geneset to be plotted in the word cloud
<code>max.words</code>	maximum words to be generated

Value

empty

Examples

```
result <- query(query.gr=query.gr,
  loci=eset.list, path=biocarta)
getWordcloud(result, min.freq.tissue=2, min.freq.gset=1)
```

`loci2pathResult-class` *loci2pathResult Class*

Description

`loci2pathResult` Class contains information for the query result from `query` function `query`. Result object contains a ranked pathway table, and a vector of gene names that are associated with loci covered by query regions

Usage

```

resultTable(x)

coveredGene(x)

## S4 method for signature 'loci2pathResult'
resultTable(x)

## S4 method for signature 'loci2pathResult'
coveredGene(x)

```

Arguments

x An geneSet object

Value

Object of CClass loci2pathResult

Slots

resultTable data.frame; contains enrichment statistics, summary of eQTL and gene numbers, pathway names and gene names, etc.

coveredGene list; each member is a vector of genes associated with one tissue, whose associating loci are covered by query regions

Examples

```

result <- query(query.gr=query.gr,
  loci=eset.list, path=biocarta)
result
resultTable(result) # a data.frame for enriched pathways
coveredGene(result)

```

query

Query enrichment in geneset through multiple eQTL sets.

Description

This is the main function for loci2path query. Query can be made on either pathway enrichment or tissue-specificity, depending on the input Class. See **Details** for more.

Usage

```

query(query.gr, loci, path, ...)

## S4 method for signature 'GenomicRanges,list,ANY'
query(query.gr, loci, N = 2897310462)

## S4 method for signature 'GenomicRanges,eqtlSet,geneSet'
query(query.gr, loci, path,
      query.score = NULL, verbose = FALSE)

## S4 method for signature 'GenomicRanges,list,geneSet'
query(query.gr, loci, path,
      query.score = NULL, parallel = FALSE, verbose = FALSE)

```

Arguments

<code>query.gr</code>	a <code>GenomicRange</code> object, representing query regions
<code>loci</code>	a list of <code>eqtlSet</code> ; each member should be an <code>eqtlSet</code> ; Or it can be a single <code>eqtlSet</code> .
<code>path</code>	Pathways or <code>geneSets</code> to be tested for enrichment
<code>...</code>	additional params
<code>N</code>	the total number of non-N nucleotides in the genome; default <code>N=2897310462</code> is for hg19
<code>query.score</code>	optional, set to <code>NULL</code> if the regions are not ordered. If the query regions are ordered, <code>query.score</code> is the quantity based on which the regions are ordered
<code>verbose</code>	bool; whether to show <code>eqtlSet</code> / <code>geneSet</code> summary information; default is <code>FALSE</code>
<code>parallel</code>	bool; whether to enable parallel computing; default is <code>FALSE</code>

Details

The user need to specify

1. Query region;
2. `loci`; one or more eQTL set; this is usually more than one eQTL set. Only multiple eQTL set derived from different cells/tissues will show cell/tissue specificity.
3. `path`; pre-defined Pathways, or gene sets. the gene sets that enrichment tests would be performed to.

`loci` must be provided; `path` is optional. When `path` is missing, the tissue-specificity query for the regions is performed.

The most common case for `loci` is an eQTL set list. This function perform enrichment test between one eQTL set and a group of gene sets. Usually query are based on eQTL set list, rather than only one eQTL set. Several result exploring functions (`getMat`, `getHeatmap`, `getPval`, etc...) are designed for query result from eQTL set list and gene sets. The class `loci2pathResult` is also designed for eQTL set list query result only. The result returns a `loci2pathResult` only the class of `loci` is a list of `eqtlSet`.

If user input one eQTL set as argument `loci`, a simple list object will be returned for specific research purpose.

Value

a data.frame showing the tissue enrichment of the query regions by binomial test.
 a list; `result.table` is the major result table showing enrichment assessment; `cover.gene` is the vector showing the genes from the eqtl Sets covered by the query region(s)
 a `loci2pathResult` class object

See Also

`loci2pathResult`

Examples

```
gr.tissue <- query(query.gr, eset.list)
#build one eqtlset
skin.eset <- eset.list$Skin
#query one egset
res.one <- query(query.gr, skin.eset, biocarta)
#enrichment result table
res.one$result.table
#all the genes associated with eQTLs covered by the query region
res.one$cover.gene
result <- query(query.gr=query.gr,
  loci=eset.list, path=biocarta)
#enrichment result table
resultTable(result)
#all the genes associated with eQTLs covered by the query region
coveredGene(result)
```

query.gr

eQTL geneset enrichment query demo data

Description

Demo Data to show how to perform eQTL-geneset enrichment query.

Usage

```
data(loci2path.demo)
```

Format

An object of class `GRanges` of length 47.

Details

`eqtl.set.list` A list of `eQTLset` objects; eQTL data are collected from GTeX.
`biocarta` A Geneset object; Geneset are from Broad Institute's MSigDB: curated gene set, category 'cp': BIOCARTE
`query.gr` A Genomic Region object; Query regions are from immunoBase, crohn's disease.

Examples

```
data(loci2path.demo)
```

Index

- * **cloud**
 - getWordcloud, 11
- * **datasets**
 - biocarta, 2
 - eset.list, 4
 - query.gr, 14
- * **heatmap**
 - getHeatmap, 6
- * **result**
 - getMat, 7
 - getPval, 9
 - getTissueDegree, 10
- * **word**
 - getWordcloud, 11
- biocarta, 2
- check.geneid, 3
- coveredGene (loci2pathResult-class), 11
- coveredGene, loci2pathResult-method (loci2pathResult-class), 11
- description (geneSet-class), 5
- description, geneSet-method (geneSet-class), 5
- eqtlGene (eqtlSet-class), 3
- eqtlGene, eqtlSet-method (eqtlSet-class), 3
- eqtlId (eqtlSet-class), 3
- eqtlId, eqtlSet-method (eqtlSet-class), 3
- eqtlRange (eqtlSet-class), 3
- eqtlRange, eqtlSet-method (eqtlSet-class), 3
- eqtlSet (eqtlSet-class), 3
- eqtlSet-class, 3
- eset.list, 4
- geneSet (geneSet-class), 5
- geneSet-class, 5
- geneSetList (geneSet-class), 5
- geneSetList, geneSet-method (geneSet-class), 5
- getHeatmap, 6
- getHeatmap, loci2pathResult-method (getHeatmap), 6
- getMat, 7
- getMat, loci2pathResult-method (getMat), 7
- getPathDescription, 8
- getPathDescription, loci2pathResult-method (getPathDescription), 8
- getPval, 9
- getPval, loci2pathResult-method (getPval), 9
- getTissueDegree, 10
- getTissueDegree, loci2pathResult-method (getTissueDegree), 10
- getWordcloud, 11
- getWordcloud, loci2pathResult-method (getWordcloud), 11
- loci2pathResult (loci2pathResult-class), 11
- loci2pathResult-class, 11
- numGene (geneSet-class), 5
- numGene, geneSet-method (geneSet-class), 5
- query, 12
- query, eqtlSet, geneSet-method (query), 12
- query, GenomicRanges, eqtlSet, geneSet-method (query), 12
- query, GenomicRanges, list, ANY-method (query), 12
- query, GenomicRanges, list, geneSet-method (query), 12
- query, list, geneSet-method (query), 12
- query, list-method (query), 12
- query.gr, 14

`resultTable (loci2pathResult-class)`, [11](#)
`resultTable, loci2pathResult-method`
 (`loci2pathResult-class`), [11](#)

`tissue (eqtlSet-class)`, [3](#)
`tissue, eqtlSet-method (eqtlSet-class)`, [3](#)