

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

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

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biocarta

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 `geneSet` of length 1.

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': 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>
--------------	--

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>
---------------	----------------------

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': BIOCARTA

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

Examples

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

geneSet-class	<i>geneSet Class</i>
---------------	----------------------

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

res	query result from function query.egset.list()
...	additional params
main	title of the heatmap, default is ""
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)
filter.quantile	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
max.ptw.gene	Filter option; minimum number of genes in a pathway; default is 5000 (pathway with >5000 genes are not included in the matrix)

Value

pathways	frequent pathways
tissues	frequent tissues

Examples

```

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

```

getMat	<i>Extract tissue/geneset enrichment matrix from query result</i>
--------	---

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

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)
filter.quantile	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
max.ptw.gene	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")
```

getPathDescription	<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

```
res          query result from function query.egset.list()
...          additional params
geneset      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 digree 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	<i>Plot word cloud using frequent terms of pathways and genes</i>
--------------	---

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

res	query result from function query.egset.list()
...	additional params
min.freq.tissue	minimum frequency of tissue/cell to be plotted in the word cloud
min.freq.gset	minimum frequency of geneset to be plotted in the word cloud
max.words	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 Class 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,eqt1Set,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/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 `eQTLSet` 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': BIOCARTA

query.gr A Genomic Region object; Query regions are from immunoBase, crohn's disease.

Examples

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

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