Package ‘RTCGAToolbox’

May 30, 2024

Type Package

Title A new tool for exporting TCGA Firehose data

Version 2.34.0

Description Managing data from large scale projects such as The Cancer Genome Atlas (TCGA) for further analysis is an important and time consuming step for research projects. Several efforts, such as Firehose project, make TCGA pre-processed data publicly available via web services and data portals but it requires managing, downloading and preparing the data for following steps. We developed an open source and extensible R based data client for Firehose pre-processed data and demonstrated its use with sample case studies. Results showed that RTCGAToolbox could improve data management for researchers who are interested with TCGA data. In addition, it can be integrated with other analysis pipelines for following data analysis.

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Depends R (>= 4.3.0)

Imports BiocGenerics, data.table, DelayedArray, GenomicRanges,
GenomeInfoDb, httr, methods, RaggedExperiment, RCurl, RJSONIO,
rvest, S4Vectors (>= 0.23.10), stats, stringr,
SummarizedExperiment, TCGAutils (>= 1.9.4), utils

Suggests BiocStyle, Homo.sapiens, knitr, readr, rmarkdown

biocViews DifferentialExpression, GeneExpression, Sequencing

URL http://mksamur.github.io/RTCGAToolbox/

BugReports https://github.com/mksamur/RTCGAToolbox/issues

VignetteBuilder knitr

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Collate 'RTCGAToolbox-Class.R' 'RTCGAToolbox.R' 'utils.R'
'biocExtract.R' 'data.R' 'getBroadSubtypes.R'
'getFirehoseAnalyzeDates.R' 'getFirehoseData.R'
'getFirehoseDatasets.R' 'getFirehoseRunningDates.R'
'getGISTICPeaks.R' 'getLinks.R' 'getMutationRate.R'
'makeSummarizedExperimentFromGISTIC.R' 'selectType.R'
Contents

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Contents

accmini ............................................................. 3
biocExtract ......................................................... 3
CorResult-class ..................................................... 5
DGEResult-class .................................................... 5
FirehoseCGHArray-class .......................................... 5
FirehoseData-class ............................................... 6
FirehoseGISTIC-class ............................................. 7
FirehoseMethylationArray-class .................................. 8
FirehoseRNAArray-class .......................................... 8
getBroadSubtypes .................................................. 9
data ............................................................... 9
getFirehoseAnalyzeDates ......................................... 10
getFirehoseData ................................................... 11
getFirehoseDatasets ............................................... 13
getFirehoseRunningDates ........................................ 14
getGISTICPeaks ................................................... 14
getLinks ............................................................ 15
getMutationRate ................................................... 16
hg19.ucsc.gene.locations ....................................... 17
makeSummarizedExperimentFromGISTIC ................................ 17
RTCGAToolbox ....................................................... 18
selectType ........................................................ 19
showResults ......................................................... 20
showResults,CorResult-method ................................... 20
showResults,DGEResult-method ................................... 21

Index  22
A subset of the Adrenocortical Carcinoma (ACC) dataset

Description
See the ‘acc_sample.R‘ script to see how the data was generated. This dataset contains real data from the The Cancer Genome Atlas for the pipeline run date and GISTIC analysis date of 2016-01-28.

Usage
data("accmini", package = "RTCGAToolbox")

Format
A FirehoseData data object

biocExtract
Extract and convert data from a FirehoseData object to a Bioconductor object

Description
This function processes data from a FirehoseData object. Raw data is converted to a conventional Bioconductor object. The function returns either a SummarizedExperiment or a RaggedExperiment class object. In cases where there are multiple platforms in a data type, an attempt to consolidate datasets will be made based on matching dimension names. For ranged data, this functionality is provided with more control as part of the RaggedExperiment features. See RaggedExperiment-class for more details.

Usage
biocExtract(
  object,
  ...
)

Arguments

object A FirehoseData object from which to extract data.
type The type of data to extract from the "FirehoseData" object, see type section.
... Additional arguments passed to lower level functions that convert tabular data into Bioconductor object such as .makeRangedSummarizedExperimentFromDataFrame or .makeRaggedExperimentFromDataFrame
Details

A typical additional argument for this function passed down to lower level functions is the names.field which indicates the row names in the data. By default, it is the "Hugo_Symbol" column in the internal code that converts data.frames to SummarizedExperiment representations (via the .makeSummarizedExperimentFromDataFrame internal function).

Value

Either an SummarizedExperiment object or a RaggedExperiment object.

type

Choices include:

- clinical - Get the clinical data slot
- RNASeqGene - RNASeqGene - RNASeq v1
- RNASeqGene - RNASeq2Gene - RNASeq v2
- RNASeq2GeneNorm - RNASeq v2 Normalized
- miRNASeqGene - micro RNA SeqGene
- CNASNP - Copy Number Alteration
- CNVSNP - Copy Number Variation
- CNASeq - Copy Number Alteration
- CNACGH - Copy Number Alteration
- Methylation - Methylation
- mRNAArray - Messenger RNA
- miRNAArray - micro RNA
- RPPAArray - Reverse Phase Protein Array
- Mutation - Mutations
- GISTICA - GISTIC v2 ("AllByGene" only)
- GISTICT - GISTIC v2 ("ThresholdedByGene" only)
- GISTICP - GISTIC v2 ("Peaks" only)
- GISTIC - GISTIC v2 scores, probabilities, and peaks

Author(s)

Marcel Ramos <marcel.ramos@roswellpark.org>

Examples

data(accmini)
biocExtract(accmini, "RNASeq2Gene")
biocExtract(accmini, "miRNASeqGene")
biocExtract(accmini, "RNASeq2GeneNorm")
biocExtract(accmini, "CNASNP")
CorResult-class

An S4 class to store correlations between gene expression level and copy number data

Description

An S4 class to store correlations between gene expression level and copy number data

Slots

Dataset A cohort name
Correlations Results data frame

DGEResult-class

An S4 class to store differential gene expression results

Description

An S4 class to store differential gene expression results

Slots

Dataset Dataset name
Toptable Results data frame

FirehoseCGHArray-class

An S4 class to store data from CGA platforms

Description

An S4 class to store data from CGA platforms

Slots

Filename Platform name
DataMatrix A data frame that stores the CGH data.
FirehoseData-class  An S4 class to store main data object from clinent function.

Description
An S4 class to store main data object from clinent function.

Usage

```r
## S4 method for signature 'FirehoseData'
show(object)
## S4 method for signature 'FirehoseData'
getData(object, type, platform)
## S4 method for signature 'FirehoseGISTIC'
getData(object, type, platform)
## S4 method for signature 'ANY'
getData(object, type, platform)
## S4 method for signature 'FirehoseData'
updateObject(object, ..., verbose = FALSE)
## S4 method for signature 'FirehoseData'
selectType(object, dataType)
```

Arguments

- `object` A FirehoseData object
- `type` A data type to be extracted
- `platform` An index for data types that may come from multiple platforms (such as mRNAArray), for GISTIC data, one of the options: 'AllByGene', 'ThresholdedByGene', or 'Peaks'
- `...` additional arguments for updateObject
- `verbose` logical (default FALSE) whether to print extra messages
- `dataType` An available data type, see object show method

Methods (by generic)

- `show(FirehoseData)`: show method
- `getData(FirehoseData)`: Get a matrix or data.frame from FirehoseData
- `getData(FirehoseGISTIC)`: Get GISTIC data from FirehoseData
- `getData(ANY)`: Default method for getting data from FirehoseData
FirehoseGISTIC-class

- `updateObject(FirehoseData)`: Update an old RTCGAToolbox FirehoseData object to the most recent API
- `selectType(FirehoseData)`: Extract data type

**Slots**

<table>
<thead>
<tr>
<th>Dataset</th>
<th>A cohort name</th>
</tr>
</thead>
<tbody>
<tr>
<td>runDate</td>
<td>Standard data run date from <code>getFirehoseRunningDates</code></td>
</tr>
<tr>
<td>gistic2Date</td>
<td>Analyze running date from <code>getFirehoseAnalyzeDates</code></td>
</tr>
<tr>
<td>clinical</td>
<td>clinical data frame</td>
</tr>
<tr>
<td>RNASeqGene</td>
<td>Gene level expression data matrix from RNAseq</td>
</tr>
<tr>
<td>RNASeq2Gene</td>
<td>Gene level expression data matrix from RNAseqV2</td>
</tr>
<tr>
<td>RNASeq2GeneNorm</td>
<td>Gene level expression data matrix from RNAseqV2 (RSEM)</td>
</tr>
<tr>
<td>miRNASeqGene</td>
<td>miRNA expression data from matrix smallRNAseq</td>
</tr>
<tr>
<td>CNASNP</td>
<td>A data frame to store somatic copy number alterations from SNP array platform</td>
</tr>
<tr>
<td>CNVSNP</td>
<td>A data frame to store germline copy number variants from SNP array platform</td>
</tr>
<tr>
<td>CNASeq</td>
<td>A data frame to store somatic copy number alterations from sequencing platform</td>
</tr>
<tr>
<td>CNACGH</td>
<td>A list that stores <code>FirehoseCGHArray</code> object for somatic copy number alterations from CGH platform</td>
</tr>
<tr>
<td>Methylation</td>
<td>A list that stores <code>FirehoseMethylationArray</code> object for methylation data</td>
</tr>
<tr>
<td>mRNAArray</td>
<td>A list that stores <code>FirehoseRNAArray</code> object for gene expression data from microarray</td>
</tr>
<tr>
<td>miRNAArray</td>
<td>A list that stores <code>FirehoseRNAArray</code> object for miRNA expression data from microarray</td>
</tr>
<tr>
<td>RPPAArray</td>
<td>A list that stores <code>FirehoseRNAArray</code> object for RPPA data</td>
</tr>
<tr>
<td>Mutation</td>
<td>A data frame for mutation information from sequencing data</td>
</tr>
<tr>
<td>GISTIC</td>
<td>A FirehoseGISTIC object to store processed copy number data</td>
</tr>
<tr>
<td>BarcodeUUID</td>
<td>A data frame that stores the Barcodes, UUIDs and Short sample identifiers</td>
</tr>
</tbody>
</table>

---

FirehoseGISTIC-class  
*An S4 class to store processed copy number data. (Data processed by using GISTIC2 algorithm)*

**Description**

An S4 class to store processed copy number data. (Data processed by using GISTIC2 algorithm)

**Usage**

```r
## S4 method for signature 'FirehoseGISTIC'
isEmpty(x)

## S4 method for signature 'FirehoseGISTIC'
updateObject(object, ..., verbose = FALSE)
```
Arguments

- x: A FirehoseGISTIC class object
- object: A FirehoseGISTIC object
- ...: additional arguments for updateObject
- verbose: logical (default FALSE) whether to print extra messages

Methods (by generic)

- isEmpty(FirehoseGISTIC): check whether the FirehoseGISTIC object has data in it or not
- updateObject(FirehoseGISTIC): Update an old FirehoseGISTIC object to the most recent API

Slots

- Dataset: Cohort name
- AllByGene: A data frame that stores continuous copy number
- ThresholdedByGene: A data frame for discrete copy number data
- Peaks: A data frame storing GISTIC peak data. See getGISTICPeaks.

FirehoseMethylationArray-class

An S4 class to store data from methylation platforms

Description

An S4 class to store data from methylation platforms

Slots

- Filename: Platform name
- DataMatrix: A data frame that stores the methylation data.

FirehosemRNAArray-class

An S4 class to store data from array (mRNA, miRNA etc.) platforms

Description

An S4 class to store data from array (mRNA, miRNA etc.) platforms

Slots

- Filename: Platform name
- DataMatrix: A data matrix that stores the expression data.
getBroadSubtypes

**Description**

Download expression-based cancer subtypes from the Broad Institute

Obtain the mRNA expression clustering results from the Broad Institute for a specific cancer code (see getFirehoseDatasets).

**Usage**

```r
getBroadSubtypes(dataset, clust.alg = c("CNMF", "ConsensusPlus"))
```

**Arguments**

- `dataset`: A TCGA cancer code, e.g. "OV" for ovarian cancer
- `clust.alg`: The selected cluster algorithm, either "CNMF" or "ConsensusPlus" (default "CNMF")

**Value**

A `data.frame` of cluster and silhouette values

**Author(s)**

Ludwig Geistlinger

**Examples**

```r
co <- getBroadSubtypes("COAD", "CNMF")
head(co)
```

getData

**Description**

Extract data from FirehoseData object

A go-to function for getting top level information from a FirehoseData object. Available datatypes for a particular object can be seen by entering the object name in the console (‘show’ method).

**Usage**

```r
data(object, type, platform)
```
getFirehoseAnalyzeDates

Get data analyze dates.

Description

getFirehoseAnalyzeDates returns the character vector for analyze release dates.

Usage

getFirehoseAnalyzeDates(last = NULL)

Arguments

last To list last n dates. (Default NULL)

Value

A character vector for dates.

Examples

getFirehoseAnalyzeDates(last=2)
getFirehoseData

Get data from Firehose portal.

Description

getFirehoseData returns FirehoseData object that stores TCGA data.

Usage

getFirehoseData(
  dataset,
  runDate = "20160128",
  gistic2Date = "20160128",
  RNASeqGene = FALSE,
  RNASeq2Gene = FALSE,
  clinical = TRUE,
  miRNASeqGene = FALSE,
  miRNASeqGeneType = c("read_count", "reads_per_million_miRNA_mapped", "cross-mapped"),
  RNASeq2GeneNorm = FALSE,
  CNASNP = FALSE,
  CNVSNP = FALSE,
  CNASeq = FALSE,
  CNACGH = FALSE,
  Methylation = FALSE,
  Mutation = FALSE,
  mRNAArray = FALSE,
  miRNAArray = FALSE,
  RPPAArray = FALSE,
  GISTIC = FALSE,
  RNAseqNorm = "raw_count",
  RNAseq2Norm = c("normalized_counts", "RSEM_normalized_log2", "raw_counts",
    "scaled_estimate"),
  forceDownload = FALSE,
  destdir = .setCache(),
  fileSizeLimit = 500,
  getUUIDs = FALSE,
  ...
)

Arguments

dataset A cohort disease code. TCGA cancer codes can be obtained via getFirehoseDatasets
runDate Standard data run dates. Date list can be accessible via getFirehoseRunningDates
gistic2Date Analysis run date for GISTIC obtained via getFirehoseAnalyzeDates
RNASeqGene Logical (default FALSE) RNAseq TPM data.
getFirehoseData

RNASeq2Gene Logical (default FALSE) RNAseq v2 (RSEM processed) data; see RNAseqNorm argument.
clinical Logical (default TRUE) clinical data.
miRNASeqGene Logical (default FALSE) smallRNAseq data.
miRNASeqGeneType Character (default "read_count") Indicate which type of data should be pulled from the miRNASeqGene data. Must be one of "reads_per_million_miRNA_mapped", "read_count", or "cross-mapped".
RNASeq2GeneNorm Logical (default FALSE) RNAseq v2 (RSEM processed) data.
CNASNP Logical (default FALSE) somatic copy number alterations data from SNP array.
CNVSNP Logical (default FALSE) germline copy number variants data from SNP array.
CNASeq Logical (default FALSE) somatic copy number alterations data from sequencing.
CNACGH Logical (default FALSE) somatic copy number alterations data from CGH.
Methylation Logical (default FALSE) methylation data.
Mutation Logical (default FALSE) mutation data from sequencing.
mRNAArray Logical (default FALSE) mRNA expression data from microarray.
miRNAArray Logical (default FALSE) miRNA expression data from microarray.
RPPAArray Logical (default FALSE) RPPA data.
GISTIC Logical (default FALSE) processed copy number data.
RNAseqNorm RNAseq data normalization method. (Default raw_count)
RNAseq2Norm RNAseq v2 data normalization method. (Default normalized_count or one of RSEM_normalized_log2, raw_count, scaled_estimate)
forceDownload A logic (Default FALSE) key to force download RTCGAToolbox every time. By default if you download files into your working directory once than RTCGAToolbox using local files next time.
destdir Directory in which to store the resulting downloaded file. Defaults to a cache directory given by RTCGAToolbox:::.setCache()
fileSizeLimit Files that are larger than set value (megabyte) won’t be downloaded (Default: 500)
getUUIDs Logical key to get UUIDs from barcode (Default: FALSE)
... Additional arguments to pass down.

Details

This is a main client function to download data from Firehose TCGA portal.

To avoid unnecessary downloads, we use tools::R_user_dir("RTCGAToolbox", "cache") to set the default destdir parameter to the cached directory. To get the actual default directory, one can run RTCGAToolbox:::.setCache().
Value

A FirehoseData data object that stores data for selected data types.

See Also

getLinks, https://gdac.broadinstitute.org/

Examples

# Sample Dataset
data(accmini)
accmini
## Not run:
BRCAdata <- getFirehoseData(dataset="BRCA",
runDate="20140416",gistic2Date="20140115",
RNASeqGene=TRUE,clinical=TRUE,mRNAArray=TRUE,Mutation=TRUE)

## End(Not run)
**getFirehoseRunningDates**

*Get standard data running dates.*

**Description**

getFirehoseRunningDates returns the character vector for standard data release dates.

**Usage**

```r
getFirehoseRunningDates(last = NULL)
```

**Arguments**

- `last` To list last n dates. (Default NULL)

**Value**

A character vector for dates.

**Examples**

```r
getFirehoseRunningDates()
getFirehoseRunningDates(last=2)
```

---

**getGISTICPeaks**

*Download GISTIC2 peak-level data from the Firehose pipeline*

**Description**

Access GISTIC2 level 4 copy number data through gdac.broadinstitute.org

**Usage**

```r
getGISTICPeaks(object, peak = c("wide", "narrow", "full"), rm.chrX = TRUE)
```

**Arguments**

- `object` A FirehoseData GISTIC type object
- `peak` The peak type, select from "wide", "narrow", "full".
- `rm.chrX` (logical default TRUE) Whether to remove observations in the X chromosome

**Value**

A data.frame of peak values
**getLinks**

**Author(s)**

Ludwig Geistlinger

**Examples**

```r
co <- getFirehoseData("COAD", clinical = FALSE, GISTIC = TRUE)
peaks <- getGISTICPeaks(co, "wide")
class(peaks)
head(peaks)[1:6]
```

---

**getLinks**

*Get resource links from inputs*

**Description**

This function provides a reference to the resources downloaded from the GDAC Firehose pipeline. Based on the input, the function returns a URL location to the resource if there exists one.

**Usage**

```r
getLinks(
  dataset,
  data_date = "20160128",
  RNASeqGene = FALSE,
  RNASeq2Gene = FALSE,
  clinical = FALSE,
  miRNASeqGene = FALSE,
  RNASeq2GeneNorm = FALSE,
  RNAseq2Norm = c("normalized_counts", "RSEM_normalized_log2", "raw_counts",
                  "scaled_estimate"),
  CNASNP = FALSE,
  CNVSNP = FALSE,
  CNASeq = FALSE,
  CNACGH = FALSE,
  Methylation = FALSE,
  Mutation = FALSE,
  mRNAArray = FALSE,
  miRNAArray = FALSE,
  RPPAArray = FALSE,
  GISTIC = FALSE
)
```

**Arguments**

- **dataset**: A cohort disease code. TCGA cancer codes can be obtained via `getFirehoseDatasets`
- **data_date**: Either a runDate or analysisDate typically entered in ‘getFirehoseData’
### RNASeqGene
Logical (default FALSE) RNAseq TPM data.

### RNASeq2Gene
Logical (default FALSE) RNAseq v2 (RSEM processed) data; see RNAseqNorm argument.

### clinical
Logical (default TRUE) clinical data.

### miRNASeqGene
Logical (default FALSE) smallRNAseq data.

### RNASeq2GeneNorm
Logical (default FALSE) RNAseq v2 (RSEM processed) data.

### RNAseq2Norm
RNAseq v2 data normalization method. (Default normalized_count or one of RSEM_normalized_log2, raw_count, scaled_estimate)

### CNASNP
Logical (default FALSE) somatic copy number alterations data from SNP array.

### CNVSNP
Logical (default FALSE) germline copy number variants data from SNP array.

### CNASeq
Logical (default FALSE) somatic copy number alterations data from sequencing.

### CNACGH
Logical (default FALSE) somatic copy number alterations data from CGH.

### Methylation
Logical (default FALSE) methylation data.

### Mutation
Logical (default FALSE) mutation data from sequencing.

### mRNAArray
Logical (default FALSE) mRNA expression data from microarray.

### miRNAArray
Logical (default FALSE) miRNA expression data from microarray.

### RPPAArray
Logical (default FALSE) RPPA data.

### GISTIC
Logical (default FALSE) processed copy number data

---

**Value**

A character URL to a dataset location

**Examples**

```r
getLinks("BRCA", CNASeq = TRUE)
```

---

**getMutationRate**

*Make a table for mutation rate of each gene in the cohort*

**Description**

Make a table for mutation rate of each gene in the cohort

**Usage**

```r
getMutationRate(dataObject)
```

**Arguments**

- `dataObject` This must be FirehoseData object.
Value

Returns a data table

Examples

data(accmini)
mutRate <- getMutationRate(dataObject=accmini)
mutRate <- mutRate[order(mutRate[,2],decreasing = TRUE),]
head(mutRate)

hg19.ucsc.gene.locations

Gene coordinates for circle plot.

Description

A dataset containing the gene coordinates. The variables are as follows:

Format

A data frame with 28454 rows and 5 variables

Details

- GeneSymbol. Gene symbols
- Chromosome. Chromosome name
- Strand. Gene strand on chromosome
- Start. Gene location on chromosome
- End. Gene location on chromosome

makeSummarizedExperimentFromGISTIC

Create a SummarizedExperiment from FireHose GISTIC

Description

Use the output of getFirehoseData to create a SummarizedExperiment. This can be done for three types of data, G-scores thresholded by gene, copy number by gene, and copy number by peak regions.
Usage

makeSummarizedExperimentFromGISTIC(
  gistic,
  dataType = c("AllByGene", "ThresholdedByGene", "Peaks"),
  rownameCol = "Gene.Symbol",
  ...
)

Arguments

gistic A FirehoseGISTIC-class object
dataType character(1) One of "ThresholdedByGene" (default), "AllByGene", or "Peaks"
rownameCol character(1) The name of the column in the data to use as rownames in the data matrix (default: 'Gene.Symbol'). The row names are only set when the column name is found in the data and all values are unique.

... Additional arguments passed to ‘getGISTICPeaks’.

Value

A SummarizedExperiment object

Author(s)

L. Geistlinger, M. Ramos

Examples

co <- getFirehoseData("COAD", clinical = FALSE, GISTIC = TRUE,
  destdir = tempdir())
makeSummarizedExperimentFromGISTIC(co, "AllByGene")

Description

Managing data from large-scale projects (such as The Cancer Genome Atlas (TCGA) for further analysis is an important and time consuming step for research projects. Several efforts, such as the Firehose project, make TCGA pre-processed data publicly available via web services and data portals, but this information must be managed, downloaded and prepared for subsequent steps. We have developed an open source and extensible R based data client for pre-processed data from the Firehose, and demonstrate its use with sample case studies. Results show that our RTCGAToolbox can facilitate data management for researchers interested in working with TCGA data. The RTCGAToolbox can also be integrated with other analysis pipelines for further data processing.
Details

The main function you’re likely to need from RTCGAToolbox is `getFirehoseData`. Otherwise refer to the vignettes to see how to use the RTCGAToolbox

Author(s)

Mehmet Kemal Samur

selectType  

Accessor function for the FirehoseData object

Description

An accessor function for the FirehoseData class. An argument will specify the data type to return. See FirehoseData-class for more details.

Usage

```r
selectType(object, dataType)
```

Arguments

- `object` A FirehoseData class object
- `dataType` A data type, see details.

Details

- clinical - Get the clinical data slot
- RNASeqGene - RNASeqGene
- RNASeq2GeneNorm - Normalized
- miRNASeqGene - micro RNA SeqGene
- CNASNP - Copy Number Alteration
- CNVSNP - Copy Number Variation
- CNASeq - Copy Number Alteration
- CNACGH - Copy Number Alteration
- Methylation - Methylation
- mRNAArray - Messenger RNA
- miRNAArray - micro RNA
- RPPAArray - Reverse Phase Protein Array
- Mutation - Mutations
- GISTIC - GISTIC v2 scores and probabilities

Value

The data type element of the FirehoseData object
showResults, CorResult-method

Description
Export toptable or correlation data frame

Usage
showResults(object)

Arguments
object A DGEResult or CorResult object

Value
Returns toptable or correlation data frame

Examples
data(accmini)
showResults,DGEResult-method

Export toptable or correlation data frame

Description
Export toptable or correlation data frame

Usage
## S4 method for signature 'DGEResult'
showResults(object)

Arguments

object A DGEResult or CorResult object

Value

Returns toptable for DGE results

Examples

data(accmini)
Index

* datasets
  accmini, 3
  biocExtract, 3
  CorResult, 20, 21
  CorResult-class, 5
  DGEResult, 20, 21
  DGEResult-class, 5
  FirehoseCGHArray-class, 5
  FirehoseData, 3, 9, 10, 19
  FirehoseData-class, 6, 19
  FirehoseGISTIC-class, 7, 18
  FirehoseMethylationArray-class, 8
  FirehosemRNAArray-class, 8
  getBroadSubtypes, 9
  getData, 9
  getData, ANY-method
    (FirehoseData-class), 6
  getData, FirehoseData-method
    (FirehoseData-class), 6
  getData, FirehoseGISTIC-method
    (FirehoseData-class), 6
  getFirehoseAnalyzeDates, 7, 10, 11
  getFirehoseData, 11, 19
  getFirehoseDatasets, 9, 11, 13, 15
  getFirehoseRunningDates, 7, 11, 14
  getGISTICPeaks, 8, 14
  getLinks, 13, 15
  getMutationRate, 16
  hg19.ucsc.gene.locations, 17
  isEmpty, FirehoseGISTIC-method
    (FirehoseGISTIC-class), 7
  makeSummarizedExperimentFromGISTIC, 17
  RaggedExperiment, 3, 4
  RTCGAToolbox, 18
  selectType, 19
  selectType, FirehoseData-method
    (FirehoseData-class), 6
  show, FirehoseData-method
    (FirehoseData-class), 6
  showResults, 20
  showResults, CorResult, CorResult-method
    (showResults, CorResult-method), 20
  showResults, CorResult-method, 20
  showResults, DGEResult, DGEResult-method
    (showResults, DGEResult-method), 21
  showResults, DGEResult-method, 21
  SummarizedExperiment, 3, 4, 17
  updateObject, FirehoseData-method
    (FirehoseData-class), 6
  updateObject, FirehoseGISTIC-method
    (FirehoseGISTIC-class), 7