Package 'RTCGAToolbox'

October 14, 2021

Type Package

Title A new tool for exporting TCGA Firehose data

Version 2.22.1

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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LazyData true

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

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Collate 'RTCGAToolbox-Class.R' 'RTCGAToolbox.R' 'utils.R' 'biocExtract.R' 'data.R' 'getBroadSubtypes.R' 'getCNGECorrelation.R' 'getDiffExpressedGenes.R' 'getFirehoseAnalyzeDates.R' 'getFirehoseData.R' 'getFirehoseDatasets.R' 'getFirehoseRunningDates.R'

'getGISTICPeaks.R' 'getLinks.R' 'getMutationRate.R'
'getReport.R' 'getSurvival.R'
'makeSummarizedExperimentFromGISTIC.R' 'selectType.R'

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R topics documented:

`accmini` *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

```
accmini
```

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,
  type = c("clinical", "RNASeqGene", "RNASeq2Gene", "miRNASeqGene", "RNASeq2GeneNorm",
    "CNASNP", "CNVSNP", "CNASeq", "CNACGH", "Methylation", "Mutation", "mRNAArray",
      "miRNAArray", "RPPAArray", "GISTIC", "GISTICA", "GISTICT", "GISTICP"),
  ...
)
```

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 .makeSummarizedExperimentFrom 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")
biocExtract(accmini, "CNVSNP")
biocExtract(accmini, "Methylation")
biocExtract(accmini, "Mutation")
biocExtract(accmini, "RPPAArray")
biocExtract(accmini, "GISTIC")
```

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

```
## 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: show method
- getData: Get a matrix or data.frame from FirehoseData
- getData: Get GISTIC data from FirehoseData
- getData: Default method for getting data from FirehoseData
- updateObject: Update an old RTCGAToolbox FirehoseData object to the most recent API
- selectType: Extract data type

Slots

Dataset A cohort name

runDate Standard data run date from getFirehoseRunningDates

gistic2Date Analyze running date from getFirehoseAnalyzeDates

clinical clinical data frame

RNASeqGene Gene level expression data matrix from RNAseq

RNASeq2Gene Gene level expression data matrix from RNAseqV2

RNASeq2GeneNorm Gene level expression data matrix from RNAseqV2 (RSEM)

miRNASeqGene miRNA expression data from matrix smallRNAseq

CNASNP A data frame to store somatic copy number alterations from SNP array platform

CNVSNP A data frame to store germline copy number variants from SNP array platform

CNASeq A data frame to store somatic copy number alterations from sequencing platform

CNACGH A list that stores FirehoseCGHArray object for somatic copy number alterations from CGH platform

Methylation A list that stores FirehoseMethylationArray object for methylation data

mRNAArray A list that stores FirehosemRNAArray object for gene expression data from microarray

miRNAArray A list that stores FirehosemRNAArray object for miRNA expression data from microarray

RPPAArray A list that stores FirehosemRNAArray object for RPPA data

Mutation A data frame for mutation infromation from sequencing data

GISTIC A FirehoseGISTIC object to store processed copy number data

BarcodeUUID A data frame that stores the Barcodes, UUIDs and Short sample identifiers

`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

```
## 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`: check whether the FirehoseGISTIC object has data in it or not
- `updateObject`: 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` *Download expression-based cancer subtypes from the Broad Institute*

Description

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

Usage

```
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

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

---

getCNGECorrelation *Perform correlation analysis between gene expression and copy number data*

Description

getCNGECorrelation returns a list that stores the results correlation between gene expression and copy number data.

Usage

```
getCNGECorrelation(
  dataObject,
  adj.method = "BH",
  adj.pval = 0.05,
  raw.pval = 0.05
)
```

Arguments

dataObject	This must be FirehoseData object.
adj.method	Raw p value adjustment methods (Default "BH")
adj.pval	Adjusted p value cut off for results table (Default 0.05)
raw.pval	raw p value cut off for results table (Default 0.05)

Value

Returns a list that stores results for each dataset

Examples

```
data(accmini)
```

getData *Extract data from FirehoseData object*

Description

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

```
getData(object, type, platform)
```

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' or 'ThresholdedByGene'

Value

Returns matrix or data.frame depending on data type

Examples

```
data(accmini)
getData(accmini, "clinical")
getData(accmini, "RNASeq2GeneNorm")
getData(accmini, "Methylation", 1)[1:4]
```

getDiffExpressedGenes *Perform differential gene expression analysis for mRNA expression data.*

Description

getDiffExpressedGenes returns a list that stores the results for each dataset.

Usage

```
getDiffExpressedGenes(
  dataObject,
  DrawPlots = TRUE,
  adj.method = "BH",
  adj.pval = 0.05,
  raw.pval = 0.05,
  logFC = 2,
  hmTopUpN = 100,
  hmTopDownN = 100,
  meanFilter = 10
)
```

Arguments

dataObject	This must be FirehoseData object.
DrawPlots	A logical parameter to draw heatmaps and volcano plots.
adj.method	Raw p value adjustment methods (Default "BH")
adj.pval	Adjusted p value cut off for results table (Default 0.05)
raw.pval	raw p value cut off for results table (Default 0.05)
logFC	log fold change cut off for results table (Default 2)
hmTopUpN	Max number of up regulated genes in heatmap (Default 100)
hmTopDownN	Max number of down regulated genes in heatmap (Default 100)
meanFilter	Mean read counts for each gene to filter not expressed genes (Default 10)

Value

Returns a list that stores results for each dataset

Examples

```
data(accmini)
```

---

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,
  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 = "normalized_count",
  forceDownload = FALSE,
  destdir = tempdir(),
  fileSizeLimit = 500,
  getUUIDs = FALSE,
  ...
)
```

Arguments

dataset	A cohort name. TCGA cancer code 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.
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.
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, 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 temporary directory given by tempdir().
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.

Value

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

See Also

getLinks

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)
```

---

getFirehoseDatasets *Get list of TCGA cohorts.*

Description

getFirehoseDatasets returns a character array for cohorts.

Usage

```
getFirehoseDatasets()
```

Value

A character string

Examples

```
getFirehoseDatasets()
```

---

getFirehoseRunningDates *Get standard data running dates.*

Description

getFirehoseRunningDates returns the character vector for standard data release dates.

Usage

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

Arguments

last	To list last n dates. (Default NULL)

Value

A character vector for dates.

Examples

```
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

```
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

Author(s)

Ludwig Geistlinger

Examples

```
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

```
getLinks(
  dataset,
  data_date = "20160128",
  RNASeqGene = FALSE,
  RNASeq2Gene = FALSE,
  clinical = FALSE,
  miRNASeqGene = FALSE,
  RNASeq2GeneNorm = FALSE,
  CNASNP = FALSE,
  CNVSNP = FALSE,
  CNASeq = FALSE,
  CNACGH = FALSE,
  Methylation = FALSE,
  Mutation = FALSE,
  mRNAArray = FALSE,
  miRNAArray = FALSE,
  RPPAArray = FALSE,
  GISTIC = FALSE
)
```

Arguments

dataset	A cohort name. TCGA cancer code 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.
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

`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

```
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)
```

getReport *Draws a circle plot into working directory*

Description

getReport draws a circle plot into your workin director to show log fold changes for differentially expressed genes, copy number alterations and mutations.

Usage

```
getReport(dataObject, DGEResult1 = NULL, DGEResult2 = NULL, geneLocations)
```

Arguments

dataObject	This must be FirehoseData object.
DGEResult1	Differential gene expression results object (Optional)
DGEResult2	Differential gene expression results object (Optional)
geneLocations	Gene coordinates.

Value

Draws a circle plot

Examples

```
data(accmini)
require("Homo.sapiens")
locations <- genes(Homo.sapiens,columns="SYMBOL")
locations <- as.data.frame(locations)
locations <- locations[,c(6,1,5,2:3)]
locations <- locations[!is.na(locations[,1]),]
locations <- locations[!duplicated(locations[,1]),]
rownames(locations) <- locations[,1]
## Not run:
  getReport(dataObject=accmini,DGEResult1=t1[[1]],geneLocations=locations)

## End(Not run)
```

getSurvival *Perform survival analysis based on gene expression data*

Description

getSurvival draws a KM plot and show survival analysis results between groups that are defined by gene expression data

Usage

```
getSurvival(dataObject, numberofGroups = 2, geneSymbols, sampleTimeCensor)
```

Arguments

dataObject	This must be FirehoseData object.
numberofGroups	Can be set as 2 or 3. (Default 2) Order and divide samples into n groups by using gene expression data.
geneSymbols	Gene symbol that is going to be tested
sampleTimeCensor	a data frame that stores clinical data. First column should store sample IDs, second column should have time and third column should have event information. For more information please see vignette.

Value

Draws a KM plot

Examples

```
## get data with  getFirehoseData function and call survival analysis
## Always check clinical data file for structural changes

data(accmini)
clinicData <- getData(accmini,"clinical")
clinicData = clinicData[,3:5]
clinicData[is.na(clinicData[,3]),3] = clinicData[is.na(clinicData[,3]),2]
survData <- data.frame(Samples=rownames(clinicData),Time=as.numeric(clinicData[,3]),
Censor=as.numeric(clinicData[,1]))
getSurvival(dataObject=accmini,geneSymbols=c("FCGBP"),sampleTimeCensor=survData)
```

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, ...)
```

Arguments

`gistic`	A FirehoseGISTIC-class object
`dataType`	Either one of "ThresholdedByGene", "AllByGene", "Peaks"
`...`	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")
```

RTCGAToolbox *RTCGAToolbox: A New Tool for Exporting TCGA Firehose Data*

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

```
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 *Export toptable or correlation data frame*

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,CorResult-method

Export toptable or correlation data frame

Description

Export toptable or correlation data frame

Usage

```
## S4 method for signature 'CorResult'
showResults(object)
```

Arguments

object	A DGEResult or CorResult object

Value

Returns correlation results 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)
```

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