

Package ‘RTCGAToolbox’

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Type Package

Title A new tool for exporting TCGA Firehose data

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Author Mehmet Kemal Samur

Maintainer Mehmet Kemal Samur <samur@jimmy.harvard.edu>

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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biocViews Sequencing, DifferentialExpression, GeneExpression

VignetteBuilder knitr

Suggests BiocStyle, knitr, rmarkdown, Homo.sapiens

Imports methods,XML,limma (>= 3.18),survival,RCircos,data.table (>= 1.9.4),RCurl,RJSONIO

Depends R (>= 3.2.0)

NeedsCompilation no

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CorResult-class	<i>An S4 class to store correlations between gene expression level and copy number data</i>
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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	<i>An S4 class to store differential gene expression results</i>
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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 clinet function.

Description

An S4 class to store main data object from clinet function.

Slots

Dataset A cohort name

Clinical Clinical data frame

RNASeqGene Gene level expression data matrix from RNAseq

RNASeq2GeneNorm Gene level expression data matrix from RNAseq (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

Mutations A data frame for mutation information 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)

Slots

Dataset Cohort name

AllByGene A data frame that stores continuous copy number

ThresholdedByGene A data frame for discrete copy number data

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.

getCNGECorrelation	<i>Perform correlation analysis between gene expression and copy number data</i>
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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(RTCGASample)  
corRes = getCNGECorrelation(RTCGASample)  
corRes  
showResults(corRes[[1]])  
## Not run:
```

getData	<i>Export data from FirehoseData object</i>
---------	---

Description

Export data from FirehoseData object

Usage

```
getData(object, type = "", platform = NULL, CN = "All")
```

Arguments

object	A FirehoseData object
type	A data type to be exported (Data types can be seen by typing <code>show(objectname)</code>)
platform	A list id for data types that may come from multiple platform (such as mRNAArray)
CN	A copy number data type (Default: 'All') (Possible values 'All' or 'Thresholed')

Value

Returns matrix or data frame depends on data type

Examples

```
data(RTCGASample)
sampleClinical = getData(RTCGASample,"Clinical")
sampleClinical = getData(RTCGASample,"RNASeqGene")
```

`getData,FirehoseData-method`

Export data from FirehoseData object

Description

Export data from FirehoseData object

Usage

```
## S4 method for signature 'FirehoseData'
getData(object, type = "", platform = NULL,
        CN = "All")
```

Arguments

object	A FirehoseData object
type	A data type to be exported (Data types can be seen by typing <code>show(objectname)</code>)
platform	A list id for data types that may come from multiple platform (such as mRNAArray)
CN	A copy number data type (Default: 'All') (Possible values 'All' or 'Thresholed')

Value

Returns matrix or data frame depends on data type

Examples

```
data(RTCGASample)
sampleClinical = getData(RTCGASample,"Clinical")
sampleClinical = getData(RTCGASample,"RNASeqGene")
```

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(RTCGASample)  
dgegenes = getDiffExpressedGenes(RTCGASample)  
dgegenes  
showResults(dgegenes[[1]])  
dgegenes = showResults(dgegenes[[1]])  
head(dgegenes)  
## Not run:
```

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()  
getFirehoseAnalyzeDates(last=2)
```

getFirehoseData

Get data from Firehose portal.

Description

getFirehoseData returns FirehoseData object that stores TCGA data.

Usage

```
getFirehoseData(dataset, runDate = NULL, gistic2_Date = NULL,  
  RNAseq_Gene = FALSE, Clinic = TRUE, miRNASeq_Gene = FALSE,  
  RNAseq2_Gene_Norm = FALSE, CNA_SNP = FALSE, CNV_SNP = FALSE,  
  CNA_Seq = FALSE, CNA_CGH = FALSE, Methylation = FALSE,  
  Mutation = FALSE, mRNA_Array = FALSE, miRNA_Array = FALSE,  
  RPPA = FALSE, RNAseqNorm = "raw_counts",  
  RNAseq2Norm = "normalized_count", forceDownload = FALSE, destdir = ".",  
  fileSizeLimit = 500, getUUIDs = FALSE)
```


Arguments

dataset	A cohort name. All dataset names can be accessible via getFirehoseDatasets
runDate	Standard data run dates. Date list can be accessible via getFirehoseRunningDates
gistic2_Date	Analyze running dates for GISTIC processed copy number data. Date list can be accessible via getFirehoseAnalyzeDates
RNAseq_Gene	Logical (default FALSE) parameter for RNAseq data.
Clinic	Logical (default TRUE) parameter for clinical data.
miRNASeq_Gene	Logical (default FALSE) parameter for smallRNAseq data.
RNAseq2_Gene_Norm	Logical (default FALSE) parameter for RNAseq v2 (RSEM processed) data.
CNA_SNP	Logical (default FALSE) parameter for somatic copy number alterations data from SNP array.
CNV_SNP	Logical (default FALSE) parameter for germline copy number variants data from SNP array.
CNA_Seq	Logical (default FALSE) parameter for somatic copy number alterations data from sequencing.
CNA_CGH	Logical (default FALSE) parameter for somatic copy number alterations data from CGH.
Methylation	Logical (default FALSE) parameter for methylation data.
Mutation	Logical (default FALSE) parameter for mutation data from sequencing.
mRNA_Array	Logical (default FALSE) parameter for mRNA expression data from microarray.
miRNA_Array	Logical (default FALSE) parameter for miRNA expression data from microarray.
RPPA	Logical (default FALSE) parameter for RPPA data
RNAseqNorm	RNAseq data normalization method. (Default raw_counts)
RNAseq2Norm	RNAseq v2 data normalization method. (Default normalized_count)
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 current working directory.
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)

Details

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

Value

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

Examples

```
#Sample Dataset
data(RTCGASample)
RTCGASample
## Not run:
BRCAdata <- getFirehoseData(dataset="BRCA",
runDate="20140416",gistic2_Date="20140115",
RNAseq_Gene=TRUE,Clinic=TRUE,mRNA_Array=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)
```

<code>getMutationRate</code>	<i>Make a table for mutation rate of each gene in the cohort</i>
------------------------------	--

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(RTCGASample)  
mutRate = getMutationRate(dataObject=RTCGASample)  
mutRate <- mutRate[order(mutRate[,2],decreasing = TRUE),]  
head(mutRate)  
## Not run:
```

getReport	<i>Draws a circle plot into working directory</i>
-----------	---

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(RTCGASample)
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]),]
rownames(locations) <- locations[,1]
t1=getDiffExpressedGenes(RTCGASample)
## Not run:
getReport(dataObject=RTCASample,DGEResult1=t1[[1]],geneLocations=locations)

## End(Not run)
```

getSurvival	<i>Perform survival analysis based on gene expression data</i>
-------------	--

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(RTCGASample)
clinicData <- getData(RTCGASample,"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=RTCASample, 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
-

RTCGASample

A sample data object for sample codes.

Description

A FirehoseData object for running sample codes. The variables are as follows:

Format

A FirehoseData data object

Details

- a2. A sample data object

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

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(RTCGASample)
dgeRes = getDiffExpressedGenes(RTCGASample)
dgeRes
showResults(dgeRes[[1]])
```

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(RTCGASample)  
corRes = getCNGECorrelation(RTCGASample,adj.pval = 1,raw.pval = 1)  
corRes  
showResults(corRes[[1]])
```

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(RTCGASample)
dgeRes = getDiffExpressedGenes(RTCGASample)
dgeRes
showResults(dgeRes[[1]])
```

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