# Package ‘RTCGAToolbox’

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**Type** Package  
**Title** A new tool for exporting TCGA Firehose data  
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**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.

**License** GPL (>= 2)  
**biocViews** Sequencing, DifferentialExpression, GeneExpression  
**VignetteBuilder** knitr  
**Suggests** BiocStyle, knitr, rmarkdown, Homo.sapiens  
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**Depends** R (>= 3.2.0)  
**NeedsCompilation** no

**R topics documented:**

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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.

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 FirehoseRNAArray object for gene expression data from microarray
- miRNAArray A list that stores FirehoseRNAArray object for miRNA expression data from microarray
- RPPAArray A list that stores FirehoseRNAArray 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.

FirehoseRNAArray-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**

**Description**

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

**Usage**

```r
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**

```r
data(RTCGASample)
corRes = getCNGECorrelation(RTCGASample)
corRes
showResults(corRes[[1]])
## Not run:
```

**getData**

**Export data from FirehoseData object**

**Description**

Export data from FirehoseData object

**Usage**

```r
getData(object, type = "", platform = NULL, CN = "All")
```
getData,FirehoseData-method

Arguments

- **object**: A FirehoseData object
- **type**: A data type to be exported (Data types can be seen by typing show(objectname))
- **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

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

Description

Export data from FirehoseData object

Usage

```r
## S4 method for signature 'FirehoseData'
ggetData(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 show(objectname))
- **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

```r
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**

```r
getFirehoseAnalyzeDates(last = NULL)
```

**Arguments**

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

**Value**

A character vector for dates.

**Examples**

```r
getFirehoseAnalyzeDates()
getFirehoseAnalyzeDates(last = 2)
```

getFirehoseData

*Get data from Firehose portal.*

**Description**

getFirehoseData returns FirehoseData object that stores TCGA data.

**Usage**

```r
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)
```
getFirehoseData

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 function to download data from Firehose TCGA portal.

Value

A FirehoseData data object that stores data for selected data types.
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 n dates. (Default NULL)

Value
A character vector for dates.
getMutationRate

Examples

getFirehoseRunningDates()
getFirehoseRunningDates(last=2)

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

getReport Draws a circle plot into working directory

Description

getReport draws a circle plot into your working directory 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.
**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

```r
## 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=RTCGASample,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
**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

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**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**

```r
data(RTCGASample)
dgeRes = getDiffExpressedGenes(RTCGASample)
dgeRes
dgeRes[[1]]
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

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