Package ‘RTCGAToolbox’

May 16, 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)

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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'
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**Description**

A subset of the Adrenocortical Carcinoma (ACC) dataset

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**

```r
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](https://bioconductor.org/packages/release/bioc/html/RaggedExperiment-class.html) for more details.

**Usage**

```r
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.frame`s to `SummarizedExperiment` representations (via the `.makeSummarizedExperimentFromData.frame` 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 client function.

Description

An S4 class to store main data object from client 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

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 FirehoseRNAArray object for RPPA data
Mutation  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)

Usage

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

## S4 method for signature 'FirehoseGISTIC'
updateObject(object, ..., verbose = FALSE)
```
**FirehosemRNAArray-class**

**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**

<table>
<thead>
<tr>
<th>Dataset</th>
<th>Cohort name</th>
</tr>
</thead>
<tbody>
<tr>
<td><strong>AllByGene</strong></td>
<td>A data frame that stores continuous copy number</td>
</tr>
<tr>
<td><strong>ThresholdedByGene</strong></td>
<td>A data frame for discrete copy number data</td>
</tr>
<tr>
<td><strong>Peaks</strong></td>
<td>A data frame storing GISTIC peak data. See <code>getGISTICPeaks</code>.</td>
</tr>
</tbody>
</table>

**FirehoseMethylationArray-class**

*An S4 class to store data from methylation platforms*

**Description**

An S4 class to store data from methylation platforms

**Slots**

<table>
<thead>
<tr>
<th>Filename</th>
<th>Platform name</th>
</tr>
</thead>
<tbody>
<tr>
<td><strong>DataMatrix</strong></td>
<td>A data frame that stores the methylation data.</td>
</tr>
</tbody>
</table>

**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**

<table>
<thead>
<tr>
<th>Filename</th>
<th>Platform name</th>
</tr>
</thead>
<tbody>
<tr>
<td><strong>DataMatrix</strong></td>
<td>A data matrix that stores the expression data.</td>
</tr>
</tbody>
</table>
**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)

---

**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)
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) small RNAseq 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().
getFirehoseDatasets

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)

getFirehoseDatasets

Get a list of TCGA disease cohorts

Description

getFirehoseDatasets returns a character vector of TCGA disease codes. A reference table can be seen at https://gdac.broadinstitute.org/.

Usage

getFirehoseDatasets()

Value

A character string

See Also

https://gdac.broadinstitute.org/

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
getLinks

Author(s)

Ludwig Geistlinger

Examples

c <- 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,
  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’
getMutationRate

**Description**

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

**Usage**

```r
getMutationRate(dataObject)
```

**Arguments**

- `dataObject` This must be FirehoseData object.
hg19.ucsc.gene.locations

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

c0 <- getFirehoseData("COAD", clinical = FALSE, GISTIC = TRUE,
destdir = tempdir())
makeSummarizedExperimentFromGISTIC(c0, "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 RTCGATool-
box 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

<table>
<thead>
<tr>
<th>Argument</th>
<th>Description</th>
</tr>
</thead>
<tbody>
<tr>
<td>object</td>
<td>A FirehoseData class object</td>
</tr>
<tr>
<td>dataType</td>
<td>A data type, see details.</td>
</tr>
</tbody>
</table>

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

---

**showResults**

*Export toptable or correlation data frame*

**Description**

Export toptable or correlation data frame

**Usage**

```r
showResults(object)
```

**Arguments**

- `object`  
  A `DGEResult` or `CorResult` object

**Value**

Returns toptable or correlation data frame

**Examples**

```r
data(accmini)
```

---

### showResults, CorResult-method

*Export toptable or correlation data frame*

**Description**

Export toptable or correlation data frame

**Usage**

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

**Arguments**

- `object`  
  A `DGEResult` or `CorResult` object

**Value**

Returns correlation results data frame

**Examples**

```r
data(accmini)
```
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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