

# Package ‘RTCGAToolbox’

April 16, 2019

**Type** Package

**Title** A new tool for exporting TCGA Firehose data

**Version** 2.12.1

**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.

**License** file LICENSE

**LazyData** true

**Depends** R (>= 3.5.0)

**Imports** BiocGenerics, data.table, DelayedArray, GenomicRanges, GenomeInfoDb, IRanges, limma, methods, RaggedExperiment, RCircos, RCurl, RJSONIO, S4Vectors, stringr, SummarizedExperiment, survival, TCGAutils, XML

**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

**RoxygenNote** 6.1.0

**Collate** 'RTCGAToolbox-Class.R' 'RTCGAToolbox.R' 'utils.R'  
'biocExtract.R' 'getBroadSubtypes.R' 'getCNGECorrelation.R'  
'getDiffExpressedGenes.R' 'getFirehoseAnalyzeDates.R'  
'getFirehoseData.R' 'getFirehoseDatasets.R'  
'getFirehoseRunningDates.R' 'getGISTICPeaks.R'  
'getMutationRate.R' 'getReport.R' 'getSurvival.R'  
'selectType.R'

**git\_url** <https://git.bioconductor.org/packages/RTCGAToolbox>

**git\_branch** RELEASE\_3\_8

**git\_last\_commit** 46aedee

**git\_last\_commit\_date** 2018-10-30

**Date/Publication** 2019-04-15

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biocExtract	<i>Extract and convert data from a FirehoseData object to a Bioconductor object</i>
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## 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](#) for more details.

## Usage

```
biocExtract(object, type = c("clinical", "RNASeqGene", "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.

## Value

Either an [SummarizedExperiment](#) object or a [RaggedExperiment](#) object.

## type

Choices include:

- 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
- GISTICA - GISTIC v2 ('AllByGene' only)
- GISTICT - GISTIC v2 ('ThresholdedByGene' only)
- GISTICP - GISTIC v2 ('Peaks' only)
- GISTIC - GISTIC v2 scores and probabilities (both)

## Author(s)

Marcel Ramos <marcel.ramos@roswellpark.org>

**Examples**

```
## Not run:
  coadmut <- getFirehoseData("COAD", Mutation = TRUE)
  biocExtract(coadmut, "Mutation")

## End(Not run)
```

---

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

---

**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>
-----------------	--

---

**Description**

An S4 class to store differential gene expression results

**Slots**

Dataset Dataset name  
Toptable Results data frame

---

FirehoseCGHArray-class	<i>An S4 class to store data from CGA platforms</i>
------------------------	---

---

**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

```
## S4 method for signature 'FirehoseData'
show(object)

## S4 method for signature 'FirehoseData'
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' or 'Thresholded-ByGene'
...	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
- updateObject: Update an old RCGAToolbox 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  
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  
 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

```

## 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	<i>Perform correlation analysis between gene expression and copy number data</i>
--------------------	--

---

**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]])
```



---

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

---

### 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 <a href="#">FirehoseData</a> 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 'Thresholded-ByGene'

### Value

Returns matrix or data.frame depending on data type

### Examples

```
data(RTCGASample)
getData(RTCGASample, "clinical")
getData(RTCGASample, "RNASeqGene")
```

---

getDiffExpressedGenes	<i>Perform differential gene expression analysis for mRNA expression data.</i>
-----------------------	--

---

### 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**

<code>dataObject</code>	This must be <code>FirehoseData</code> object.
<code>DrawPlots</code>	A logical parameter to draw heatmaps and volcano plots.
<code>adj.method</code>	Raw p value adjustment methods (Default "BH")
<code>adj.pval</code>	Adjusted p value cut off for results table (Default 0.05)
<code>raw.pval</code>	raw p value cut off for results table (Default 0.05)
<code>logFC</code>	log fold change cut off for results table (Default 2)
<code>hmTopUpN</code>	Max number of up regulated genes in heatmap (Default 100)
<code>hmTopDownN</code>	Max number of down regulated genes in heatmap (Default 100)
<code>meanFilter</code>	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)
```

---

`getFirehoseAnalyzeDates`

*Get data analyze dates.*

---

**Description**

`getFirehoseAnalyzeDates` returns the character vector for analyze release dates.

**Usage**

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

**Arguments**

<code>last</code>	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, 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_counts", RNAseq2Norm = "normalized_count",
  forceDownload = FALSE, destdir = ".", fileSizeLimit = 500,
  getUUIDs = FALSE, ...)
```

## Arguments

dataset	A cohort name. TCGA cancer code obtained via <a href="#">getFirehoseDatasets</a>
runDate	Standard data run dates. Date list can be accessible via <a href="#">getFirehoseRunningDates</a>
gistic2Date	Analysis run date for GISTIC obtained via <a href="#">getFirehoseAnalyzeDates</a>
RNASeqGene	Logical (default FALSE) RNAseq data.
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_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.

<code>destdir</code>	Directory in which to store the resulting downloaded file. Defaults to current working directory.
<code>fileSizeLimit</code>	Files that are larger than set value (megabyte) won't be downloaded (Default: 500)
<code>getUUIDs</code>	Logical key to get UUIDs from barcode (Default: FALSE)
<code>...</code>	Additional arguments to pass down. See details.

**Details**

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

The `...` argument allows for selection of GISTIC peaks when calling `getGISTICPeaks`.

**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",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](http://gdac.broadinstitute.org)

**Usage**

```
getGISTICPeaks(dataset, peak = c("wide", "narrow", "full"),  
  rm.chrX = TRUE, gistic2Date = "20160128", destdir = tempdir())
```

**Arguments**

`dataset` A TCGA cancer code  
`peak` The peak type, select from "wide", "narrow", "full".  
`rm.chrX` (logical default TRUE) Whether to remove observations in the X chromosome  
`gistic2Date` (character default "20160128") Data of the analysis pipeline run  
`destdir` Directory location to save the downloaded file (default `tempdir()`)

**Value**

A `data.frame` of peak values

**Author(s)**

Ludwig Geistlinger

**Examples**

```
co <- getGISTICPeaks("COAD", "wide")
class(co)
head(co)[1:6]
```

---

getMutationRate	<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]),]
locations <- locations[!duplicated(locations[,1]),]
rownames(locations) <- locations[,1]
t1 <- getDiffExpressedGenes(RTCGASample)
## Not run:
getReport(dataObject=RTCGASample,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=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:

Example dataset not biologically meaningful

**Usage**

RTCGASample



**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

---

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(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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