

Package ‘TCGAbiolinks’

February 10, 2015

Type Package

Title Download data from TCGA

Version 1.0

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Depends R (>= 3.1.1), RCurl

Description Query Download and Preprocess data from TCGA portal

License GPL (>= 3)

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TCGAbiolinks-package	<i>TCGAbiolinks</i>
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Description

More about what it does (maybe more than one line) ~~ A concise (1-5 lines) description of the package ~~

Details

Package: TCGAbiolinks
Type: Package
Version: 1.0
Date: 2015-01-21
License: What license is it under?

~~ An overview of how to use the package, including the most important functions ~~

Author(s)

Who wrote it

Maintainer: Who to complain to <yourfault@somewhere.net> ~~ The author and/or maintainer of the package ~~

References

~~ Literature or other references for background information ~~

See Also

~~ Optional links to other man pages, e.g. ~~ <pkg> ~~

createDirectory

createDirectory

Usage

createDirectory(base)

Arguments

base

Examples

createDirectory

DownloadDmageTAB	<i>DownloadDmageTAB</i>
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Usage

```
DownloadDmageTAB(Description, TumorDataList, keySpecies, startK, stopK, typeProtein = F)
```

Arguments

```
Description  
TumorDataList  
keySpecies  
startK  
stopK  
typeProtein
```

DownloadDmageTAB_sdrf	<i>DownloadDmageTAB_sdrf</i>
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Usage

```
DownloadDmageTAB_sdrf(Description, keySpecies, KeyGrep1 = "mage-tab", KeyGrep2 = "sdrf")
```

Arguments

```
Description  
keySpecies  
KeyGrep1  
KeyGrep2
```

DownloadManifest	<i>DownloadManifest</i>
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Usage

```
DownloadManifest(siteNewLevel)
```

Arguments

```
siteNewLevel
```

DownloadSdrf	<i>DownloadSdrf</i>
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Usage

DownloadSdrf(siteNewLevel)

Arguments

siteNewLevel

DownloadTypeFile	<i>DownloadTypeFile</i>
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Usage

DownloadTypeFile(siteNewLevel, keyDown)

Arguments

siteNewLevel
keyDown

DownloadURL	<i>DownloadURL</i>
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Usage

DownloadURL(Site)

Arguments

Site

FindGrepSite	<i>FindGrepSite</i>
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Usage

FindGrepSite(x, Key, Description)

Arguments

x
Key
Description

Examples

FindGrepSite

TCGADownload

*TCGADownload***Description**

Download data of samples from TCGA specified by tumor,type, species and platform type.

Usage

```
TCGADownload(Tumor, Type, Species, PlatformAndAssociatedData, downloadFolder = "", PlatformType, n
```

Arguments

Tumor	character containing tumor to analyze
Type	character containing biological data type to analyze
Species	character containing technology from which you want to get the data
PlatformAndAssociatedData	data frame 615 observations of 12 variables, indicating the different characteristics of the data e.g. tumour, type, species.
downloadFolder	path folder where data will be stored
PlatformType	character containing platform type from which you want to get the data
nsample	number of samples to be analyzed, default all samples
listSample	

Details

TCGA download retrieves and stores data of samples belonging to the specified cancer type and measured by the specified assay platform.

Value

TCGADownload returns a matrix with Samples in columns with barcode and probeID in rows. ProbeID and values changes with platforms.

humanmethylation27

If platform is humanmethylation27 returns values as Hybridization.RE

illuminahiseq_rnaseq

If platform is humanmethylation27 returns values as raw_counts

agilentg4502a_07_3

If platform is humanmethylation27 returns values as Hybridization.REF

illuminahiseq_rnaseqv2

I

humanmethylation450

If platform is humanmethylation27 returns values as Hybridization.REF

illuminaga_mirnaseq

If platform is humanmethylation27 returns values as read_count

illuminahiseq_mirnaseq

If platform is humanmethylation27 returns values as read_count

genome_wide_snp_6

If platform is humanmethylation27 returns values as Segment_Mean

mda_rppa_core I

Author(s)

Antonio Colaprico, Luciano Garofano, Claudia Cava, Gianluca Bontempi, Michele Ceccarelli

TCGAQuery	<i>TCGAQuery</i>
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Description

TCGAQuery retrieves TCGA in order to find

Usage

```
TCGAQuery(Tumor, siteTCGA)
```

Arguments

Tumor
siteTCGA

TCGAVersion	<i>TCGAVersion</i>
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Description

TCGAVersion downloads automatically the latest version of data samples from TCGA specified by tumor and platform type.

Usage

```
TCGAVersion(Tumor, PlatformType, PlatformAndAssociatedData)
```

Arguments

Tumor character containing tumor to analyze
PlatformType character containing platform type from which you want to get the data
PlatformAndAssociatedData
 data frame 615 observations of 12 variables, indicating the different characteristics of the data e.g. tumour, type, species.

Value

TCGADownload returns a matrix with Samples in columns with barcode and probeID in rows. ProbeID and values changes with platforms.

humanmethylation27

If platform is humanmethylation27 returns values as Hybridization.RE

illuminahiseq_rnaseq

If platform is humanmethylation27 returns values as raw_counts

agilentg4502a_07_3

If platform is humanmethylation27 returns values as Hybridization.REF

illuminahiseq_rnaseqv2

I

humanmethylation450

If platform is humanmethylation27 returns values as Hybridization.REF

illuminaga_mirnaseq

If platform is humanmethylation27 returns values as read_count

illuminahiseq_mirnaseq

If platform is humanmethylation27 returns values as read_count

genome_wide_snp_6

If platform is humanmethylation27 returns values as Segment_Mean

mda_rppa_core I

Author(s)

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