Package 'RnaSeqSampleSizeData'

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Type Package

Title RnaSeqSampleSizeData

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Description RnaSeqSampleSizeData package provides the read counts and
dispersion distribution from real RNA-seq experiments. It can
be used by RnaSeqSampleSize package to estimate sample size and
power for RNA-seq experiment design.

License GPL (>= 2)

LazyLoad yes

LazyData false

Depends edgeR,R (>= 2.10)

VignetteBuilder knitr

Suggests BiocStyle, knitr

biocViews ExperimentData, CancerData, RNASeqData

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TCGA_BLCA   *Read counts and dispersion distribution for genes in TCGA BLCA data.*

Description

Read counts and dispersion distribution for genes in TCGA BLCA data.

Usage

```
TCGA_BLCA
```

Value

A class 'DGEList' from edgeR package.

Source

https://tcga-data.nci.nih.gov/tcgafiles/ftp_auth/distro_ftpusers/anonymous/tumor/
blca/cgcc/unc.edu/illuminahiseq_rnaseqv2/rnaseqv2/unc.edu_BLCA.IlluminaHiSeq_RNASeqV2.
Level_3.1.17.0/

TCGA_BRCA   *Read counts and dispersion distribution for genes in TCGA BRCA data.*

Description

Read counts and dispersion distribution for genes in TCGA BRCA data.

Usage

```
TCGA_BRCA
```

Value

A class 'DGEList' from edgeR package.

Source

https://tcga-data.nci.nih.gov/tcgafiles/ftp_auth/distro_ftpusers/anonymous/tumor/
brca/cgcc/unc.edu/illuminahiseq_rnaseqv2/rnaseqv2/unc.edu_BRCA.IlluminaHiSeq_RNASeqV2.
Level_3.1.10.0/

TCGA_CESC	*Read counts and dispersion distribution for genes in TCGA CESC data.*

Description

Read counts and dispersion distribution for genes in TCGA CESC data.

Usage

```
TCGA_CESC
```

Value

A class 'DGEList' from edgeR package.

Source

https://tcga-data.nci.nih.gov/tcgafiles/ftp_auth/distro_ftpusers/anonymous/tumor/
[cesc/cgcc/unc.edu/illuminahiseq_rnaseqv2/rnaseqv2/](https://tcga-data.nci.nih.gov/tcgafiles/ftp_auth/distro_ftpusers/anonymous/tumor/cesc/cgcc/unc.edu/illuminahiseq_rnaseqv2/rnaseqv2/)

TCGA_COAD	*Read counts and dispersion distribution for genes in TCGA COAD data.*

Description

Read counts and dispersion distribution for genes in TCGA COAD data.

Usage

```
TCGA_COAD
```

Value

A class 'DGEList' from edgeR package.

Source

https://tcga-data.nci.nih.gov/tcgafiles/ftp_auth/distro_ftpusers/anonymous/tumor/
[coad/cgcc/unc.edu/illuminahiseq_rnaseqv2/rnaseqv2/unc.edu_COAD.IlluminaHiSeq_RNASeqV2.](https://tcga-data.nci.nih.gov/tcgafiles/ftp_auth/distro_ftpusers/anonymous/tumor/coad/cgcc/unc.edu/illuminahiseq_rnaseqv2/rnaseqv2/unc.edu_COAD.IlluminaHiSeq_RNASeqV2.Level_3.1.9.0/)
[Level_3.1.9.0/](https://tcga-data.nci.nih.gov/tcgafiles/ftp_auth/distro_ftpusers/anonymous/tumor/coad/cgcc/unc.edu/illuminahiseq_rnaseqv2/rnaseqv2/unc.edu_COAD.IlluminaHiSeq_RNASeqV2.Level_3.1.9.0/)

TCGA_HNSC	*Read counts and dispersion distribution for genes in TCGA HNSC data.*

Description

Read counts and dispersion distribution for genes in TCGA HNSC data.

Usage

```
TCGA_HNSC
```

Value

A class 'DGEList' from edgeR package.

Source

https://tcga-data.nci.nih.gov/tcgafiles/ftp_auth/distro_ftpusers/anonymous/tumor/
[hnsc/cgcc/unc.edu/illuminahiseq_rnaseqv2/rnaseqv2/unc.edu_HNSC.IlluminaHiSeq_RNASeqV2.](https://tcga-data.nci.nih.gov/tcgafiles/ftp_auth/distro_ftpusers/anonymous/tumor/hnsc/cgcc/unc.edu/illuminahiseq_rnaseqv2/rnaseqv2/unc.edu_HNSC.IlluminaHiSeq_RNASeqV2.)
[Level_3.1.7.0/](https://tcga-data.nci.nih.gov/tcgafiles/ftp_auth/distro_ftpusers/anonymous/tumor/hnsc/cgcc/unc.edu/illuminahiseq_rnaseqv2/rnaseqv2/unc.edu_HNSC.IlluminaHiSeq_RNASeqV2.Level_3.1.7.0/)

TCGA_KIRC	*Read counts and dispersion distribution for genes in TCGA KIRC data.*

Description

Read counts and dispersion distribution for genes in TCGA KIRC data.

Usage

```
TCGA_KIRC
```

Value

A class 'DGEList' from edgeR package.

Source

https://tcga-data.nci.nih.gov/tcgafiles/ftp_auth/distro_ftpusers/anonymous/tumor/
[kirc/cgcc/unc.edu/illuminahiseq_rnaseqv2/rnaseqv2/unc.edu_KIRC.IlluminaHiSeq_RNASeqV2.](https://tcga-data.nci.nih.gov/tcgafiles/ftp_auth/distro_ftpusers/anonymous/tumor/kirc/cgcc/unc.edu/illuminahiseq_rnaseqv2/rnaseqv2/unc.edu_KIRC.IlluminaHiSeq_RNASeqV2.)
[Level_3.1.5.0/](https://tcga-data.nci.nih.gov/tcgafiles/ftp_auth/distro_ftpusers/anonymous/tumor/kirc/cgcc/unc.edu/illuminahiseq_rnaseqv2/rnaseqv2/unc.edu_KIRC.IlluminaHiSeq_RNASeqV2.Level_3.1.5.0/)

TCGA_LGG	*Read counts and dispersion distribution for genes in TCGA LGG data.*

Description

Read counts and dispersion distribution for genes in TCGA LGG data.

Usage

```
TCGA_LGG
```

Value

A class 'DGEList' from edgeR package.

Source

https://tcga-data.nci.nih.gov/tcgafiles/ftp_auth/distro_ftpusers/anonymous/tumor/
lgg/cgcc/unc.edu/illuminahiseq_rnaseqv2/rnaseqv2/unc.edu_LGG.IlluminaHiSeq_RNASeqV2.
Level_3.1.12.0/

TCGA_LUAD	*Read counts and dispersion distribution for genes in TCGA LUAD data.*

Description

Read counts and dispersion distribution for genes in TCGA LUAD data.

Usage

```
TCGA_LUAD
```

Value

A class 'DGEList' from edgeR package.

Source

https://tcga-data.nci.nih.gov/tcgafiles/ftp_auth/distro_ftpusers/anonymous/tumor/
luad/cgcc/unc.edu/illuminahiseq_rnaseqv2/rnaseqv2/unc.edu_LUAD.IlluminaHiSeq_RNASeqV2.
Level_3.1.13.0/

TCGA_LUSC	*Read counts and dispersion distribution for genes in TCGA LUSC data.*

Description

Read counts and dispersion distribution for genes in TCGA LUSC data.

Usage

```
TCGA_LUSC
```

Value

A class 'DGEList' from edgeR package.

Source

[https://tcga-data.nci.nih.gov/tcgafiles/ftp_auth/distro_ftpusers/anonymous/tumor/](https://tcga-data.nci.nih.gov/tcgafiles/ftp_auth/distro_ftpusers/anonymous/tumor/lusc/cgcc/unc.edu/illuminahiseq_rnaseqv2/rnaseqv2/unc.edu_LUSC.IlluminaHiSeq_RNASeqV2.Level_3.1.9.0/)
[lusc/cgcc/unc.edu/illuminahiseq_rnaseqv2/rnaseqv2/unc.edu_LUSC.IlluminaHiSeq_RNASeqV2.](https://tcga-data.nci.nih.gov/tcgafiles/ftp_auth/distro_ftpusers/anonymous/tumor/lusc/cgcc/unc.edu/illuminahiseq_rnaseqv2/rnaseqv2/unc.edu_LUSC.IlluminaHiSeq_RNASeqV2.Level_3.1.9.0/)
[Level_3.1.9.0/](https://tcga-data.nci.nih.gov/tcgafiles/ftp_auth/distro_ftpusers/anonymous/tumor/lusc/cgcc/unc.edu/illuminahiseq_rnaseqv2/rnaseqv2/unc.edu_LUSC.IlluminaHiSeq_RNASeqV2.Level_3.1.9.0/)

TCGA_PRAD	*Read counts and dispersion distribution for genes in TCGA PRAD data.*

Description

Read counts and dispersion distribution for genes in TCGA PRAD data.

Usage

```
TCGA_PRAD
```

Value

A class 'DGEList' from edgeR package.

Source

[https://tcga-data.nci.nih.gov/tcgafiles/ftp_auth/distro_ftpusers/anonymous/tumor/](https://tcga-data.nci.nih.gov/tcgafiles/ftp_auth/distro_ftpusers/anonymous/tumor/prad/cgcc/unc.edu/illuminahiseq_rnaseqv2/rnaseqv2/unc.edu_PRAD.IlluminaHiSeq_RNASeqV2.Level_3.1.12.0/)
[prad/cgcc/unc.edu/illuminahiseq_rnaseqv2/rnaseqv2/unc.edu_PRAD.IlluminaHiSeq_RNASeqV2.](https://tcga-data.nci.nih.gov/tcgafiles/ftp_auth/distro_ftpusers/anonymous/tumor/prad/cgcc/unc.edu/illuminahiseq_rnaseqv2/rnaseqv2/unc.edu_PRAD.IlluminaHiSeq_RNASeqV2.Level_3.1.12.0/)
[Level_3.1.12.0/](https://tcga-data.nci.nih.gov/tcgafiles/ftp_auth/distro_ftpusers/anonymous/tumor/prad/cgcc/unc.edu/illuminahiseq_rnaseqv2/rnaseqv2/unc.edu_PRAD.IlluminaHiSeq_RNASeqV2.Level_3.1.12.0/)

TCGA_READ	*Read counts and dispersion distribution for genes in TCGA READ data.*

Description

Read counts and dispersion distribution for genes in TCGA READ data.

Usage

```
TCGA_READ
```

Value

A class 'DGEList' from edgeR package.

Source

https://tcga-data.nci.nih.gov/tcgafiles/ftp_auth/distro_ftpusers/anonymous/tumor/ [read/cgcc/unc.edu/illuminahiseq_rnaseqv2/rnaseqv2/unc.edu_READ.IlluminaHiSeq_RNASeqV2.](https://tcga-data.nci.nih.gov/tcgafiles/ftp_auth/distro_ftpusers/anonymous/tumor/read/cgcc/unc.edu/illuminahiseq_rnaseqv2/rnaseqv2/unc.edu_READ.IlluminaHiSeq_RNASeqV2.Level_3.1.8.0/) [Level_3.1.8.0/](https://tcga-data.nci.nih.gov/tcgafiles/ftp_auth/distro_ftpusers/anonymous/tumor/read/cgcc/unc.edu/illuminahiseq_rnaseqv2/rnaseqv2/unc.edu_READ.IlluminaHiSeq_RNASeqV2.Level_3.1.8.0/)

TCGA_THCA	*Read counts and dispersion distribution for genes in TCGA THCA data.*

Description

Read counts and dispersion distribution for genes in TCGA THCA data.

Usage

```
TCGA_THCA
```

Value

A class 'DGEList' from edgeR package.

Source

https://tcga-data.nci.nih.gov/tcgafiles/ftp_auth/distro_ftpusers/anonymous/tumor/ [thca/cgcc/unc.edu/illuminahiseq_rnaseqv2/rnaseqv2/unc.edu_THCA.IlluminaHiSeq_RNASeqV2.](https://tcga-data.nci.nih.gov/tcgafiles/ftp_auth/distro_ftpusers/anonymous/tumor/thca/cgcc/unc.edu/illuminahiseq_rnaseqv2/rnaseqv2/unc.edu_THCA.IlluminaHiSeq_RNASeqV2.Level_3.1.12.0/) [Level_3.1.12.0/](https://tcga-data.nci.nih.gov/tcgafiles/ftp_auth/distro_ftpusers/anonymous/tumor/thca/cgcc/unc.edu/illuminahiseq_rnaseqv2/rnaseqv2/unc.edu_THCA.IlluminaHiSeq_RNASeqV2.Level_3.1.12.0/)

TCGA_UCEC	*Read counts and dispersion distribution for genes in TCGA UCEC data.*

Description

Read counts and dispersion distribution for genes in TCGA UCEC data.

Usage

```
TCGA_UCEC
```

Value

A class 'DGEList' from edgeR package.

Source

https://tcga-data.nci.nih.gov/tcgafiles/ftp_auth/distro_ftpusers/anonymous/tumor/ucec/cgcc/unc.edu/illuminahiseq_rnaseqv2/rnaseqv2/unc.edu_UCEC.IlluminaHiSeq_RNASeqV2.Level_3.1.10.0/

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