Package ‘shinyMethylData’

October 8, 2016

Version 0.106.0

Title Example dataset of input data for shinyMethyl

Description Extracted data from 369 TCGA Head and Neck Cancer DNA methylation samples. The extracted data serve as an example dataset for the package shinyMethyl. Original samples are from 450k methylation arrays, and were obtained from The Cancer Genome Atlas (TCGA). 310 samples are from tumor, 50 are matched normals and 9 are technical replicates of a control cell line.

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Depends R (>= 3.0.0)

LazyData yes

biocViews Genome, CancerData

Url https://github.com/Jfortin1/shinyMethylData

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NeedsCompilation no

R topics documented:

`summary.tcga.norm` *Example dataset of input data for shinyMethyl*

Description

Extracted data from 369 TCGA Head and Neck Cancer DNA methylation samples. The extracted data serve as an example dataset for the package shinyMethyl. Original samples are from 450k methylation arrays, and were obtained from The Cancer Genome Atlas (TCGA). 310 samples are from tumor, 50 are matched normals and 9 are technical replicates of a control cell line.

Usage

```
data(summary.tcga.norm)
```

Format

A `list` containing the necessary information to launch a shinyMethyl session. See the links below for more details on the data.

References

The Cancer Genome Atltas (TCGA) Head and Neck Cancer dataset: http://cancergenome.nih.gov/cancersselected/headandne

See Also

These data objects were created by See `shinySummarize` for details on how to perform the data extraction. See `runShinyMethyl` for how to launch a shinyMethyl session.

Examples

```
data(summary.tcga.norm)
## Not run:
runShinyMethyl(summary.tcga.norm)

## End(Not run)
```

`summary.tcga.raw` *Example dataset of input data for shinyMethyl*

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Usage

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data(summary.tcga.raw)
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A `list` containing the necessary information to launch a shinyMethyl session. See the links below for more details on the data.

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See `shinySummarize` for details on how to perform the data extraction. See `runShinyMethyl` for how to launch a shinyMethyl session.

Examples

```
data(summary.tcga.raw)
## Not run:
runShinyMethyl(summary.tcga.raw)

## End(Not run)
```

Index