Package 'shinyMethylData'

July 10, 2025

Version 1.29.0

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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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/headan

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)
```

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summary.tcga.raw   *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.raw)
```

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/headar

See Also

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)
```

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