

Package ‘shinyMethylData’

November 18, 2025

Version 1.30.0

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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git_url <https://git.bioconductor.org/packages/shinyMethylData>

git_branch RELEASE_3_22

git_last_commit fa68252

git_last_commit_date 2025-10-29

Repository Bioconductor 3.22

Date/Publication 2025-11-18

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summary.tcga.norm

Example dataset of input data for shinyMethyl

Description

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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 Atlas (TCGA) Head and Neck Cancer dataset: <http://cancergenome.nih.gov/cancersselected/headandneck/>

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

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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

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data(summary.tcga.raw)
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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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