Package 'shinyMethylData'

January 21, 2025

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. Maintainer Jean-Philippe Fortin <jfortin@jhsph.edu> Depends R (>= 3.0.0) Depends R (>= 3.0.0) Depends Genome, CancerData Jrl https://github.com/Jfortin1/shinyMethylData Buthor Jean-Philippe Fortin [cre, aut], Kasper Daniel Hansen [aut] Bit_url https://git.bioconductor.org/packages/shinyMethylData Bit_last_commit_late 2024-10-29 Repository Bioconductor 3.21 Date/Publication 2025-01-21</jfortin@jhsph.edu>
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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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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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Usage

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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)
```

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