Package ‘shinyMethylData’

February 1, 2017

Version 0.108.0

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.

Maintainer Jean-Philippe Fortin <jfortin@jhsph.edu>

License Artistic-2.0

Depends R (>= 3.0.0)

LazyData yes

biocViews Genome, CancerData

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

Author Jean-Philippe Fortin [cre, aut], Kasper Daniel Hansen [aut]

NeedsCompilation no

R topics documented:

summary.tcga.norm 1
summary.tcga.raw 2

Index 4

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


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

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


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)
Index

*Topic datasets
  summary.tcga.norm, 1
  summary.tcga.raw, 2

runShinyMethyl, 2
shinySummarize, 2
summary.tcga.norm, 1
summary.tcga.raw, 2