Package 'nanotubes'

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Type Package

Title Mouse nanotube CAGE data

Version 1.24.0

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Description Cap Analysis of Gene Expression (CAGE) data from ``Identification of Gene Transcription Start Sites and Enhancers Responding to Pulmonary Carbon Nanotube Exposure in Vivo" by Bornholdt et al. supplied as CAGE Transcription Start Sites (CTSSs).

URL https://github.com/MalteThodberg/nanotubes

BugReports https://github.com/MalteThodberg/nanotubes/issues

License GPL-3

Encoding UTF-8

LazyData FALSE

Depends R (>= 3.6)

Suggests knitr, rmarkdown, BiocStyle, GenomicRanges, rtracklayer, CAGEfightR

RoxygenNote 6.1.1

VignetteBuilder knitr

biocViews ExperimentData, SequencingData, ExpressionData

git_url https://git.bioconductor.org/packages/nanotubes

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Repository Bioconductor 3.21

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nanotubes *CAGE data from mouse nanotube experiment*

Description

Overview of the mouse nanotube CAGE experiment by Bornholdt et al. This experiment involved exposing mice to carbon nanotubes and performing Cap Analysis of Gene Expression (CAGE) on lung biopsies. The resulting CAGE Transcription Start Sites (CTSSs), the number of CAGE tag 5'-ends mapping to each genomic position, are supplied as BigWig-files (on mm9).

Usage

```
nanotubes
```

Format

Study design as a data.frame:

Class Experimental group (factor): Ctrl (Untreated) or Nano (Treated with nanotubes)

Name Name of sample

BigWigPlus BigWig-file holding plus-strand CTSSs

BigWigPlus BigWig-file holding plus-strand CTSSs

Source

https://pubs.acs.org/doi/10.1021/acsnano.6b07533

Examples

```
# BigWig import is only supported on non-windows platforms:
if (.Platform$OS.type != "windows") {
    library(GenomicRanges)
    library(rtracklayer)
    data(nanotubes)
    bw_path <- system.file("extdata",
                           nanotubes$BigWigMinus[1],
                           package="nanotubes",
                           mustWork = TRUE)
import(bw_path)
}
```

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