Package 'vulcandata'

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Type Package

Title VirtUaL ChIP-Seq data Analysis using Networks, dummy dataset

Version 1.34.0

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Description This package provides a dummy regulatory network and ChIP-Seq dataset for running examples in the vulcan package

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LazyData TRUE

biocViews ExperimentData, Homo_sapiens_Data, CancerData, ChIPSeqData

NeedsCompilation no

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RoxygenNote 6.0.1

Imports utils

Suggests viper

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vulcanexample *Function to load an example VULCAN dataset into the workspace*

Description

This function loads a dummy ChIP-Seq dataset used for VULCAN examples.

Usage

```
vulcanexample()
```

Value

A list of components:

peakcounts A matrix of raw peak counts, peaks as rows, samples as columns

peakrpkms A matrix of peak RPKMs, peaks as rows, samples as columns

samples A vector of sample names and conditions

Examples

```
vobj<-vulcanexample()
names(vobj)
vobj$peakcounts[1:5,]
```

vulcansheet *FUnction to generate an import sheet CSV file for the vulcan test set*

Description

This function generates a user-specific example sheet with appropriate paths on a dummy ChIP-Seq dataset

Usage

```
vulcansheet(outfile = "sheetfile.csv")
```

Arguments

outfile	Path and file name for the CSV sheet file

Value

nothing

Examples

```
vfile<-tempfile()
vulcansheet(vfile)
tmp<-read.csv(vfile)
head(tmp)
unlink(vfile)
```

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