Package ‘vulcandata’

March 27, 2025

Type Package

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

Version 1.28.0

Author Federico M. Giorgi, Andrew N. Holding, Florian Markowetz

Maintainer Federico M. Giorgi <`federico.giorgi@gmail.com`>

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

License LGPL-3

LazyData TRUE

biocViews ExperimentData, Homo_sapiens_Data, CancerData, ChIPSeqData

NeedsCompilation no

Encoding UTF-8

RoxygenNote 6.0.1

Imports utils

Suggests viper

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

git_branch RELEASE_3_20

git_last_commit 2e76783

git_last_commit_date 2024-10-29

Repository Bioconductor 3.20

Date/Publication 2025-03-27

Contents

vulcanexample 2
vulcansheet 2

Index **3**

`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)
```

Index

`vulcanexample`, 2
`vulcansheet`, 2