

Package ‘vulcandata’

September 11, 2025

Type Package
Title VirtUaL ChIP-Seq data Analysis using Networks, dummy dataset
Version 1.30.0
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_21
git_last_commit be1b0ad
git_last_commit_date 2025-04-15
Repository Bioconductor 3.21
Date/Publication 2025-09-11

Contents

vulcanexample	2
vulcansheet	2
Index	4

`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

peakrpkm 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](#)