

Package ‘vulcandata’

December 16, 2025

Type Package
Title VirtUaL ChIP-Seq data Analysis using Networks, dummy dataset
Version 1.32.0
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_22
git_last_commit 41aa5dd
git_last_commit_date 2025-10-29
Repository Bioconductor 3.22
Date/Publication 2025-12-16

Contents

vulcanexample	2
vulcansheet	2
Index	3

vulcanexample	<i>Function to load an example VULCAN dataset into the workspace</i>
---------------	--

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	<i>Function to generate an import sheet CSV file for the vulcan test set</i>
-------------	--

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](#)