

# Package ‘vulcandata’

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**Type** Package  
**Title** VirtUaL ChIP-Seq data Analysis using Networks, dummy dataset  
**Version** 1.28.0  
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**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  
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## Contents

|                         |          |
|-------------------------|----------|
| vulcanexample . . . . . | 2        |
| vulcansheet . . . . .   | 2        |
| <b>Index</b>            | <b>3</b> |

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|---------------|----------------------------------------------------------------------|
| vulcanexample | <i>Function to load an example VULCAN dataset into the workspace</i> |
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**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,]
```

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

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**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](#)