

Package ‘CVE’

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Title Cancer Variant Explorer

Version 1.0.0

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Description Shiny app for interactive variant prioritisation in precision cancer medicine. The input file for CVE is the output file of the recently released Oncotator Variant Annotation tool summarising variant-centric information from 14 different publicly available resources relevant for cancer researches. Interactive prioritisation in CVE is based on known germline and cancer variants, DNA repair genes and functional prediction scores. An optional feature of CVE is the exploration of the tumour-specific pathway context that is facilitated using co-expression modules generated from publicly available transcriptome data. Finally druggability of prioritised variants is assessed using the Drug Gene Interaction Database (DGIdb).

Depends R (>= 3.3), shiny, ConsensusClusterPlus, RColorBrewer, gplots, plyr, ggplot2, jsonlite, ape, WGCNA

License GPL-3

Encoding UTF-8

LazyData true

RoxygenNote 5.0.1

Suggests knitr, rmarkdown, testthat, BiocStyle

VignetteBuilder knitr

biocViews BiomedicalInformatics

NeedsCompilation no

R topics documented:

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genes_WGCNA	<i>Top 5000 most variant genes in TCGA RNAseq data</i>
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Description

A dataset containing the top 5000 most variant genes in TCGA RNAseq data for WGCNAmelanoma extension

GS_lscore	<i>Lymphocyte score gene significance (GS)</i>
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Description

A dataset containing the lymphocyte score gene significance for WGCNAmelanoma extension

GS_pmet	<i>Primary vs metastasis gene significance (GS)</i>
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Description

A dataset containing the primary vs metastases gene significance for WGCNAmelanoma extension

GS_survival	<i>Survival gene significance (GS)</i>
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Description

A dataset containing the survival gene significance for WGCNAmelanoma extension

GS_UV	<i>UV signature gene significance (GS)</i>
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Description

A dataset containing the UV signature gene significance for WGCNA melanoma extension

GS_Vem	<i>Vemurafenib resistance gene significance (GS)</i>
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Description

A dataset containing the vemurafenib resistance gene significance for WGCNA melanoma extension

label_order	<i>Label order of co-expression modules</i>
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Description

A dataset containing the label order of co-expression modules for WGCNA melanoma extension

METree_G0	<i>Gene tree of co-expression network</i>
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Description

A dataset containing the gene tree of co-expression network for WGCNA melanoma extension

MM	<i>Module membership</i>
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Description

A dataset containing the module membership for WGCNA melanoma extension

modules	<i>Module assignment of top 5000 most variant genes in TCGA RNAseq data</i>
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Description

A dataset containing the module assignment top 5000 most variant genes in TCGA RNAseq data for WGCNA melanoma extension

MS_lscore_bar	<i>Lymphocyte score module significance scaled for barplot</i>
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Description

A dataset containing the lymphocyte score module significance scaled for barplot for WGCNA melanoma extension

MS_pmet_bar	<i>Primary vs metastasis module significance scaled for barplot</i>
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Description

A dataset containing the primary vs metastases module significance scaled for barplot for WGCNA melanoma extension

MS_survival_bar	<i>Survival module significance scaled for barplot</i>
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Description

A dataset containing the survival module significance scaled for barplot for WGCNA melanoma extension

MS_UV_bar	<i>UV signature module significance scaled for barplot</i>
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Description

A dataset containing the UV signature module significance scaled for barplot for WGCNA melanoma extension

MS_Vem_bar	<i>Vemurafenib resistance module significance scaled for barplot</i>
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Description

A dataset containing the vemurafenib resistance module significance scaled for barplot for WGCNA melanoma extension

oncotator_example	<i>Example Oncotator output for the case study described in the paper</i>
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Description

A dataset containing the example Oncotator output for the case study described in the paper

openCVE	<i>Open Cancer Variant Explorer (CVE) Shiny app</i>
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Description

The openCVE function opens the CVE Shiny app. The function to supplement the R package with the Shiny app was suggested by Dean Attali (<http://deanattali.com>). Currently, the only extension available is a melanoma co-expression network (WGCNAmelanoma).

Usage

```
openCVE(x, sample_names, extension = FALSE)
```

Arguments

x	A dataframe (for single file) or list (for multiple oncotator output files)
sample_names	A character vector with sample name(s)
extension	A character vector of extension name

Value

opens CVE Shiny app

Examples

```
openCVE(oncotator_example,"case study")  
openCVE(oncotator_example,"case study WGCNA","WGCNAmelanoma")
```

WGCNAmelanoma_extension

Melanoma co-expression network CVE extension

Description

A dataset containing the files to explore variant genes in melanoma-specific co-expression networks within CVE. A proof of principle how the files were generated is described in the vignette WGCNA_from_TCGA_RNAseq. In summary the files are:

Gene significance measures: GS_lscore, GS_pmet, GS_survival, GS_UV, GS_Vem

Module membership: MM

Module significance measures: MS_lscore_bar, MS_pmet_bar, MS_survival_bar, MS_UV_bar, MS_Vem_bar

Top 5000 mad genes of WGCNA: genes_WGCNA

label order of modules: label_order

gene tree of co-expression network: METree_GO

module assignment of genes: modules

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