

Package ‘CVE’

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Title Cancer Variant Explorer

Version 1.8.0

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Description Shiny app for interactive variant prioritisation in precision oncology. 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 (>= 3.4.0), tidyverse, plyr, ggplot2

Imports shiny, ConsensusClusterPlus, RColorBrewer, gplots, jsonlite, ape, WGCNA

License GPL-3

Encoding UTF-8

LazyData true

RoxygenNote 6.0.1

Suggests knitr, rmarkdown, RTCGAToolbox, testthat, BiocStyle

VignetteBuilder knitr

biocViews BiomedicalInformatics

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crcCase	<i>Example Oncotator output for the single-patient colorectal cancer sample</i>
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Description

An Oncotator MAF file

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 WGCNA melanoma extension

get.oncotator.anno *Open Cancer Variant Explorer (CVE) Shiny app*

Description

The get.oncotator.anno retrieves annotation from the Oncotator database.

Usage

```
get.oncotator.anno(x)
```

Arguments

x A matrix containing the columns chromosome, start, end, reference_allele and observed_allele.

Examples

```
exCase <- data.frame(chr = rep(10, 3),
  start = c("100894110", "100985376", "101137905"),
  end = c("100894110", "100985376", "101137905"),
  ref_allele = c("T", "C", "G"),
  obs_allele = c("G", "A", "A"))
get.oncotator.anno(exCase)
```

GS_lscore *Lymphocyte score gene significance (GS)*

Description

A dataset containing the lymphocyte score gene significance for WGCNA melanoma extension

GS_pmet *Primary vs metastasis gene significance (GS)*

Description

A dataset containing the primary vs metastases gene significance for WGCNA melanoma extension

GS_survival *Survival gene significance (GS)*

Description

A dataset containing the survival gene significance for WGCNA melanoma 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

melanomaCase	<i>Example Oncotator output for the melanoma cohort study described in the paper</i>
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Description

An Oncotator MAF file

METree_GO	<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	<i>Lymphocyte score module significance (MS)</i>
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Description

A dataset containing the lymphocyte score module significance 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	<i>Primary vs metastasis module significance (MS)</i>
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Description

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

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

Description

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

MS_survival	<i>Survival module significance (MS)</i>
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Description

A dataset containing the survival module significance for WGCNAmelanoma extension

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

Description

A dataset containing the survival module significance scaled for barplot for WGCNAmelanoma extension

MS_UV	<i>UV signature module significance (MS)</i>
-------	--

Description

A dataset containing the UV signature module significance for WGCNAmelanoma 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 WGCNAmelanoma extension

MS_vem	<i>Vemurafenib resistance module significance (MS)</i>
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Description

A dataset containing the vemurafenib resistance module significance for WGCNAmelanoma 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

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 (WGCNA melanoma).

Usage

```
openCVE(x, sample_names = NULL, 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

Examples

```
openCVE(crcCase,"case study")  
openCVE(melanomaCase,"case study WGCNA",extension="WGCNA melanoma")
```

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