Package 'CVE'

April 11, 2018

Title Cancer Variant Explorer

Version 1.4.0

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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 priortisation 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)

Imports shiny, ConsensusClusterPlus, RColorBrewer, gplots, plyr, ggplot2, 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

NeedsCompilation no

R topics documented:

`crcCase` *Example Oncotator output for the single-patient colorectal cancer sample*

Description

An Oncotator MAF file

`genes_WGCNA` *Top 5000 most variant genes in TCGA RNAseq data*

Description

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

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`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 signficance for WGCNAmelanoma extension

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`GS_pmet` *Primary vs metastasis gene significance (GS)*

Description

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

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`GS_survival` *Survival gene significance (GS)*

Description

A dataset containing the survival gene signficance for WGCNAmelanoma extension

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`GS_UV` *UV signature gene significance (GS)*

Description

A dataset containing the UV signature gene signficance for WGCNAmelanoma extension

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`GS_Vem` *Vemurafenib resistance gene significance (GS)*

Description

A dataset containing the vemurafenib resistance gene signficance for WGCNAmelanoma extension

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`label_order` *Label order of co-expression modules*

Description

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

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`melanomaCase` *Example Oncotator output for the melanoma cohort study described in the paper*

Description

An Oncotator MAF file

`METree_GO` *Gene tree of co-expression network*

Description

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

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`MM` *Module membership*

Description

A dataset containing the module membership for WGCNAmelanoma extension

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`modules` *Module assignment of top 5000 most variant genes in TCGA RNAseq data*

Description

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

`MS_lscore` *Lymphocyte score module significance (MS)*

Description

A dataset containing the lymphocyte score module signficance for WGCNAmelanoma extension

`MS_lscore_bar` *Lymphocyte score module significance scaled for barplot*

Description

A dataset containing the lymphocyte score module signficance scaled for barplot for WGCNAmelanoma extension

`MS_pmet` *Primary vs metastasis module significance (MS)*

Description

A dataset containing the primary vs metastases module signficance for WGCNAmelanoma extension

`MS_pmet_bar` *Primary vs metastasis module significance scaled for barplot*

Description

A dataset containing the primary vs metastases module signficance scaled for barplot for WGCNAmelanoma extension

`MS_survival` *Survival module significance (MS)*

Description

A dataset containing the survival module signficance for WGCNAmelanoma extension

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`MS_survival_bar` *Survival module significance scaled for barplot*

Description

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

---

`MS_UV` *UV signature module significance (MS)*

Description

A dataset containing the UV signature module signficance for WGCNAmelanoma extension

---

`MS_UV_bar` *UV signature module significance scaled for barplot*

Description

A dataset containing the UV signature module signficance scaled for barplot for WGCNAmelanoma extension

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`MS_vem` *Vemurafenib resistance module significance (MS)*

Description

A dataset containing the vemurafenib resistance module signficance for WGCNAmelanoma extension

---

`MS_Vem_bar` *Vemurafenib resistance module significance scaled for barplot*

Description

A dataset containing the vemurafenib resistance module signficance scaled for barplot for WGCNAmelanoma extension

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openCVE *Open Cancer Variant Explorer (CVE) Shiny app*

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 = 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 extention name

Examples

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

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