

# Package ‘CVE’

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**Title** Cancer Variant Explorer

**Version** 1.2.0

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

**License** GPL-3

**Encoding** UTF-8

**LazyData** true

**RoxygenNote** 5.0.1

**Suggests** knitr, rmarkdown, testthat, BiocStyle

**VignetteBuilder** knitr

**biocViews** BiomedicalInformatics

**NeedsCompilation** no

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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

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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 WGCNA melanoma extension

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get.oncotator.anno	<i>Open Cancer Variant Explorer (CVE) Shiny app</i>
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### 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.
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**Examples**

```
get.oncotator.anno(crcCase_input)
```

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

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

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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 WGCNA melanoma extension

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

A dataset containing the survival gene significance for WGCNA melanoma extension

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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

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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

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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

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

An Oncotator MAF file

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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

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MM	<i>Module membership</i>
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**Description**

A dataset containing the module membership for WGCNA melanoma extension

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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

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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

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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

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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>
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**Description**

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

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

A dataset containing the survival module significance for WGCNA melanoma extension

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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 WGCNAmelanoma extension

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

A dataset containing the UV signature module significance for WGCNAmelanoma extension

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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

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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

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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 WGCNAmelanoma extension

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

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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 = NULL, extension = FALSE)
```

**Arguments**

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

**Examples**

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

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