Package 'oncoEnrichR'

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Type Package

Title Functional annotation and enrichment analysis of genesets in the context of cancer

Version 0.6.8

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URL https://github.com/sigven/oncoEnrichR

BugReports https://github.com/sigven/oncoEnrichR/issues

Description oncoEnrichR performs annotation and prioritization of genesets discovered from high-throughput experiments within
cancer biology. The tool queries a number of high-
quality resources, including Project Score (cellular fitness in genome-scale
drop-out screens), Open Targets Platform (comprehensive target-drug and target-
disease associations), TCGA (genetic aberrations
and gene expression patterns in human tumor samples), STRING (protein-
protein interaction networks), CORUM (curated protein complexes),
COMPPI (subcellular compartments), and Gene Ontology/MSigDB/REACTOME/KEGG (func-
tional enrichment/over-representation analysis
with respect to gene function and cellular pathways). The package outputs an interac-
tive HTML report in which the user
can interrogate the the various types of annotations and analyses performed with the geneset.

Depends R (>= 3.5)

biocViews

Imports tidyverse (>= 1.3.0), visNetwork (>= 2.0.9), plotly (>= 4.9.1), pals (>= 1.5),
org.Hs.eg.db, clusterProfiler, igraph, reshape2 (>= 1.4.4), rlogging, gganatogram, openxlsx,
speed2

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Encoding UTF-8

Remotes mjkallen/rlogging, jespermaag/gganatogram, molsysbio/speed2

LazyData true

RoxygenNote 7.1.0

Roxygen list(markdown = TRUE)

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R topics documented:

onco_enrich	*Function that interrogates and analyzes a list of human protein-coding genes for cancer relevance*

Description

Function that interrogates and analyzes a list of human protein-coding genes for cancer relevance

Usage

```
onco_enrich(
  query,
  query_source = "symbol",
  ignore_unknown = FALSE,
  p_title = "Project Title",
  p_owner = "Project Owner",
  background_fname = NULL,
  background_enrichment = NULL,
  background_enrichment_source = "symbol",
  background_enrichment_description = "All protein-coding genes",
  p_value_cutoff_enrichment = 0.05,
  p_value_adjustment_method = "BH",
  q_value_cutoff_enrichment = 0.2,
  min_geneset_size = 10,
  max_geneset_size = 500,
  simplify_go = F,
  ppi_add_nodes = 50,
  ppi_score_threshold = 900,
  show_gene_summary = F,
  show_ppi = T,
  show_drugs_in_ppi = F,
  show_disease = T,
  show_enrichment = T,
  show_tcga_aberration = T,
  show_tcga_coexpression = T,
  show_subcell_comp = T,
  show_crispr_lof = T,
  show_complex = T
)
```

Arguments

query	character vector with gene/query identifiers
query_source	character indicating source of query (one of "uniprot_acc", "symbol", "entrez-gene", or "ensembl_gene_id")

ignore_unknown	logical indicating if analysis should continue when uknown query identifiers are encountered
p_title	title of report
p_owner	name of project owner
background_fname	
	filename for simple text file with project background information, one line per background item
background_enrichment	
	character vector with gene identifiers, used as reference/background for enrichment/over-representation analysis
background_enrichment_source	
	character indicating source of background ("uniprot_acc","symbol","entrezgene","ensembl_gene_id"
background_enrichment_description	
	character indicating type of background (e.g. "All lipid-binding proteins (n = 200)")
p_value_cutoff_enrichment	
	cutoff p-value for enrichment/over-representation analysis
p_value_adjustment_method	
	one of "holm", "hochberg", "hommel", "bonferroni", "BH", "BY", "fdr", "none"
q_value_cutoff_enrichment	
	cutoff q-value for enrichment analysis
min_geneset_size	
	minimal size of geneset annotated by term for testing in enrichment/over-representation analysis
max_geneset_size	
	maximal size of geneset annotated by term for testing in enrichment/over-representation analysis
simplify_go	remove highly similar GO terms in results from GO enrichment/over-representation analysis
ppi_add_nodes	number of nodes to add to query set when computing the protein-protein interaction network (STRING)
ppi_score_threshold	
	minimum score (0-1000) for retrieval of protein-protein interactions (STRING)
show_gene_summary	
	logical indicating if report should fetch summary of gene function (from RefSeq/mygene.info, will increase processing time)
show_ppi	logical indicating if report should contain protein-protein interaction data (STRING)
show_drugs_in_ppi	
	logical indicating if targeted drugs (> phase 3) should be displayed in protein-protein interaction network (Open Targets Platform)
show_disease	logical indicating if report should contain disease associations (Open Targets Platform)
show_enrichment	
	logical indicating if report should contain functional enrichment/over-representation analysis (MSigDB, GO, KEGG, REACTOME etc.)
show_tcga_aberration	
	logical indicating if report should contain TCGA aberration plots (amplifications/deletions)

```
show_tcga_coexpression
                    logical indicating if report should contain TCGA co-expression data (RNAseq)
                    of queryset with oncogenes/tumor suppressor genes
show_subcell_comp
                    logical indicating if report should list subcellular compartment annotations (ComPPI)
show_crispr_lof
                    logical indicating if report should list results from CRISPR/Cas9 loss-of-fitness
                    screens (Project Score)
show_complex        logical indicating if report should list proteins in known protein complexes (CO-
                    RUM)
```

| write | *Function that writes the contents in the oncoEnrichR report object to an interactive HTML report* |

Description

Function that writes the contents in the oncoEnrichR report object to an interactive HTML report

Usage

```
write(report, project_directory, report_name, format = "html")
```

Arguments

```
report              object with oncoEnrichR report data (returned by oncoEnrichR::onco_enrich)
project_directory
                    working directory
report_name         prefix filename for report output
format              file format of output (html/json)
```

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