

Package ‘DFD’

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Type Package

Title Extract Drugs from Differential Expression Data from LINCS Database

Version 0.4.0

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Description Get Drug information from given differential expression profile. The package search for the bioactive compounds from reference databases such as LINCS containing the genome-wide gene expression signature (GES) from tens of thousands of drug and genetic perturbations (Subramanian et al. (2017) <[DOI:10.1016/j.cell.2017.10.049](https://doi.org/10.1016/j.cell.2017.10.049)>).

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Encoding UTF-8

Imports stringr, gprofiler2, scales, ggplot2, gridExtra, ggpubr

Suggests signatureSearch, signatureSearchData

URL <https://github.com/MohmedSoudy/DFD>

BugReports <https://github.com/MohmedSoudy/DFD/issues>

RoxygenNote 7.2.3

NeedsCompilation no

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convert_id	<i>Convert Gene Symbols to ENTREZ IDs</i>
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Description

The function is used to convert gene symbols to entrez ids and map the genes to human orthologs

Usage

```
convert_id(gene_symbols)
```

Arguments

gene_symbols gene symbols

Value

IDs that are converted from gene symbols to ENTREZ gene ids

Author(s)

Mohamed Soudy <Mohmedsoudy2009@gmail.com>

Examples

```
convert_id(c("TP53", "A2M"))
```

filter_drugs	<i>Re-rank drugs based on the number of targets</i>
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Description

The function is used to re-rank drugs based on their targets

Usage

```
filter_drugs(drug_frame)
```

Arguments

drug_frame drugs data frame returned by 'get_drugs' function

Value

re-ranked drug data frame based on their number of targets

Author(s)

Mohamed Soudy <Mohmedsoudy2009@gmail.com>

get_drugs

Get Drugs associated with the differential expression profile

Description

The function is used to get list of drugs that are associated with differential expression profile

Usage

```
get_drugs(up_regulated, down_regulated)
```

Arguments

up_regulated up-regulated genes returned by 'prepare_ids' function

down_regulated down-regulated genes returned by 'prepare_ids' function

Value

significant drugs data frame that contains list of drugs with their targets

Author(s)

Mohamed Soudy <Mohmedsoudy2009@gmail.com>

get_pert_by_type

Filter the drug based on the tested cell-line

Description

The function is used to re-rank drugs based on their targets

Usage

```
get_pert_by_type(perts, perts_type = c("cancer", "Normal"), high_targets = TRUE)
```

Arguments

perts drugs data frame returned by 'get_drugs' function

perts_type type of drug, whether it's from a normal or cancerous cell line

high_targets Boolean paramter to rank their drugs per the number of targets

Value

re-ranked drug data frame based on their number of targets and cell line

Author(s)

Mohamed Soudy <Mohmedsoudy2009@gmail.com>

parse_perts	<i>Parse the perturbagens to find out their frequency of occurrence.</i>
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Description

The function is used to parse drugs based on their targets

Usage

```
parse_perts(perts)
```

Arguments

perts drugs data frame returned by 'get_drugs' function

Value

re-ranked drug data frame based on their number of targets and cell line

Author(s)

Mohamed Soudy <Mohmedsoudy2009@gmail.com>

plot_activities	<i>Visualise the number of perturbagens and the top activities</i>
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Description

The function is used to provide a handy visualization of the top activities

Usage

```
plot_activities(perts, top = 10, directorypath = NULL)
```

Arguments

perts drugs data frame returned by 'get_drugs' function or 'get_pert_by_type' function

top Number of activities to be visualised (N) The default value is set to 10.

directorypath path to save the output figure

Value

re-ranked drug data frame based on their number of targets and cell line

Author(s)

Mohamed Soudy <Mohmedsoudy2009@gmail.com>

prepare_ids	<i>Prepare IDs for CMAP Search</i>
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Description

The function is used to prepare the ids for the CMAP search

Usage

```
prepare_ids(up_regulated, down_regulated)
```

Arguments

up_regulated up regulated gene symbols
down_regulated down regulated gene symbols

Value

list containing up_regulated and down_regulated genes ENTREZ gene ids

Author(s)

Mohamed Soudy <Mohmedsoudy2009@gmail.com>

read_id	<i>Read Gene Symbols from CSV file into up and down regulated lists</i>
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Description

The function is used to read symbols from a CSV file. The gene symbols should be in the first column

Usage

```
read_id(csv_path)
```

Arguments

csv_path absolute path of CSV file containing gene symbols and sign

Value

list containing up_regulated and down_regulated genes symbols

Author(s)

Mohamed Soudy <Mohmedsoudy2009@gmail.com>

run_pipeline	<i>Run the main pipeline for getting drugs from differential expression profile</i>
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Description

The function is used to run the main pipeline by extracting the drug list given differential expressed genes

Usage

```
run_pipeline(degs_path, output_path = NULL)
```

Arguments

degs_path	path to csv file containing degs see example file at https://raw.githubusercontent.com/MohmedSoudy/datas expression.csv
output_path	absolute path to output directory

Value

significant drug data frame after the re-ranking step

Author(s)

Mohamed Soudy <Mohmedsoudy2009@gmail.com>

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