Package: DFD (via r-universe)

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Type Package

Title Extract Drugs from Differential Expression Data

Version 0.1.0

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Description Extract Drugs from Differential Expression Data using the Connectivity Map (CMAP) Approach and Library of Integrated Network-Based Cellular Signatures (LINCS) Database.

License GPL-3

Encoding UTF-8

LazyData true

Imports stringr, gprofiler2, signatureSearch, signatureSearchData

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

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

RoxygenNote 7.2.3

Repository https://mohmedsoudy.r-universe.dev

RemoteUrl https://github.com/mohmedsoudy/dfd

RemoteRef HEAD

RemoteSha d9b4a857c730165c1b658aa6b5f1c380174a800e

Contents

convert_id *Convert Gene Symbols to ENTREZ IDs*

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

ENTREZ gene ids

Author(s)

Mohamed Soudy <Mohmedsoudy2009@gmail.com>

Examples

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

filter_drugs *Re-rank drugs based on the number of targets*

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

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

Author(s)

Mohamed Soudy <Mohmedsoudy2009@gmail.com>

prepare_ids *Prepare IDs for CMAP Search*

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

ENTREZ gene ids

Author(s)

Mohamed Soudy <Mohmedsoudy2009@gmail.com>

`read_id` *Read Gene IDs from CSV file*

Description

The function is used to read IDs from a CSV file

Usage

```
read_id(csv_path)
```

Arguments

`csv_path`	absolute path of CSV file containing gene symbols and sign

Value

up_regulated and down_regulated genes

Author(s)

Mohamed Soudy <Mohmedsoudy2009@gmail.com>

`run_pipeline` *Run the main pipeline for getting drugs from differentail expression profile*

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

Author(s)

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