

Package: DFD (via r-universe)

October 10, 2026

Type Package

Title Extract Drugs from Differential Expression Data

Version 0.1.0

Author Mohamed Soudy [aut, cre]

Maintainer Mohamed Soudy <MohmedSoudy2009@gmail.com>

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

Config/pak/sysreqs

cmake make libicu-dev libpng-dev libuv1-dev libxml2-dev libssl-dev libx11-dev zlib1g-dev

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

Date/Publication 2023-10-11 10:31:59 UTC

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

RemoteRef HEAD

RemoteSha d9b4a857c730165c1b658aa6b5f1c380174a800e

Contents

convert_id	2
filter_drugs	2
get_drugs	3
prepare_ids	3
read_id	4
run_pipeline	4

Index**5**

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

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

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	<i>Read Gene IDs from CSV file</i>
---------	------------------------------------

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	<i>Run the main pipeline for getting drugs from differentail expression profile</i>
--------------	---

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/master/deg_expression.csv
output_path	absolute path to output directory

Author(s)

Mohamed Soudy <Mohmedsoudy2009@gmail.com>

Index

`convert_id`, [2](#)
`filter_drugs`, [2](#)
`get_drugs`, [3](#)
`prepare_ids`, [3](#)
`read_id`, [4](#)
`run_pipeline`, [4](#)