

Package ‘phexpo’

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Type Package

Title Bi-directional enrichment analysis of phenotypes and chemicals

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Description A package for phenotype and chemical enrichment of gene lists using data from the Comparative Toxicogenomics Database and the Human Phenotype Ontology.

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LazyData true

Encoding UTF-8

Imports dplyr,tibble,ggplot2,magrittr,rlang

Depends R (>= 2.10),shiny

RoxygenNote 6.1.1

Suggests testthat

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chem2gene

*Chemical and gene interactions***Description**

Dataset of chemicals and their gene interactions. Original data set downloaded on 11-Feb-2019. Version Feb-05-2019. Dataset has been filtered to contain only the organisms Homo sapiens, Mus musculus, Rattus norvegicus, Rattus rattus, Danio rerio, Macaca fascicularis, Macaca mulatta and human gene IDs. Genes were checked that they belonged to humans using the Homo sapiens gene info from NCBI (downloaded 19-March-2019). For gene IDs not belonging to Homo sapiens, gene IDs were checked that they belonged to their respective organism using All Mammalia gene info from NCBI (15-March-2019) and Danio rerio gene info from NCBI (15-March-2019). All orthologs for these gene IDs were found using NCBI Homologene (version 06-May-2014) and outdated ortholog gene IDs were updated to the latest gene ID using NCBI gene_history (15-March-2019) and updated gene symbols were taken from Homo sapiens gene info.

Usage

chem2gene

Format

An object of class `tbl_df` (inherits from `tbl`, `data.frame`) with 1575035 rows and 11 columns.

Details

@format A data frame of 1,575,035 rows and 11 columns.

@source <http://ctdbase.org/downloads/#cg>

perfFishTestChemMultiple

*Enriched HPO terms for multiple chemicals***Description**

Enriched HPO terms for multiple chemicals

Usage

```
perfFishTestChemMultiple(cname, enrich_1S = TRUE)
```

Arguments

cname	List of chemical characters
enrich_1S	Enrichment one-sided. Automatically set to true for enrichment, where the one-sided Fisher's exact is set to alternative = 'greater.' If enrich = FALSE, Fisher's exact is set to alternative = 'two.sided' for two-sided.

Value

Dataframe with enrichment

Note

Enrichment for multiple chemicals is a simplistic exploratory function, where we take an additive approach. Chemical names and synonyms used are dependent on the chemical names within CTD.

Examples

```
## Not run:  
x <- list("Chemical1", "Chemical2", "Chemical3")  
perfFishTestChemMultiple(x)  
  
## End(Not run)
```

perfFishTestChemSingle

Enriched HPO terms for a single chemical's associated gene list

Description

Enriched HPO terms for a single chemical's associated gene list

Usage

```
perfFishTestChemSingle(cname, enrich_1S = TRUE)
```

Arguments

cname	Chemical character
enrich_1S	Enrichment one-sided. Automatically set to true for enrichment, where the one-sided Fisher's exact is set to alternative = 'greater.' If enrich_1S = FALSE, Fisher's exact is set to alternative = "two.sided" for two-sided.

Value

Dataframe with enrichment.

Note

Chemical names and synonyms used are dependent on the chemical names within CTD.

Examples

```
perfFishTestChemSingle("Iodine")
```

`perfFishTestHPOMultiple`*Chemical enrichment for multiple phenotype terms*

Description

Chemical enrichment for multiple phenotype terms

Usage

```
perfFishTestHPOMultiple(HPO, enrich_1S = TRUE)
```

Arguments

HPO	List of Human Phenotype Ontology terms
enrich_1S	Enrichment one-sided. Automatically set to true for enrichment, where the one-sided Fisher's exact is set to alternative = 'greater.' If enrich_1S = FALSE, Fisher's exact is set to alternative = 'two.sided' for two.sided.

Value

Dataframe with enrichment.

Note

Chemical enrichment for multiple HPO terms is a simplistic exploratory function, where we take an additive approach. HPO terms used should be phenotypic abnormality terms within the HPO release 2019-02-12.

Examples

```
## Not run:  
x <- list("HPO term1", "HPO term2", "HPO term3")  
perfFishTestHPOMultiple(x)  
  
## End(Not run)
```

`perfFishTestHPOSingle` *Enriched Chemicals for a single phenotype term's associated gene list*

Description

Enriched Chemicals for a single phenotype term's associated gene list

Usage

```
perfFishTestHPOSingle(HPO, enrich_1S = TRUE)
```

Arguments

HPO	Human Phenotype Ontology term
enrich_1S	Enrichment one-sided. Automatically set to true for enrichment, where the one-sided Fisher's exact is set to alternative = 'greater.' If enrich_1S = FALSE, Fisher's exact is set to alternative = 'two.sided' for two-sided.

Value

Dataframe with enrichment.

Note

HPO terms used should be phenotypic abnormality terms within the HPO release 2019-02-12.

Examples

```
perfFishTestHPOSingle("Rickets")
```

pheno2gene	<i>Phenotype and gene association</i>
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Description

Dataset of phenotype and their gene associations. Original data set downloaded on 28-Feb-2019. Version 2019-02-12. Dataset has been filtered to only contain Phenotypic abnormality terms.

Usage

```
pheno2gene
```

Format

An object of class `data.frame` with 472515 rows and 4 columns.

Details

@format A data frame of 472,515 rows and 4 columns.

@source <https://hpo.jax.org/app/download/annotation>

sym_tbl	<i>Chemical vocabulary</i>
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Description

Dataset of chemicals and their synonyms. Data has been modified from original data, to contain synonyms only for chemicals with gene interactions, synonyms have been changed to lower-case and duplicate synonyms have been removed. Downloaded on 11-Feb-2019. Version Feb-05-2019.

Usage

```
sym_tbl
```

Format

An object of class `data.frame` with 63818 rows and 2 columns.

Details

@format A data frame of 63,818 rows and 2 columns.

@source <http://ctdbase.org/downloads/#allchems>

visEnrich	<i>Enrichment visualisation</i>
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Description

Enrichment visualisation

Usage

```
visEnrich(x)
```

Arguments

x	Dataframe of enrichment data
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Value

Shiny app.

Examples

```
## Not run:  
x <- perfFishTestHPOSingle("Iodine")  
visEnrich(x)  
## End(Not run)
```

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