

Package ‘phexpo’

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Type Package

Title Bidirectional 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. Phexpo is for research purposes only.

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LazyData true

Encoding UTF-8

Imports dplyr,tibble,ggplot2,magrittr,rlang,tidyr

Depends R (>= 2.10),shiny

RoxygenNote 6.1.1

Suggests testthat

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checkChemical	<i>Check chemicals are supported for analysis</i>
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Description

Check chemicals are supported for analysis

Usage

```
checkChemical(cname)
```

Arguments

cname	List of chemical characters.
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Value

Tibble data frame with chemicals and if they are supported or not.

Examples

```
checkChemical(list("Ethanol", "Iodine", "Zinc"))
```

checkHPO	<i>Check HPO terms are supported for analysis</i>
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Description

Check HPO terms are supported for analysis

Usage

```
checkHPO(HPO)
```

Arguments

HPO	List of Human Phenotype Ontology terms characters.
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Value

Tibble data frame with HPO terms and if they are supported or not.

Examples

```
checkHPO(list("Rickets", "Breast carcinoma", "Preeclampsia"))
```

chem2gene*Chemical and gene interactions*

Description

Dataset of chemicals and their gene interactions. Original dataset 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 sapien gene info from National Center for Biotechnology Information (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 All orthologues for these gene IDs were found using NCBI Homologene (version 06-May-2014) and outdated orthologue gene IDs were updated to the latest gene ID using NCBI gene_history (15-March-2019) and updated gene symbols were retrieved from Homo sapien gene info. Tibble, dplyr, readr, tidyr, magrittr and annotationTools were used in the generation of this dataset.

Usage

```
chem2gene
```

Format

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

Details

@format A tibble 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

<code>cname</code>	List of chemical characters.
<code>enrich_1S</code>	Enrichment one-sided. Default set to true for enrichment, where the one-sided Fisher's exact is set to alternative = "greater." If <code>enrich_1S = FALSE</code> , Fisher's exact is set to alternative = "two.sided" for two-sided.

Value

Tibble data frame 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

```
perfFishTestChemMultiple(list("bisphenol A", "bisphenol F", "bisphenol B"))
```

```
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. Default 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

Tibble data frame 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 characters
enrich_1S	Enrichment one-sided. Default 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

Tibble data frame 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

```
perfFishTestHPOMultiple(list("Increased circulating ACTH level",  
  "Androgen insufficiency",  
  "Decreased circulating aldosterone level"))
```

`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 character.
enrich_1S	Enrichment one-sided. Default 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

Tibble data frame 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 dataset downloaded on 28-Feb-2019. Version 2019-02-12. Dataset has been filtered to only contain phenotypic abnormality terms. Generation of this dataset used the Human Phenotype Ontology OBO file (2019-02-12 version) and the R packages ontologyIndex, tibble, magrittr and dplyr.

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*Chemical vocabulary*

Description

Dataset of chemicals and their synonyms. Data has been modified from original data to contain synonyms only for chemicals with gene interactions. Duplicated synonyms for tetrachlorodibenzodioxin and polychlorinated dibenzodioxins were removed from polychlorinated dibenzodioxins, synonyms have been changed to lowercase and duplicate synonyms have been removed. Downloaded on 11-Feb-2019. Version Feb-05-2019. The R packages dplyr, tidyr, stringr, magrittr and tibble were used in the generation of this dataset.

Usage

```
sym_tbl
```

Format

An object of class `data.frame` with 63819 rows and 2 columns.

Details

@format A data frame of 63,819 rows and 2 columns.

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

visEnrich*Enrichment visualisation*

Description

Enrichment visualisation

Usage

```
visEnrich(x)
```

Arguments

x Enrichment results tibble data frame.

Value

Shiny app.

Examples

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


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