Package 'RichR'

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Type Package

Title Enrichment for Diseases in a Set of Genes

Version 1.0.0

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Description

It provides a list of genes associated to diseases (g2d$clean and g2d$complete) based on the following 4 publications (GS2D, Fontaine (2016) <doi:10.18547/gcb.2016.vol2.iss1.e33>, DisGeNET, Pinero (2016) <doi:10.1093/nar/gkw943> Berto2016, Berto (2016) <doi:10.3389/fgene.2016.00031> and PsyGeNET, Sacristan (2015) <doi:10.1093/bioinformatics/btv301>). Those lists were combined and manually curated to have matching disease names. When provided a list of gene names, it calculates the disease enrichment of the gene set. The enrichment is calculated using proportion test and Fisher's exact test. Adjusted fdr p-values are returned alongside with p-values combined using the Fisher's method.

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Imports plyr, reshape2, magrittr, stats, metap

Encoding UTF-8

LazyData true

Depends R (>= 3.1)

RoxygenNote 6.1.1

NeedsCompilation no

Repository CRAN

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R topics documented:

Enrichment *Enrichment*

Description

Given a list of genes associated to diseases and a background list, it calculates the diseases enrichment. It calculates both pvalues from proportion test and Fisher's exact test. Adjusted BH pvalues are returned.

Usage

```
Enrichment(Background, Genes2Dis = g2d$clean, Genes)
```

Arguments

Background	The background list of genes. In generela is the list of genes expressed.
Genes2Dis	A data.frame with the Gene names and the Diseases. The package has two inbuild lists. g2d_clean and g2d_complete. Both lists contains data from 4 publications (GS2D, DisGeNET, Berto2016 and PsyGeNET), however in the clean similar names were treated as the same disease.
Genes	A list of genes to test for enrichment

Value

a list contating the enrichment of diseases

Author(s)

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Examples

```
data('g2d')

g2d_clean = g2d$clean

# The user can choose a particular disorder, or use the whole disease set to compare to

g2d_ASD = subset(g2d_clean, g2d_clean$Disease %in% c('AUTISM'))
Enrichment(Background = g2d_clean$Gene.symbol,
Genes2Dis = g2d_ASD,
Genes = g2d_ASD$Gene.symbol[1:100])
```

g2d g2d

Description

g2d is a list with two data.frames based on the following 4 publications (GS2D, Fontaine (2016) <doi:10.18547/gcb.2016.vol2.iss1.e33>, DisGeNET, Pinero (2016) <doi:10.1093/nar/gkw943>, Berto2016, Berto (2016) <doi:10.3389/fgene.2016.00031> and PsyGeNET, Sacristan (2015) <doi:10.1093/bioinformatics/btv301>). Those lists were combined and manually curated to have matching disease names. The first list, clean, contains the curated data, the list complete contains complete data. In the former disease names might not match.

Usage

```
g2d
```

Format

An object of class `list` of length 2.

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