

Package: aliases2entrez (via r-universe)

October 12, 2024

Title Converts Human gene symbols to entrez IDs

Version 0.1.2

Description Queries multiple resources authors HGNC (2019) <<https://www.genenames.org>>, authors limma (2015) <[doi:10.1093/nar/gkv007](https://doi.org/10.1093/nar/gkv007)> to find the correspondence between evolving nomenclature of human gene symbols, aliases, previous symbols or synonyms with stable, curated gene entrezID from NCBI database. This allows fast, accurate and up-to-date correspondence between human gene expression datasets from various date and platform (e.g: gene symbol: BRCA1 - ID: 672).

BugReports <https://github.com/peyronlab/aliases2entrez/issues>

Imports doParallel, limma, utils, org.Hs.eg.db, AnnotationDbi, parallel, foreach, readr, RCurl

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Encoding UTF-8

LazyData true

RoxygenNote 7.1.1

Suggests spelling

Language en-US

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

RemoteUrl <https://github.com/peyronlab/aliases2entrez>

RemoteRef HEAD

RemoteSha 6e38d7e7891426bb75ad818461be5a1650bc6415

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convert_symbols	<i>Multi resources gene symbols conversion to entrez ID (Human)</i>
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Description

This function is used to convert gene symbols, previous symbols or aliases to gene entrez ID

It performs :

- a gene query to limma::alias2Symbol to map gene alias to official symbols
- looks for LOC* symbols
- tries to find correspondence within HGNC database
- queries org.Hs.eg.db
- checks again with adaptive symbol parsing (e.g. transforms BRCA-1 to BRCA1)

Usage

```
convert_symbols(symbols, HGNC, c=1)
```

Arguments

symbols	gene matrix from which rownames (gene symbols) are extracted
HGNC	HGNC correspondence file.
c	number of cores to use for parallel processes

Value

returns a vector containing IDs if match were found or NA if unknown or withdrawn symbol

Examples

```
# import the correspondence file
file <- system.file("extdata", "HGNC.txt", package = "aliases2entrez")
HGNC <- read.delim(file)
# alternatively update a new one with update_symbols()
symbols <- c("BRCA1", "TP53")
# run the main function
ids <- convert_symbols(symbols, HGNC)
```

update_symbols	<i>Update last HGNC correspondence database</i>
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Description

This function is used to update gene symbol correspondence from HGNC database

Usage

```
update_symbols(url=NULL)
```

Arguments

`url` user can provide url (default is NULL)

Value

returns a data.frame containing gene symbols with status, previous symbols and synonyms as well as their corresponding entrezIDs

Examples

```
HGNC <- update_symbols()
```

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