

Package ‘babelgene’

March 30, 2022

Type Package

Title Gene Orthologs for Model Organisms in a Tidy Data Format

Version 22.3

Description Genomic analysis of model organisms frequently requires the use of databases based on human data or making comparisons to patient-derived resources. This requires harmonization of gene names into the same gene space. The 'babelgene' R package converts between human and non-human gene orthologs/homologs. The package integrates orthology assertion predictions sourced from multiple databases as compiled by the HGNC Comparison of Orthology Predictions (HCOP) (Wright et al. 2005 <[doi:10.1007/s00335-005-0103-2](https://doi.org/10.1007/s00335-005-0103-2)>, Eyre et al. 2007 <[doi:10.1093/bib/bbl030](https://doi.org/10.1093/bib/bbl030)>, Seal et al. 2011 <[doi:10.1093/nar/gkq892](https://doi.org/10.1093/nar/gkq892)>).

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URL <https://igordot.github.io/babelgene/>

BugReports <https://github.com/igordot/babelgene/issues>

Depends R (>= 3.4)

Imports dplyr, methods, rlang

Suggests covr, knitr, rmarkdown, testthat (>= 3.0.0)

VignetteBuilder knitr

Config/testthat/edition 3

Encoding UTF-8

RoxygenNote 7.1.2

NeedsCompilation no

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Repository CRAN

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orthologs	<i>Retrieve gene orthologs/homologs</i>
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Description

Retrieve gene orthologs/homologs for a set of genes. Converts between human and non-human analogs.

Usage

```
orthologs(genes, species, human = TRUE, min_support = 3, top = TRUE)
```

Arguments

genes	A vector of gene symbols or Entrez/Ensembl IDs.
species	Species name, such as <i>Mus musculus</i> or mouse (see <code>species()</code> for options).
human	A logical scalar indicating if the input genes are human. If TRUE, the input genes are human. If FALSE, the input genes correspond to the non-human species and the output will be the human equivalents.
min_support	Minimum number of supporting source databases.
top	For each gene, output only the match with the highest support level if there are multiple hits.

Value

A data frame of gene pairs (human and given species).

References

Wright MW, Eyre TA, Lush MJ, Povey S, Bruford EA. HCOP: the HGNC comparison of orthology predictions search tool. *Mamm Genome*. 2005 Nov;16(11):827-8. doi: [10.1007/s0033500501032](https://doi.org/10.1007/s0033500501032)

Eyre TA, Wright MW, Lush MJ, Bruford EA. HCOP: a searchable database of human orthology predictions. *Brief Bioinform*. 2007 Jan;8(1):2-5. doi: [10.1093/bib/bbl030](https://doi.org/10.1093/bib/bbl030)

Seal RL, Gordon SM, Lush MJ, Wright MW, Bruford EA. genenames.org: the HGNC resources in 2011. *Nucleic Acids Res*. 2011 Jan;39:D514-9. doi: [10.1093/nar/gkq892](https://doi.org/10.1093/nar/gkq892)

Examples

```
orthologs(genes = "TP53", species = "mouse", human = TRUE)
orthologs(genes = c("Ptprc", "Cd34"), species = "mouse", human = FALSE)
```

species	<i>Retrieve the available species</i>
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Description

List the species with available human orthologs.

Usage

```
species(species = NULL)
```

Arguments

species	Species name, such as <i>Mus musculus</i> or mouse. If specified, will return results for the given species only.
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Value

A data frame of the available species.

Examples

```
species()  
species("Mus musculus")  
species("mouse")  
species("rat")
```

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