Package 'biolink'

August 21, 2023

Type Package

Title Create Hyperlinks to Biological Databases and Resources

Description Generate urls and hyperlinks to commonly used biological databases and resources based on standard identifiers. This is primarily useful when writing dynamic reports that reference things like gene symbols in text or tables, allowing you to, for example, convert gene identifiers to hyperlinks pointing to their entry in the 'NCBI' Gene database. Currently supports 'NCBI' Gene, 'PubMed', Gene Ontology, 'KEGG', CRAN and Bioconductor.

Version 0.1.8

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Encoding UTF-8

Imports rentrez, xml2, DBI, RMySQL, glue, memoise

Suggests testthat, lintr, httr, covr

RoxygenNote 7.2.3

NeedsCompilation no

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R topics documented:

build_link *Construct hypertext links*

Description

Convert a bare url to a valid hyperlink formatted for a Markdown, HTML or LaTeX document.

Usage

```
build_link(url, text = NULL, title = NULL, format = "markdown")
```

Arguments

url	URL where you want the link to point
text	displayed text
title	link title, often used in tooltips
format	generate links using "html", "markdown" or "latex" syntax

Examples

```
build_link("https://r-project.org", "R", "The R Project")
```

links *Construct hyperlinks to online resources*

Description

These resource-specific functions return a hyperlink to the relevant online database/resource based on the provided identifier (id).

Usage

```
link_go(id, text = id, title = NULL, format = "html")

link_kegg(id, text = id, title = NULL, format = "html")

link_pubmed(id, text = id, title = NULL, format = "html")

link_entrez(id, text = id, title = NULL, format = "html")

link_cran(id, text = id, title = NULL, format = "html")

link_bioc(id, text = id, title = NULL, format = "html")
```

Arguments

id	valid identifier for the relevant online database
text	displayed text
title	link title, often used in tooltips
format	generate links using "html", "markdown" or "latex" syntax

Functions

- link_go(): to Gene Ontology Consortium
- link_kegg(): to KEGG Pathway Database
- link_pubmed(): to PubMed based on PMID (PubMed identifier)
- link_entrez(): to NCBI's database for gene-specific information based on Entrez ID
- link_cran(): for R packages available from CRAN
- link_bioc(): for R packages available from Bioconductor

Link Customization

By default the hyperlinked text is just the id, so link_pubmed("22066989") becomes 22066989. The text argument allows you to customize the hyperlinked text. To display a hyperlinked URL (e.g., https://www.r-project.org), set text = NULL.

Data Tags

For a few supported online resources, specially formatted tags can be passed to the text and title arguments to display live data obtained from the corresponding resource. For example, link_entrez("4609", text = "<symbol>"), produces MYC, displaying the gene symbol rather than the Entrez ID. We could also set title = "<description>" to produce a link that reveals the gene's description when a user hovers over the link (using a supported browser).

Currently supported data tags:

NCBI Entrez:

- symbol: Gene symbol
- description: Gene description
- location: Cytogenetic location

NCBI PubMed:

- title: Article title
- year: Publication year
- journal: Journal title

Gene Ontology:

- name: GO term name
- definition: GO term definition

References

- Gene Ontology Consortium
- KEGG Pathway Database
- NCBI PubMed
- NCBI Gene

Examples

```
link_go("GO:0005539", format = "html")
link_kegg("hsa04915", format = "html")
link_pubmed("22066989", format = "html")
link_entrez("4609", format = "html")
```

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urls *Construct urls to online resources*

Description

These resource-specific functions return a bare url (i.e., not a hyperlink) to the relevant online database/resource based on the provided identifier.

Usage

```
url_go(id)

url_kegg(id)

url_pubmed(id)

url_entrez(id)

url_cran(id)

url_bioc(id)
```

Arguments

id	valid identifier for the relevant online database

Functions

- `url_go()`: for Gene Ontology Consortium
- `url_kegg()`: for KEGG Pathway Database
- `url_pubmed()`: for PubMed based on PMID (PubMed identifier)
- `url_entrez()`: for NCBI's database for gene-specific information based on Entrez ID
- `url_cran()`: for R packages available from CRAN
- `url_bioc()`: for R packages available from Bioconductor

Examples

```
# gene ontology url
url_go("GO:0005539")

# KEGG pathway url
url_kegg("hsa04915")

# PubMed article url
url_pubmed("23193287")
```

Index