

Package ‘biorxivr’

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Type Package

Title Search and Download Papers from the bioRxiv Preprint Server

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LazyLoad yes

LazyData yes

Description The bioRxiv preprint server (<http://www.biorxiv.org>) is a website where scientists can post preprints of scholarly texts in biology. Users can search and download PDFs in bulk from the preprint server. The text of abstracts are stored as raw text within R, and PDFs can easily be saved and imported for text mining with packages such as 'tm'.

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Depends XML

Suggests knitr

VignetteBuilder knitr

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NeedsCompilation no

Repository CRAN

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bx_download	<i>Download PDF's</i>
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Description

Download PDF's of all the papers in your search results.

Usage

```
bx_download(bxso, directory, create = TRUE)
```

Arguments

bxso	search results from bx_search()
directory	The location you want to download the PDF's to.
create	TRUE or FALSE. If true create the directory if it doesn't exist

Examples

```
## Not run:  
bxEco <- bx_search("ecology", limit=20)  
bx_download(bxEco, "~/biorxivPDF")  
  
## End(Not run)
```

bx_extract	<i>Extract data from search results</i>
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Description

Extract information about each paper in search results, returning author info, abstract and download metrics

Usage

```
bx_extract(bxso)
```

Arguments

bxso	search results from bx_search()
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Details

The metrics field will return a month by month data frame with abstract views and pdf downloads

Value

a list holding the details about all the papers from search results. Each element in the list is an S3 object that holds all the salient details about the paper

Examples

```
## Not run:
bxEco <- bx_search("ecology",limit=5)
bxEcoData <- bx_extract(bxEco)
## See a plot of abstract views
plot(bxEcoData[[1]],type="abs")

## See a plot of downloads
plot(bxEcoData[[1]],type="dl")

## End(Not run)
```

bx_extract_single	<i>Extract data from a single record</i>
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Description

Generate an S3 object that represents a single paper

Usage

```
bx_extract_single(bxso_url)
```

Arguments

bxso_url the URL of a single biorxiv paper

Value

a single S3 object with all the salient details about a paper

bx_search	<i>Search biorxiv.org</i>
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Description

return a list of URLs, IDS and number of results found from search of biorxiv.org

Usage

```
bx_search(query, limit = 10)
```

Arguments

query	the terms to search for in biorxiv
limit	the number of results to return

Details

This uses the generic search interface, therefore be aware that you'll have to do post download filtering if you want terms in a specific field

Value

a list with the following elements: a vector of URL's for bioRxiv papers from the search terms, and the maximum number of results

Examples

```
## Not run:
### Get search results
bxEco <- bx_search("ecology", limit=20)
summary(bxEco)

## End(Not run)
```

plot.biorxiv_paper	<i>plot metric details for a paper</i>
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Description

plot a summary of the views a paper has had

Usage

```
## S3 method for class 'biorxiv_paper'
plot(x, type = "abs", ...)
```

Arguments

x the paper to plot a summary of
type the data to plot, 'abs' for abstract views, 'dl' for PDF downloads
... extra parameters to pass

`print.summary.biorxiv_search`
Print summary results

Description

print a summary of search results

Usage

```
## S3 method for class 'summary.biorxiv_search'  
print(x, ...)
```

Arguments

x the biorxiv search object to print
... extra parameters to the print function

`summary.biorxiv_search`
Summary of search results

Description

create a summary of search results

Usage

```
## S3 method for class 'biorxiv_search'  
summary(object, ...)
```

Arguments

object the search object to create a summary of
... extra parameters to pass

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