

Package: BiocResourceStats (via r-universe)

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Type Package

Title What the Package Does (Title Case)

Version 0.1.1

Author Who wrote it

Maintainer The package maintainer <yourself@somewhere.net>

Description More about what it does (maybe more than one line) Use four spaces when indenting paragraphs within the Description.

License What license is it under?

Encoding UTF-8

LazyData true

Roxygen list(markdown = TRUE)

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Repository <https://link-ny.r-universe.dev>

RemoteUrl <https://github.com/Bioconductor/BiocResourceStats>

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hello	<i>Hello, World!</i>
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Description

Prints 'Hello, world!'.

Usage

```
hello()
```

Examples

```
hello()
```

HubHits	<i>Quantify topic occurrence in *Hub resources and combine package related resources</i>
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Description

Quantify topic occurrence in *Hub resources and combine package related resources

Usage

```
HubHits(topics, pkg_pattern, hub = c("ExperimentHub", "AnnotationHub"))
```

```
prop.HubHits(x)
```

```
## S3 method for class 'HubHits'
print(x)
```

Arguments

topics	character() A vector of topics to query ExperimentHub resources with
pkg_pattern	character(1) A pattern to use for searching through packages that expose ExperimentHub resources related to topics
hub	character(1) Either 'ExperimentHub' or 'AnnotationHub' indicating which hub to query resources from
x	HubHits An instance of HubHits as returned by the eponymous constructor function

Value

- HubHits: A HubHits instance
- prop.HubHits: The proportion of search hits to all resources in the specified hub

Methods (by generic)

- `print(HubHits)`:

Functions

- `prop.HubHits()`:

Examples

```
if (interactive()) {  
  et <- HubHits(c("cancer", "tumor"), "curated*", hub = "ExperimentHub")  
}  
if (interactive()) {  
  # proportion of hits in all *Hub  
  prop.HubHits(et)  
}  
if (interactive()) {  
  # print HubHits  
  et  
}
```

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