

# Package: BiocPkgStats (via r-universe)

August 27, 2024

**Title** Use templates to create package stats reports

**Version** 0.0.15

**Description** Create package reports as RMarkdown documents. Rendering RMarkdown documents will provide a brief summary of package statistics. A starting date must be specified.

**License** Artistic-2.0

**Imports** BiocBaseUtils, BiocPkgTools, biocViews, graphics, lubridate, stats, tools, utils, whisker

**Suggests** BiocStyle, knitr

**Encoding** UTF-8

**Roxygen** list(markdown = TRUE)

**RoxygenNote** 7.3.1

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

**RemoteUrl** <https://github.com/Bioconductor/BiocPkgStats>

**RemoteRef** HEAD

**RemoteSha** da6323c0f866da309c6ec323405aa2d4322c11c3

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downloadTrend                      *Plot the download activity for a package*

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### Description

Plot the download activity for a package

### Usage

```
downloadTrend(package, since_date, include_recent = FALSE)
```

### Arguments

package                      character(1) The package to download activity for

since\_date                    character() The date from when to start looking at commit and issue history. This should be specified in the year, month, and day format, 'YYYY-MM-DD'. It can be a vector of dates that match the length packages.

include\_recent               logical(1) Whether to include the latest month of download data. Usually, the data for the most recent month has incomplete numbers and is excluded (default is FALSE).

### Examples

```
if (interactive()) {  
  downloadTrend("MultiAssayExperiment", "2017-05-01")  
  downloadTrend("cBioPortalData", "2017-05-01")  
  downloadTrend("RaggedExperiment", "2017-05-01")  
  
  downloadTrend("SingleCellMultiModal", "2017-05-01")  
  downloadTrend("curatedTCGAData", "2017-05-01")  
  
  # low downloads  
  downloadTrend("TENxIO", "2017-05-01")  
  downloadTrend("terraTCGAdata", "2017-05-01")  
}
```

---

generateReport                    *Create a report for a given set of packages*

---

### Description

The function compiles statistics for Bioconductor packages that have GitHub repositories. It uses functionality in BiocPkgTools to extract commit and issue history. A token is required to access the GitHub commit and issue history.

**Usage**

```
generateReport(packages, gh_org, since_date, outdir = ".", overwrite = FALSE)
```

**Arguments**

packages	character()	A vector of valid package names that are installed
gh_org	character()	The GitHub organization from which to read issue and commit data from. It can be either a scalar character to be recycled to the length of packages or a vector the length of packages for instances where packages are hosted under different GitHub organizations.
since_date	character()	The date from when to start looking at commit and issue history. This should be specified in the year, month, and day format, 'YYYY-MM-DD'. It can be a vector of dates that match the length packages.
outdir	character(1)	The directory in which to place rendered RMarkdown documents, by default they will be placed in the current working directory.
overwrite	logical(1)	Whether to overwrite an existing rendered product, i.e., a runnable RMarkdown document.

**Details**

Note that packages must be installed in order to determine the package type via the `biocViews` field.

**Authentication**

The package uses the `gh` package calls from `BiocPkgTools`. Users must authenticate with a GitHub Fine Grained Token and add the token using `gitcreds::gitcreds_set()`.

**Examples**

```
if (interactive()) {  
  
  generateReport(  
    c(  
      "MultiAssayExperiment", "cBioPortalData", "SingleCellMultiModal"  
    ),  
    gh_org = "waldronlab",  
    since_date = "2017-05-01",  
    overwrite = TRUE  
  )  
  
}
```

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generateTable	<i>Create a table of package metrics</i>
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### Description

The function compiles statistics for Bioconductor packages that have GitHub repositories. It uses functionality in BiocPkgTools to extract commit and issue history. A token is required to access the GitHub commit and issue history. See the `.token` argument in `?gh::gh` for details on its use.

### Usage

```
generateTable(packages, gh_org, since_date)
```

### Arguments

<code>packages</code>	<code>character()</code> A vector of valid package names that are installed
<code>gh_org</code>	<code>character()</code> The GitHub organization from which to read issue and commit data from. It can be either a scalar character to be recycled to the length of <code>packages</code> or a vector the length of <code>packages</code> for instances where packages are hosted under different GitHub organizations.
<code>since_date</code>	<code>character()</code> The date from when to start looking at commit and issue history. This should be specified in the year, month, and day format, 'YYYY-MM-DD'. It can be a vector of dates that match the length <code>packages</code> .

### Details

Note that pull requests are a type of "issue" on GitHub; therefore, issues and pull requests are combined when reporting the number of closed issues since a specific date. For more information on how the queries are performed, see the GitHub API documentation for the `/repos/{owner}/{repo}/issues` endpoint at <https://docs.github.com/en/rest/issues> and the `gh` R package. The following list describes each column in the returned data frame:

- `download.rank`: The percentile rank of the package in its respective repository, e.g., software, data-experiment etc.
- `avg.downloads`: The average number of monthly downloads from distinct IP addresses since the given date
- `med.downloads`: The median number of monthly downloads from distinct IP addresses since the given date
- `num.revdeps`: The number of "all" reverse dependencies including "Depends", "Imports", "LinkingTo", "Suggests", and "Enhances"
- `issues.since`: The number of closed issues (including pull requests) since the date given
- `commits.since`: The number of commits since the given date

### Value

A data frame of metrics, see the `details` section for specifics

**Examples**

```
if (interactive()) {  
  
  generateTable(  
    packages = c(  
      "MultiAssayExperiment", "cBioPortalData", "SingleCellMultiModal"  
    ),  
    gh_org = "waldronlab",  
    since_date = "2019-05-01"  
  )  
}
```

---

supportSiteStats	<i>Gather support site statistics for a given period</i>
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**Description**

Gather support site statistics for a given period

**Usage**

```
supportSiteStats(from = "2021-01-01", to = "2021-12-31")  
  
## S3 method for class 'bioc_support_stats'  
print(x, ...)
```

**Arguments**

from	character(1) date in ISO 8601 format ("YYYY-MM-DD")
to	character(1) date in ISO 8601 format ("YYYY-MM-DD")
x	bioc_support_stats The class object that has a print method
...	Additional arguments to the print method. Not used.

**Value**

a bioc\_support\_stats list class with components userdiff, toplevdiff, questdiff, and respdiff

**Author(s)**

Vincent J. Carey

**Examples**

```
if (interactive()) {  
  supportSiteStats()  
}
```

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