Package: BiocPkgDash (via r-universe)

May 30, 2026

Type Package

Title An interactive Shiny dashboard for Bioconductor package maintainers

Version 1.1.0

Description This package provides an interactive Shiny dashboard for Bioconductor package maintainers. It visualizes various package statuses, metadata, and development metrics, offering insights into package health and activity. This tool aims to support maintainers of multiple packages by filtering packages via maintainer email.

Depends R (>= 4.5.0), shiny

Imports BiocBaseUtils, BiocPkgTools (>= 1.27.6), BiocManager, bsicons, bslib, dplyr, DT, ggplot2, gh, htmlwidgets, plotly, rmarkdown, shinybiocloader, shinyjs, tibble, tidyr, utils, whisker, yaml

Suggests BiocStyle, knitr, sessioninfo, tinytest

biocViews Software, Infrastructure, Visualization, GUI

VignetteBuilder knitr

License Artistic-2.0

Encoding UTF-8

URL https://github.com/Bioconductor/BiocPkgDash

BugReports https://github.com/Bioconductor/BiocPkgDash/issues

RoxygenNote 7.3.3

Roxygen list(markdown = TRUE)

Date 2026-03-23

Config/pak/sysreqs
cmake git libglpk-dev make libicu-dev libuv1-dev libxml2-dev libssl-dev libx11-dev zlib1g-dev

Repository https://bioc.r-universe.dev

Date/Publication 2026-04-28 13:06:39 UTC

RemoteUrl https://github.com/bioc/BiocPkgDash

RemoteRef HEAD

RemoteSha 489cd3b5067d2b051c81fb706db659a393ce3a35

Contents

`BiocPkgDash` *The Bioconductor Package Dashboard*

Description

A dashboard for Bioconductor package maintainers to monitor the status of their packages. The key input to the dashboard is the email the maintainer uses in their package's `DESCRIPTION` file. The dashboard displays the badge statuses of the package in both the `release` or `devel` branches of Bioconductor. The status is determined by the results of the Bioconductor nightly builds. The dashboard also provides a visualization of the status of the package checks on either the `release` or `devel` branches of Bioconductor.

Usage

```
BiocPkgDash(email = NULL, ...)
```

Arguments

`email`	`character(1)` vector providing the email of the maintainer. By default, the package will look for the email in the URL query.
`...`	Additional parameters to pass to the `shiny::shinyApp()` function.

Value

called for the side effect of initializing a shiny app

Examples

```
BiocPkgDash()
```

`pkgStatusPlot` *A Summary Plot for Package Statuses*

Description

This function generates a stacked bar plot of package statuses for a given Bioconductor version and email combination. It is mainly used for the Bioconductor Package Dashboard.

Usage

```
pkgStatusPlot(
  data = NULL,
  status = c("OK", "WARNINGS", "ERROR", "TIMEOUT", "skipped"),
  stage = c("install", "buildsrc", "checksrc", "buildbin")
)
```

Arguments

`data`	`tibble()` / `data.frame()` A data frame of maintained packages. This is used internally to avoid repeated calls to the `BiocPkgTools::biocMaintained()` function.
`status`	`character()` A vector of `INSTALL`, `build` and `check` statuses to include in the plot. These values are obtained from the `result` column in `BiocPkgTools::biocBuildReport()`. The default is all: `c("OK", "WARNINGS", "ERROR", "TIMEOUT", "skipped")`.
`stage`	`character()` A vector of the Bioconductor Build System (BBS) stages to include in the plot. These values are obtained from the `stage` `BiocPkgTools::biocBuildReport()`. The default is all stages: `c("install", "buildsrc", "checksrc", "buildbin")`.

Details

Note that binary build stages for the Linux builders are not included in the plot. This is because the binaries are built on GitHub Actions and their result are not included in the Bioconductor Build System (BBS) database.

Value

An interactive `ggplotly` object.

Examples

```
data <- BiocPkgTools::biocMaintained(
    "maintainer@bioconductor.org", pkgType = "software"
)
pkgStatusPlot(data)
```

`pkgStatusTable` *Build a table of package build statuses*

Description

This function builds a table of package build statuses for a given Bioconductor version and email combination. It is mainly used for the Bioconductor Package Dashboard.

Usage

```
pkgStatusTable(
  data = NULL,
  status = c("OK", "WARNINGS", "ERROR", "TIMEOUT", "skipped"),
  stage = c("install", "buildsrc", "checksrc", "buildbin")
)
```

Arguments

`data`	`tibble()` / `data.frame()` A table of maintained packages. This is used internally to avoid repeated calls to the `BiocPkgTools::biocMaintained()` function.
`status`	`character()` The status of the builders to include in the table. These values are obtained from the `result` column in `BiocPkgTools::biocBuildReport()`. The default is all: `c("OK", "WARNINGS", "ERROR", "TIMEOUT", "skipped")`.
`stage`	`character()` A vector of the Bioconductor Build System (BBS) stages to include in the plot. These values are obtained from the `stage` `BiocPkgTools::biocBuildReport()`. The default is all stages: `c("install", "buildsrc", "checksrc", "buildbin")`.

Details

Note that binary build stages for the Linux builders are marked as `skipped` in the table. This is because the binaries are built on GitHub Actions and their result are not included in the Bioconductor Build System (BBS) database. Provide the `data` argument to avoid recomputing the list of maintained packages for a given email and Bioconductor version. Annotation packages are not included in the table because they are not built regularly by the BBS.

Value

A `tibble()` / `data.frame()` with the package build statuses for the given `data` input.

Examples

```
data <- BiocPkgTools::biocMaintained("maintainer@bioconductor.org")
pkgStatusTable(data)
```

Index