Package dissemination

Physalia course 2023

Instructor: Jacques Serizay

Incentivize other people to use your package

Your computer:

```
myPackage/
    R/
      functions.R
      utils.R
   man/
      myfunction.Rd
   tests/
      testthat.R
      testthat/
         test–myfun.R
   inst/
      extdata/
         <raw–data–file>
   data/
      <data>.Rda
   vignettes/
      myPackage.Rmd
   DESCRIPTION
   NAMESPACE
   README.md
   NEWS
   LICENSE
```

Many computers:

```
myPackage/
    R/
      functions.R
      utils.R
   man/
      myfunction.Rd
   tests/
      testthat.R
      testthat/
         test–myfun.R
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   data/
      <data>.Rda
   vignettes/
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   DESCRIPTION
   NAMESPACE
   README.md
   NEWS
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```

Incentivize other people to use your package

- By providing high-quality public resources

- By serving a polished documentation website for your package

Implement documentation website for your package

Once again, a package is
available in R to help you!

pkgdown let’s you easily create
a documentation website.

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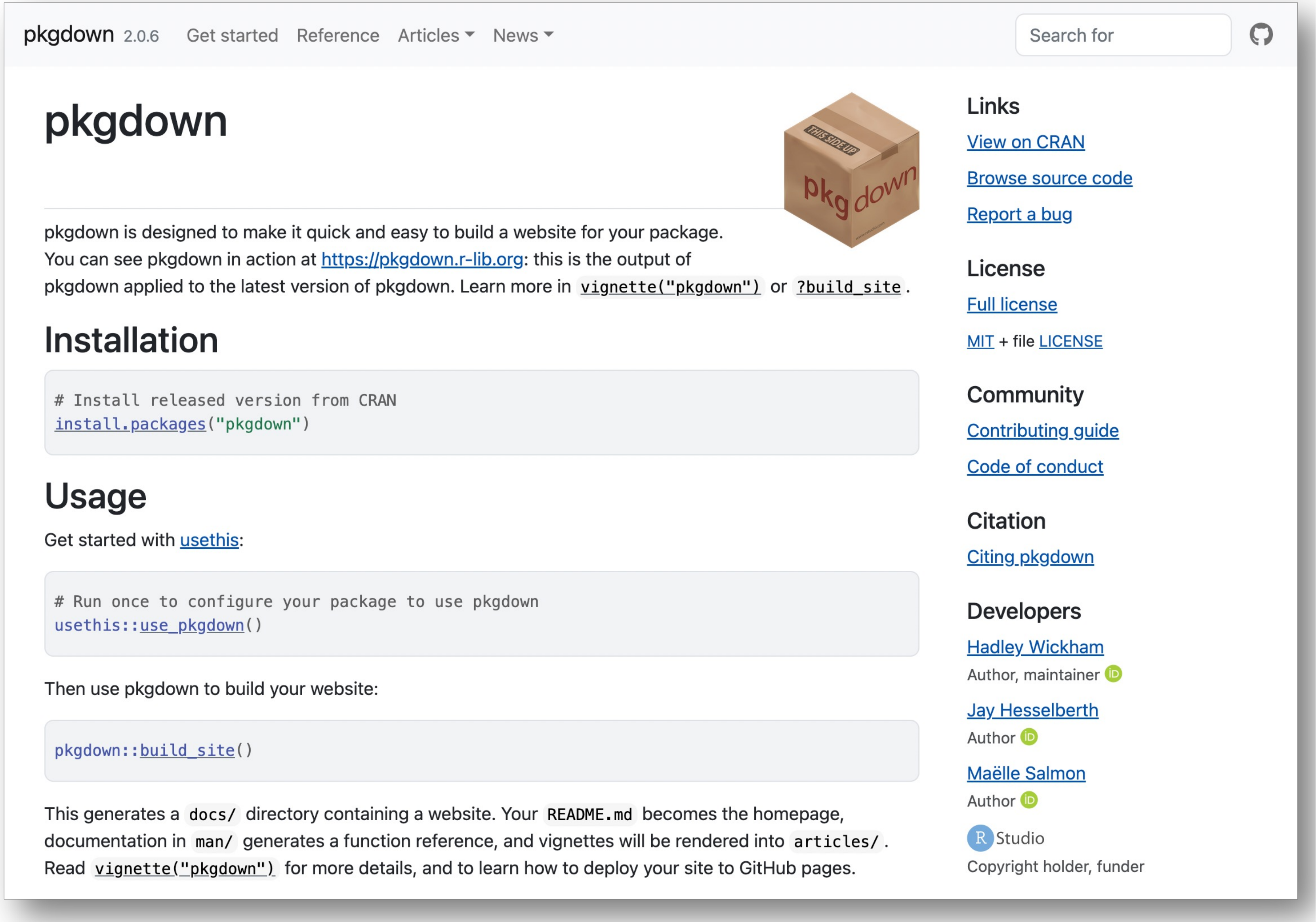


pkgdown

pkgdown is designed to make it quick and easy to build a website for your package. You can see pkgdown in action at https://pkgdown.r-lib.org: this is the output of pkgdown applied to the latest version of pkgdown. Learn more in `vignette("pkgdown")` or `?build_site`.

Installation

```
# Install released version from CRAN
install.packages("pkgdown")
```

Usage

Get started with usethis:

```
# Run once to configure your package to use pkgdown
usethis::use_pkgdown()
```

Then use pkgdown to build your website:

```
pkgdown::build_site()
```

This generates a `docs/` directory containing a website. Your `README.md` becomes the homepage, documentation in `man/` generates a function reference, and vignettes will be rendered into `articles/`. Read `vignette("pkgdown")` for more details, and to learn how to deploy your site to GitHub pages.

Links

View on CRAN

Browse source code

Report a bug

License

Full license

MIT + file LICENSE

Community

Contributing guide

Code of conduct

Citation

Citing pkgdown

Developers

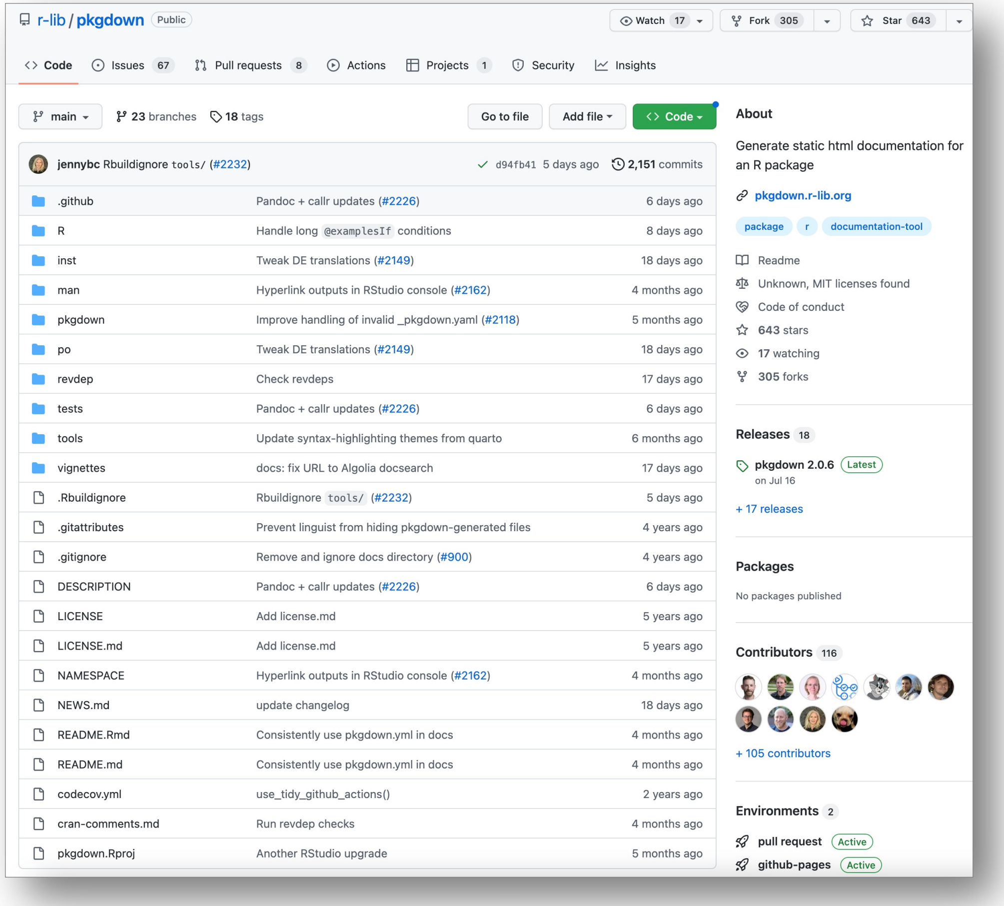
Hadley Wickham
Author, maintainer

Jay Hesselberth
Author

Maëlle Salmon
Author

RStudio
Copyright holder, funder

Implement documentation website for your package



jennybc Rbuildignore `tools/` (#2232) ✓ d94fb41 5 days ago 2,151 commits

.github	Pandoc + callr updates (#2226)	6 days ago
R	Handle long `@examplesIf` conditions	8 days ago
inst	Tweak DE translations (#2149)	18 days ago
man	Hyperlink outputs in RStudio console (#2162)	4 months ago
pkgdown	Improve handling of invalid _pkgdown.yaml (#2118)	5 months ago
po	Tweak DE translations (#2149)	18 days ago
revdep	Check revdeps	17 days ago
tests	Pandoc + callr updates (#2226)	6 days ago
tools	Update syntax-highlighting themes from quarto	6 months ago
vignettes	docs: fix URL to Algolia docsearch	17 days ago
.Rbuildignore	Rbuildignore `tools/` (#2232)	5 days ago
.gitattributes	Prevent linguist from hiding pkgdown-generated files	4 years ago
.gitignore	Remove and ignore docs directory (#900)	4 years ago
DESCRIPTION	Pandoc + callr updates (#2226)	6 days ago
LICENSE	Add license.md	5 years ago
LICENSE.md	Add license.md	5 years ago
NAMESPACE	Hyperlink outputs in RStudio console (#2162)	4 months ago
NEWS.md	update changelog	18 days ago
README.Rmd	Consistently use pkgdown.yml in docs	4 months ago
README.md	Consistently use pkgdown.yml in docs	4 months ago
codecov.yml	use_tidy_github_actions()	2 years ago
cran-comments.md	Run revdep checks	4 months ago
pkgdown.Rproj	Another RStudio upgrade	5 months ago

About

Generate static html documentation for an R package

pkgdown.r-lib.org

package r documentation-tool

Readme
Unknown, MIT licenses found
Code of conduct
643 stars
17 watching
305 forks

Releases 18

pkgdown 2.0.6 Latest
on Jul 16

+ 17 releases

Packages

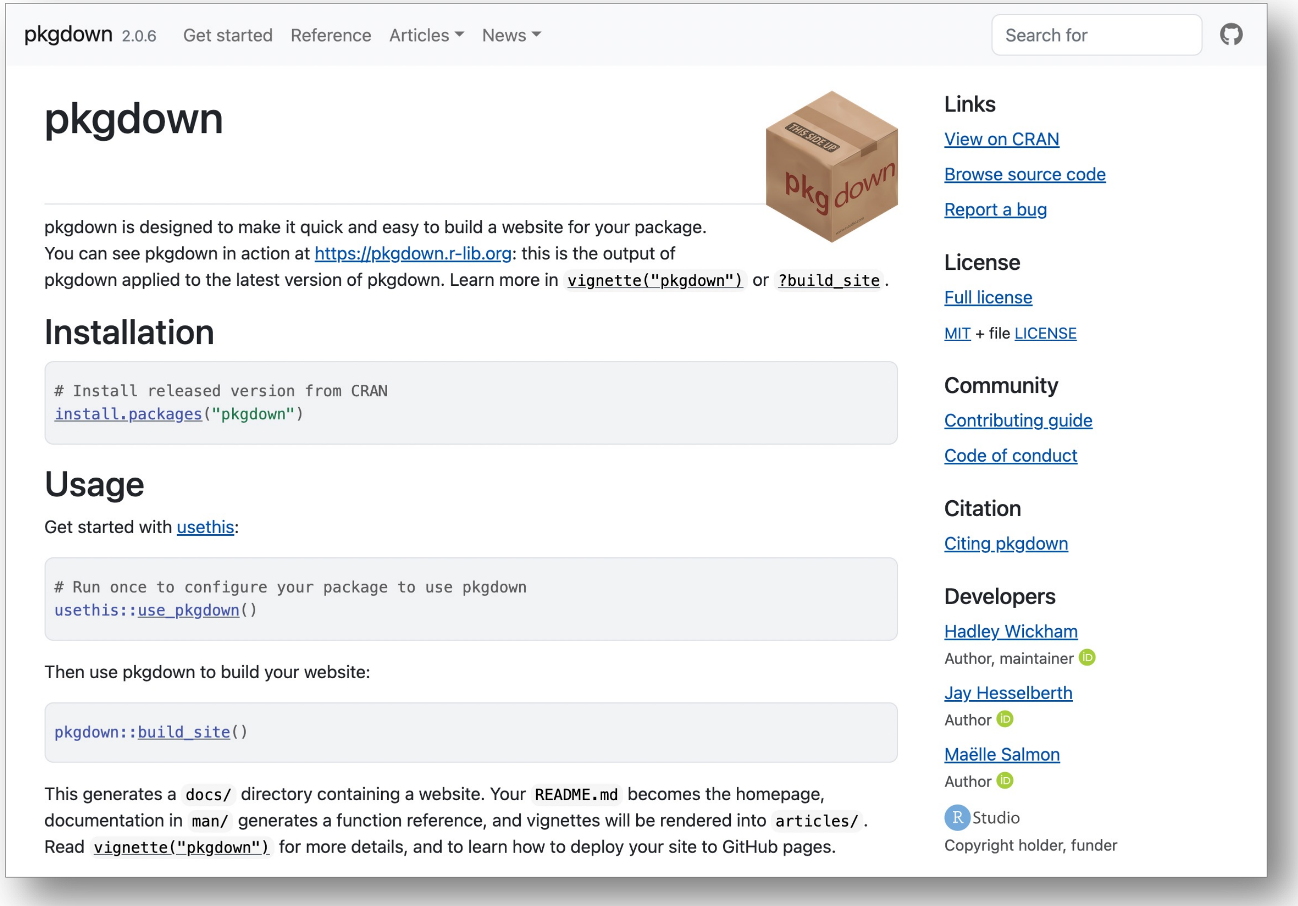
No packages published

Contributors 116

+ 105 contributors

Environments 2

pull request Active
github-pages Active



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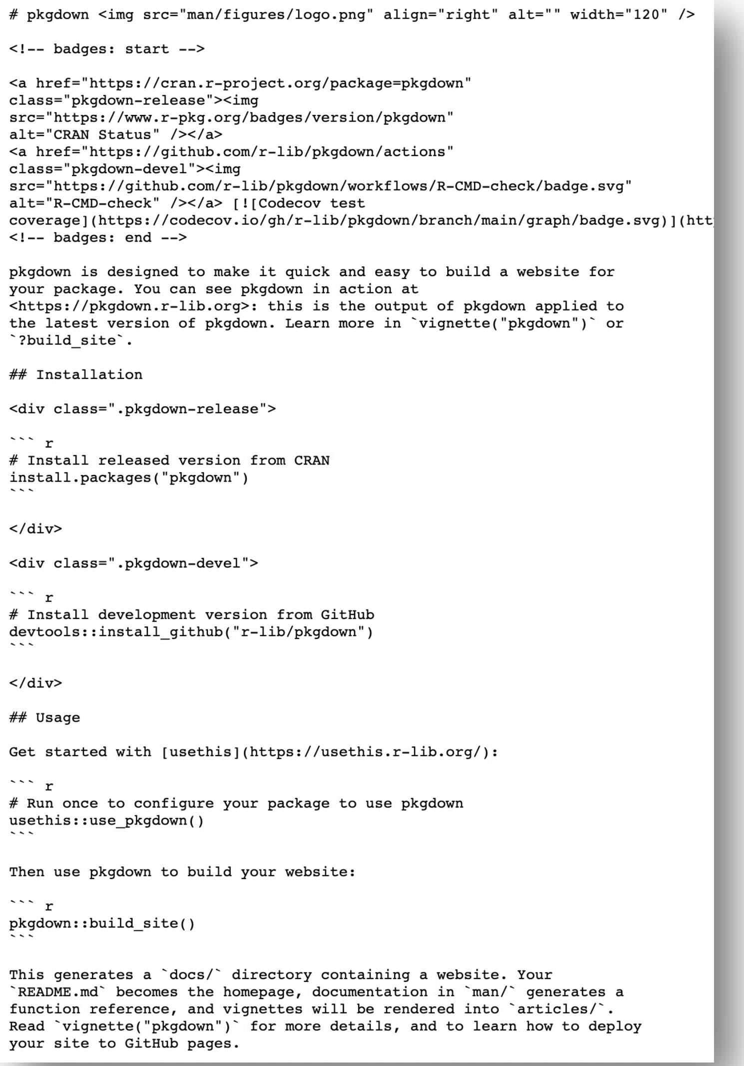
Pkgdown functionalities

1. Parsing of R package files in html code

README.md



~~~
# pkgdown <img src="man/figures/logo.png" align="right" alt="" width="120" />

<!-- badges: start -->

<a href="https://cran.r-project.org/package=pkgdown"
class="pkgdown-release"><img
src="https://www.r-pkg.org/badges/version/pkgdown"
alt="CRAN Status" /></a>
<a href="https://github.com/r-lib/pkgdown/actions"
class="pkgdown-devel"><img
src="https://github.com/r-lib/pkgdown/workflows/R-CMD-check/badge.svg"
alt="R-CMD-check" /></a> [![Codecov test
coverage](https://codecov.io/gh/r-lib/pkgdown/branch/main/graph/badge.svg)](htt
<!-- badges: end -->

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your package. You can see pkgdown in action at
<https://pkgdown.r-lib.org>: this is the output of pkgdown applied to
the latest version of pkgdown. Learn more in `vignette("pkgdown")` or
`?build_site`.

## Installation

<div class=".pkgdown-release">

``` r
# Install released version from CRAN
install.packages("pkgdown")
```

</div>

<div class=".pkgdown-devel">

``` r
# Install development version from GitHub
devtools::install_github("r-lib/pkgdown")
```

</div>

## Usage

Get started with [usethis](https://usethis.r-lib.org/):

``` r
# Run once to configure your package to use pkgdown
usethis::use_pkgdown()
```

Then use pkgdown to build your website:

``` r
pkgdown::build_site()
```

This generates a `docs/` directory containing a website. Your
`README.md` becomes the homepage, documentation in `man/` generates a
function reference, and vignettes will be rendered into `articles/`.
Read `vignette("pkgdown")` for more details, and to learn how to deploy
your site to GitHub pages.
~~~
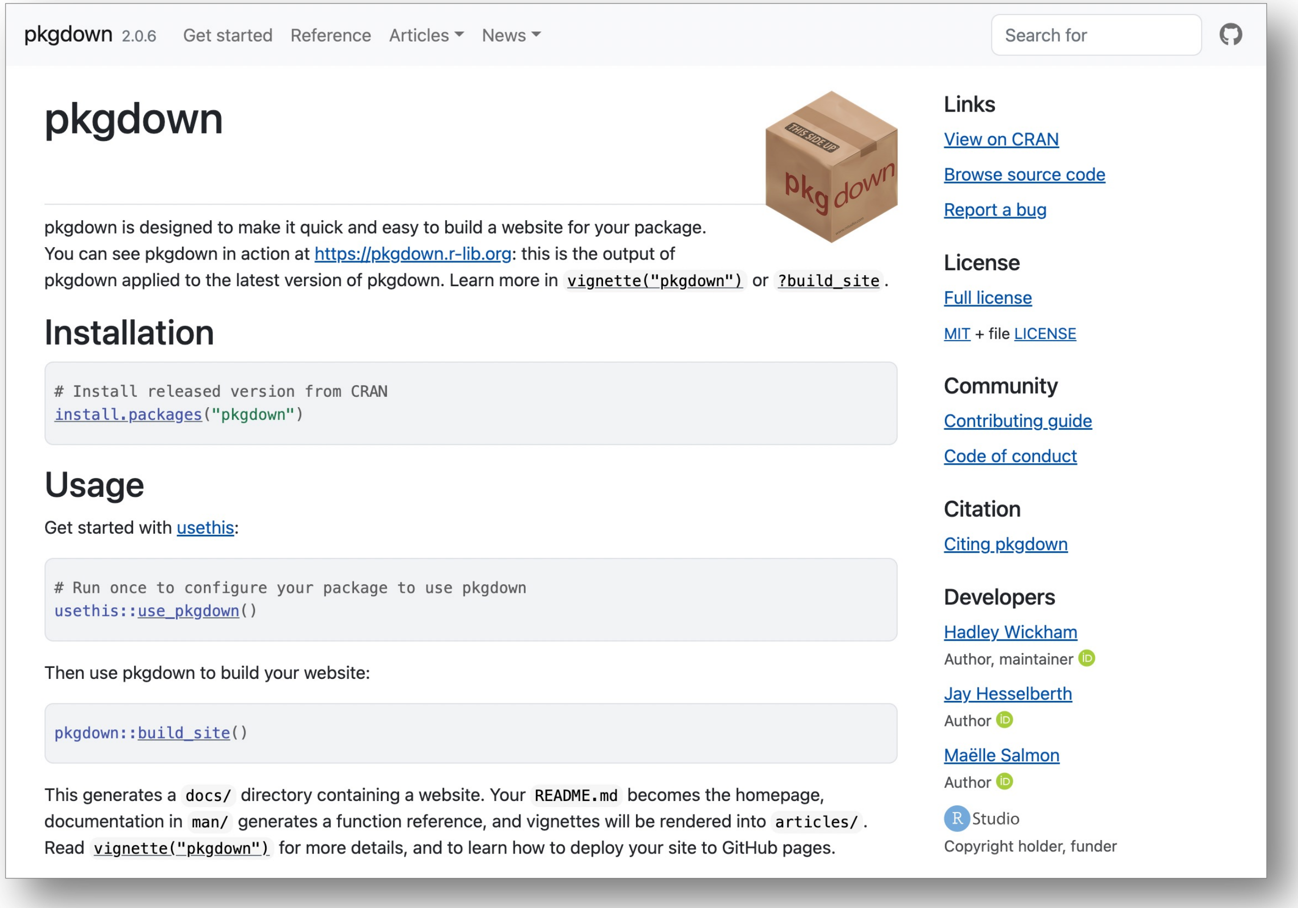

pkgdown.r-lib.org/



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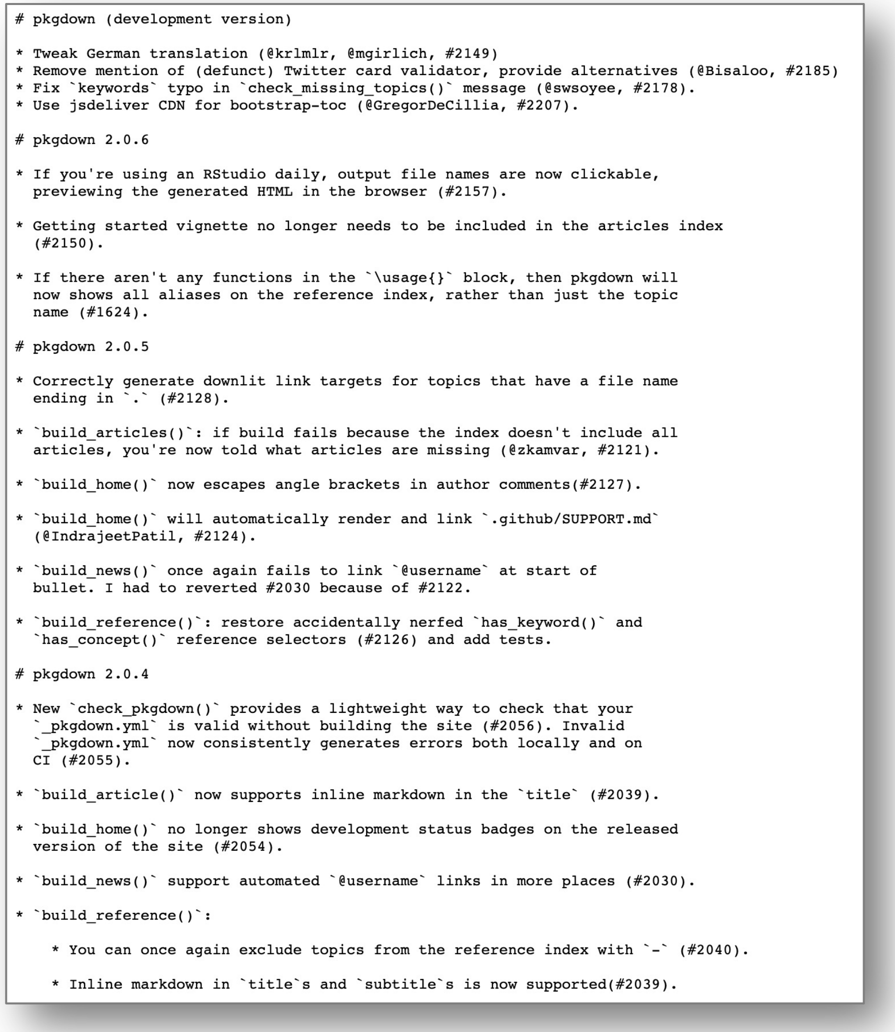
Pkgdown functionalities

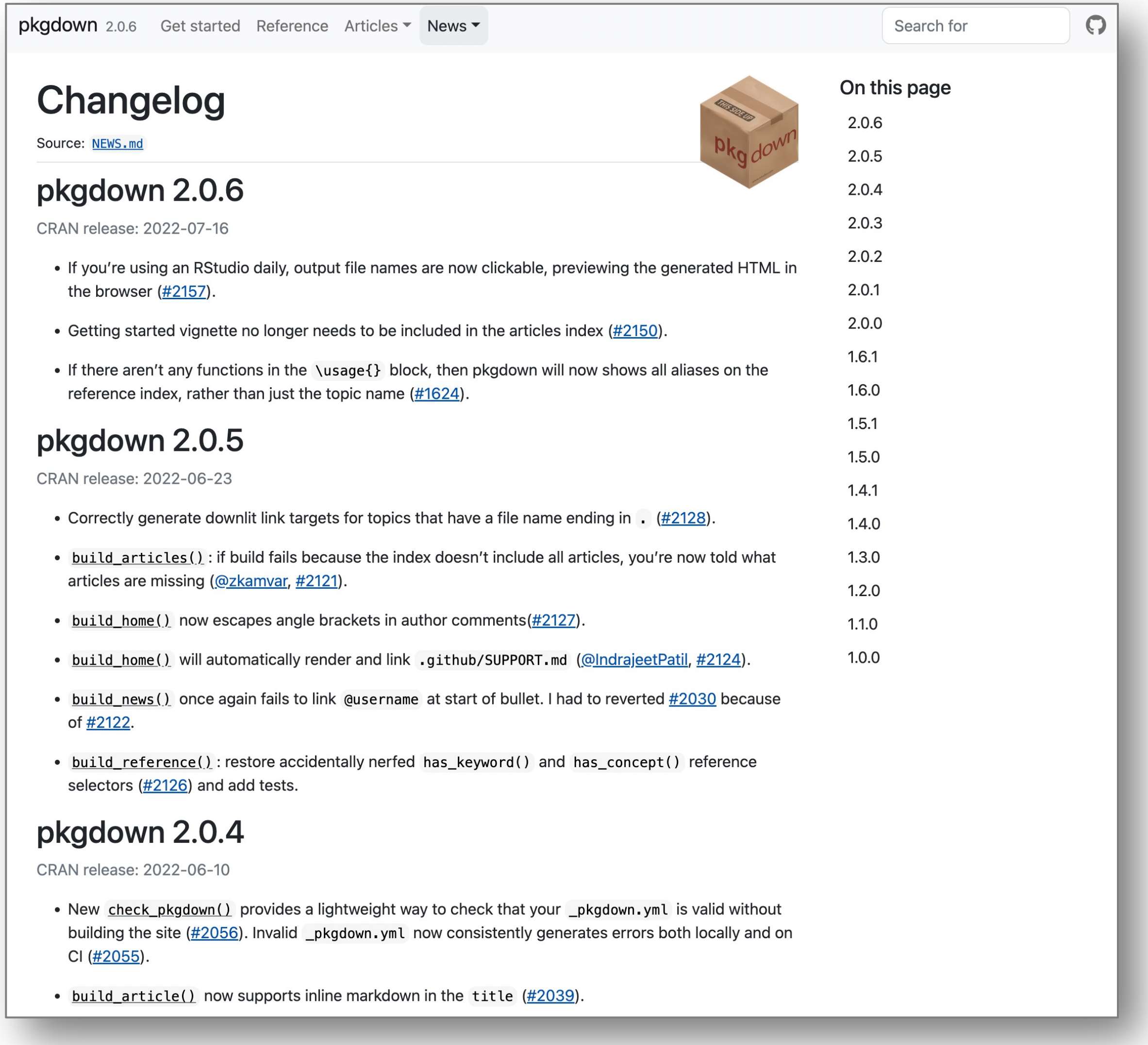
1. Parsing of R package files in html code

NEWS.md



```
# pkgdown (development version)

* Tweak German translation (@krlmlr, @mgirlich, #2149)
* Remove mention of (defunct) Twitter card validator, provide alternatives (@Bisaloo, #2185)
* Fix `keywords` typo in `check_missing_topics()` message (@swsoyee, #2178).
* Use jsdeliver CDN for bootstrap-toc (@GregorDeCillia, #2207).

# pkgdown 2.0.6

* If you're using an RStudio daily, output file names are now clickable,
  previewing the generated HTML in the browser (#2157).

* Getting started vignette no longer needs to be included in the articles index
  (#2150).

* If there aren't any functions in the `\usage{}` block, then pkgdown will
  now shows all aliases on the reference index, rather than just the topic
  name (#1624).

# pkgdown 2.0.5

* Correctly generate downlit link targets for topics that have a file name
  ending in `.` (#2128).

* `build_articles()`: if build fails because the index doesn't include all
  articles, you're now told what articles are missing (@zkamvar, #2121).

* `build_home()` now escapes angle brackets in author comments(#2127).

* `build_home()` will automatically render and link `.github/SUPPORT.md`
  (@IndrajeetPatil, #2124).

* `build_news()` once again fails to link `@username` at start of
  bullet. I had to reverted #2030 because of #2122.

* `build_reference()`: restore accidentally nerfed `has_keyword()` and
  `has_concept()` reference selectors (#2126) and add tests.

# pkgdown 2.0.4

* New `check_pkgdown()` provides a lightweight way to check that your
  `_pkgdown.yml` is valid without building the site (#2056). Invalid
  `_pkgdown.yml` now consistently generates errors both locally and on
  CI (#2055).

* `build_article()` now supports inline markdown in the `title` (#2039).

* `build_home()` no longer shows development status badges on the released
  version of the site (#2054).

* `build_news()` support automated `@username` links in more places (#2030).

* `build_reference()`:

    * You can once again exclude topics from the reference index with `-` (#2040).

    * Inline markdown in `title`s and `subtitle`s is now supported(#2039).
```

pkgdown.r-lib.org/news



Changelog

Source: `NEWS.md`

pkgdown 2.0.6

CRAN release: 2022-07-16

- If you're using an RStudio daily, output file names are now clickable, previewing the generated HTML in the browser (#2157).
- Getting started vignette no longer needs to be included in the articles index (#2150).
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pkgdown 2.0.5

CRAN release: 2022-06-23

- Correctly generate downlit link targets for topics that have a file name ending in `.` (#2128).
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pkgdown 2.0.4

CRAN release: 2022-06-10

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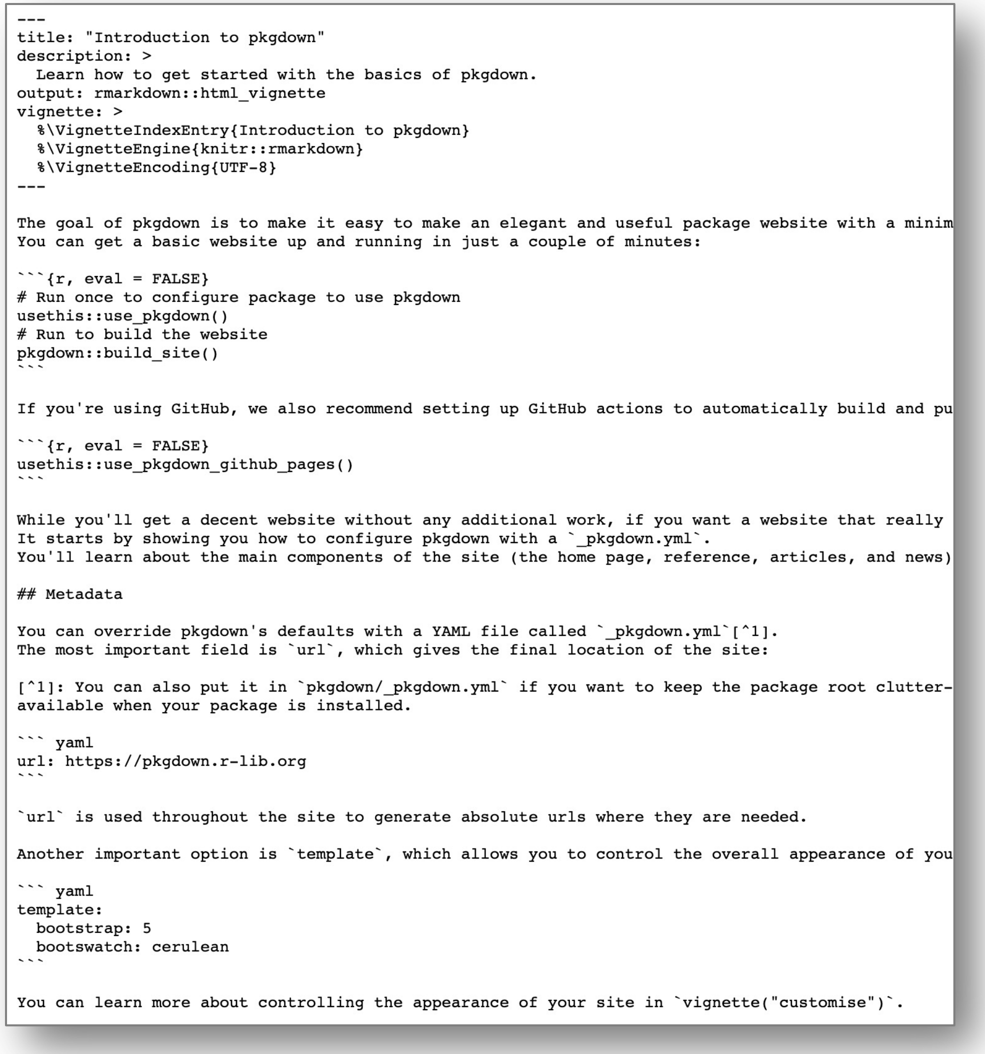
Pkgdown functionalities

1. Parsing of R package files in html code

vignettes/pkgdown.Rmd



~~~
---
title: "Introduction to pkgdown"
description: >
  Learn how to get started with the basics of pkgdown.
output: rmarkdown::html_vignette
vignette: >
  %\VignetteIndexEntry{Introduction to pkgdown}
  %\VignetteEngine{knitr::rmarkdown}
  %\VignetteEncoding{UTF-8}
---

The goal of pkgdown is to make it easy to make an elegant and useful package website with a minim
You can get a basic website up and running in just a couple of minutes:

```{r, eval = FALSE}
# Run once to configure package to use pkgdown
usethis::use_pkgdown()
# Run to build the website
pkgdown::build_site()
~~~

If you're using GitHub, we also recommend setting up GitHub actions to automatically build and pu

```{r, eval = FALSE}
usethis::use_pkgdown_github_pages()
```

While you'll get a decent website without any additional work, if you want a website that really
It starts by showing you how to configure pkgdown with a `_pkgdown.yml`.
You'll learn about the main components of the site (the home page, reference, articles, and news)

Metadata

You can override pkgdown's defaults with a YAML file called `_pkgdown.yml`[^1].
The most important field is `url`, which gives the final location of the site:

[^1]: You can also put it in `pkgdown/_pkgdown.yml` if you want to keep the package root clutter-
available when your package is installed.

``` yaml
url: https://pkgdown.r-lib.org
```

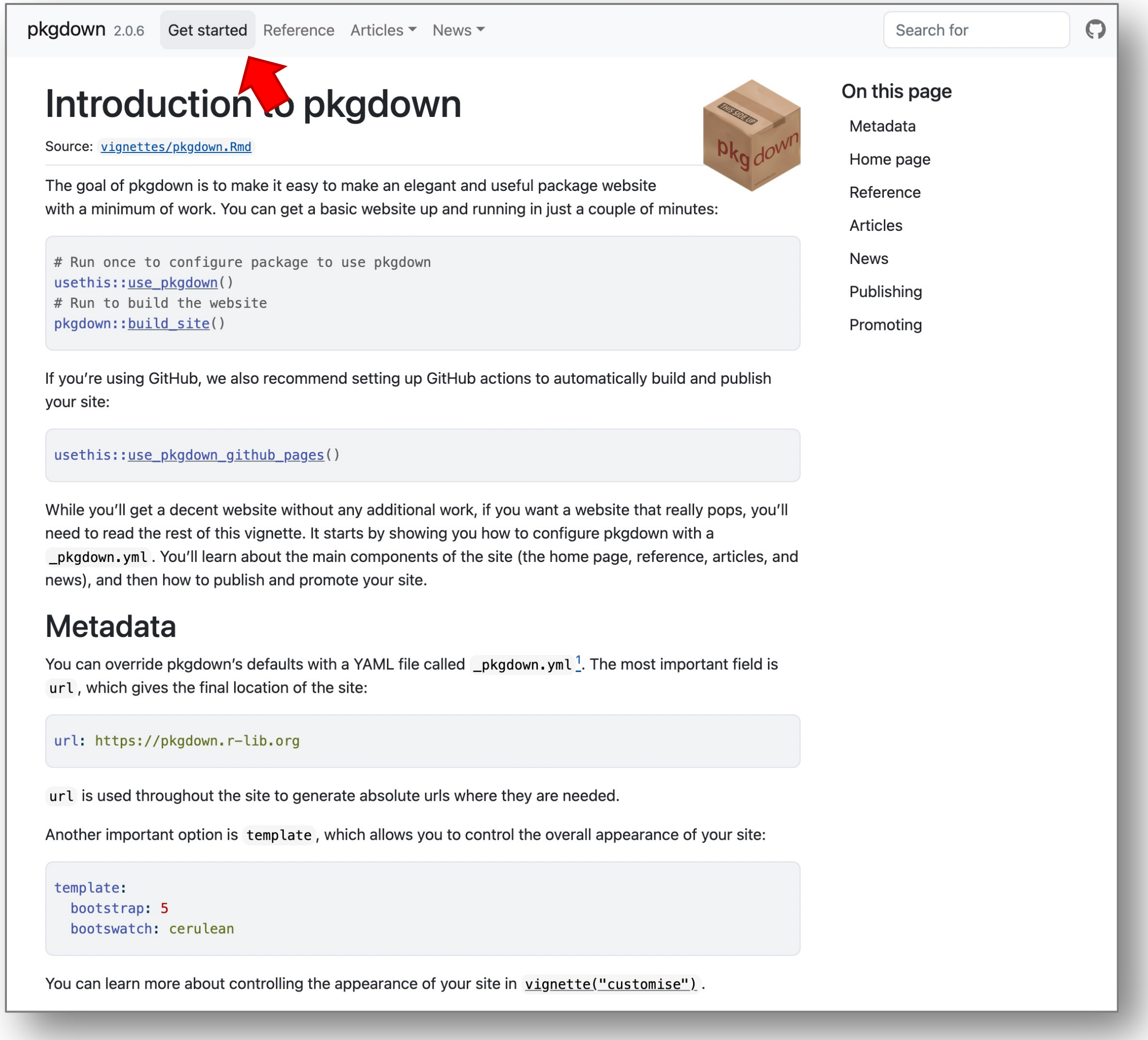
`url` is used throughout the site to generate absolute urls where they are needed.

Another important option is `template`, which allows you to control the overall appearance of you

``` yaml
template:
  bootstrap: 5
  bootswatch: cerulean
```

You can learn more about controlling the appearance of your site in `vignette("customise")`.
```

pkgdown.r-lib.org/articles/pkgdown.html


pkgdown 2.0.6
Get started
Reference
Articles
News
Search for
On this page
Metadata
Home page
Reference
Articles
News
Publishing
Promoting

Introduction to pkgdown

Source: vignettes/pkgdown.Rmd

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```
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  bootswatch: cerulean
```

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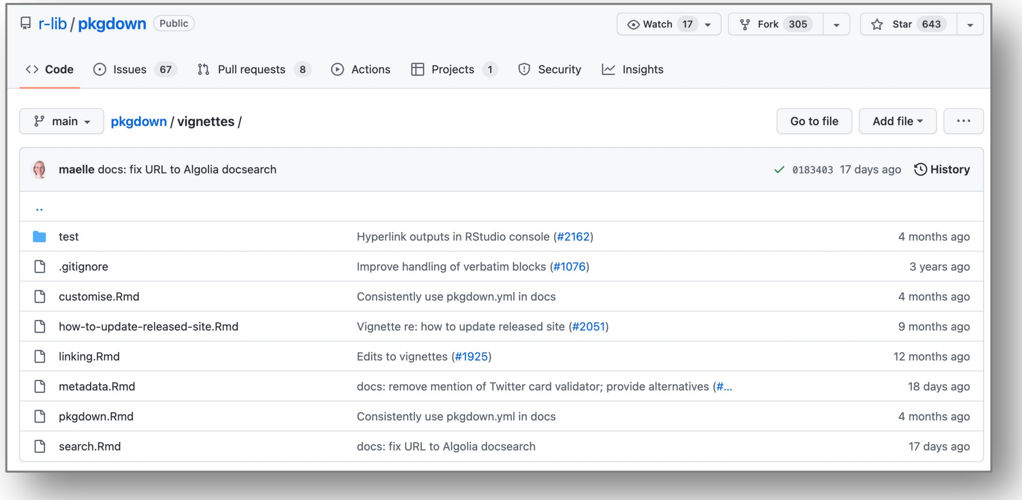
# Pkgdown functionalities

1. Parsing of R package files in html code

**vignettes/*.Rmd**

**pkgdown.r-lib.org/articles/pkgdown.html**



r-lib / pkgdown Public

Watch 17 · Fork 305 · Star 643

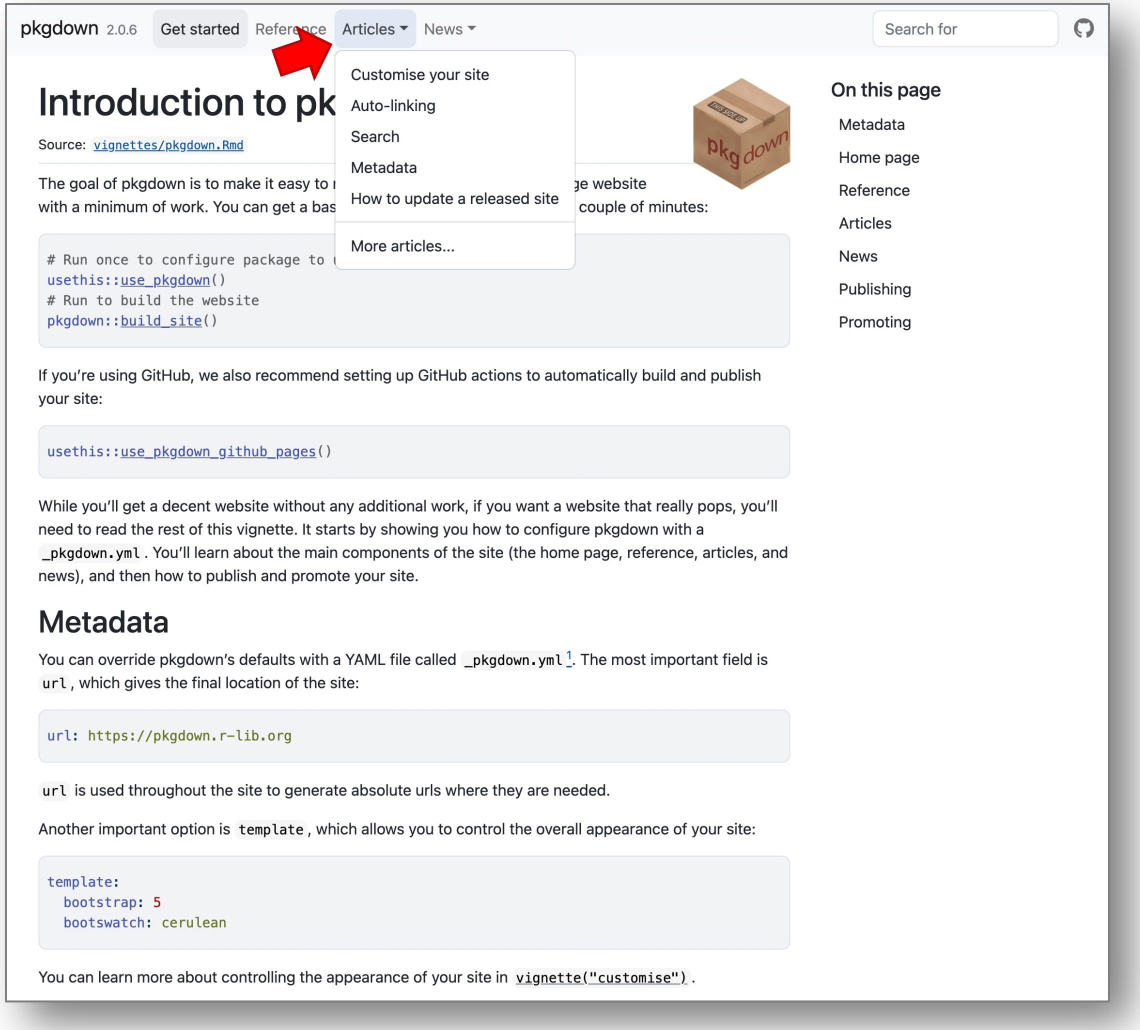
Code · Issues 67 · Pull requests 8 · Actions · Projects 1 · Security · Insights

main · pkgdown / vignettes / · Go to file · Add file

maelle docs: fix URL to Algolia docsearch ✓ 0183403 17 days ago History

..

| | | |
|---|---|---|
| test | Hyperlink outputs in RStudio console (#2162) | 4 months ago |
| .gitignore | Improve handling of verbatim blocks (#1076) | 3 years ago |
| customise.Rmd | Consistently use pkgdown.yml in docs | 4 months ago |
| how-to-update-released-site.Rmd | Vignette re: how to update released site (#2051) | 9 months ago |
| linking.Rmd | Edits to vignettes (#1925) | 12 months ago |
| metadata.Rmd | docs: remove mention of Twitter card validator; provide alternatives (#... | 18 days ago |
| pkgdown.Rmd | Consistently use pkgdown.yml in docs | 4 months ago |
| search.Rmd | docs: fix URL to Algolia docsearch | 17 days ago |



pkgdown 2.0.6 · Get started · Reference · Articles · News · Search for

Customise your site
Auto-linking
Search
Metadata
How to update a released site
More articles...

On this page
Metadata
Home page
Reference
Articles
News
Publishing
Promoting

## Introduction to pk

Source: vignettes/pkgdown.Rmd

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usethis::use_pkgdown()
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If you're using GitHub, we also recommend setting up GitHub actions to automatically build and publish your site:

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usethis::use_pkgdown_github_pages()
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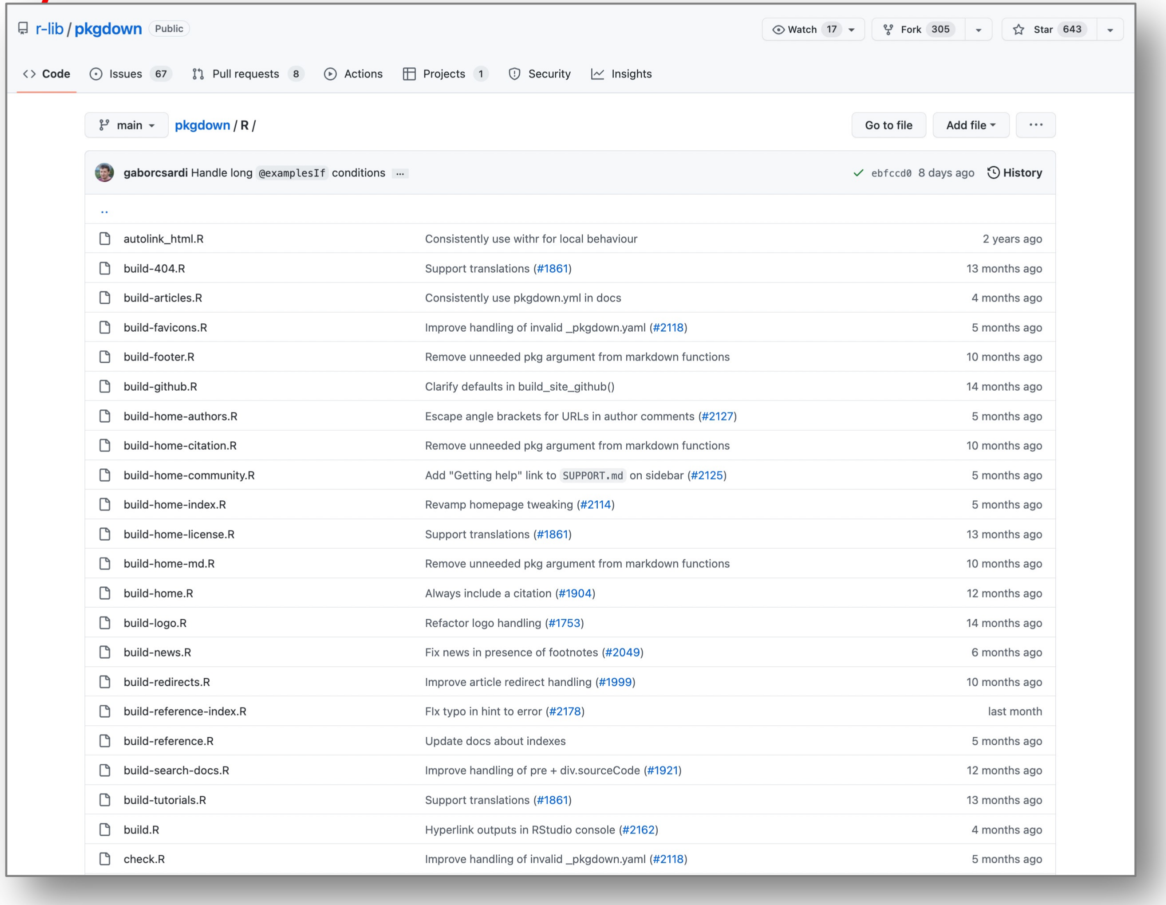
Pkgdown functionalities

1. Parsing of R package files in html code

2. List each function and link to its documentation

R/*.R

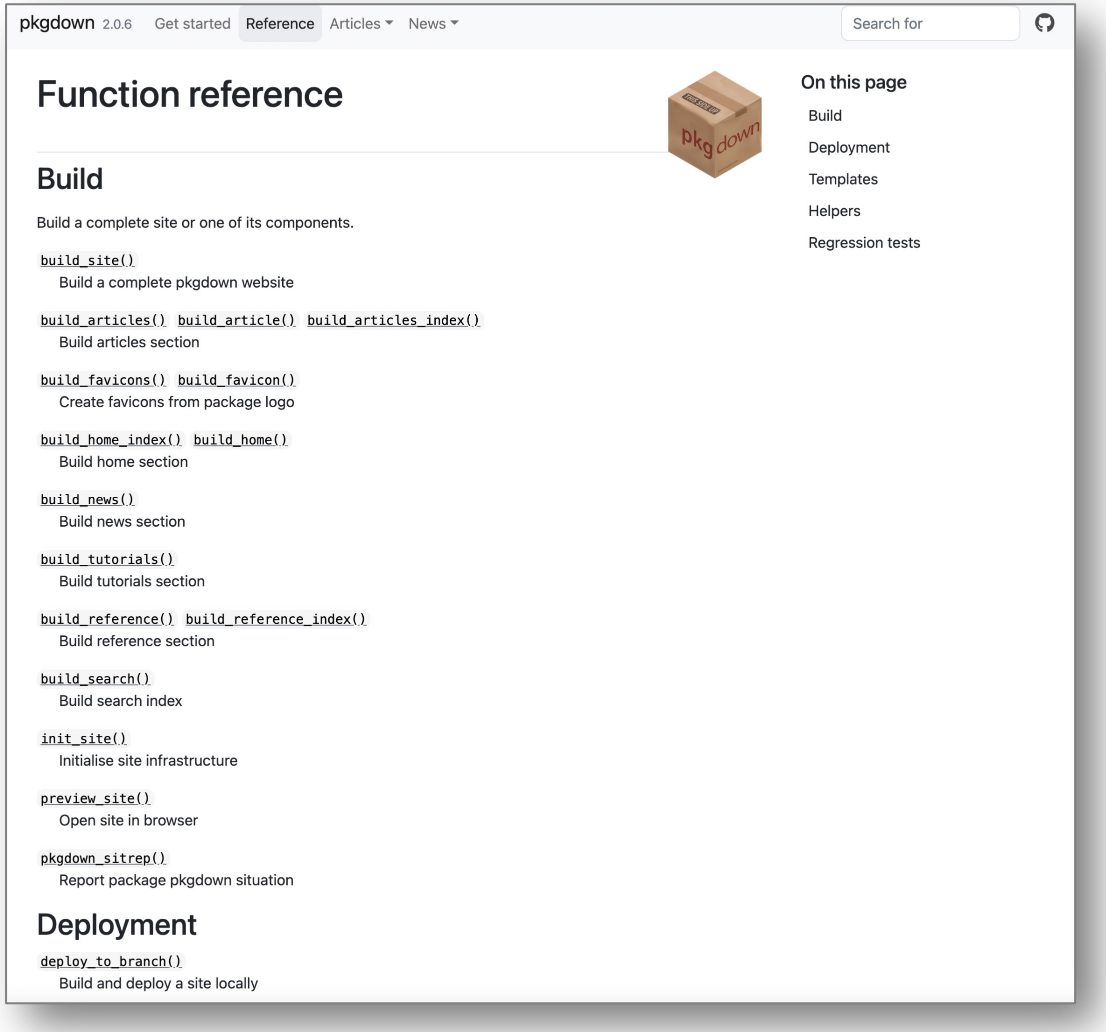


gaborcsardi Handle long `@examplesIf` conditions … ebfccd0 8 days ago

..

autolink_html.R	Consistently use withr for local behaviour	2 years ago
build-404.R	Support translations (#1861)	13 months ago
build-articles.R	Consistently use pkgdown.yml in docs	4 months ago
build-favicons.R	Improve handling of invalid _pkgdown.yaml (#2118)	5 months ago
build-footer.R	Remove unneeded pkg argument from markdown functions	10 months ago
build-github.R	Clarify defaults in build_site_github()	14 months ago
build-home-authors.R	Escape angle brackets for URLs in author comments (#2127)	5 months ago
build-home-citation.R	Remove unneeded pkg argument from markdown functions	10 months ago
build-home-community.R	Add "Getting help" link to `SUPPORT.md` on sidebar (#2125)	5 months ago
build-home-index.R	Revamp homepage tweaking (#2114)	5 months ago
build-home-license.R	Support translations (#1861)	13 months ago
build-home-md.R	Remove unneeded pkg argument from markdown functions	10 months ago
build-home.R	Always include a citation (#1904)	12 months ago
build-logo.R	Refactor logo handling (#1753)	14 months ago
build-news.R	Fix news in presence of footnotes (#2049)	6 months ago
build-redirects.R	Improve article redirect handling (#1999)	10 months ago
build-reference-index.R	FIx typo in hint to error (#2178)	last month
build-reference.R	Update docs about indexes	5 months ago
build-search-docs.R	Improve handling of pre + div.sourceCode (#1921)	12 months ago
build-tutorials.R	Support translations (#1861)	13 months ago
build.R	Hyperlink outputs in RStudio console (#2162)	4 months ago
check.R	Improve handling of invalid _pkgdown.yaml (#2118)	5 months ago

pkgdown.r-lib.org/reference



Function reference

Build

Build a complete site or one of its components.

`build_site()`
Build a complete pkgdown website

`build_articles()` `build_article()` `build_articles_index()`
Build articles section

`build_favicons()` `build_favicon()`
Create favicons from package logo

`build_home_index()` `build_home()`
Build home section

`build_news()`
Build news section

`build_tutorials()`
Build tutorials section

`build_reference()` `build_reference_index()`
Build reference section

`build_search()`
Build search index

`init_site()`
Initialise site infrastructure

`preview_site()`
Open site in browser

`pkgdown_sitrep()`
Report package pkgdown situation

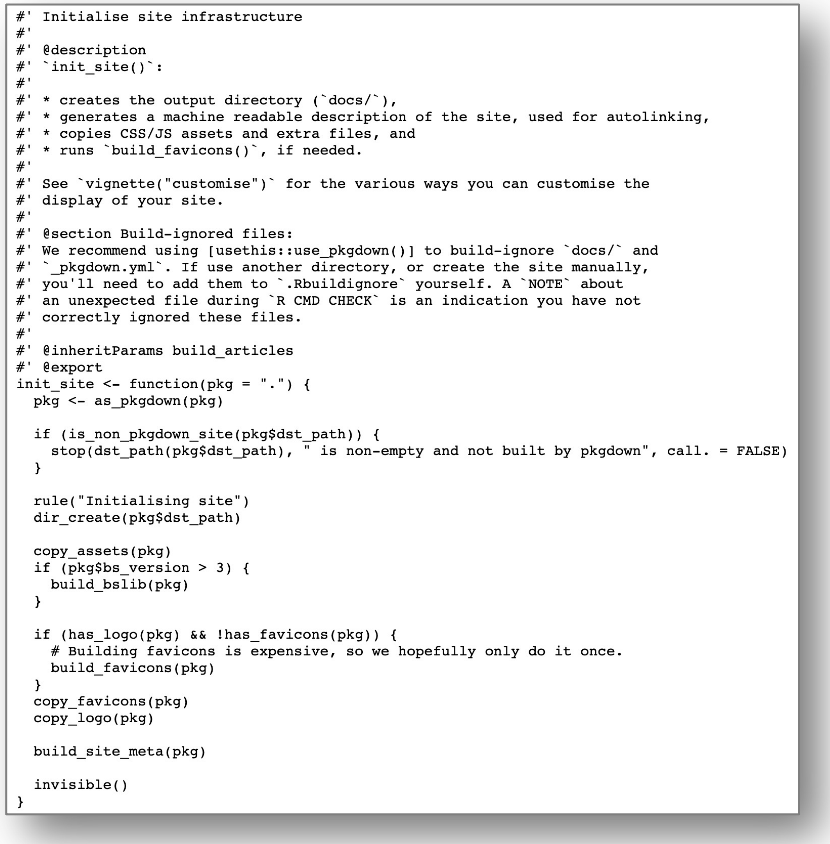
Deployment

`deploy_to_branch()`
Build and deploy a site locally

Pkgdown functionalities

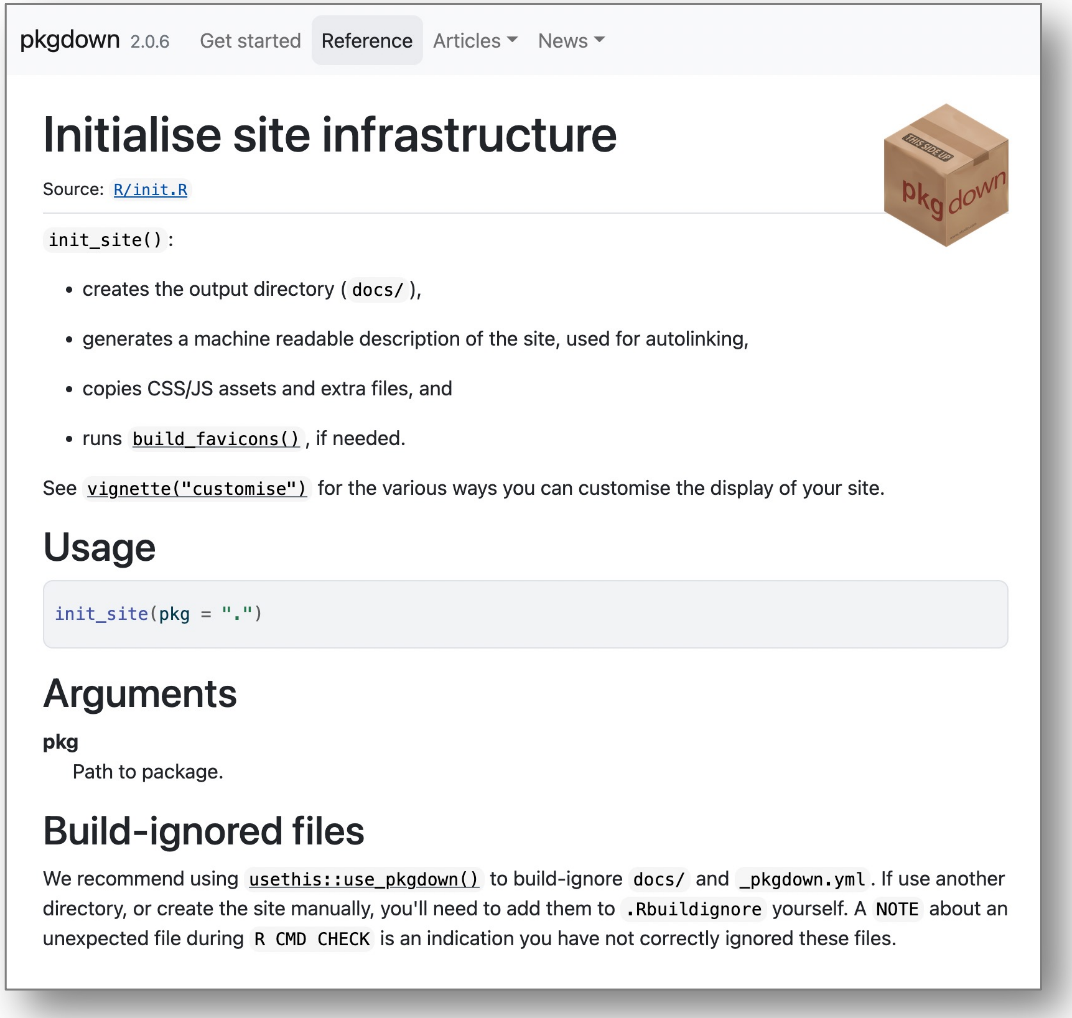
1. Parsing of R package files in html code
2. List each function and link to its documentation

R/init.R



```r
#' Initialise site infrastructure
#'
#' @description
#' `init_site()`:
#'
#' * creates the output directory (`docs/`),
#' * generates a machine readable description of the site, used for autolinking,
#' * copies CSS/JS assets and extra files, and
#' * runs `build_favicons()`, if needed.
#'
#' See `vignette("customise")` for the various ways you can customise the
#' display of your site.
#'
#' @section Build-ignored files:
#' We recommend using [usethis::use_pkgdown()] to build-ignore `docs/` and
#' `_pkgdown.yml`. If use another directory, or create the site manually,
#' you'll need to add them to `.Rbuildignore` yourself. A `NOTE` about
#' an unexpected file during `R CMD CHECK` is an indication you have not
#' correctly ignored these files.
#'
#' @inheritParams build_articles
#' @export
init_site <- function(pkg = ".") {
  pkg <- as_pkgdown(pkg)

  if (is_non_pkgdown_site(pkg$dst_path)) {
    stop(dst_path(pkg$dst_path), " is non-empty and not built by pkgdown", call. = FALSE)
  }

  rule("Initialising site")
  dir_create(pkg$dst_path)

  copy_assets(pkg)
  if (pkg$bs_version > 3) {
    build_bslib(pkg)
  }

  if (has_logo(pkg) && !has_favicons(pkg)) {
    # Building favicons is expensive, so we hopefully only do it once.
    build_favicons(pkg)
  }
  copy_favicons(pkg)
  copy_logo(pkg)

  build_site_meta(pkg)

  invisible()
}
```

pkgdown.r-lib.org/reference/init_site.html



Initialise site infrastructure

Source: R/init.R

`init_site()`:

- creates the output directory (`docs/`),
- generates a machine readable description of the site, used for autolinking,
- copies CSS/JS assets and extra files, and
- runs `build_favicons()` , if needed.

See `vignette("customise")` for the various ways you can customise the display of your site.

Usage

```r
init_site(pkg = ".")
```

Arguments

pkg
Path to package.

Build-ignored files

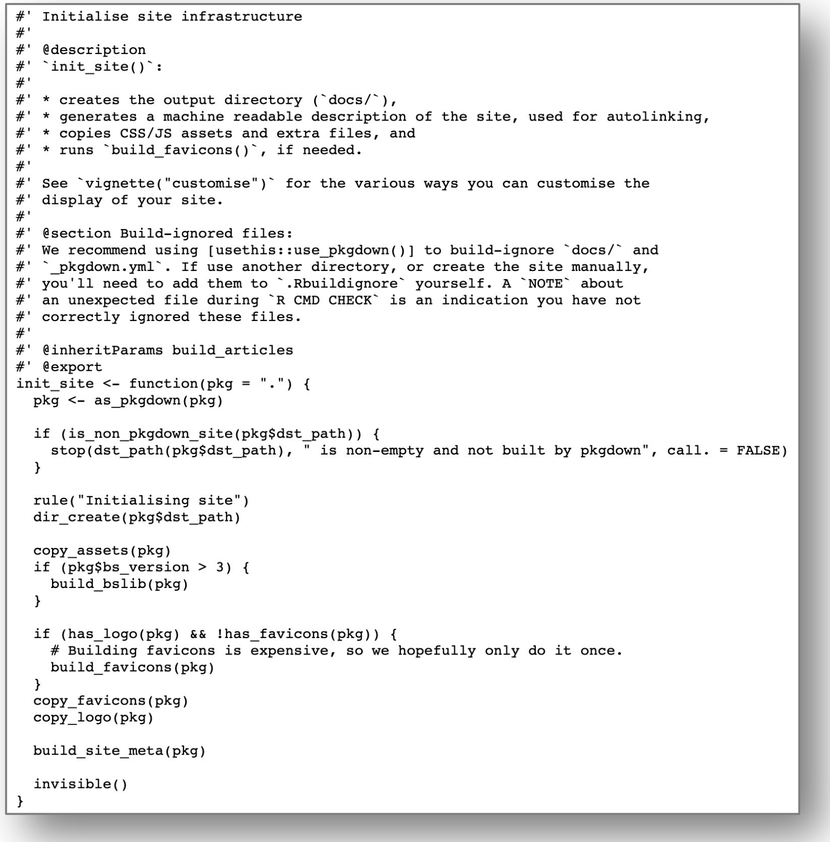
We recommend using `usethis::use_pkgdown()` to build-ignore `docs/` and `_pkgdown.yml`. If use another directory, or create the site manually, you'll need to add them to `.Rbuildignore` yourself. A `NOTE` about an unexpected file during `R CMD CHECK` is an indication you have not correctly ignored these files.

Pkgdown functionalities

1. Parsing of R package files in html code

2. List each function and link to its documentation

3. Auto-linking to useful resources



```r
#' Initialise site infrastructure
#'
#' @description
#' `init_site()`:
#'
#' * creates the output directory (`docs/`),
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#' We recommend using [usethis::use_pkgdown()] to build-ignore `docs/` and
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#' an unexpected file during `R CMD CHECK` is an indication you have not
#' correctly ignored these files.
#'
#' @inheritParams build_articles
#' @export
init_site <- function(pkg = ".") {
  pkg <- as_pkgdown(pkg)

  if (is_non_pkgdown_site(pkg$dst_path)) {
    stop(dst_path(pkg$dst_path), " is non-empty and not built by pkgdown", call. = FALSE)
  }

  rule("Initialising site")
  dir_create(pkg$dst_path)

  copy_assets(pkg)
  if (pkg$bs_version > 3) {
    build_bslib(pkg)
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  copy_logo(pkg)

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  invisible()
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```

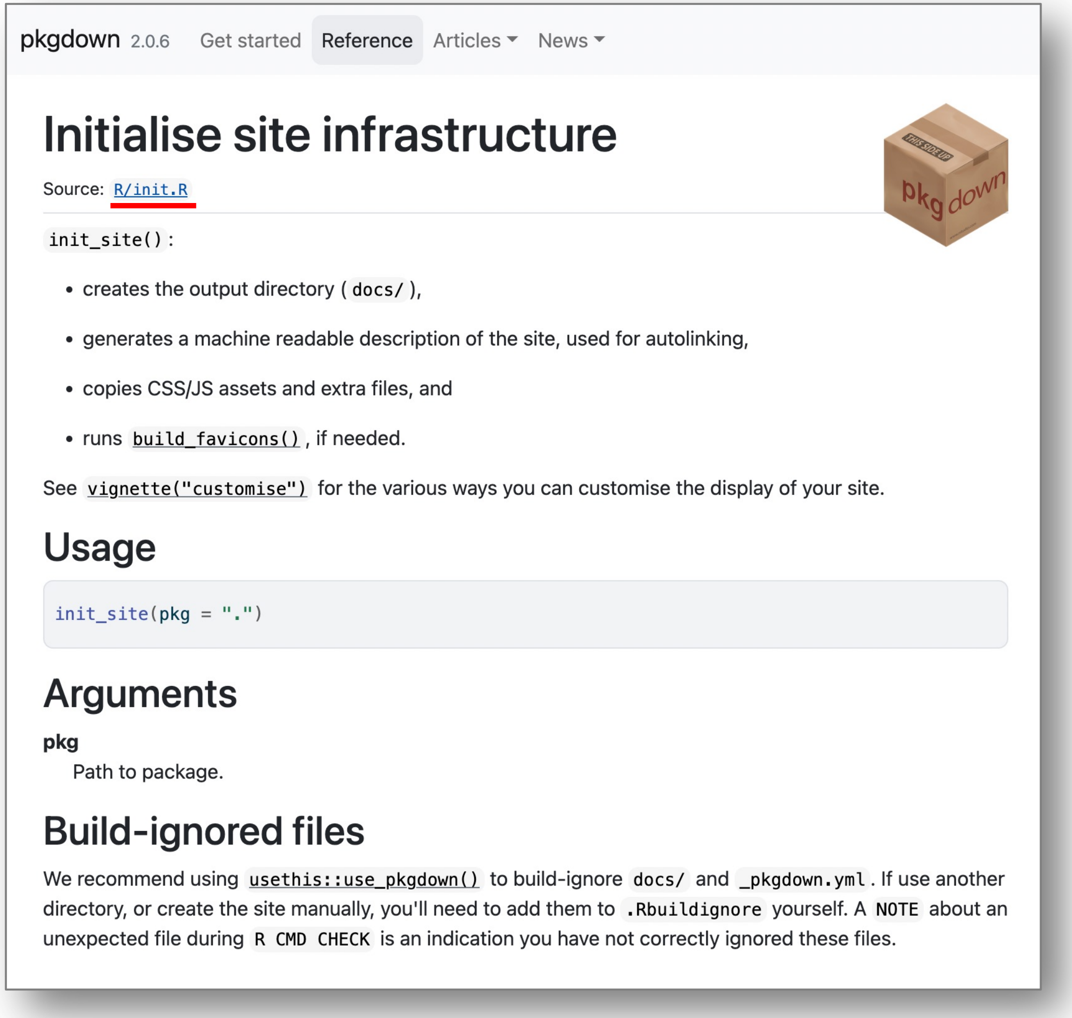

Initialise site infrastructure

Source: R/init.R

`init_site()`:

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Usage

```r
init_site(pkg = ".")
```

Arguments

pkg

Path to package.

Build-ignored files

We recommend using `usethis::use_pkgdown()` to build-ignore `docs/` and `_pkgdown.yml` . If use another directory, or create the site manually, you'll need to add them to `.Rbuildignore` yourself. A `NOTE` about an unexpected file during `R CMD CHECK` is an indication you have not correctly ignored these files.

Pkgdown functionalities

1. Parsing of R package files in html code

2. List each function and link to its documentation

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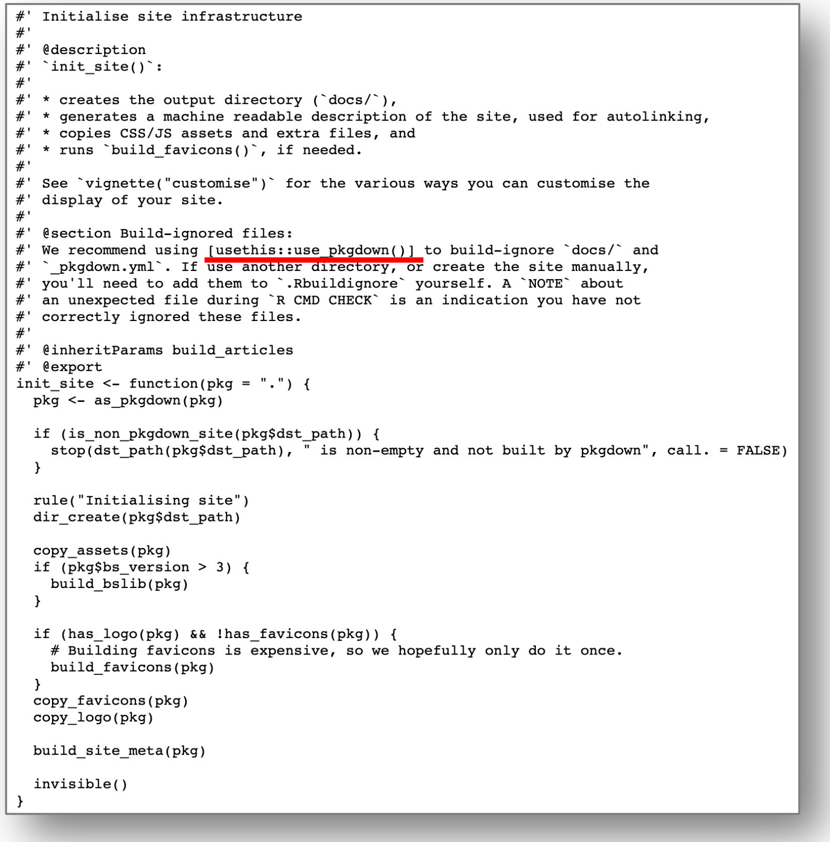

```r
#' Initialise site infrastructure
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#' @description
#' `init_site()`:
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#' * creates the output directory (`docs/`),
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init_site <- function(pkg = ".") {
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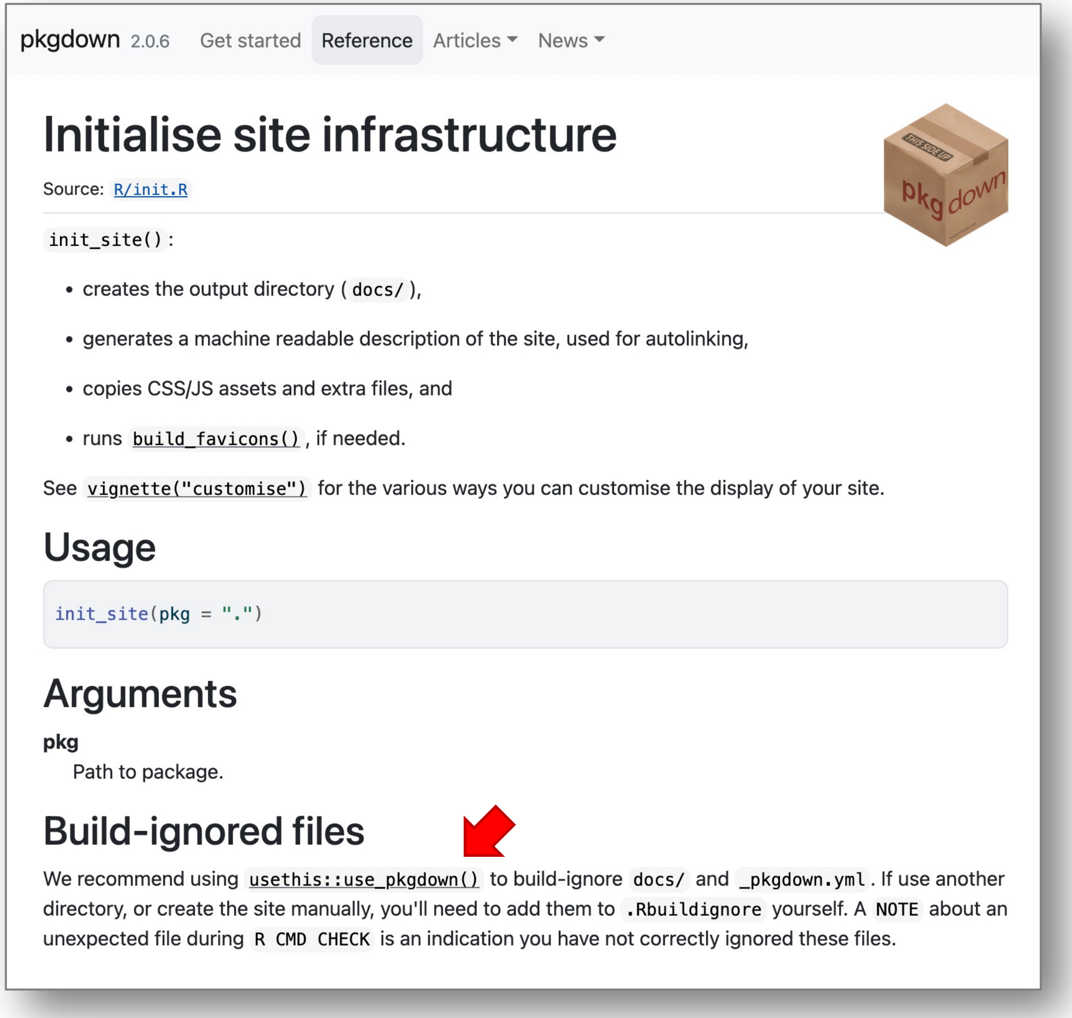

Initialise site infrastructure

Source: R/init.R

`init_site()`:

- creates the output directory (`docs/`),
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See `vignette("customise")` for the various ways you can customise the display of your site.

Usage

```r
init_site(pkg = ".")
```

Arguments

pkg
Path to package.

Build-ignored files

We recommend using `usethis::use_pkgdown()` to build-ignore `docs/` and `_pkgdown.yml`. If use another directory, or create the site manually, you'll need to add them to `.Rbuildignore` yourself. A `NOTE` about an unexpected file during `R CMD CHECK` is an indication you have not correctly ignored these files.

Pkgdown functionalities

1. Parsing of R package files in html code
2. List each function and link to its documentation
3. Auto-linking to useful resources

Use pkgdown

Source: R/pkgdown.R

pkgdown makes it easy to turn your package into a beautiful website. usethis provides two functions to help you use pkgdown:

- `use_pkgdown()` : creates a pkgdown config file and adds relevant files or directories to `.Rbuildignore` and `.gitignore`.
- `use_pkgdown_github_pages()` : implements the GitHub setup needed to automatically publish your pkgdown site to GitHub pages:
  - (first, it calls `use_pkgdown()`)
  - `use_github_pages()` prepares to publish the pkgdown site from the `gh-pages` branch
  - `use_github_action("pkgdown")` configures a GitHub Action to automatically build the pkgdown site and deploy it via GitHub Pages
  - The pkgdown site's URL is added to the pkgdown configuration file, to the URL field of DESCRIPTION, and to the GitHub repo.
  - Packages owned by certain GitHub organizations (tidyverse, r-lib, and tidymodels) get some special treatment, in terms of anticipating the (eventual) site URL and the use of a pkgdown template.

`use_pkgdown_travis()` is deprecated; we no longer recommend that you use Travis-CI.

Usage

```
use_pkgdown(config_file = "_pkgdown.yml", destdir = "docs")

use_pkgdown_github_pages()

use_pkgdown_travis()
```

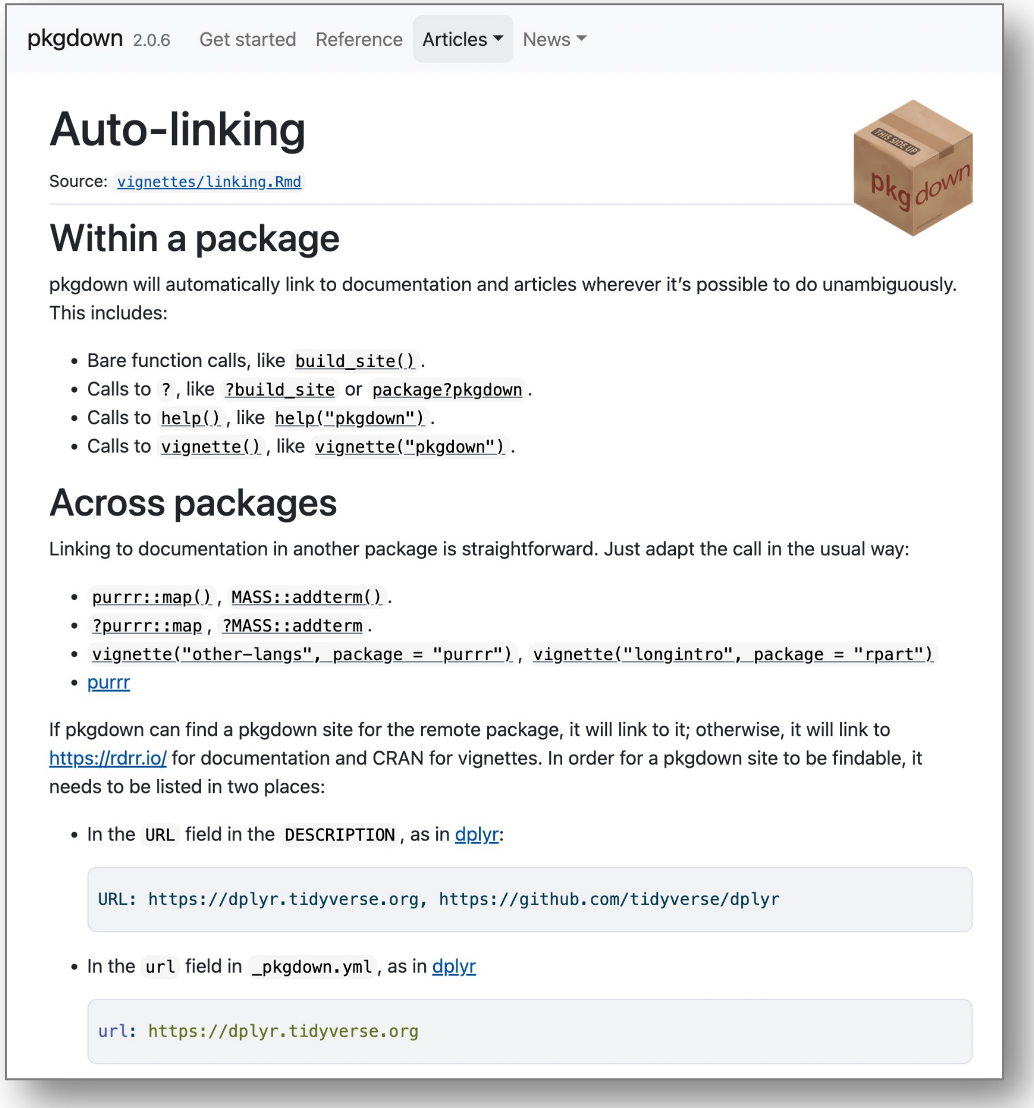
Arguments

config_file

Path to the pkgdown yaml config file

Pkgdown functionalities

1. Parsing of R package files in html code
2. List each function and link to its documentation
3. Auto-linking to useful resources



Auto-linking

Source: `vignettes/linking.Rmd`

Within a package

pkgdown will automatically link to documentation and articles wherever it's possible to do unambiguously. This includes:

- Bare function calls, like `build_site()`.
- Calls to `?`, like `?build_site` or `package?pkgdown`.
- Calls to `help()`, like `help("pkgdown")`.
- Calls to `vignette()`, like `vignette("pkgdown")`.

Across packages

Linking to documentation in another package is straightforward. Just adapt the call in the usual way:

- `purrr::map()`, `MASS::addterm()`.
- `?purrr::map`, `?MASS::addterm`.
- `vignette("other-langs", package = "purrr")`, `vignette("longintro", package = "rpart")`
- purrr

If pkgdown can find a pkgdown site for the remote package, it will link to it; otherwise, it will link to https://rdrr.io/ for documentation and CRAN for vignettes. In order for a pkgdown site to be findable, it needs to be listed in two places:

- In the `URL` field in the `DESCRIPTION`, as in dplyr:

```
URL: https://dplyr.tidyverse.org, https://github.com/tidyverse/dplyr
```

- In the `url` field in `_pkgdown.yml`, as in dplyr

```
url: https://dplyr.tidyverse.org
```

How to enable pkgdown for your own package

```
> install.packages("pkgdown")
```

How to enable pkgdown for your own package

```
> install.packages("pkgdown")
> usethis::use_pkgdown()
```

_pkgdown.yml

```
url: ~
template:
  bootstrap: 5
```

How to enable pkgdown for your own package

```
> install.packages("pkgdown")
> usethis::use_pkgdown()
> pkgdown::build_site()
```

_pkgdown.yml

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url: ~
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  bootstrap: 5
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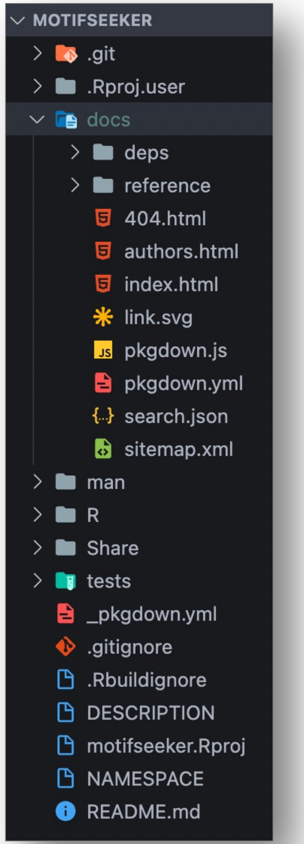


- MOTIFSEEKER
  - .git
  - .Rproj.user
  - docs
    - deps
    - reference
    - 404.html
    - authors.html
    - index.html
    - link.svg
    - pkgdown.js
    - pkgdown.yml
    - search.json
    - sitemap.xml
  - man
  - R
  - Share
  - tests
  - _pkgdown.yml
  - .gitignore
  - .Rbuildignore
  - DESCRIPTION
  - motifseeker.Rproj
  - NAMESPACE
  - README.md

How to enable pkgdown for your own package

```
> install.packages("pkgdown")
> usethis::use_pkgdown()
> pkgdown::build_site()
```

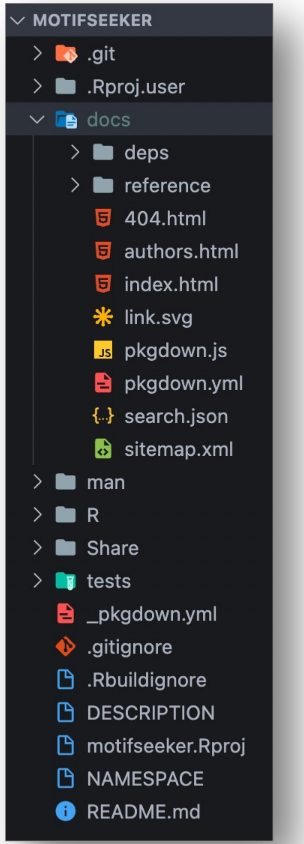
!!!

```
Git commit
Git push
```

!!!

_pkgdown.yml

```
url: ~
template:
  bootstrap: 5
```



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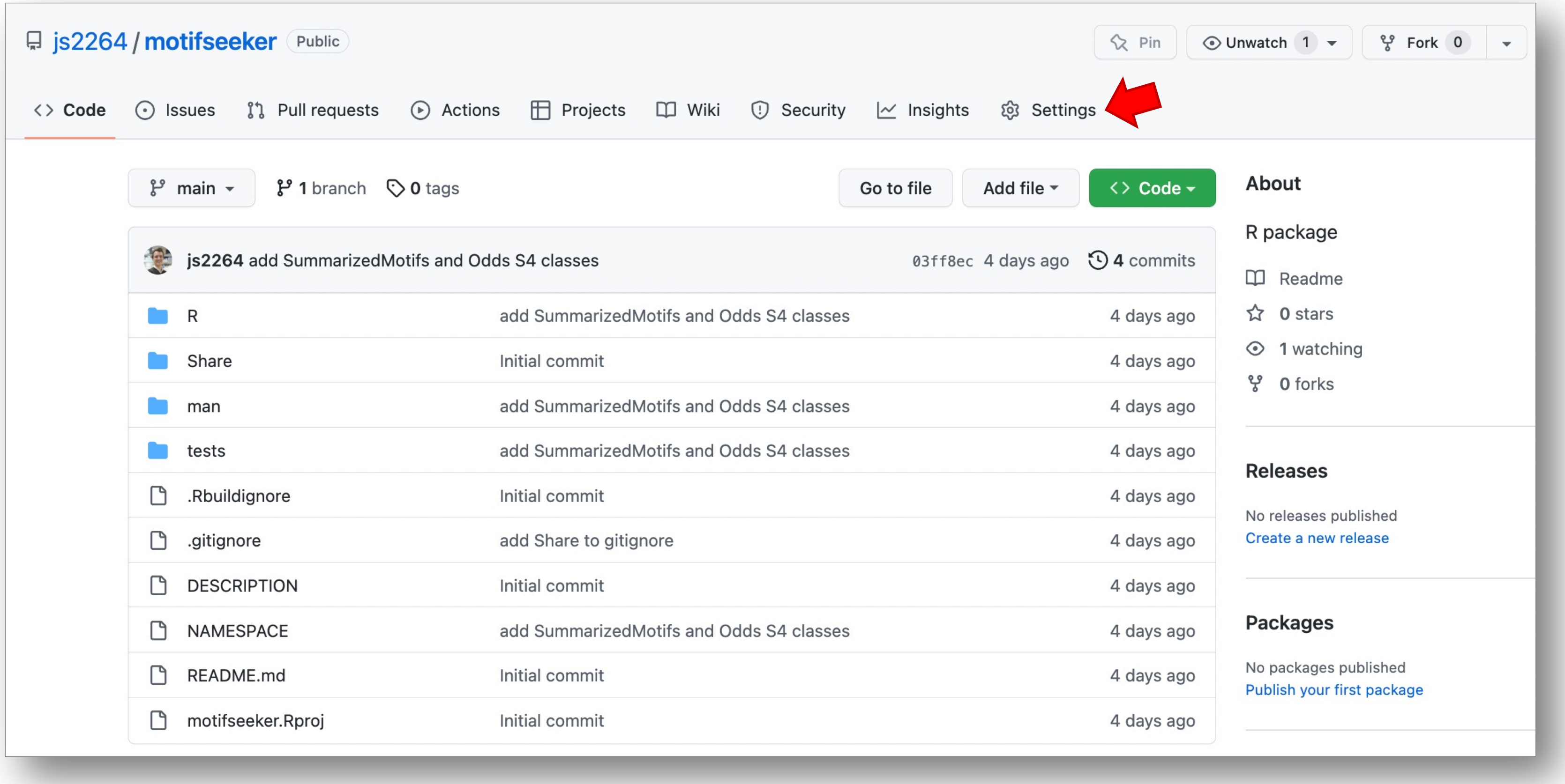
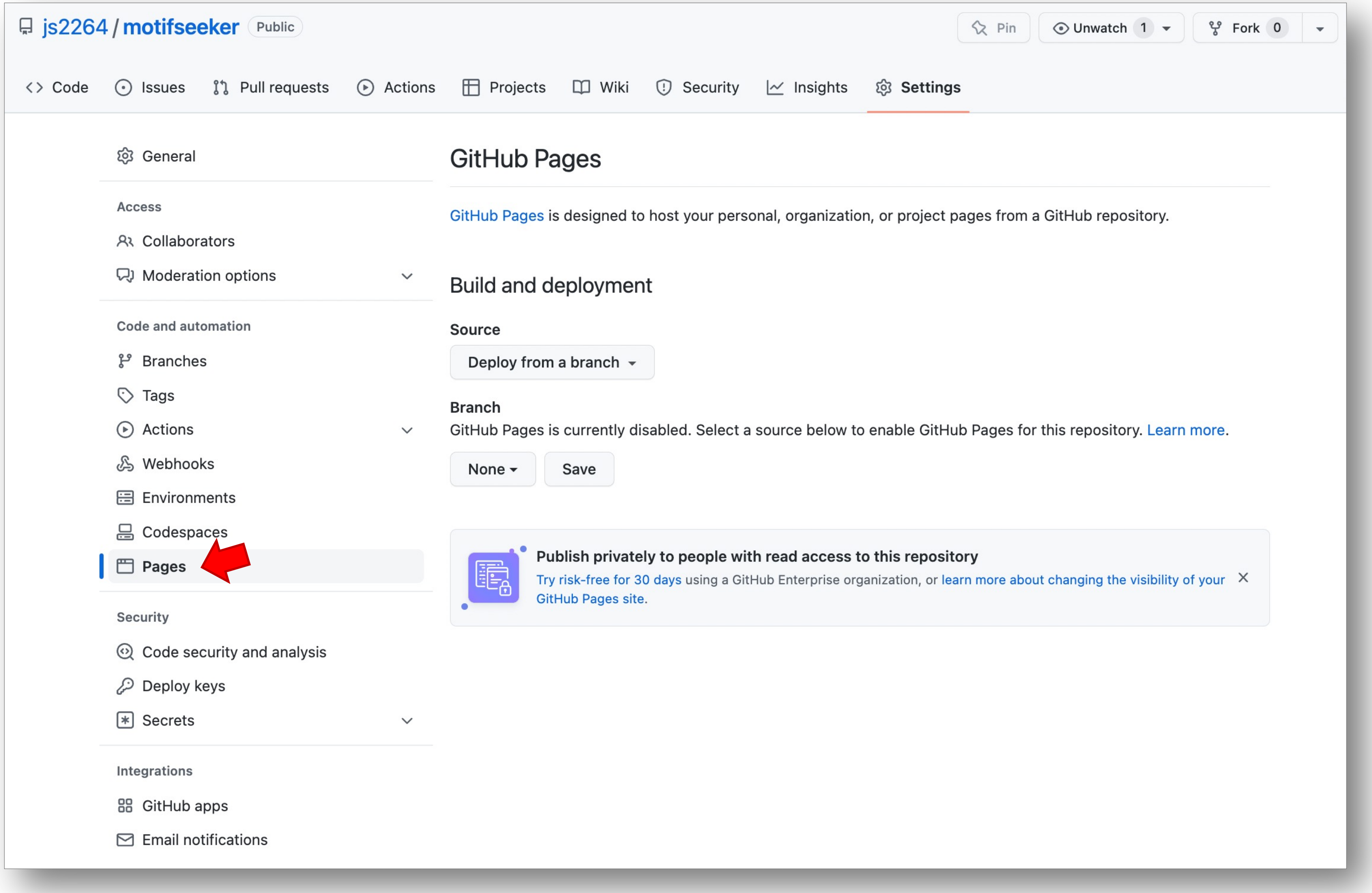
How to enable pkgdown for your own package



js2264 add SummarizedMotifs and Odds S4 classes 03ff8ec 4 days ago 4 commits

R	add SummarizedMotifs and Odds S4 classes	4 days ago
Share	Initial commit	4 days ago
man	add SummarizedMotifs and Odds S4 classes	4 days ago
tests	add SummarizedMotifs and Odds S4 classes	4 days ago
.Rbuildignore	Initial commit	4 days ago
.gitignore	add Share to gitignore	4 days ago
DESCRIPTION	Initial commit	4 days ago
NAMESPACE	add SummarizedMotifs and Odds S4 classes	4 days ago
README.md	Initial commit	4 days ago
motifseeker.Rproj	Initial commit	4 days ago

How to enable pkgdown for your own package



GitHub Pages

GitHub Pages is designed to host your personal, organization, or project pages from a GitHub repository.

Build and deployment

Source

Deploy from a branch

Branch

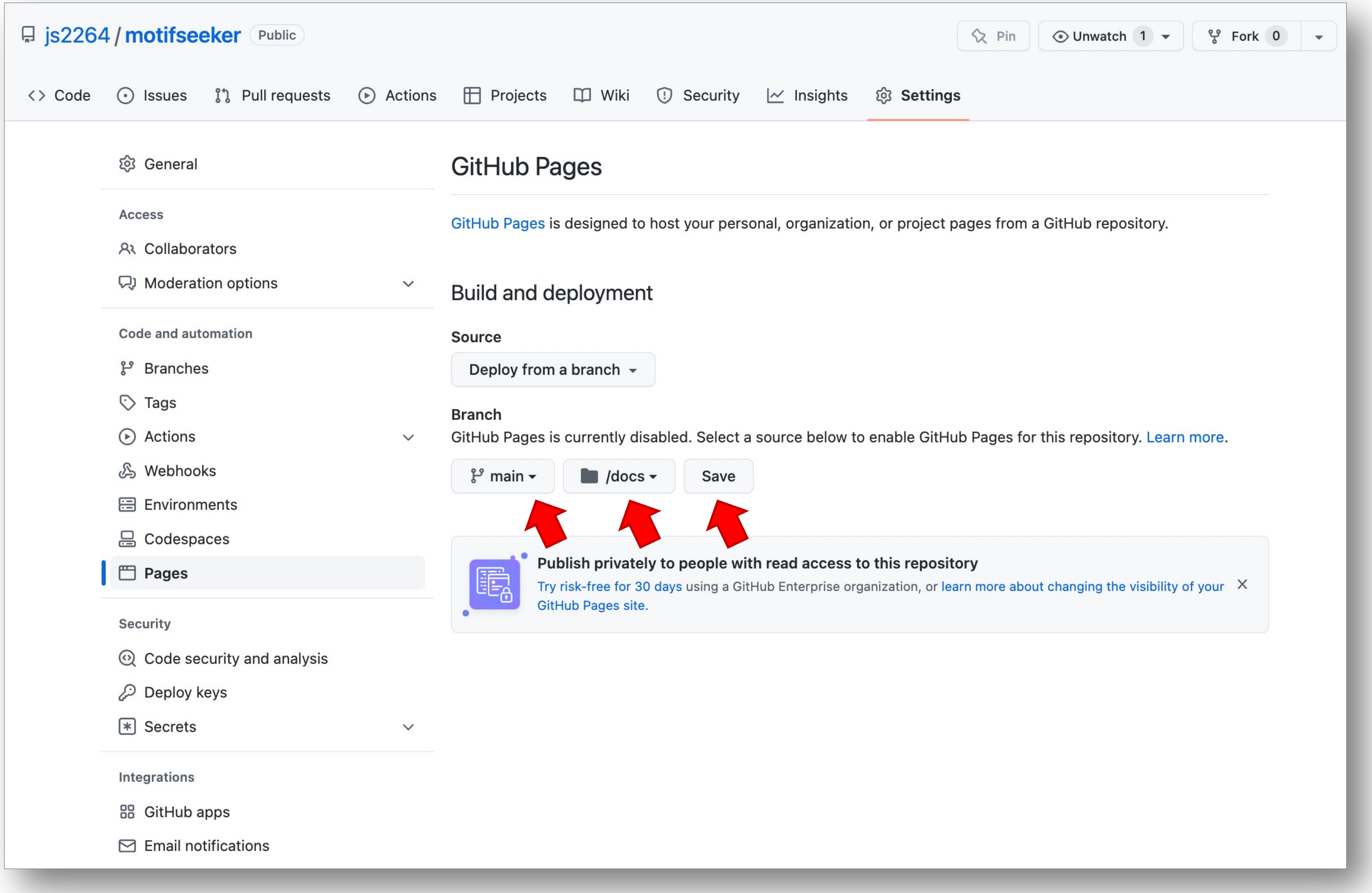
GitHub Pages is currently disabled. Select a source below to enable GitHub Pages for this repository. Learn more.

None | Save

Publish privately to people with read access to this repository

Try risk-free for 30 days using a GitHub Enterprise organization, or learn more about changing the visibility of your GitHub Pages site.

How to enable pkgdown for your own package



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Build and deployment

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GitHub Pages is currently disabled. Select a source below to enable GitHub Pages for this repository. Learn more.

main | /docs | Save

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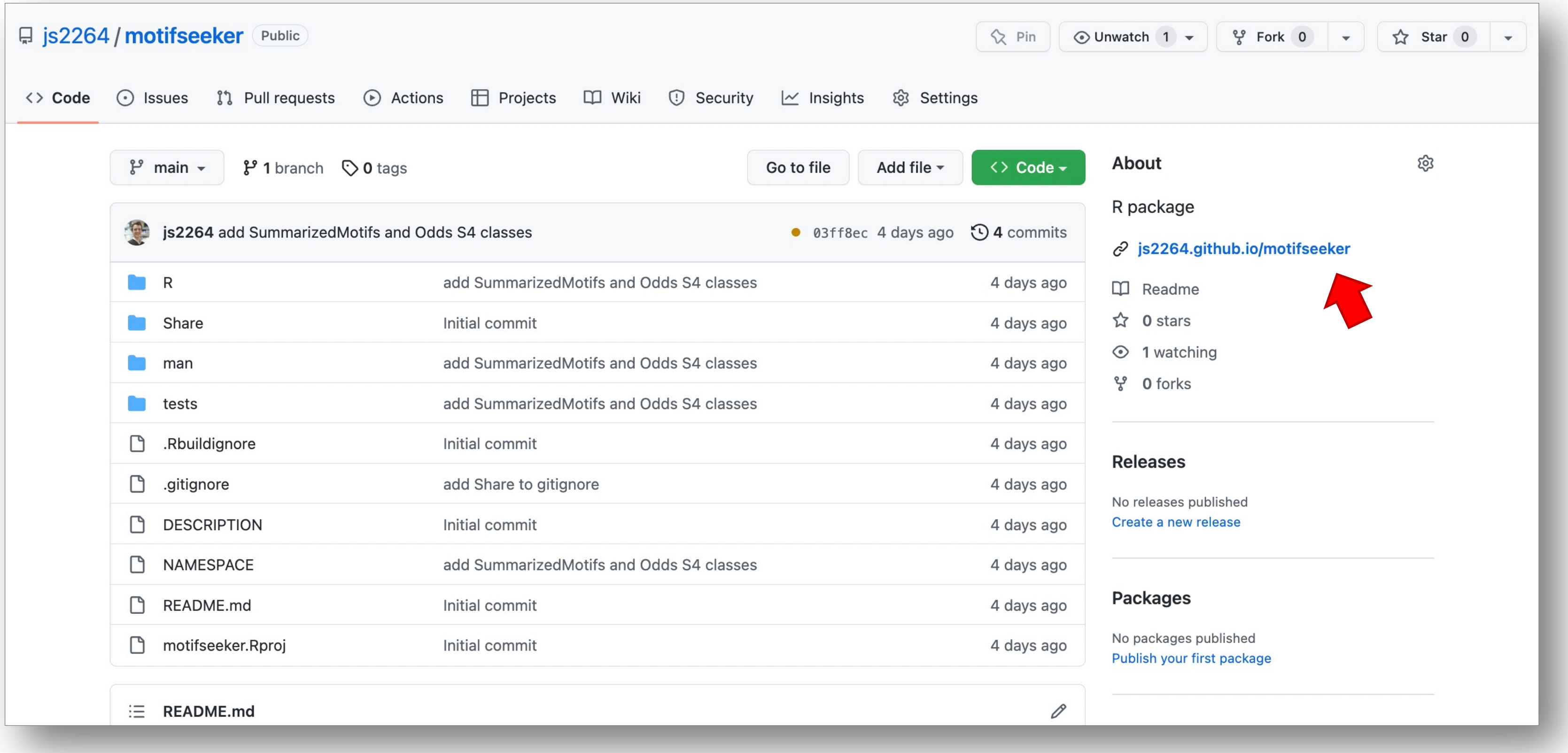

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README.md	Initial commit	4 days ago
motifseeker.Rproj	Initial commit	4 days ago

README.md

About

R package

js2264.github.io/motifseeker

Readme

0 stars

1 watching

0 forks

Releases

No releases published

Create a new release

Packages

No packages published

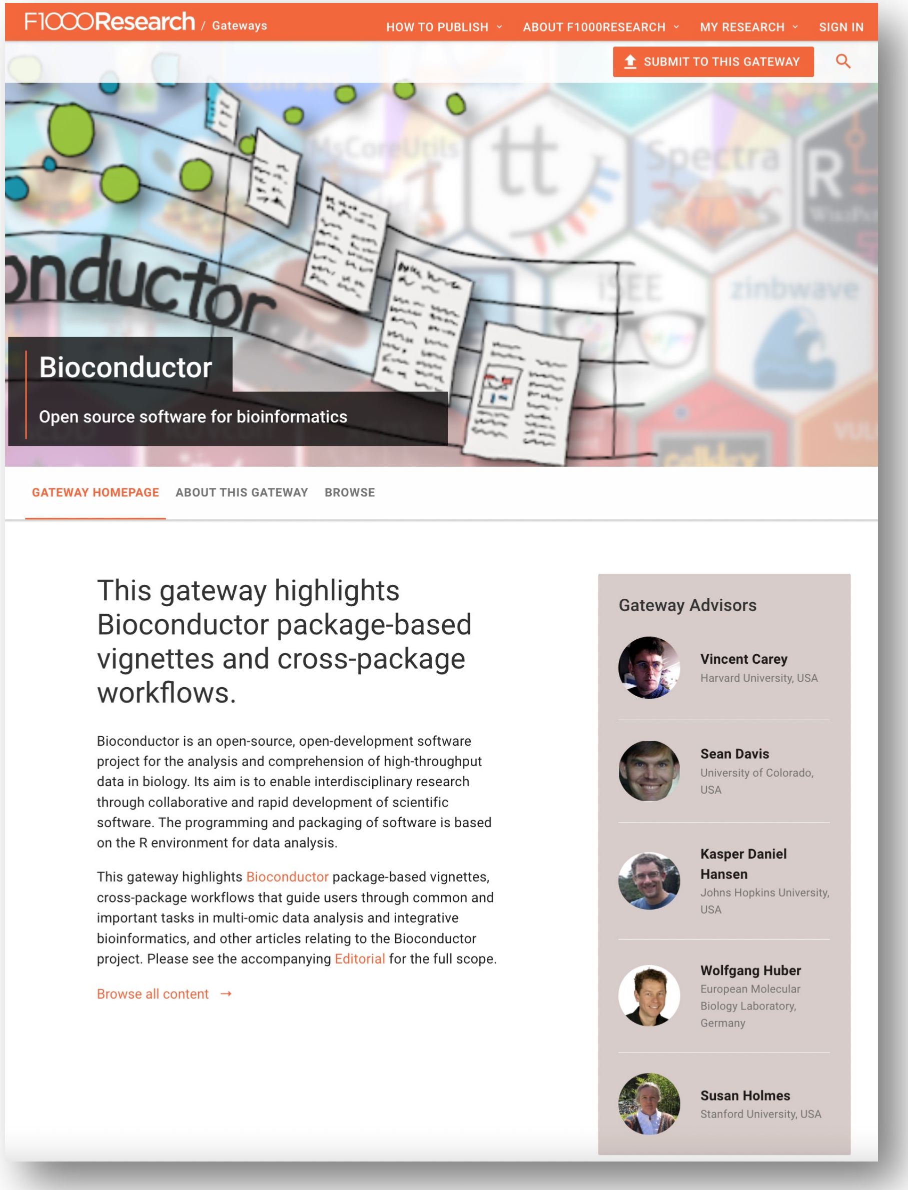
Publish your first package

Disseminating your package

Several journals will consider submission of manuscripts describing package functionalities, e.g.:

- Bioinformatics
- Bioinformatics and Biology Insights
- BMC Bioinformatics
- BMC Systems Biology
- Current Protocols in Bioinformatics
- eLife (Tools and Resources)
- F1000 Research
- Nature Methods
- PeerJ
- PLoS Computational Biology: Software collection

F1000 Research & Bioconductor gateway



Bioconductor

Open source software for bioinformatics

This gateway highlights Bioconductor package-based vignettes and cross-package workflows.

Bioconductor is an open-source, open-development software project for the analysis and comprehension of high-throughput data in biology. Its aim is to enable interdisciplinary research through collaborative and rapid development of scientific software. The programming and packaging of software is based on the R environment for data analysis.

This gateway highlights Bioconductor package-based vignettes, cross-package workflows that guide users through common and important tasks in multi-omic data analysis and integrative bioinformatics, and other articles relating to the Bioconductor project. Please see the accompanying Editorial for the full scope.

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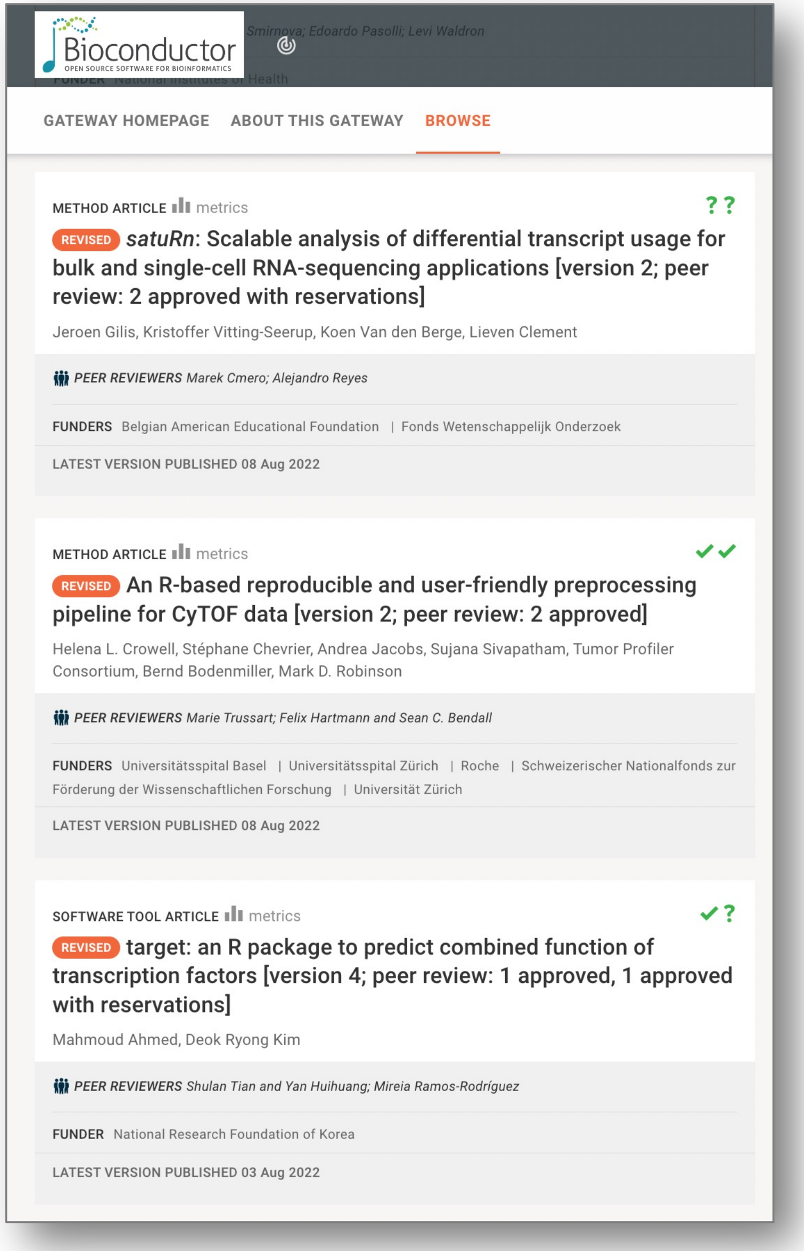


Smirnova; Edoardo Pasolli; Levi Waldron

FUNDER National Institutes of Health

METHOD ARTICLE metrics ? ?

REVISED *satuRn*: Scalable analysis of differential transcript usage for bulk and single-cell RNA-sequencing applications [version 2; peer review: 2 approved with reservations]

Jeroen Gilis, Kristoffer Vitting-Seerup, Koen Van den Berge, Lieven Clement

PEER REVIEWERS Marek Cmero; Alejandro Reyes

FUNDERS Belgian American Educational Foundation | Fonds Wetenschappelijk Onderzoek

LATEST VERSION PUBLISHED 08 Aug 2022

METHOD ARTICLE metrics ✓ ✓

REVISED An R-based reproducible and user-friendly preprocessing pipeline for CyTOF data [version 2; peer review: 2 approved]

Helena L. Crowell, Stéphane Chevrier, Andrea Jacobs, Sujana Sivapatham, Tumor Profiler Consortium, Bernd Bodenmiller, Mark D. Robinson

PEER REVIEWERS Marie Trussart; Felix Hartmann and Sean C. Bendall

FUNDERS Universitätsspital Basel | Universitätsspital Zürich | Roche | Schweizerischer Nationalfonds zur Förderung der Wissenschaftlichen Forschung | Universität Zürich

LATEST VERSION PUBLISHED 08 Aug 2022

SOFTWARE TOOL ARTICLE metrics ✓ ?

REVISED target: an R package to predict combined function of transcription factors [version 4; peer review: 1 approved, 1 approved with reservations]

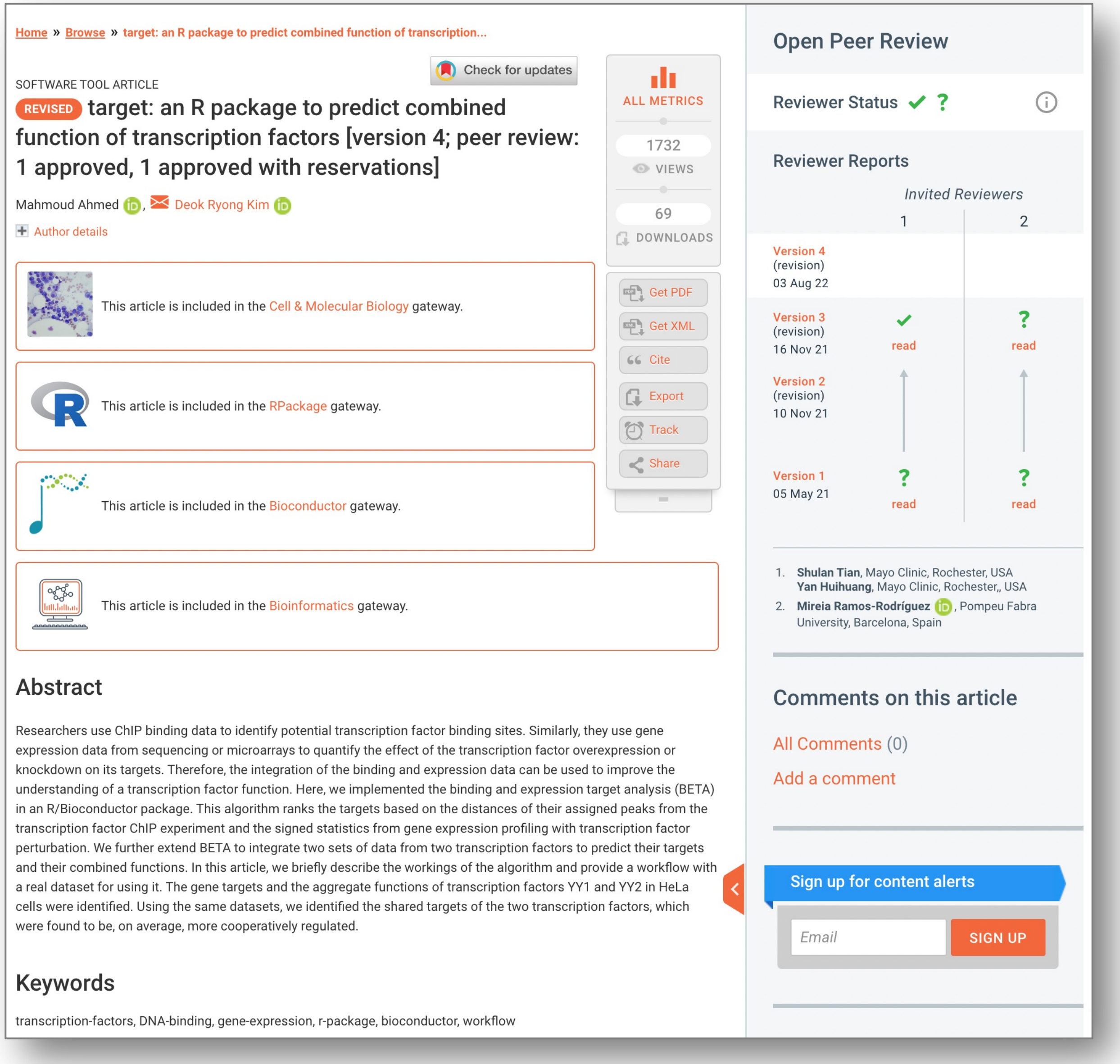
Mahmoud Ahmed, Deok Ryong Kim

PEER REVIEWERS Shulan Tian and Yan Huihuang; Mireia Ramos-Rodríguez

FUNDER National Research Foundation of Korea

LATEST VERSION PUBLISHED 03 Aug 2022

F1000 Research & Bioconductor gateway



SOFTWARE TOOL ARTICLE

REVISED target: an R package to predict combined function of transcription factors [version 4; peer review: 1 approved, 1 approved with reservations]

Mahmoud Ahmed, Deok Ryong Kim

This article is included in the Cell & Molecular Biology gateway.

This article is included in the RPackage gateway.

This article is included in the Bioconductor gateway.

This article is included in the Bioinformatics gateway.

Abstract

Researchers use ChIP binding data to identify potential transcription factor binding sites. Similarly, they use gene expression data from sequencing or microarrays to quantify the effect of the transcription factor overexpression or knockdown on its targets. Therefore, the integration of the binding and expression data can be used to improve the understanding of a transcription factor function. Here, we implemented the binding and expression target analysis (BETA) in an R/Bioconductor package. This algorithm ranks the targets based on the distances of their assigned peaks from the transcription factor ChIP experiment and the signed statistics from gene expression profiling with transcription factor perturbation. We further extend BETA to integrate two sets of data from two transcription factors to predict their targets and their combined functions. In this article, we briefly describe the workings of the algorithm and provide a workflow with a real dataset for using it. The gene targets and the aggregate functions of transcription factors YY1 and YY2 in HeLa cells were identified. Using the same datasets, we identified the shared targets of the two transcription factors, which were found to be, on average, more cooperatively regulated.

Keywords

transcription-factors, DNA-binding, gene-expression, r-package, bioconductor, workflow

Open Peer Review

Reviewer Status ✓ ?

Reviewer Reports

	Invited Reviewers 1	2
Version 4 (revision) 03 Aug 22		
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Version 2 (revision) 10 Nov 21	↑	↑
Version 1 05 May 21	? read	? read

1. **Shulan Tian**, Mayo Clinic, Rochester, USA
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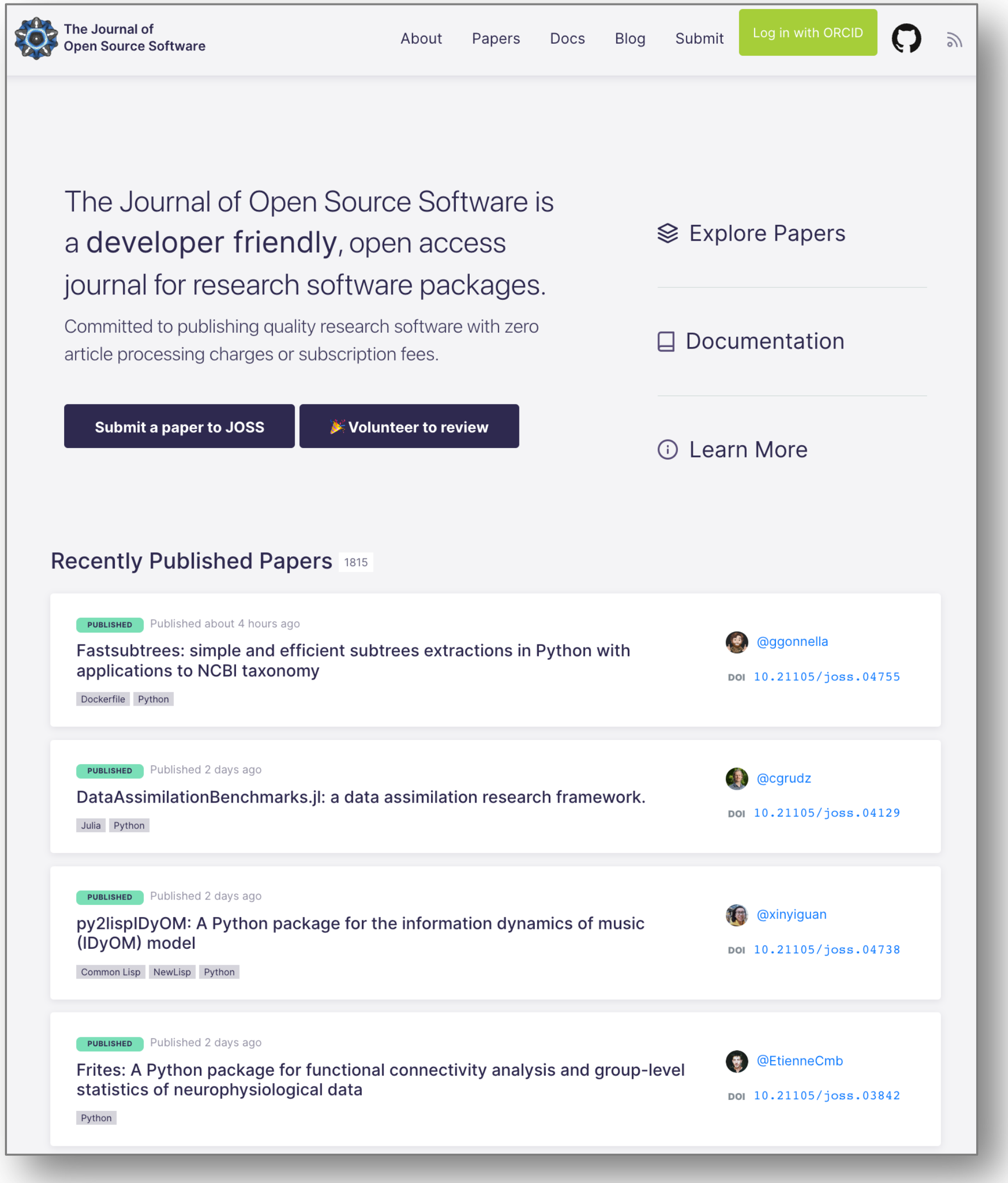

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basilisk: a Bioconductor package for managing Python environments

R Python Submitted 18 August 2022 • Published 04 November 2022

basilisk: a Bioconductor package for managing Python environments

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1 Genentech Inc., South San Francisco, USA

DOI: 10.21105/joss.04742

Software

- Review
- Repository
- Archive

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Submitted: 18 August 2022
Published: 04 November 2022

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Summary

`basilisk` is an R/Bioconductor package for managing Python environments within the Bioconductor package ecosystem. Developers of other Bioconductor packages can use `basilisk` to automatically provision and load custom Python environments, providing a streamlined experience for their end-users by avoiding the need for any manual system configuration. `basilisk` also enables robust execution of Python code via `reticulate` in complex analysis workflows involving multiple Python environments. This package aims to provide a standardized mechanism for integration of Python functionality into the Bioconductor code base.

Statement of need

The Python package ecosystem provides a large number of algorithms and tools that are relevant to R/Bioconductor users. Interoperability between R and Python is facilitated by several popular tools - this includes the `reticulate` package to seamlessly call Python code from an R session (Ushey et al., 2022), and the conda package manager to provision environments with the appropriate Python packages (Anaconda Inc., 2022). However, the configuration and management of the Python instances is typically the responsibility of the end user. R/Bioconductor packages with Python functionality often rely on the user to manually ensure that the correct versions of all Python packages are installed. This is burdensome, error-prone, and does not scale to widespread integration of Python code into the Bioconductor ecosystem. Moreover, `reticulate` only supports one Python environment for each R session. This compromises interoperability between multiple R/Bioconductor packages that have different (and possibly incompatible) Python dependencies. The `basilisk` package aims to automate the management of Python environments required by “client” R/Bioconductor packages, simplifying their installation and enabling their integration into complex analysis workflows.

Usage

A developer of a client package is expected to define one or more `BasiliskEnvironment` objects that describe the Python environments required by the package. I show an small example below from the `snifter` Bioconductor package (O'Callaghan & Lun, 2022):

```
snifter.env <- BasiliskEnvironment(
    "fitsne",
    pkgname = "snifter",
    packages = c(
      "opentsne=0.4.3",
      "scikit-learn=0.23.1",
      if (basilisk.utils::isWindows()) "scipy=1.5.0" else "scipy=1.5.1",
      "numpy=1.19.0",
```

Lun. (2022). basilisk: a Bioconductor package for managing Python environments. *Journal of Open Source Software*, *7*(79), 4742. https://doi.org/10.21105/joss.04742. 1

Review
Editor: @Nikoleta-v3 (all papers)
Reviewers: @jsun (all reviews), @gtonkinhill (all reviews)

Authors
Aaron T. L. Lun (0000-0002-3564-4813)

Citation
Lun, A. T., (2022). basilisk: a Bioconductor package for managing Python environments. Journal of Open Source Software, 7(79), 4742, https://doi.org/10.21105/joss.04742
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basilisk: a Bioconductor package for managing Python environments

R Python Submitted 18 August 2022 • Published 04 November 2022

basilisk: a Bioconductor package for managing Python environments

Aaron T. L. Lun[1]

1 Genentech Inc., South San Francisco, USA

DOI: 10.21105/joss.04742

Software

- Review
- Repository
- Archive

Editor: Nikoleta Glynatsi

Reviewers:

- @jsun
- @gtonkinhill

Submitted: 18 August 2022
Published: 04 November 2022

Summary

`basilisk` is an R/Bioconductor package for managing Python environments within the Bioconductor package ecosystem. Developers of other Bioconductor packages can use `basilisk` to automatically provision and load custom Python environments, providing a streamlined experience for their end-users by avoiding the need for any manual system configuration. `basilisk` also enables robust execution of Python code via `reticulate` in complex analysis workflows involving multiple Python environments. This package aims to provide a standardized mechanism for integration of Python functionality into the Bioconductor code base.

Statement of need

The Python package ecosystem provides a large number of algorithms and tools that are relevant to R/Bioconductor users. Interoperability between R and Python is facilitated by several popular tools - this includes the `reticulate` package to seamlessly call Python code from an R session (Ushey et al., 2022), and the conda package manager to provision environments with the appropriate Python packages (Anaconda Inc., 2022). However, the configuration and management of the Python instances is typically the responsibility of the end user. R/Bioconductor packages with Python functionality often rely on the user to manually ensure that the correct versions of all Python packages are installed. This is burdensome, error-prone, and does not scale to widespread integration of Python code into the Bioconductor ecosystem. Moreover, `reticulate` only supports one Python environment for each R session. This compromises interoperability between multiple R/Bioconductor packages that have different (and possibly incompatible) Python dependencies. The `basilisk` package aims to automate the management of Python environments required by “client” R/Bioconductor packages, simplifying their installation and enabling their integration into complex analysis workflows.

Usage

A developer of a client package is expected to define one or more `BasiliskEnvironment` objects that describe the Python environments required by the package. I show an small example below from the `snifter` Bioconductor package (O’Callaghan & Lun, 2022):

```
snifter.env <- BasiliskEnvironment(
    ”fitsne”,
    pkgname = ”snifter”,
    packages = c(
      ”opentsne=0.4.3”,
      ”scikit-learn=0.23.1”,
      if (basilisk.utils::isWindows()) ”scipy=1.5.0” else ”scipy=1.5.1”,
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```

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Submitted 18 August 2022 • Published 04 November 2022

The Journal of Open Source Software

basilisk: a Bioconductor package for managing Python environments

Aaron T. L. Lun[1]

1 Genentech Inc., South San Francisco, USA

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Software

- Review
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Editor: Nikoleta Glynatsi

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Submitted: 18 August 2022
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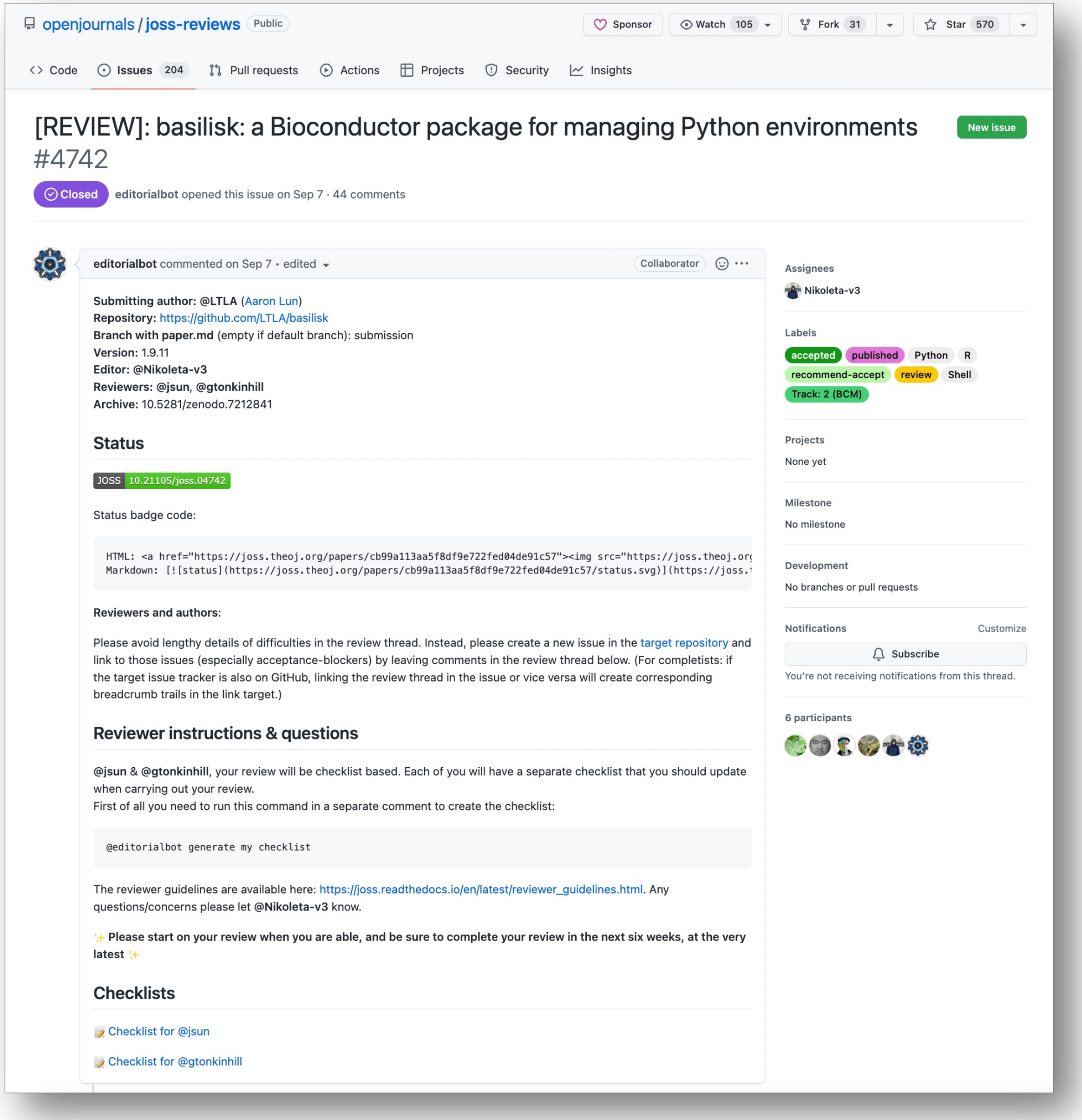

[REVIEW]: basilisk: a Bioconductor package for managing Python environments #4742

editorialbot opened this issue on Sep 7 · 44 comments

editorialbot commented on Sep 7 • edited

Submitting author: @LTLA (Aaron Lun)
Repository: https://github.com/LTLA/basilisk
Branch with paper.md (empty if default branch): submission
Version: 1.9.11
Editor: @Nikoleta-v3
Reviewers: @jsun, @gtonkinhill
Archive: 10.5281/zenodo.7212841

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📝 Checklist for @jsun

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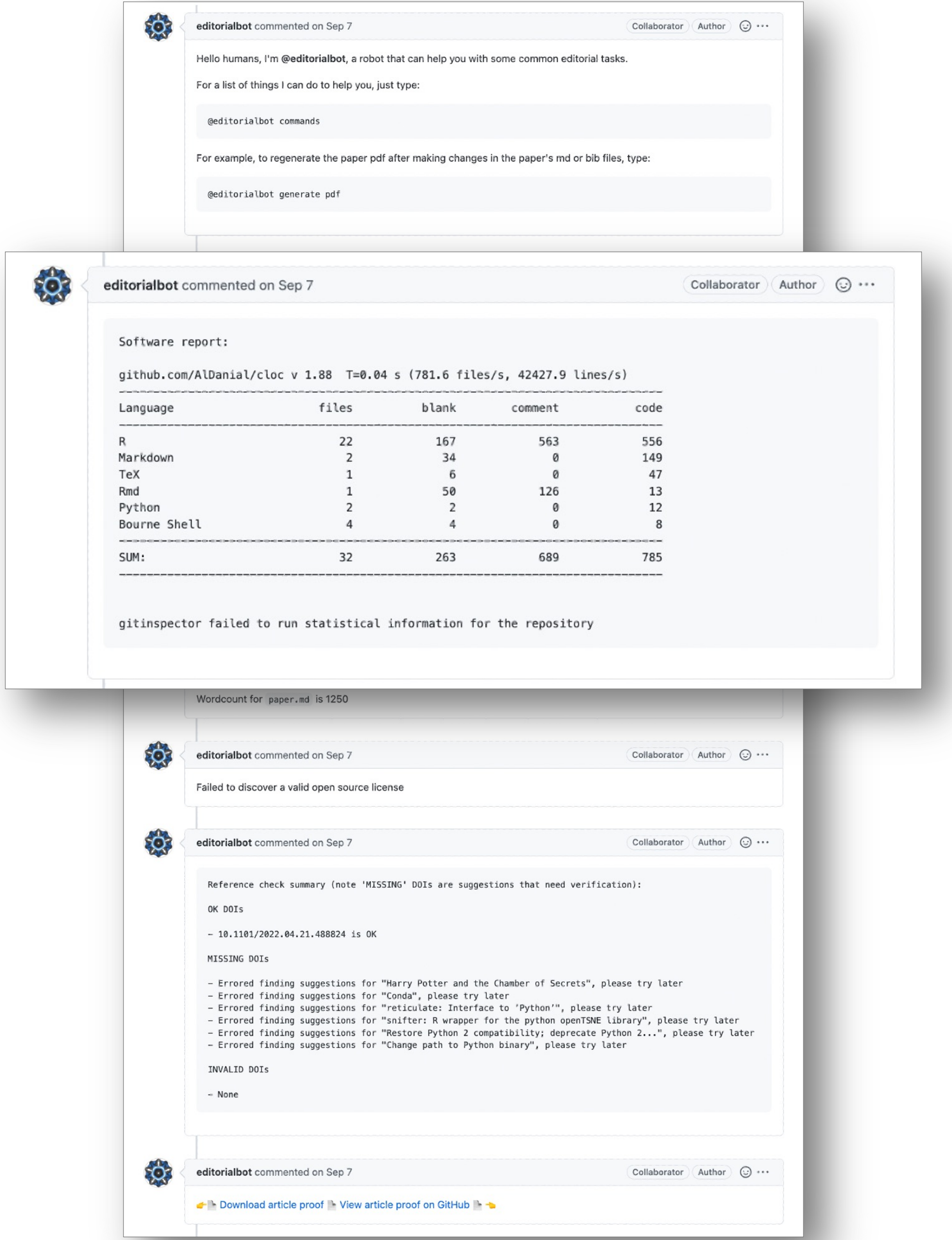

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-------------------------------------------------------------------------------
Language                     files          blank        comment           code
-------------------------------------------------------------------------------
R                               22            167            563            556
Markdown                         2             34              0            149
TeX                              1              6              0             47
Rmd                              1             50            126             13
Python                           2              2              0             12
Bourne Shell                     4              4              0              8
-------------------------------------------------------------------------------
SUM:                            32            263            689            785
-------------------------------------------------------------------------------


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- Errored finding suggestions for "reticulate: Interface to 'Python'", please try later
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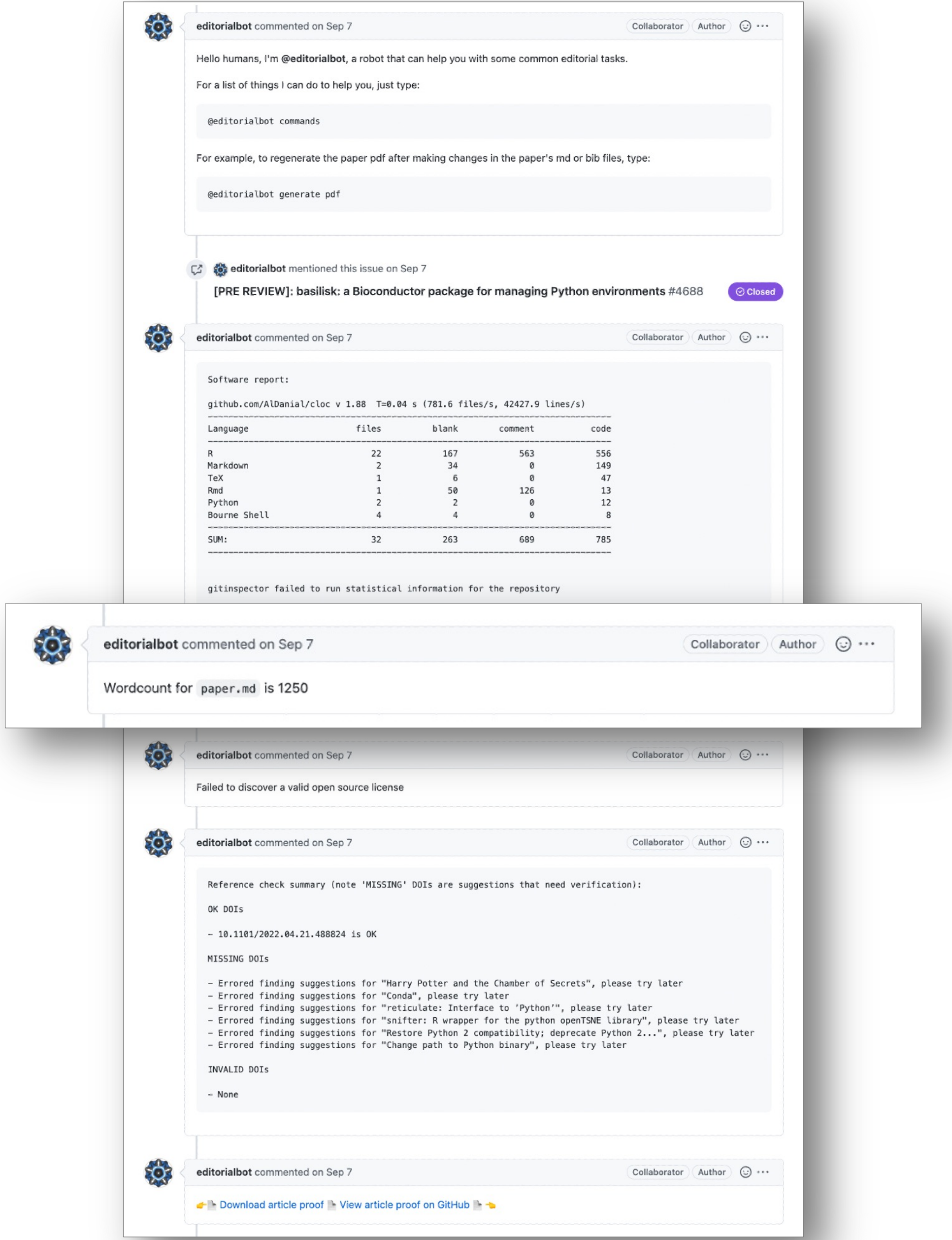

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[PRE REVIEW]: basilisk: a Bioconductor package for managing Python environments #4688

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-------------------------------------------------------------------------------
Language                     files          blank        comment           code
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R                               22            167            563            556
Markdown                         2             34              0            149
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Bourne Shell                     4              4              0              8
-------------------------------------------------------------------------------
SUM:                            32            263            689            785
-------------------------------------------------------------------------------


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- Errored finding suggestions for "Change path to Python binary", please try later

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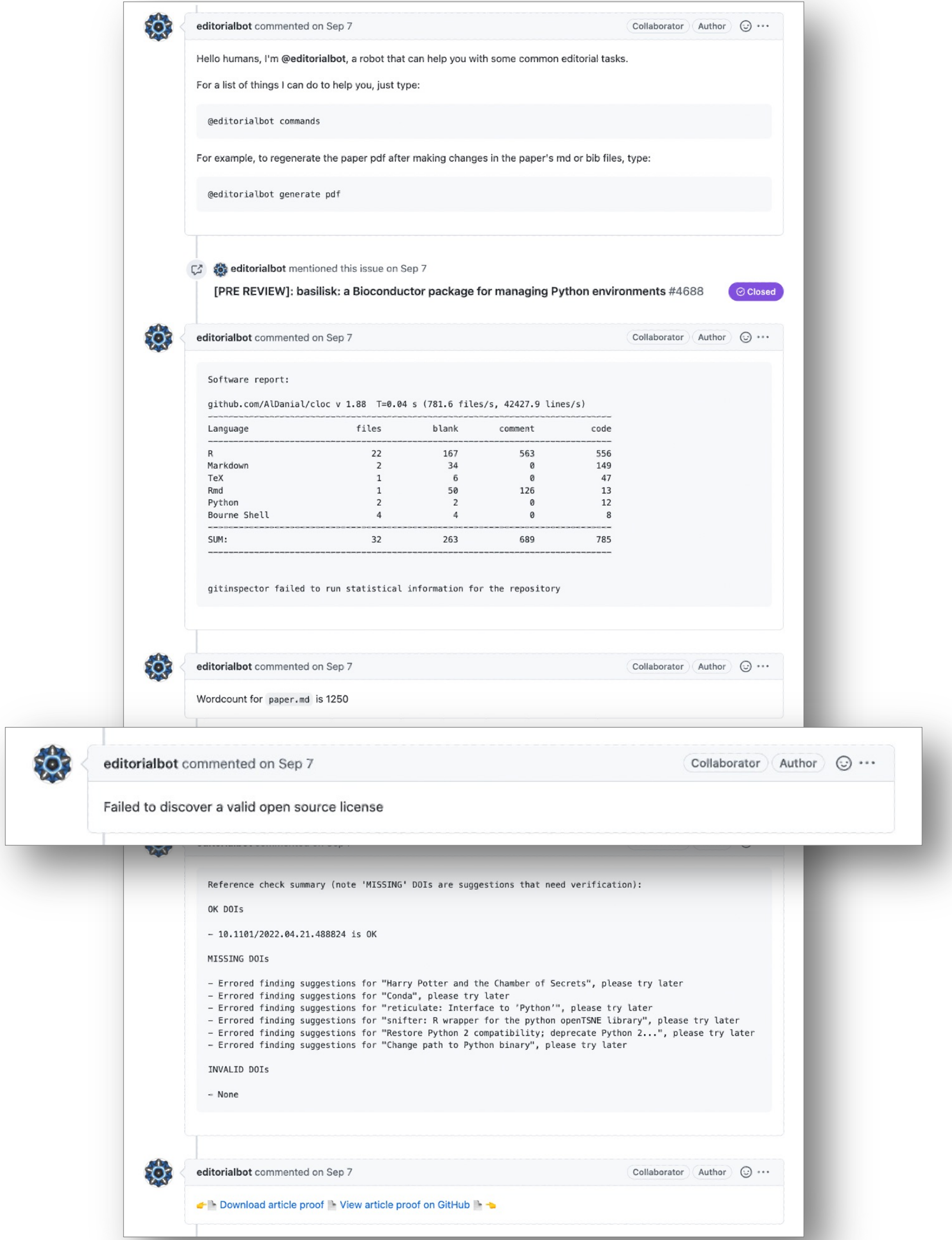

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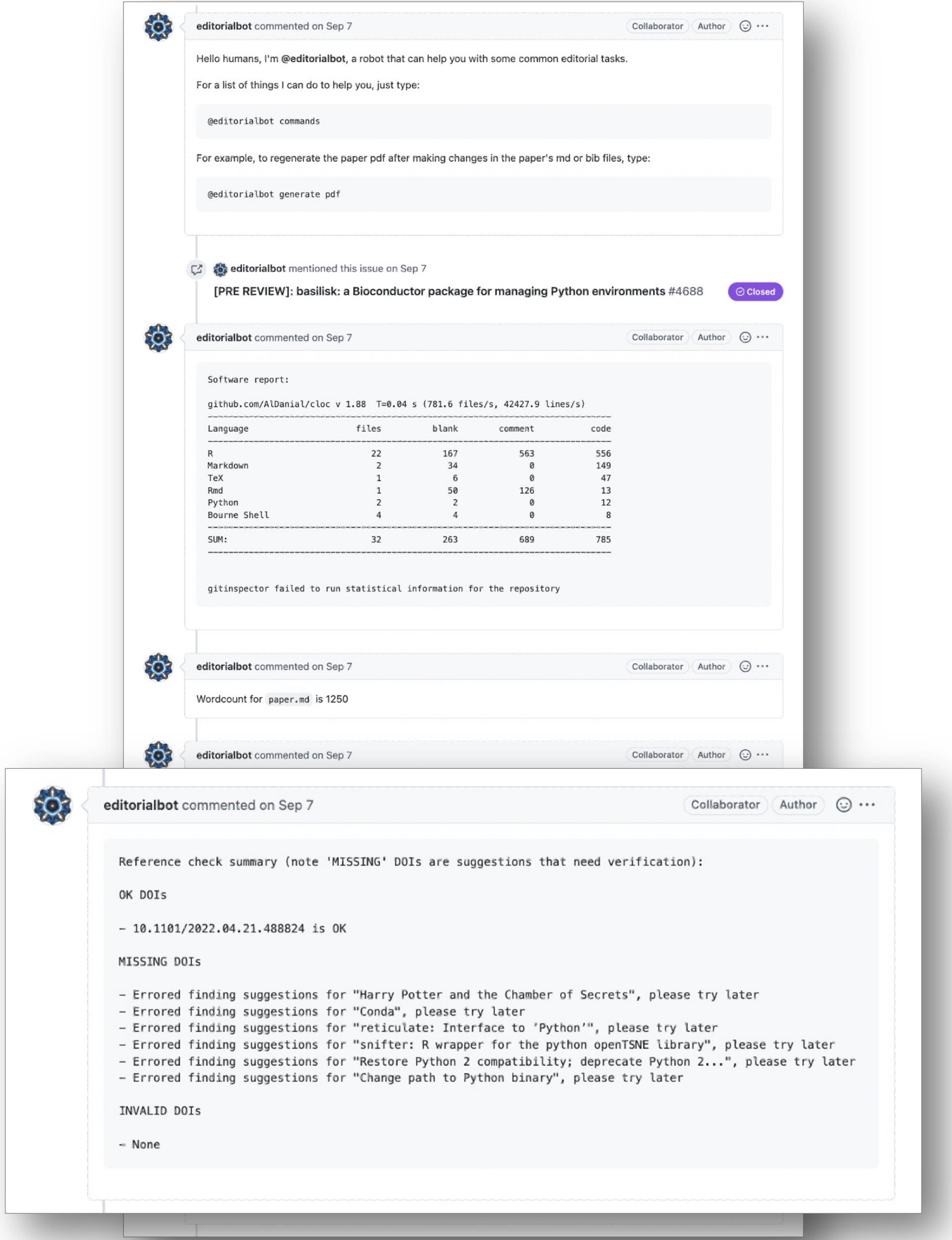

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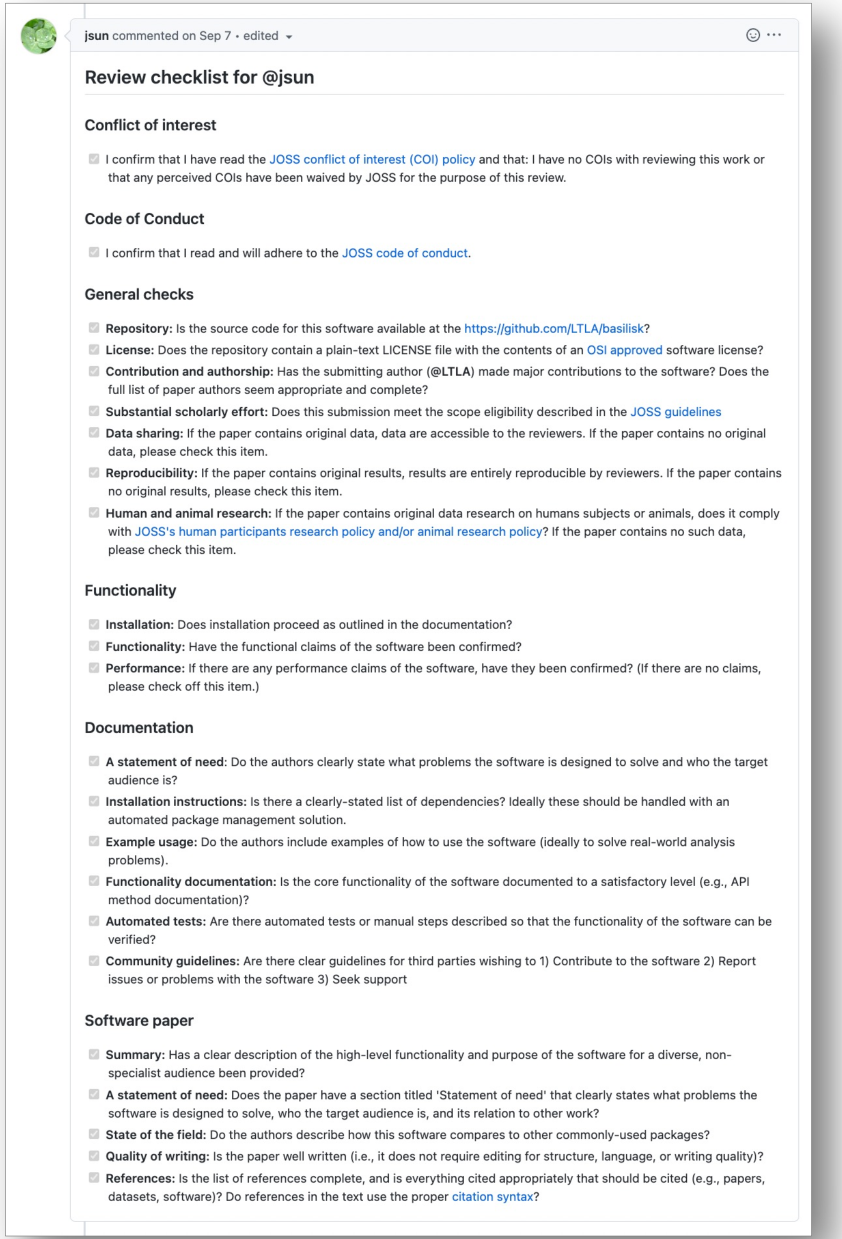

jsun commented on Sep 7 • edited

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- ☑ **Repository:** Is the source code for this software available at the https://github.com/LTLA/basilisk?
- ☑ **License:** Does the repository contain a plain-text LICENSE file with the contents of an OSI approved software license?
- ☑ **Contribution and authorship:** Has the submitting author (@LTLA) made major contributions to the software? Does the full list of paper authors seem appropriate and complete?
- ☑ **Substantial scholarly effort:** Does this submission meet the scope eligibility described in the JOSS guidelines
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- ☑ **Functionality:** Have the functional claims of the software been confirmed?
- ☑ **Performance:** If there are any performance claims of the software, have they been confirmed? (If there are no claims, please check off this item.)

Documentation

- ☑ **A statement of need:** Do the authors clearly state what problems the software is designed to solve and who the target audience is?
- ☑ **Installation instructions:** Is there a clearly-stated list of dependencies? Ideally these should be handled with an automated package management solution.
- ☑ **Example usage:** Do the authors include examples of how to use the software (ideally to solve real-world analysis problems).
- ☑ **Functionality documentation:** Is the core functionality of the software documented to a satisfactory level (e.g., API method documentation)?
- ☑ **Automated tests:** Are there automated tests or manual steps described so that the functionality of the software can be verified?
- ☑ **Community guidelines:** Are there clear guidelines for third parties wishing to 1) Contribute to the software 2) Report issues or problems with the software 3) Seek support

Software paper

- ☑ **Summary:** Has a clear description of the high-level functionality and purpose of the software for a diverse, non-specialist audience been provided?
- ☑ **A statement of need:** Does the paper have a section titled 'Statement of need' that clearly states what problems the software is designed to solve, who the target audience is, and its relation to other work?
- ☑ **State of the field:** Do the authors describe how this software compares to other commonly-used packages?
- ☑ **Quality of writing:** Is the paper well written (i.e., it does not require editing for structure, language, or writing quality)?
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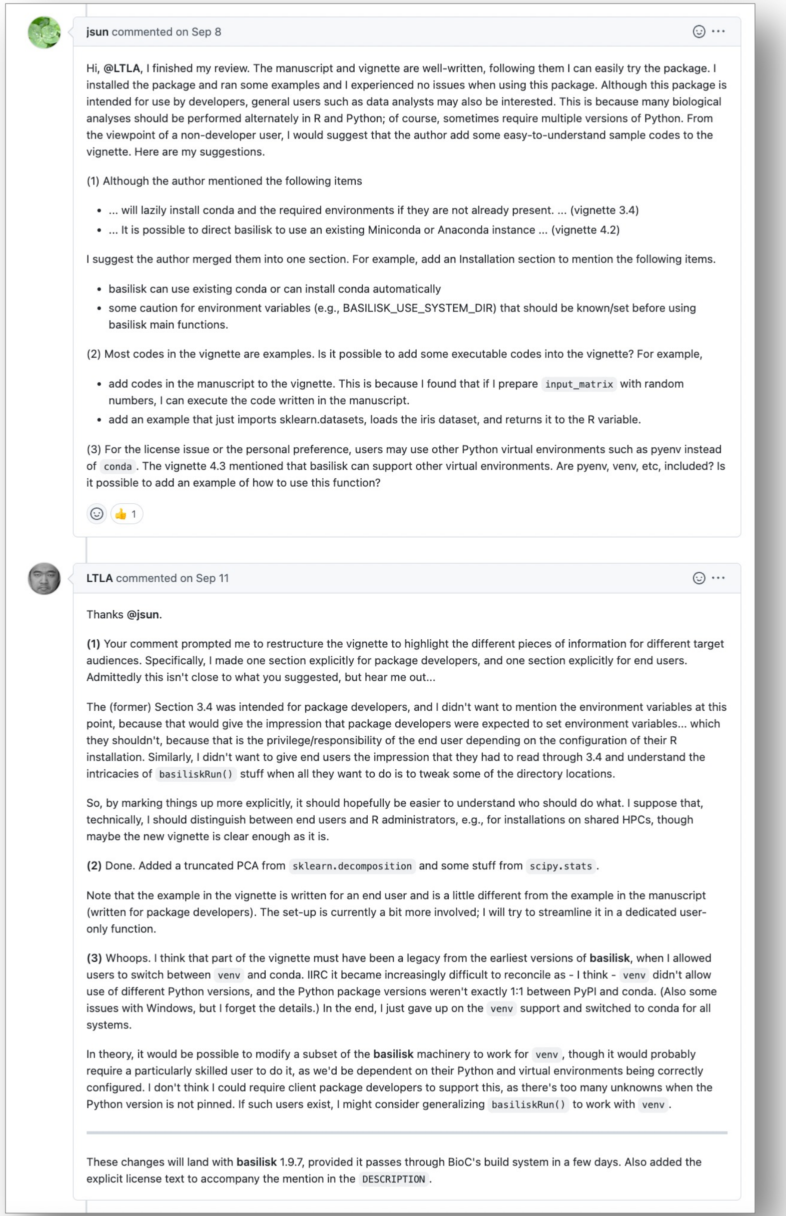

jsun commented on Sep 8

Hi, **@LTLA**, I finished my review. The manuscript and vignette are well-written, following them I can easily try the package. I installed the package and ran some examples and I experienced no issues when using this package. Although this package is intended for use by developers, general users such as data analysts may also be interested. This is because many biological analyses should be performed alternately in R and Python; of course, sometimes require multiple versions of Python. From the viewpoint of a non-developer user, I would suggest that the author add some easy-to-understand sample codes to the vignette. Here are my suggestions.

(1) Although the author mentioned the following items

- ... will lazily install conda and the required environments if they are not already present. ... (vignette 3.4)
- ... It is possible to direct basilisk to use an existing Miniconda or Anaconda instance ... (vignette 4.2)

I suggest the author merged them into one section. For example, add an Installation section to mention the following items.

- basilisk can use existing conda or can install conda automatically
- some caution for environment variables (e.g., BASILISK_USE_SYSTEM_DIR) that should be known/set before using basilisk main functions.

(2) Most codes in the vignette are examples. Is it possible to add some executable codes into the vignette? For example,

- add codes in the manuscript to the vignette. This is because I found that if I prepare `input_matrix` with random numbers, I can execute the code written in the manuscript.
- add an example that just imports sklearn.datasets, loads the iris dataset, and returns it to the R variable.

(3) For the license issue or the personal preference, users may use other Python virtual environments such as pyenv instead of `conda`. The vignette 4.3 mentioned that basilisk can support other virtual environments. Are pyenv, venv, etc, included? Is it possible to add an example of how to use this function?

👍 1

LTLA commented on Sep 11

Thanks **@jsun**.

(1) Your comment prompted me to restructure the vignette to highlight the different pieces of information for different target audiences. Specifically, I made one section explicitly for package developers, and one section explicitly for end users. Admittedly this isn't close to what you suggested, but hear me out...

The (former) Section 3.4 was intended for package developers, and I didn't want to mention the environment variables at this point, because that would give the impression that package developers were expected to set environment variables... which they shouldn't, because that is the privilege/responsibility of the end user depending on the configuration of their R installation. Similarly, I didn't want to give end users the impression that they had to read through 3.4 and understand the intricacies of `basiliskRun()` stuff when all they want to do is to tweak some of the directory locations.

So, by marking things up more explicitly, it should hopefully be easier to understand who should do what. I suppose that, technically, I should distinguish between end users and R administrators, e.g., for installations on shared HPCs, though maybe the new vignette is clear enough as it is.

(2) Done. Added a truncated PCA from `sklearn.decomposition` and some stuff from `scipy.stats`.

Note that the example in the vignette is written for an end user and is a little different from the example in the manuscript (written for package developers). The set-up is currently a bit more involved; I will try to streamline it in a dedicated user-only function.

(3) Whoops. I think that part of the vignette must have been a legacy from the earliest versions of **basilisk**, when I allowed users to switch between `venv` and conda. IIRC it became increasingly difficult to reconcile as - I think - `venv` didn't allow use of different Python versions, and the Python package versions weren't exactly 1:1 between PyPI and conda. (Also some issues with Windows, but I forget the details.) In the end, I just gave up on the `venv` support and switched to conda for all systems.

In theory, it would be possible to modify a subset of the **basilisk** machinery to work for `venv`, though it would probably require a particularly skilled user to do it, as we'd be dependent on their Python and virtual environments being correctly configured. I don't think I could require client package developers to support this, as there's too many unknowns when the Python version is not pinned. If such users exist, I might consider generalizing `basiliskRun()` to work with `venv`.

These changes will land with **basilisk** 1.9.7, provided it passes through BioC's build system in a few days. Also added the explicit license text to accompany the mention in the `DESCRIPTION`.

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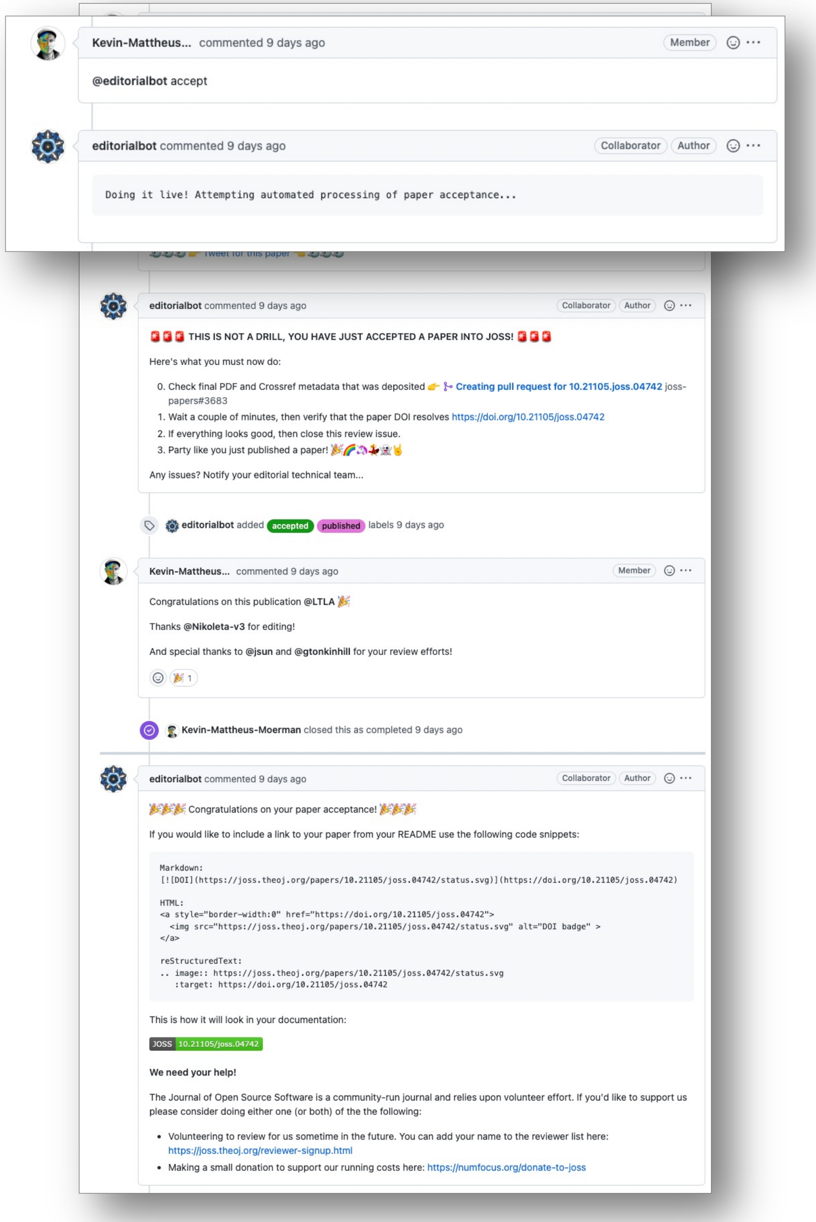

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Thanks **@Nikoleta-v3** for editing!

And special thanks to **@jsun** and **@gtonkinhill** for your review efforts!

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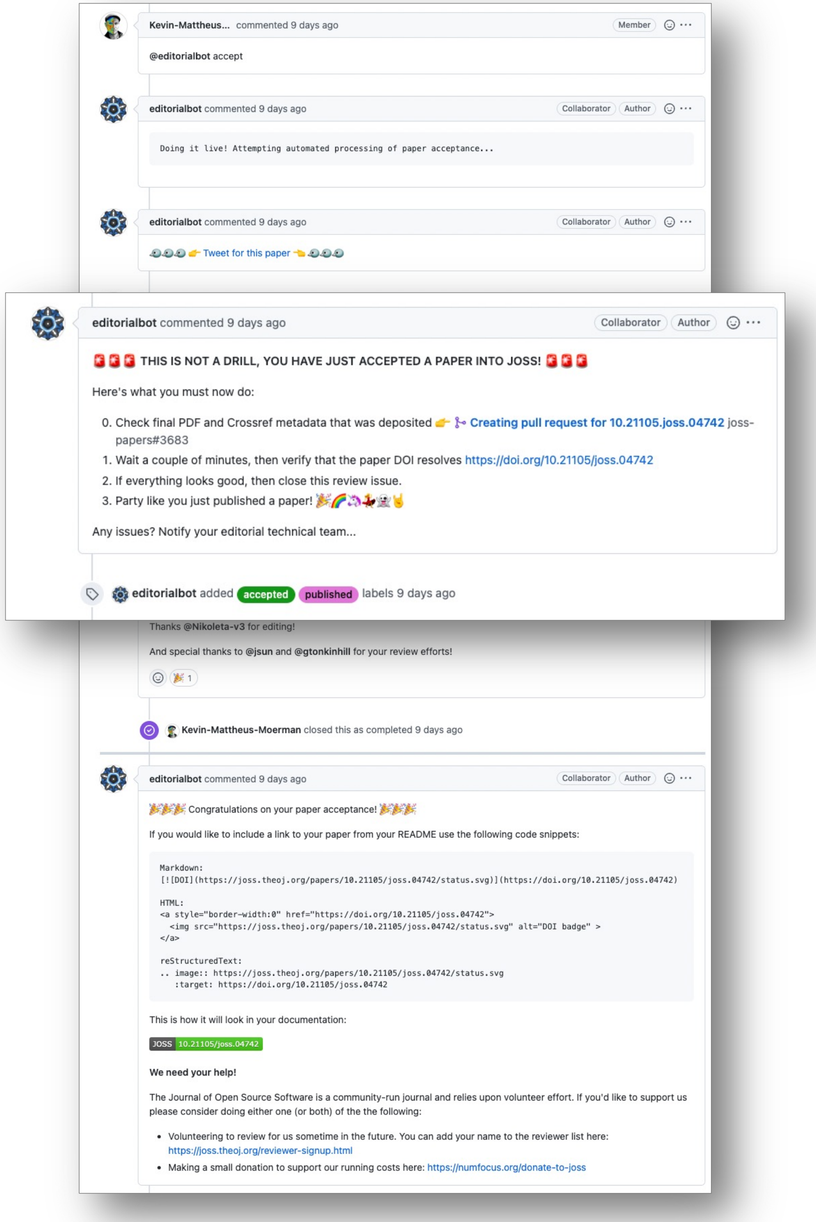

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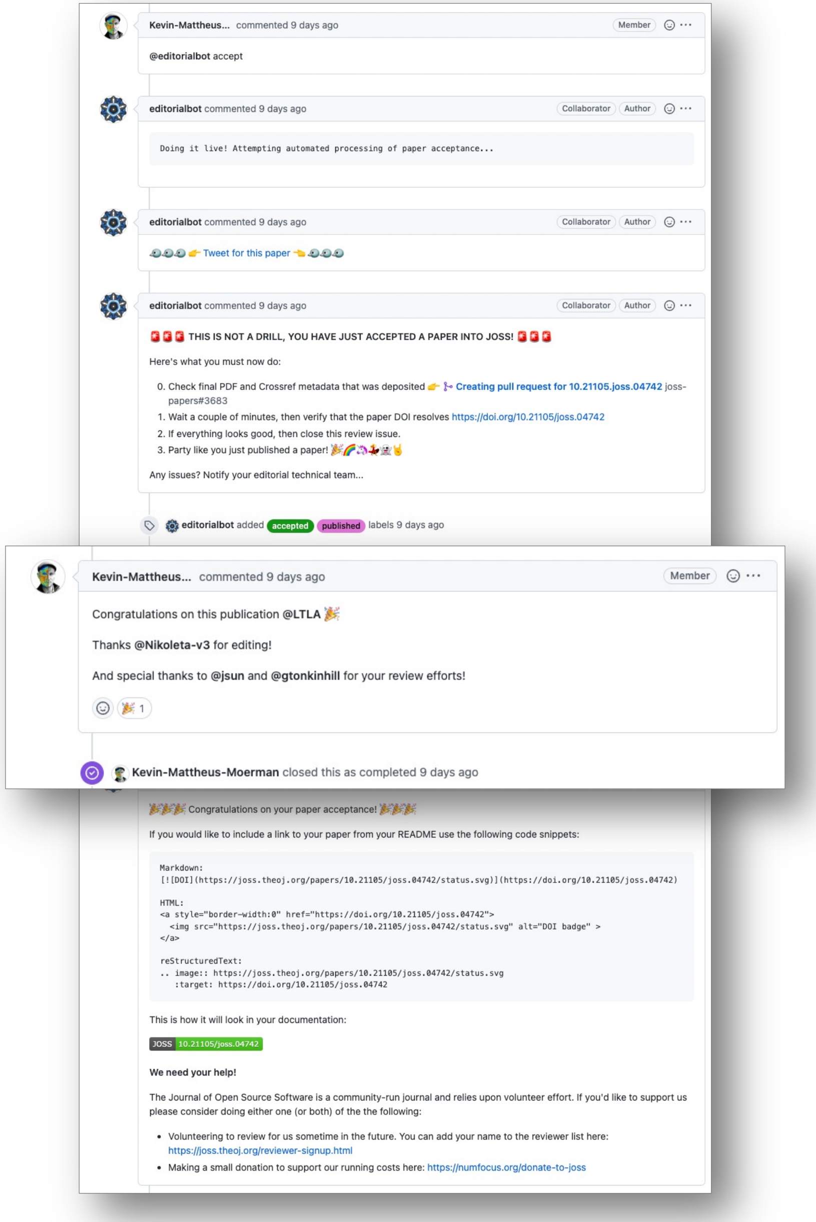

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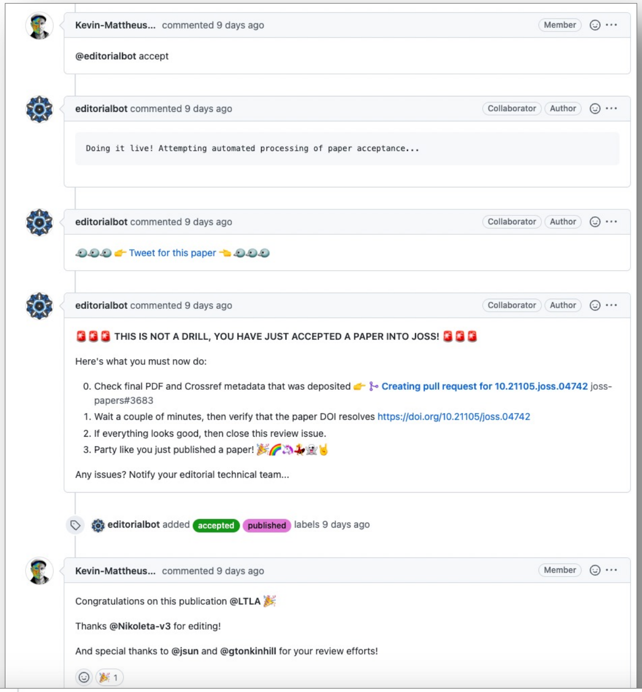

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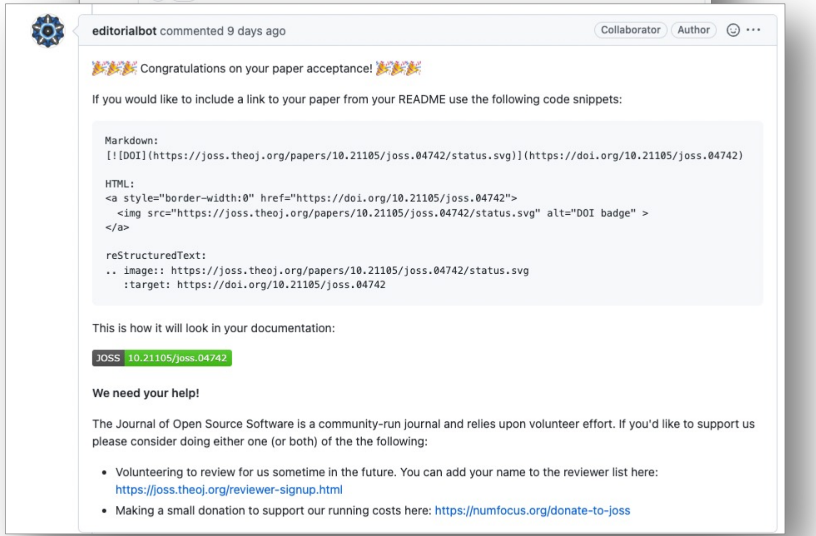

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