Bioconductor submission

Physalia course 2023

Instructor: Jacques Serizay

Standard package submission process

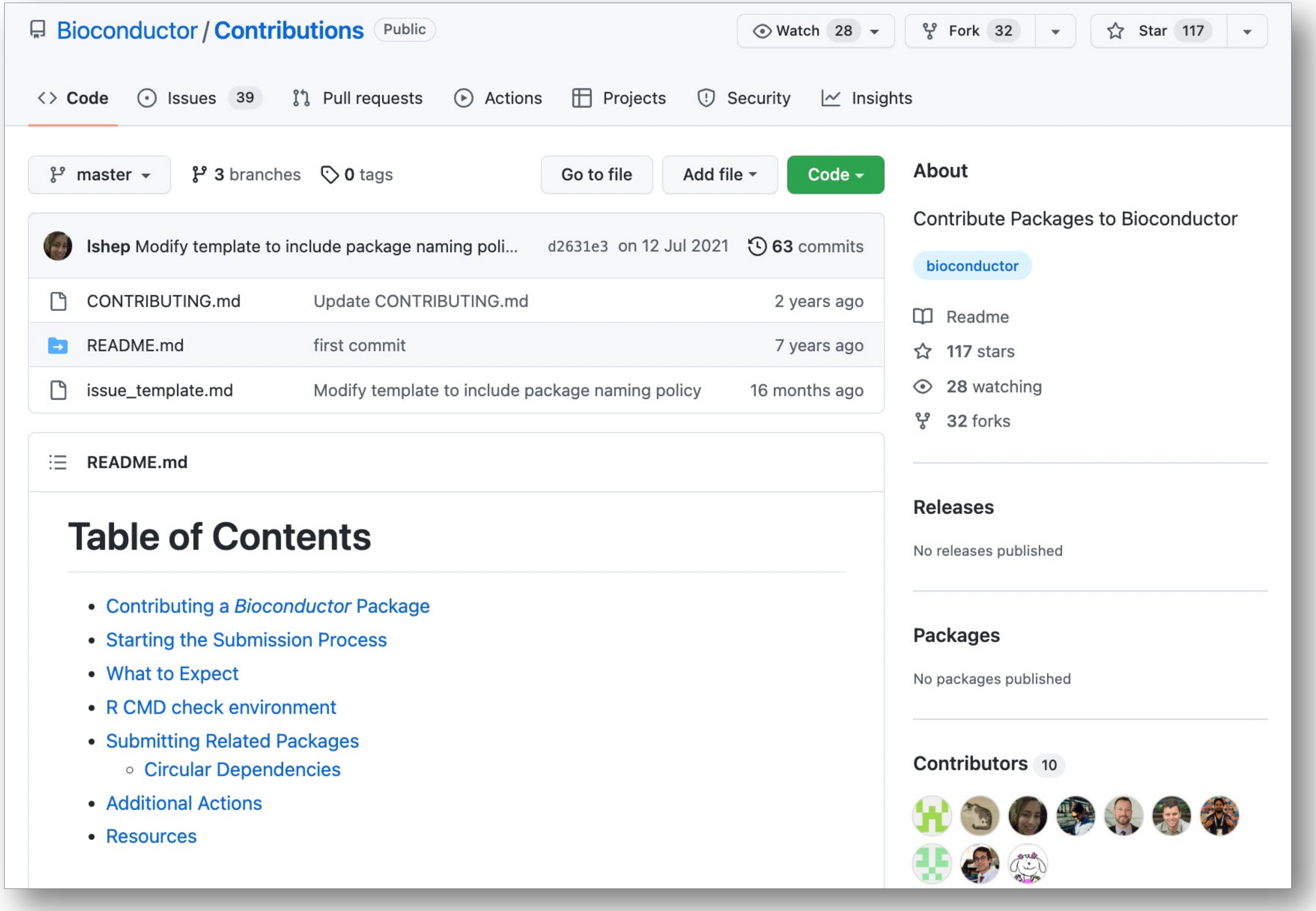
This is the main page (I recommend) to get information regarding submission process:

→ https://contributions.bioconductor.org/bioconductor-package-submissions.html

TL;DR:

→ https://github.com/Bioconductor/Contributions

Standard package submission process



lshep Modify template to include package naming poli... d2631e3 on 12 Jul 2021 63 commits

CONTRIBUTING.md	Update CONTRIBUTING.md	2 years ago
README.md	first commit	7 years ago
issue_template.md	Modify template to include package naming policy	16 months ago

README.md

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- Contributing a *Bioconductor* Package
- Starting the Submission Process
- What to Expect
- R CMD check environment
- Submitting Related Packages
  - Circular Dependencies
- Additional Actions
- Resources

About

Contribute Packages to Bioconductor

Releases

No releases published

Packages

No packages published

Contributors 10

Standard package submission process

0. Make sure your package works fine

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0d. Make sure your package works fine `Github Actions`

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  - Version number? **HAS TO BE 0.99.0**
  - Your SSH key?

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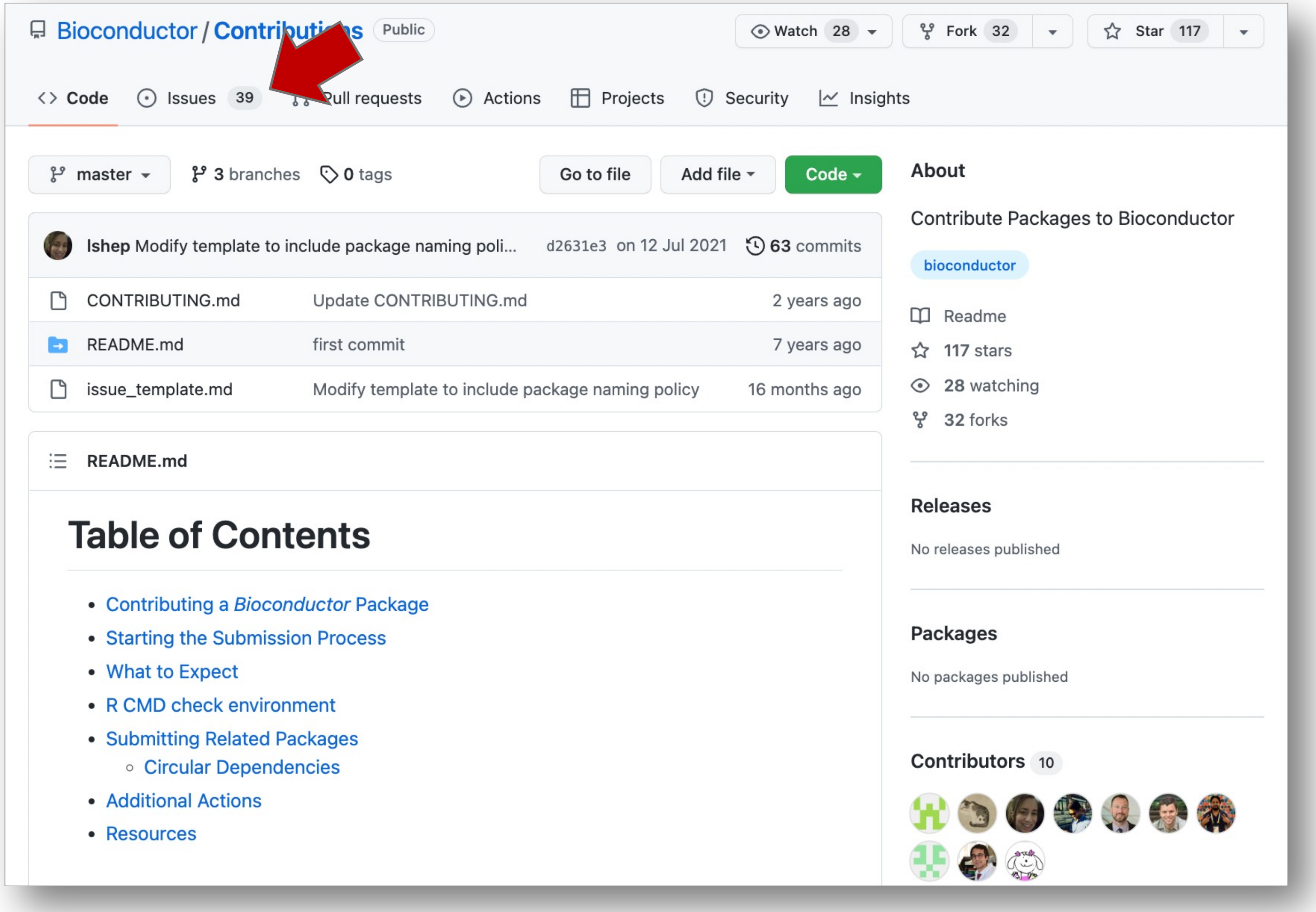
And then…

Submitting initial issue to Bioconductor

1. Submit an **issue** to [Bioconductor/Contributions](https://github.com/Bioconductor/Contributions)



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bioconductor

Readme
117 stars
28 watching
32 forks

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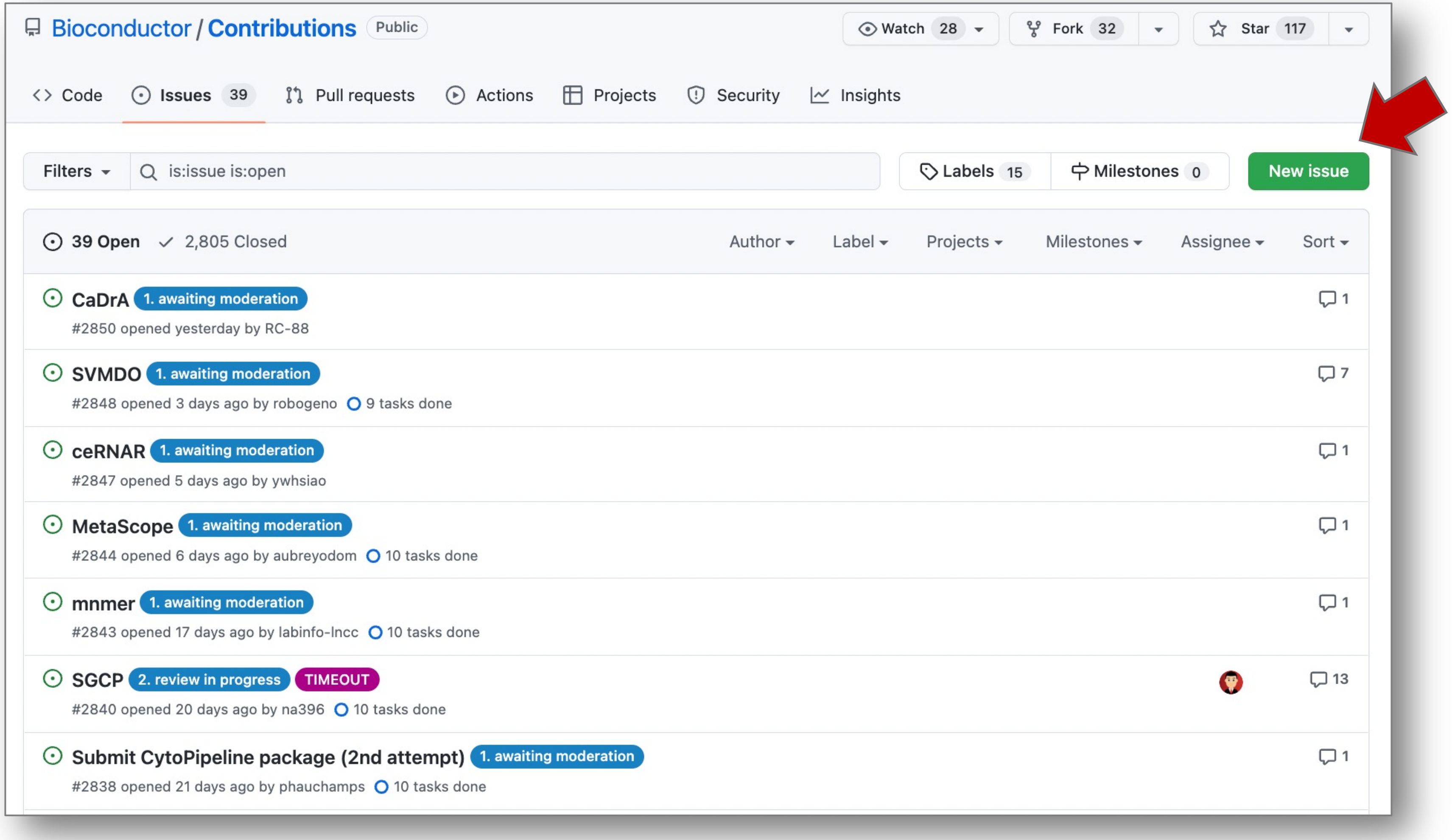

Bioconductor / Contributions Public

Watch 28 · Fork 32 · Star 117

Code · Issues 39 · Pull requests · Actions · Projects · Security · Insights

Filters · is:issue is:open · Labels 15 · Milestones 0 · New issue

39 Open · ✓ 2,805 Closed · Author · Label · Projects · Milestones · Assignee · Sort

- CaDrA `1. awaiting moderation` — #2850 opened yesterday by RC-88 — 1
- SVMDO `1. awaiting moderation` — #2848 opened 3 days ago by robogeno ○ 9 tasks done — 7
- ceRNAR `1. awaiting moderation` — #2847 opened 5 days ago by ywhsiao — 1
- MetaScope `1. awaiting moderation` — #2844 opened 6 days ago by aubreyodom ○ 10 tasks done — 1
- mnmer `1. awaiting moderation` — #2843 opened 17 days ago by labinfo-lncc ○ 10 tasks done — 1
- SGCP `2. review in progress` `TIMEOUT` — #2840 opened 20 days ago by na396 ○ 10 tasks done — 13
- Submit CytoPipeline package (2nd attempt) `1. awaiting moderation` — #2838 opened 21 days ago by phauchamps ○ 10 tasks done — 1

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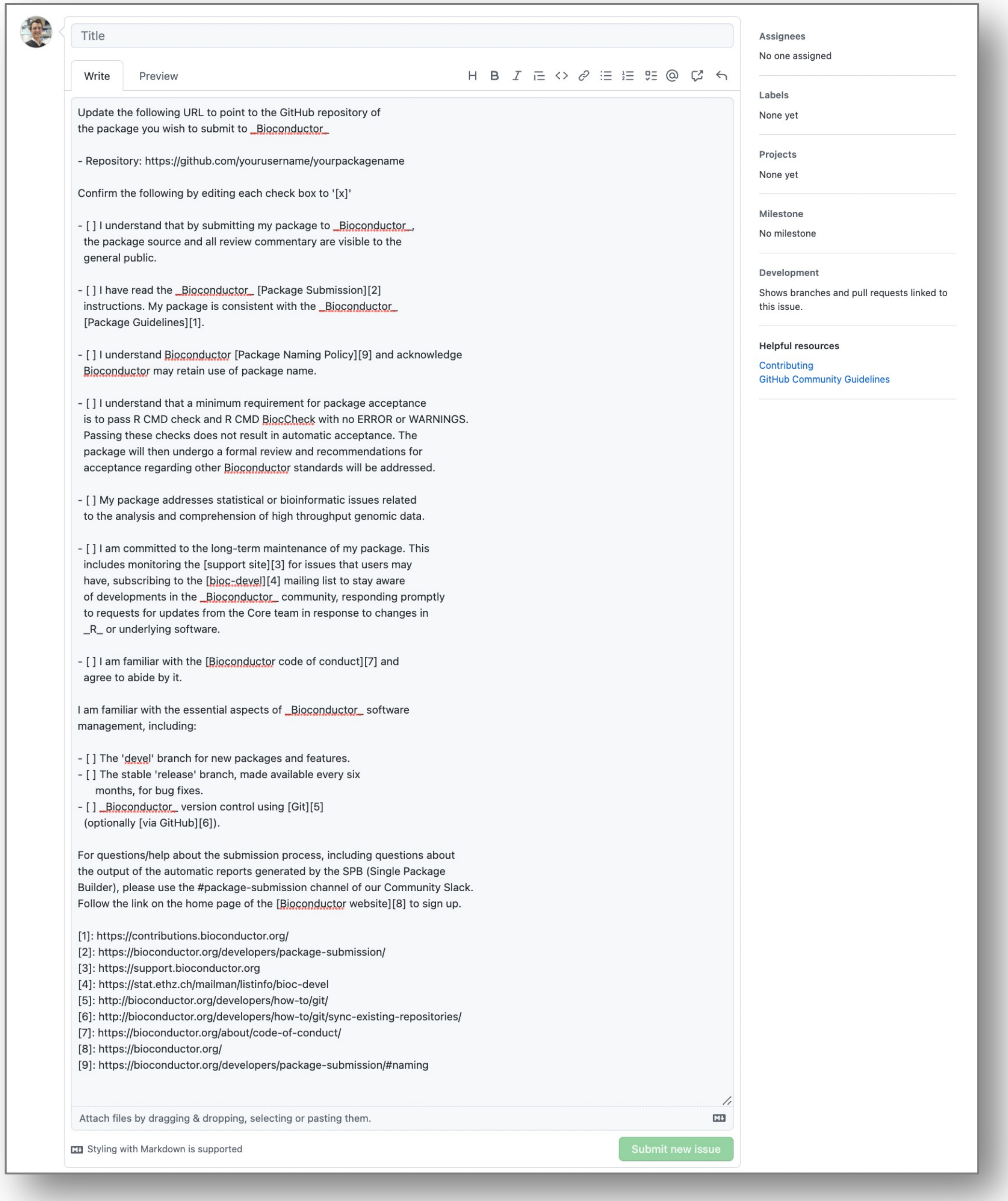

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Assignees
No one assigned

Labels
None yet

Projects
None yet

Milestone
No milestone

Development
Shows branches and pull requests linked to this issue.

Helpful resources
Contributing
GitHub Community Guidelines

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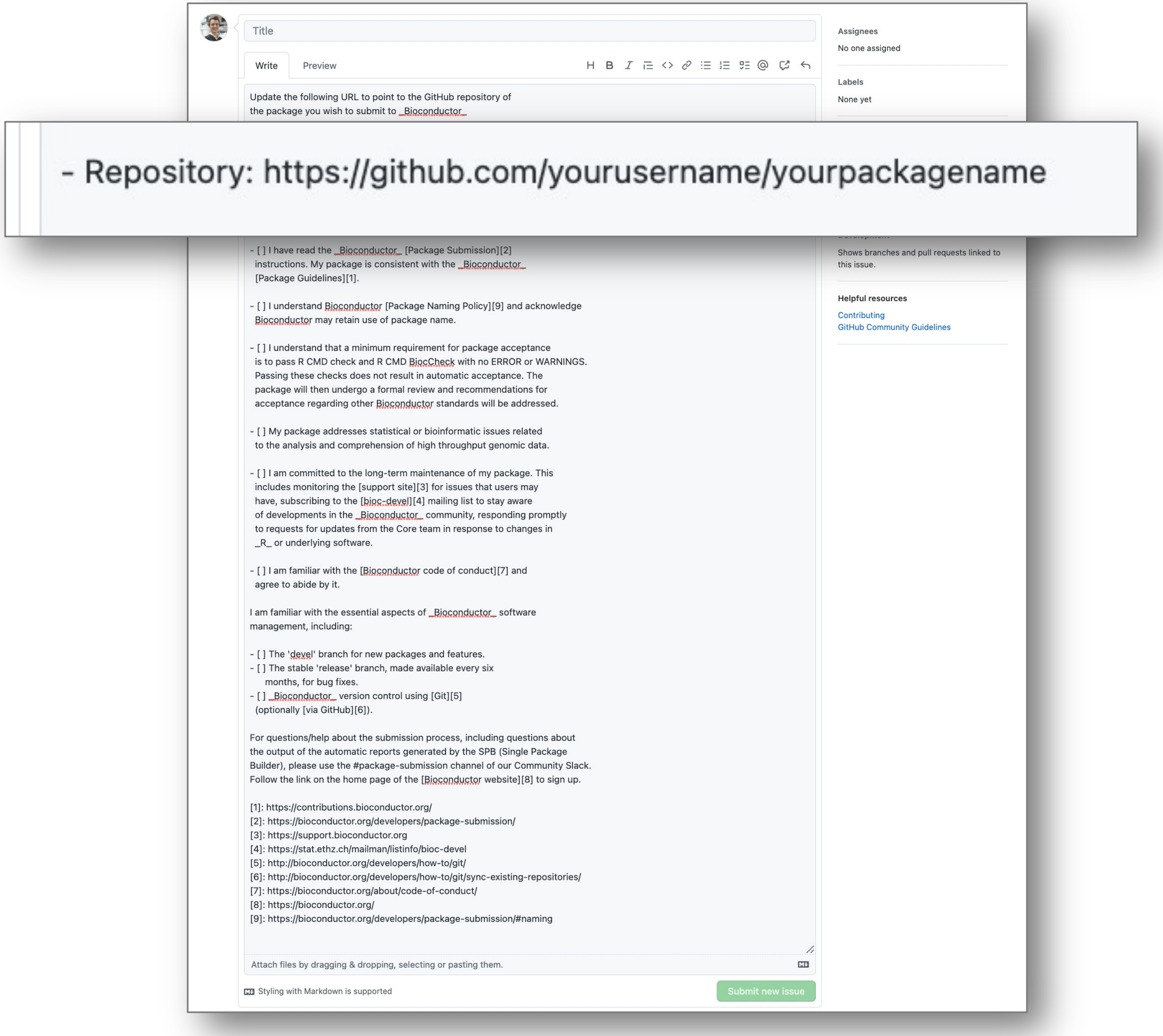

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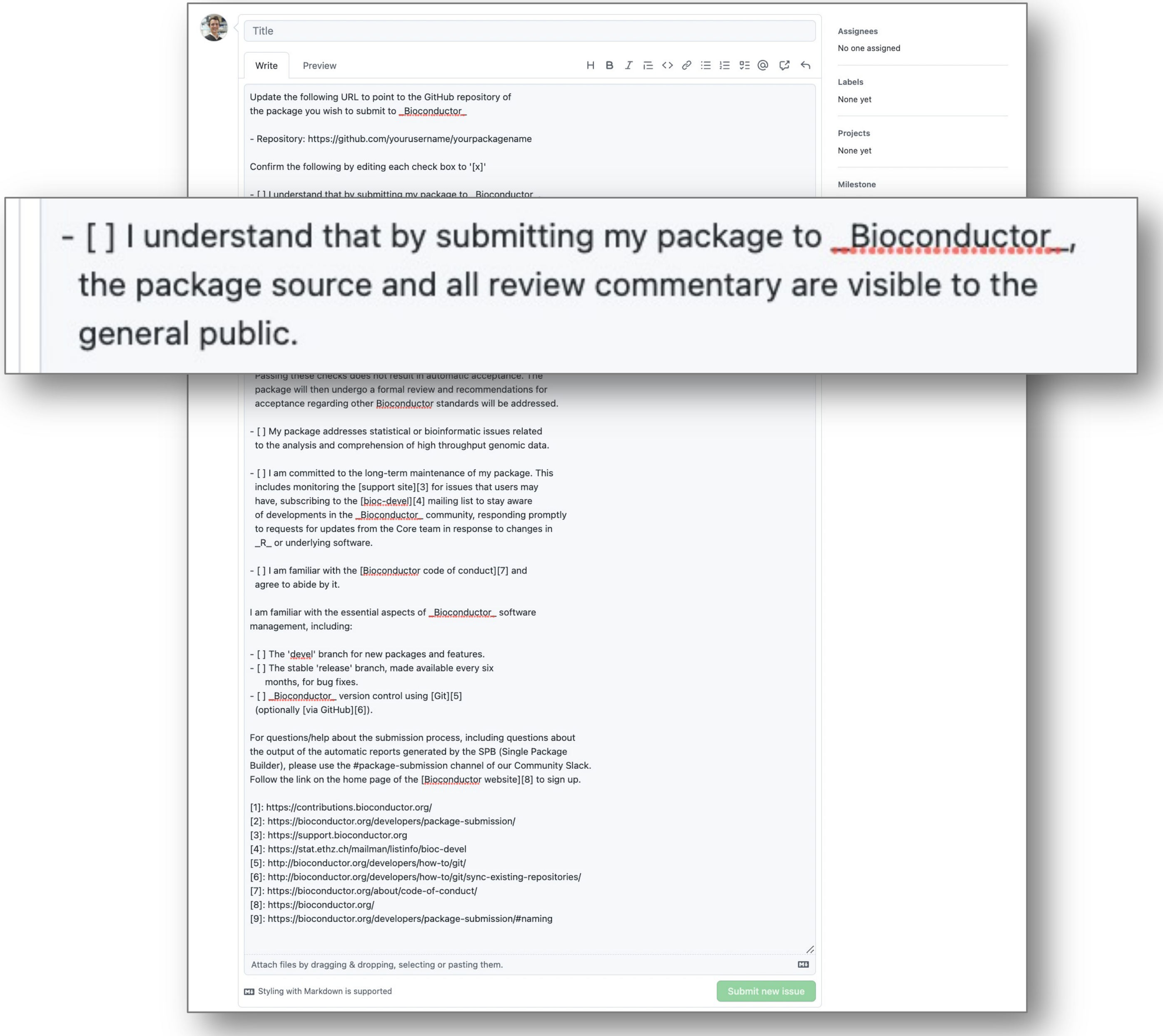

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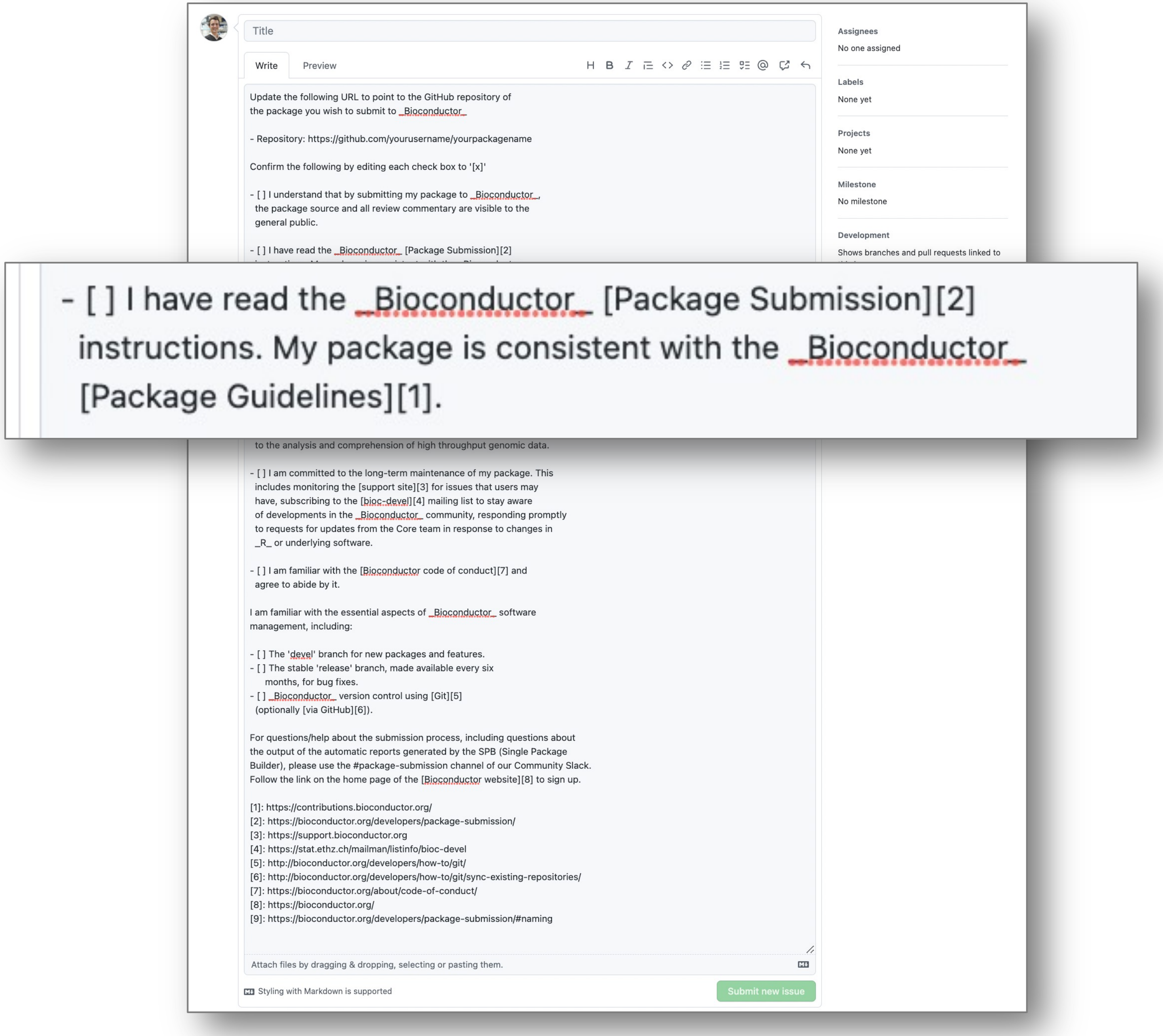

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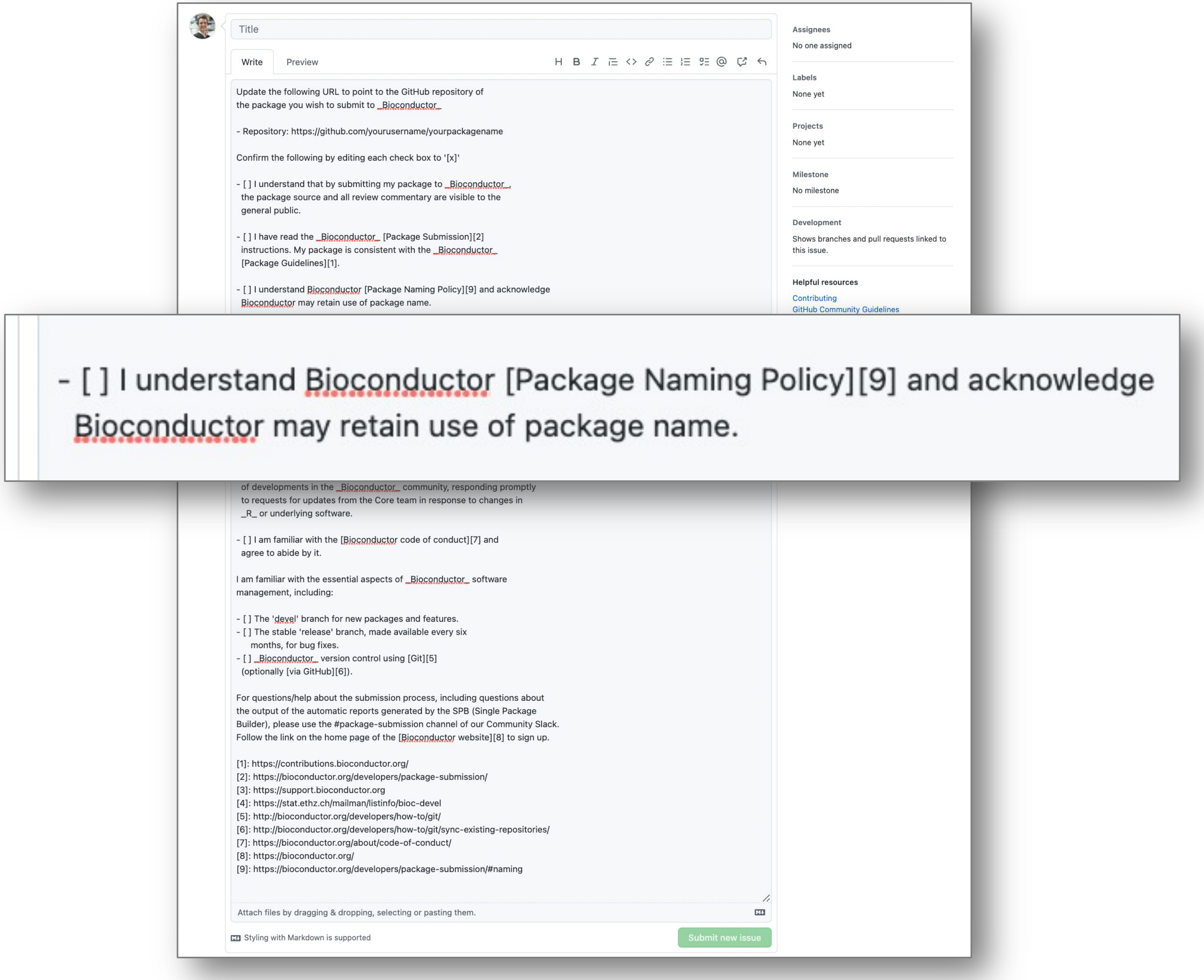

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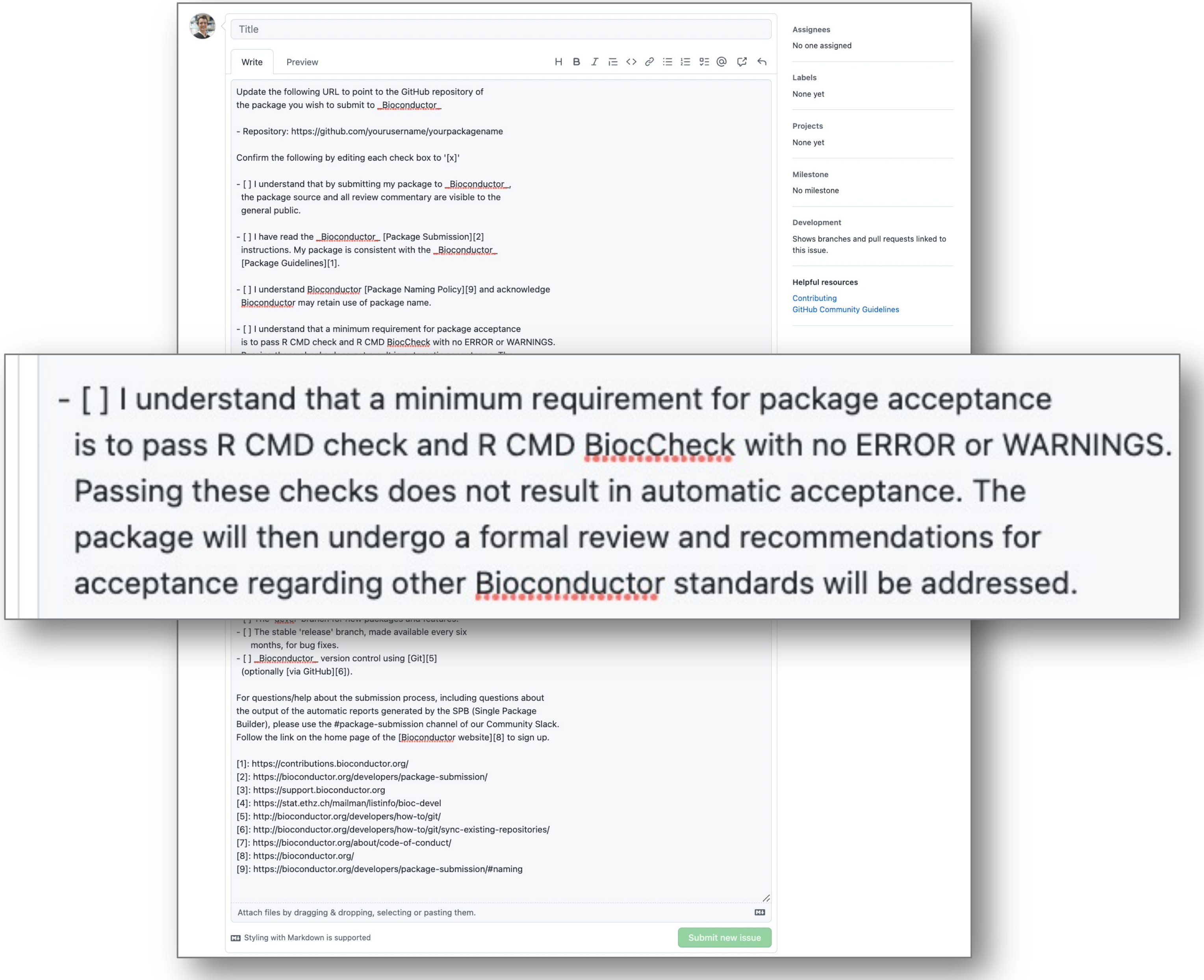

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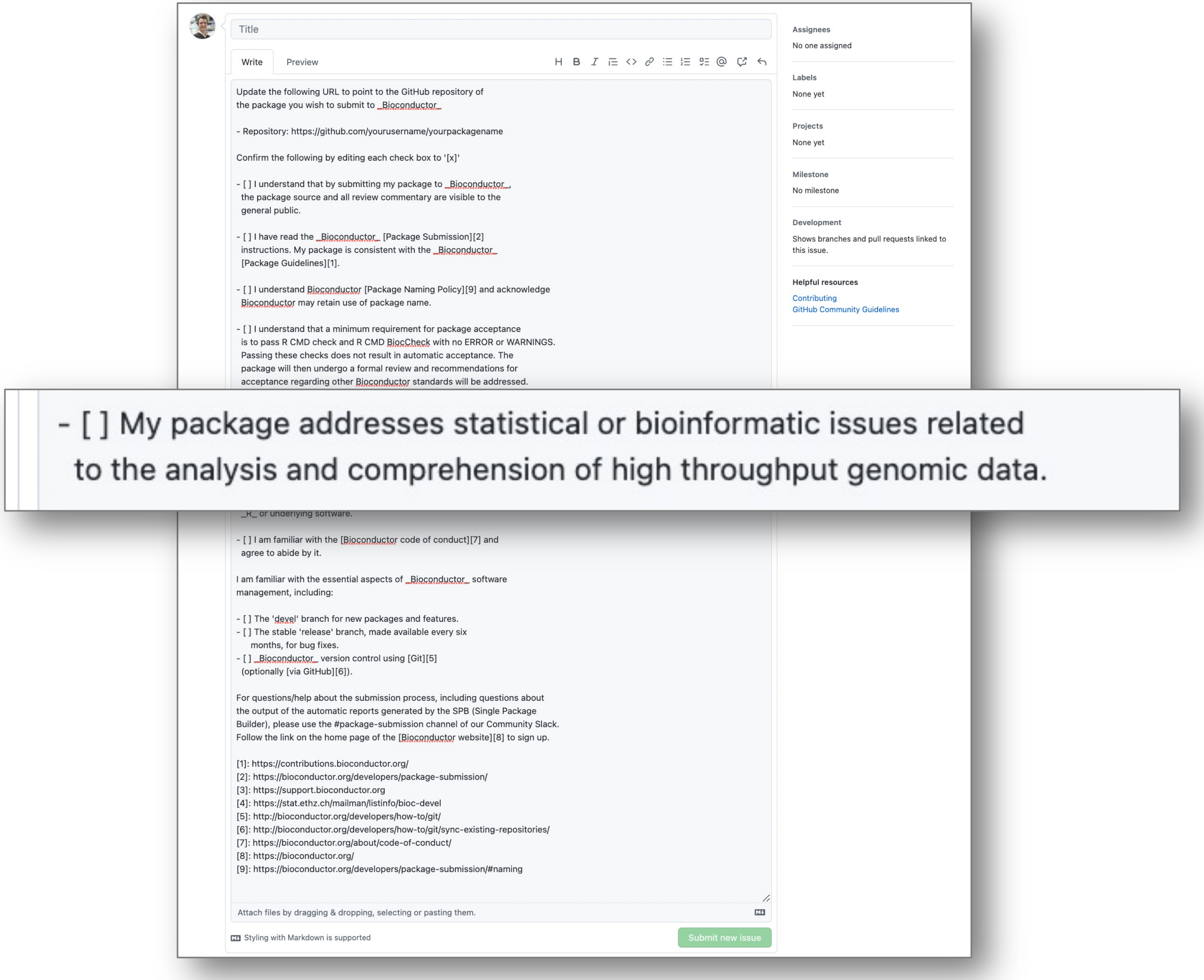

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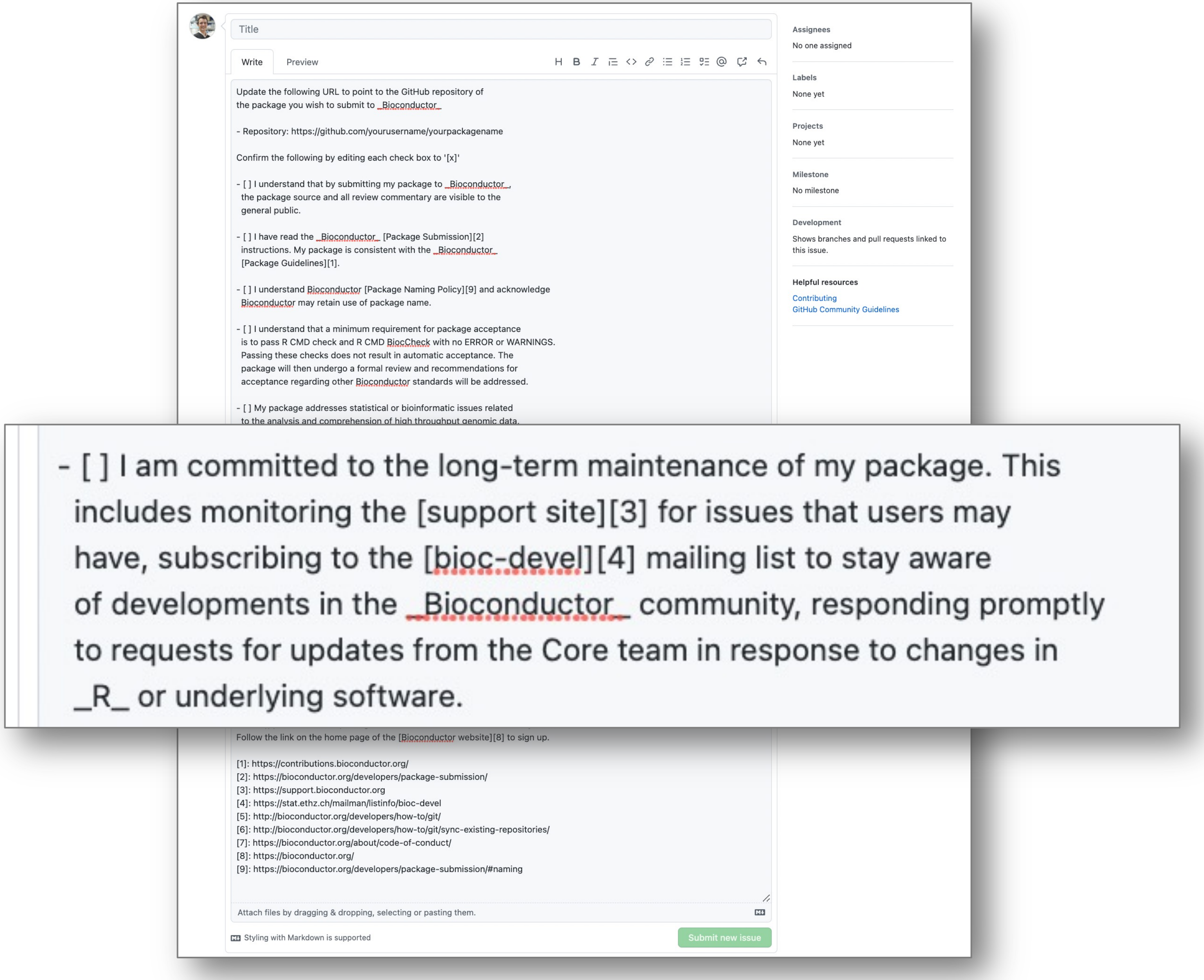

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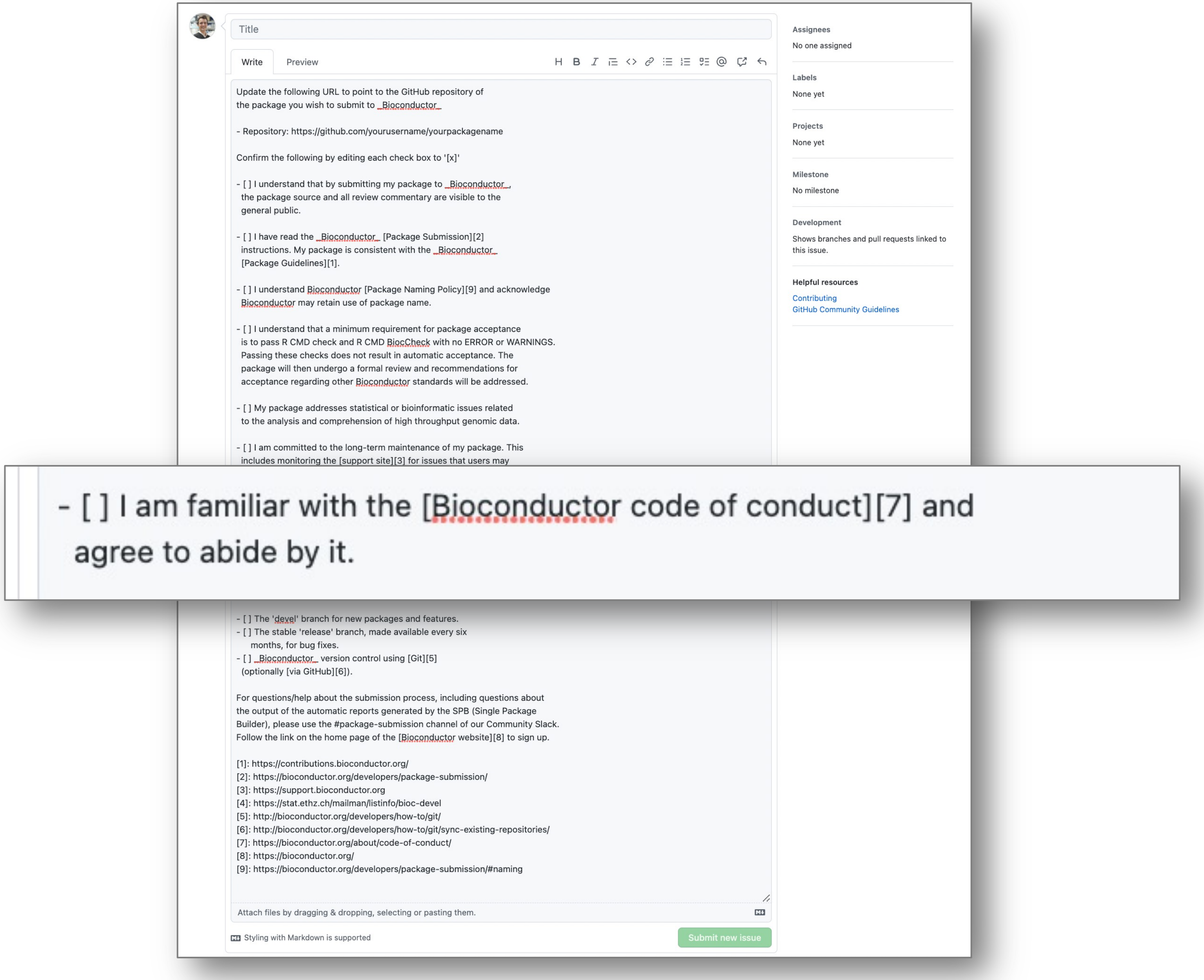
Attach files by dragging & dropping, selecting or pasting them.

Submitting initial issue to Bioconductor



Update the following URL to point to the GitHub repository of
the package you wish to submit to _Bioconductor_

- Repository: https://github.com/yourusername/yourpackagename

Confirm the following by editing each check box to '[x]'

- [ ] I understand that by submitting my package to _Bioconductor_,
  the package source and all review commentary are visible to the
  general public.

- [ ] I have read the _Bioconductor_ [Package Submission][2]
  instructions. My package is consistent with the _Bioconductor_
  [Package Guidelines][1].

- [ ] I understand Bioconductor [Package Naming Policy][9] and acknowledge
  Bioconductor may retain use of package name.

- [ ] I understand that a minimum requirement for package acceptance
  is to pass R CMD check and R CMD BiocCheck with no ERROR or WARNINGS.
  Passing these checks does not result in automatic acceptance. The
  package will then undergo a formal review and recommendations for
  acceptance regarding other Bioconductor standards will be addressed.

- [ ] My package addresses statistical or bioinformatic issues related
  to the analysis and comprehension of high throughput genomic data.

- [ ] I am committed to the long-term maintenance of my package. This
  includes monitoring the [support site][3] for issues that users may

- [ ] I am familiar with the [Bioconductor code of conduct][7] and
  agree to abide by it.

- [ ] The 'devel' branch for new packages and features.
- [ ] The stable 'release' branch, made available every six
    months, for bug fixes.
- [ ] _Bioconductor_ version control using [Git][5]
  (optionally [via GitHub][6]).

For questions/help about the submission process, including questions about
the output of the automatic reports generated by the SPB (Single Package
Builder), please use the #package-submission channel of our Community Slack.
Follow the link on the home page of the [Bioconductor website][8] to sign up.

[1]: https://contributions.bioconductor.org/
[2]: https://bioconductor.org/developers/package-submission/
[3]: https://support.bioconductor.org
[4]: https://stat.ethz.ch/mailman/listinfo/bioc-devel
[5]: http://bioconductor.org/developers/how-to/git/
[6]: http://bioconductor.org/developers/how-to/git/sync-existing-repositories/
[7]: https://bioconductor.org/about/code-of-conduct/
[8]: https://bioconductor.org/
[9]: https://bioconductor.org/developers/package-submission/#naming

Attach files by dragging & dropping, selecting or pasting them.

Assignees
No one assigned

Labels
None yet

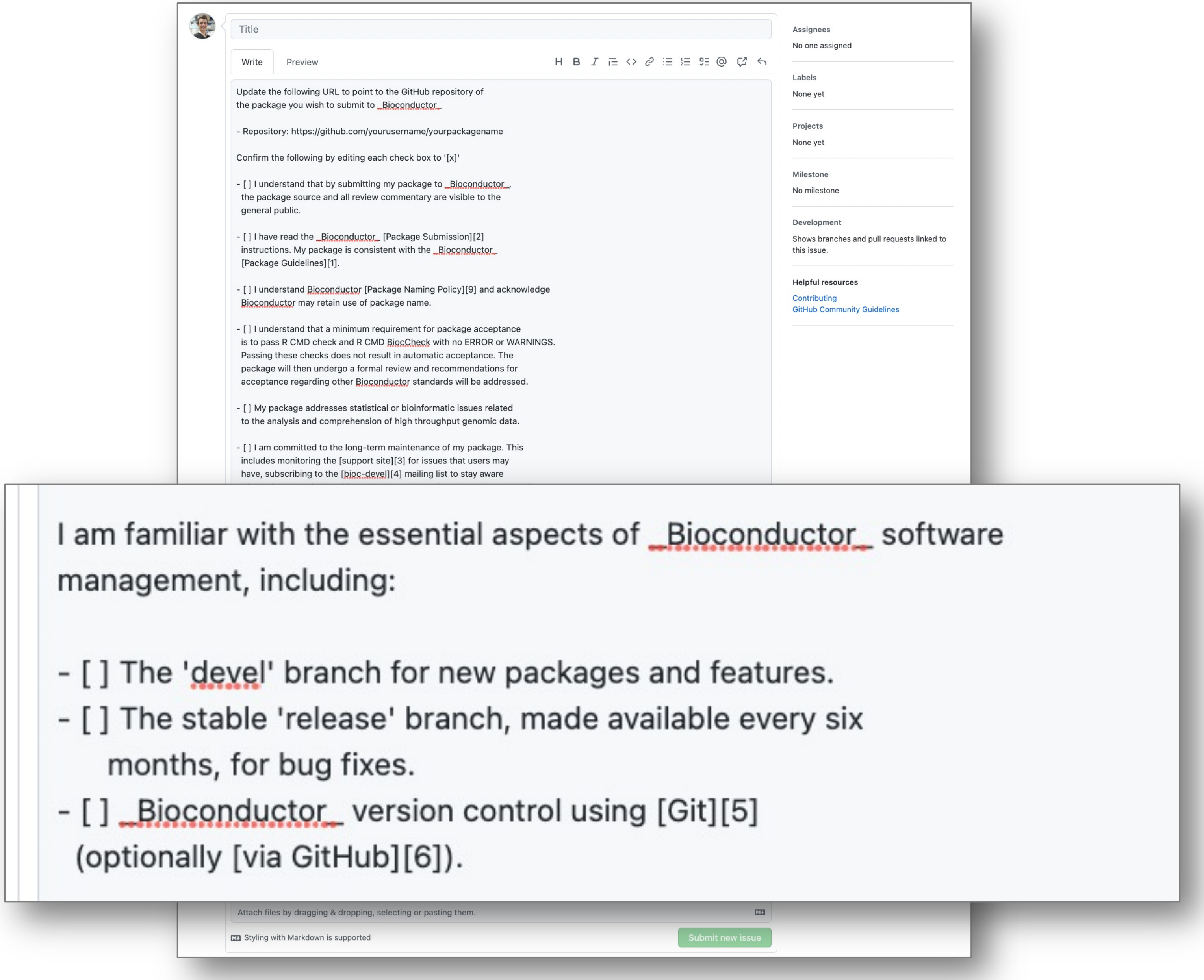
Projects
None yet

Milestone
No milestone

Development
Shows branches and pull requests linked to this issue.

Helpful resources
Contributing
GitHub Community Guidelines

Submitting initial issue to Bioconductor



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  is to pass R CMD check and R CMD BiocCheck with no ERROR or WARNINGS.
  Passing these checks does not result in automatic acceptance. The
  package will then undergo a formal review and recommendations for
  acceptance regarding other Bioconductor standards will be addressed.

- [ ] My package addresses statistical or bioinformatic issues related
  to the analysis and comprehension of high throughput genomic data.

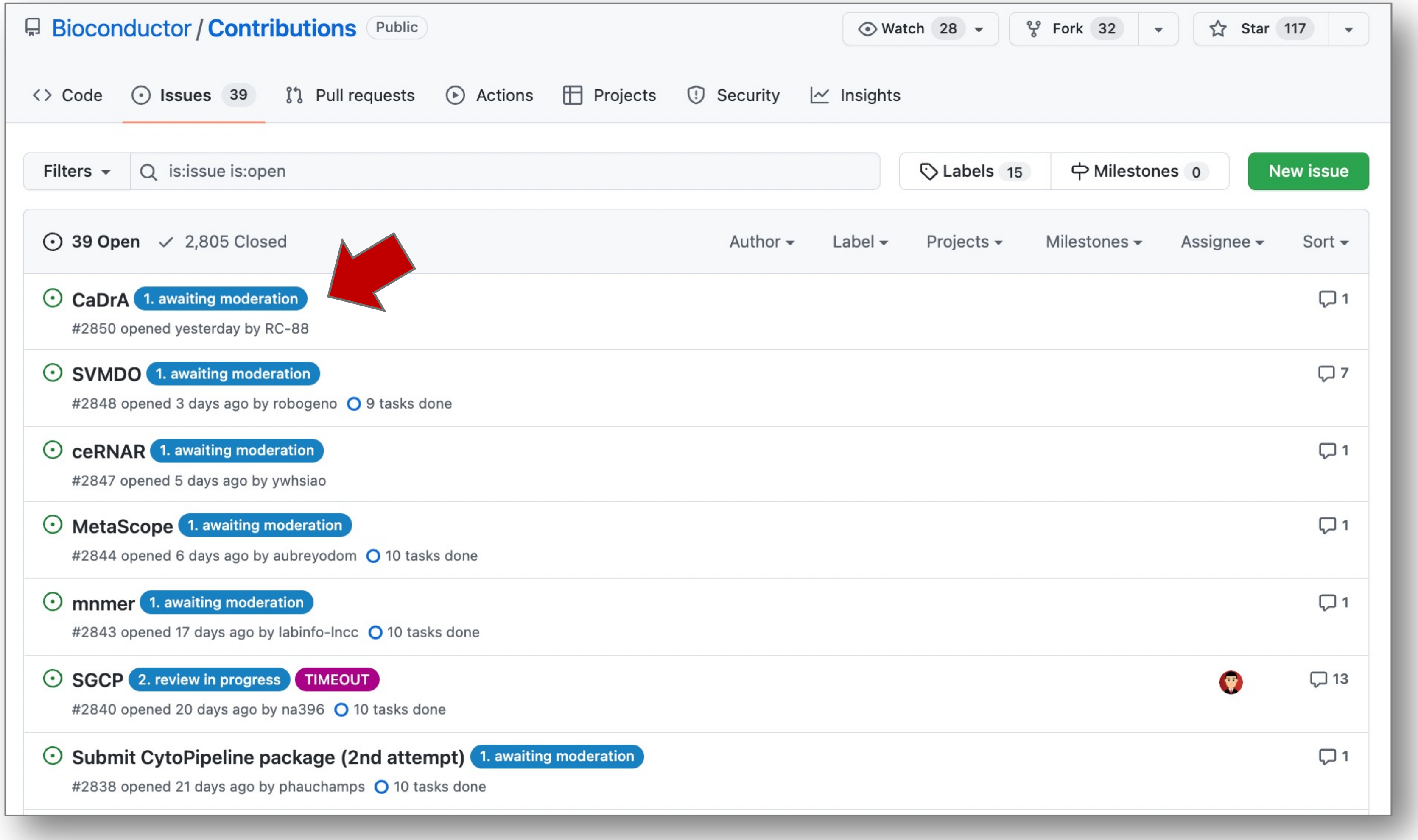
- [ ] I am committed to the long-term maintenance of my package. This
  includes monitoring the [support site][3] for issues that users may
  have, subscribing to the [bioc-devel][4] mailing list to stay aware

I am familiar with the essential aspects of _Bioconductor_ software
management, including:

- [ ] The 'devel' branch for new packages and features.
- [ ] The stable 'release' branch, made available every six
    months, for bug fixes.
- [ ] _Bioconductor_ version control using [Git][5]
  (optionally [via GitHub][6]).

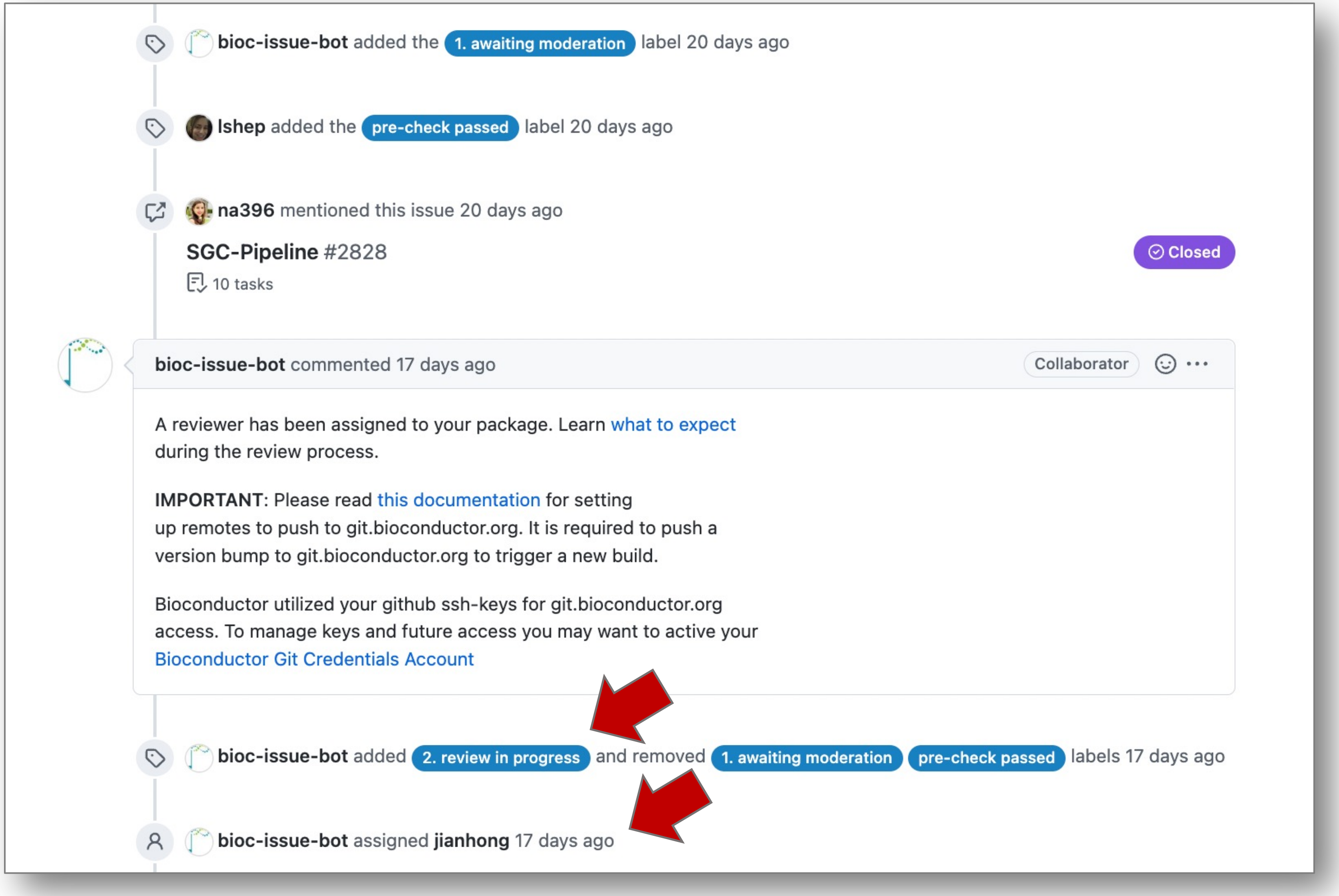
Await for a Bioconductor team member to be selected to review your package

2. Patiently await for moderators to pre-check your package



- CaDrA 1. awaiting moderation — #2850 opened yesterday by RC-88 — 1
- SVMDO 1. awaiting moderation — #2848 opened 3 days ago by robogeno 9 tasks done — 7
- ceRNAR 1. awaiting moderation — #2847 opened 5 days ago by ywhsiao — 1
- MetaScope 1. awaiting moderation — #2844 opened 6 days ago by aubreyodom 10 tasks done — 1
- mnmer 1. awaiting moderation — #2843 opened 17 days ago by labinfo-lncc 10 tasks done — 1
- SGCP 2. review in progress TIMEOUT — #2840 opened 20 days ago by na396 10 tasks done — 13
- Submit CytoPipeline package (2nd attempt) 1. awaiting moderation — #2838 opened 21 days ago by phauchamps 10 tasks done — 1

Await for a Bioconductor team member to be selected to review your package



bioc-issue-bot added the 1. awaiting moderation label 20 days ago

lshep added the pre-check passed label 20 days ago

na396 mentioned this issue 20 days ago

SGC-Pipeline #2828

bioc-issue-bot commented 17 days ago

A reviewer has been assigned to your package. Learn what to expect during the review process.

IMPORTANT: Please read this documentation for setting up remotes to push to git.bioconductor.org. It is required to push a version bump to git.bioconductor.org to trigger a new build.

Bioconductor utilized your github ssh-keys for git.bioconductor.org access. To manage keys and future access you may want to active your Bioconductor Git Credentials Account

bioc-issue-bot added 2. review in progress and removed 1. awaiting moderation pre-check passed labels 17 days ago

bioc-issue-bot assigned **jianhong** 17 days ago

Moving to (pre-)review process

The “2. review in progress” tag is slightly mis-leading.

Your reviewer is not likely to have a look at your package as soon as they are assigned to review it.

Moving to (pre-)review process

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Your reviewer is not likely to have a look at your package as soon as they are assigned to review it.

And this is because of…

Moving to (pre-)review process

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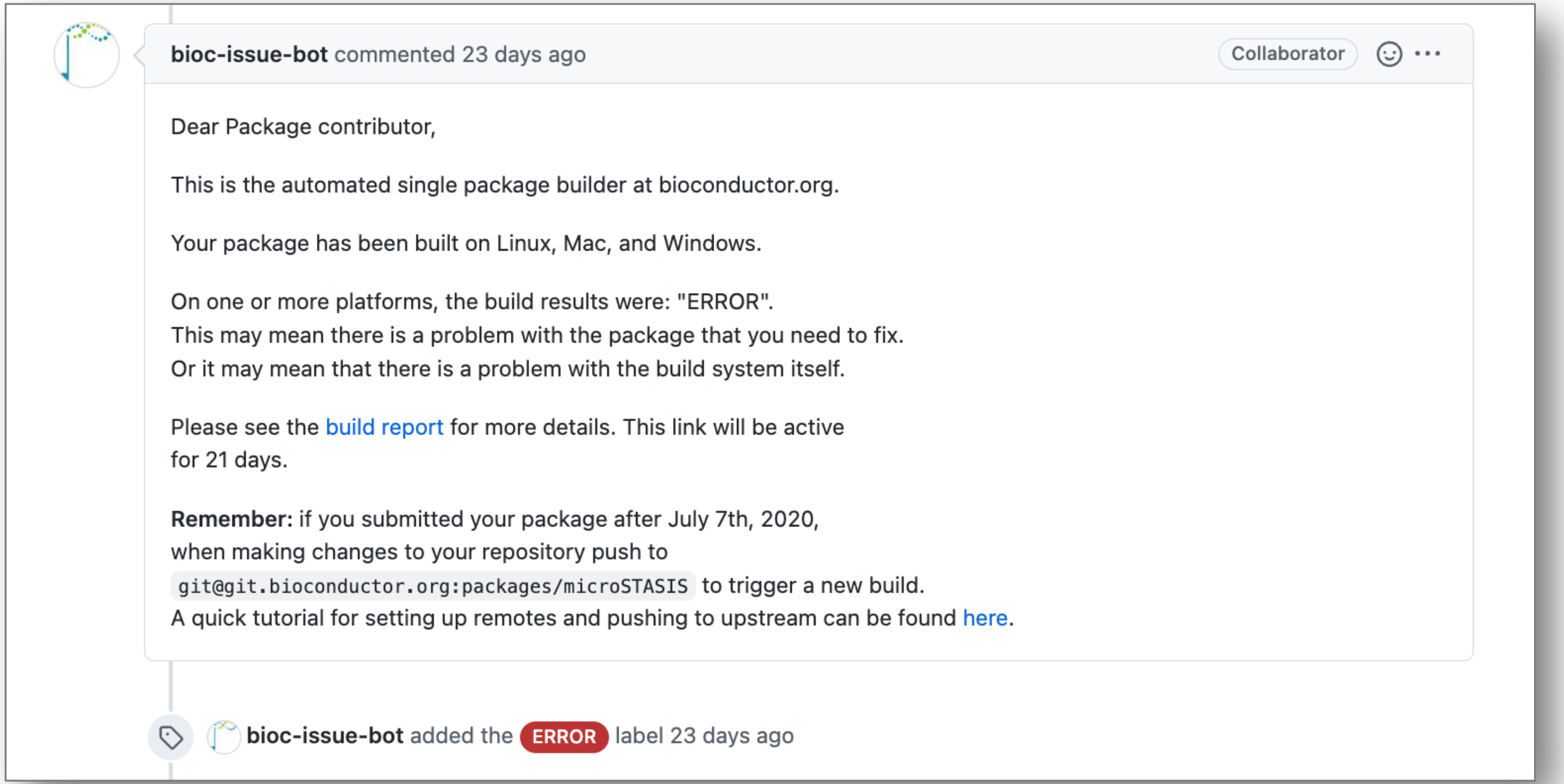


bioc-issue-bot commented 23 days ago

Dear Package contributor,

This is the automated single package builder at bioconductor.org.

Your package has been built on Linux, Mac, and Windows.

On one or more platforms, the build results were: "ERROR".
This may mean there is a problem with the package that you need to fix.
Or it may mean that there is a problem with the build system itself.

Please see the build report for more details. This link will be active for 21 days.

Remember: if you submitted your package after July 7th, 2020, when making changes to your repository push to `git@git.bioconductor.org:packages/microSTASIS` to trigger a new build.
A quick tutorial for setting up remotes and pushing to upstream can be found here.

bioc-issue-bot added the ERROR label 23 days ago

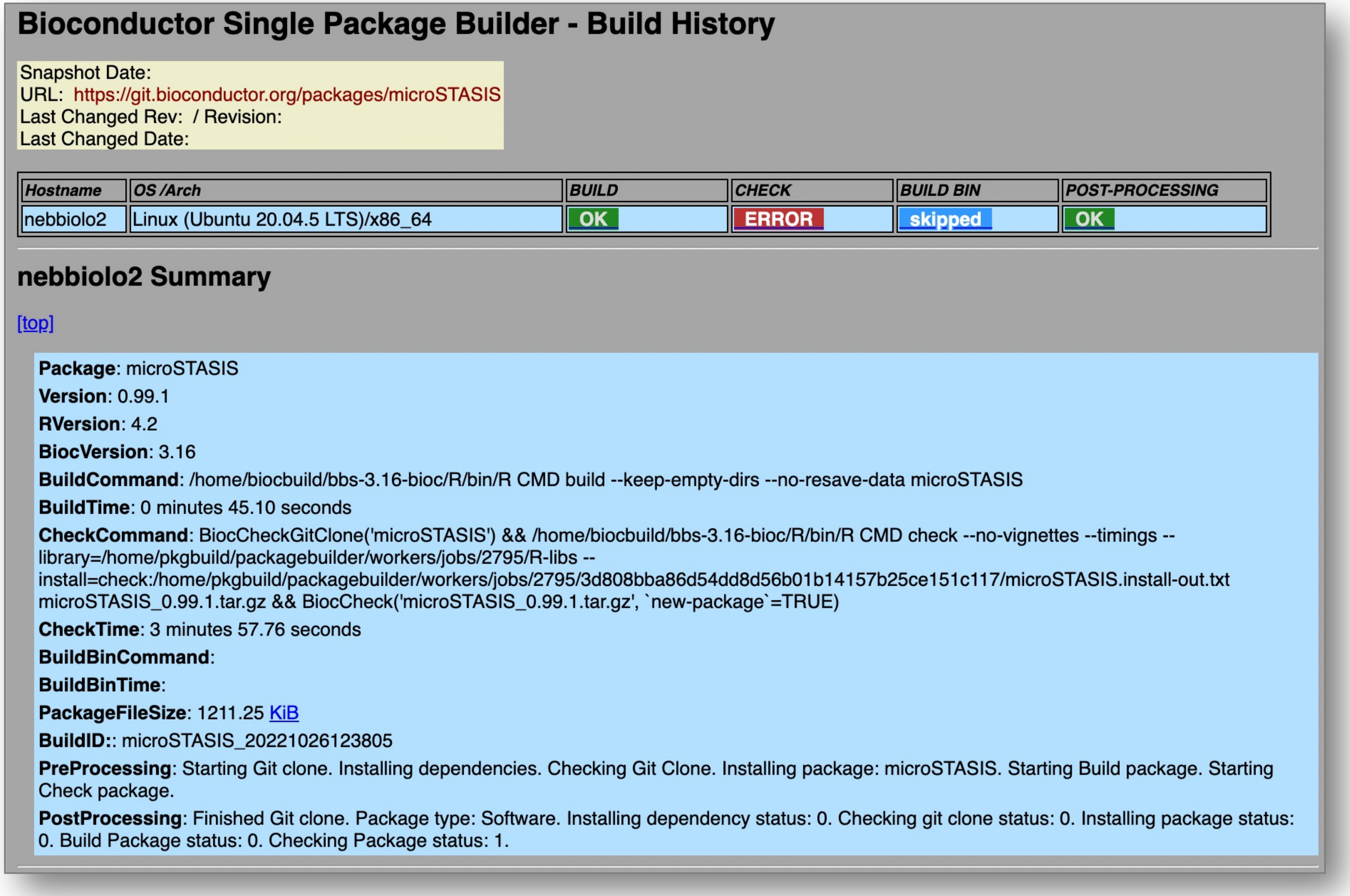
The most dreaded Bioconductor Build System (BBS)

Once your package is in review, a new ”sub-repo” is created in Bioconductor’s GitHub (in the `packages` repo), synchronized with your own GitHub.

```
> git clone git@git.bioconductor.org:packages/microSTASIS.git
Cloning into 'microSTASIS'...
remote: Enumerating objects: 283, done.
remote: Counting objects: 100% (283/283), done.
remote: Compressing objects: 100% (164/164), done.
remote: Total 283 (delta 183), reused 154 (delta 103), pack-
reused 0
Receiving objects: 100% (283/283), 1012.15 KiB | 2.80 MiB/s,
done.
Resolving deltas: 100% (183/183), done.
```

The most dreaded Bioconductor Build System (BBS)

Then Bioconductor heavy machines (the Single Package Builder) run-run-run.



Bioconductor Single Package Builder - Build History

Snapshot Date:
URL: https://git.bioconductor.org/packages/microSTASIS
Last Changed Rev: / Revision:
Last Changed Date:

Hostname	*OS /Arch*	*BUILD*	*CHECK*	*BUILD BIN*	*POST-PROCESSING*
nebbiolo2	Linux (Ubuntu 20.04.5 LTS)/x86_64	OK	ERROR	skipped	OK

nebbiolo2 Summary

[top]

Package: microSTASIS

Version: 0.99.1

RVersion: 4.2

BiocVersion: 3.16

BuildCommand: /home/biocbuild/bbs-3.16-bioc/R/bin/R CMD build --keep-empty-dirs --no-resave-data microSTASIS

BuildTime: 0 minutes 45.10 seconds

CheckCommand: BiocCheckGitClone('microSTASIS') && /home/biocbuild/bbs-3.16-bioc/R/bin/R CMD check --no-vignettes --timings --library=/home/pkgbuild/packagebuilder/workers/jobs/2795/R-libs --install=check:/home/pkgbuild/packagebuilder/workers/jobs/2795/3d808bba86d54dd8d56b01b14157b25ce151c117/microSTASIS.install-out.txt microSTASIS_0.99.1.tar.gz && BiocCheck('microSTASIS_0.99.1.tar.gz', `new-package`=TRUE)

CheckTime: 3 minutes 57.76 seconds

BuildBinCommand:

BuildBinTime:

PackageFileSize: 1211.25 KiB

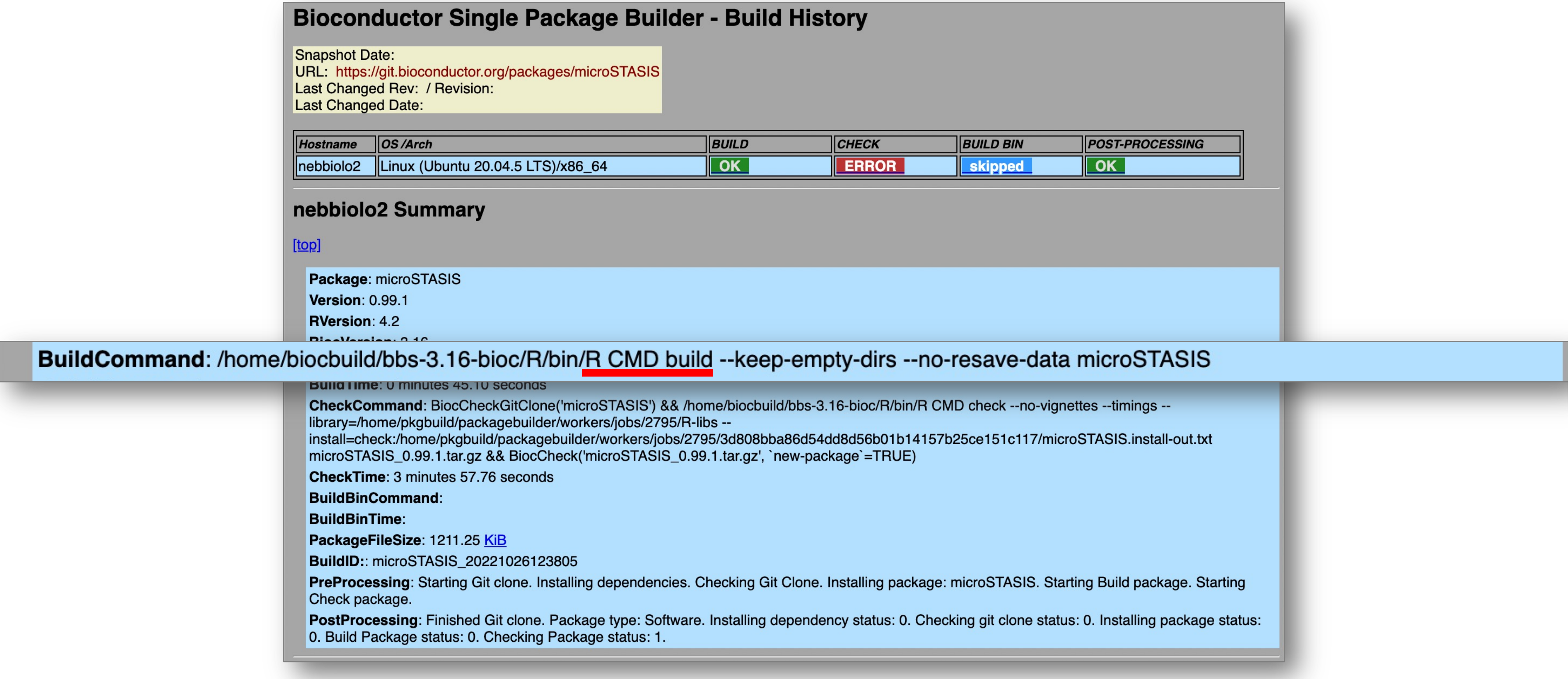
BuildID:: microSTASIS_20221026123805

PreProcessing: Starting Git clone. Installing dependencies. Checking Git Clone. Installing package: microSTASIS. Starting Build package. Starting Check package.

PostProcessing: Finished Git clone. Package type: Software. Installing dependency status: 0. Checking git clone status: 0. Installing package status: 0. Build Package status: 0. Checking Package status: 1.

The most dreaded Bioconductor Build System (BBS)

Then Bioconductor heavy machines (the Single Package Builder) run-run-run.



Bioconductor Single Package Builder - Build History

Snapshot Date:
URL: https://git.bioconductor.org/packages/microSTASIS
Last Changed Rev: / Revision:
Last Changed Date:

Hostname	*OS /Arch*	*BUILD*	*CHECK*	*BUILD BIN*	*POST-PROCESSING*
nebbiolo2	Linux (Ubuntu 20.04.5 LTS)/x86_64	OK	ERROR	skipped	OK

nebbiolo2 Summary

[top]

Package: microSTASIS

Version: 0.99.1

RVersion: 4.2

BiocVersion: 3.16

BuildCommand: /home/biocbuild/bbs-3.16-bioc/R/bin/R CMD build --keep-empty-dirs --no-resave-data microSTASIS

BuildTime: 0 minutes 45.10 seconds

CheckCommand: BiocCheckGitClone('microSTASIS') && /home/biocbuild/bbs-3.16-bioc/R/bin/R CMD check --no-vignettes --timings --library=/home/pkgbuild/packagebuilder/workers/jobs/2795/R-libs --install=check:/home/pkgbuild/packagebuilder/workers/jobs/2795/3d808bba86d54dd8d56b01b14157b25ce151c117/microSTASIS.install-out.txt microSTASIS_0.99.1.tar.gz && BiocCheck('microSTASIS_0.99.1.tar.gz', `new-package`=TRUE)

CheckTime: 3 minutes 57.76 seconds

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BuildBinTime:

PackageFileSize: 1211.25 KiB

BuildID:: microSTASIS_20221026123805

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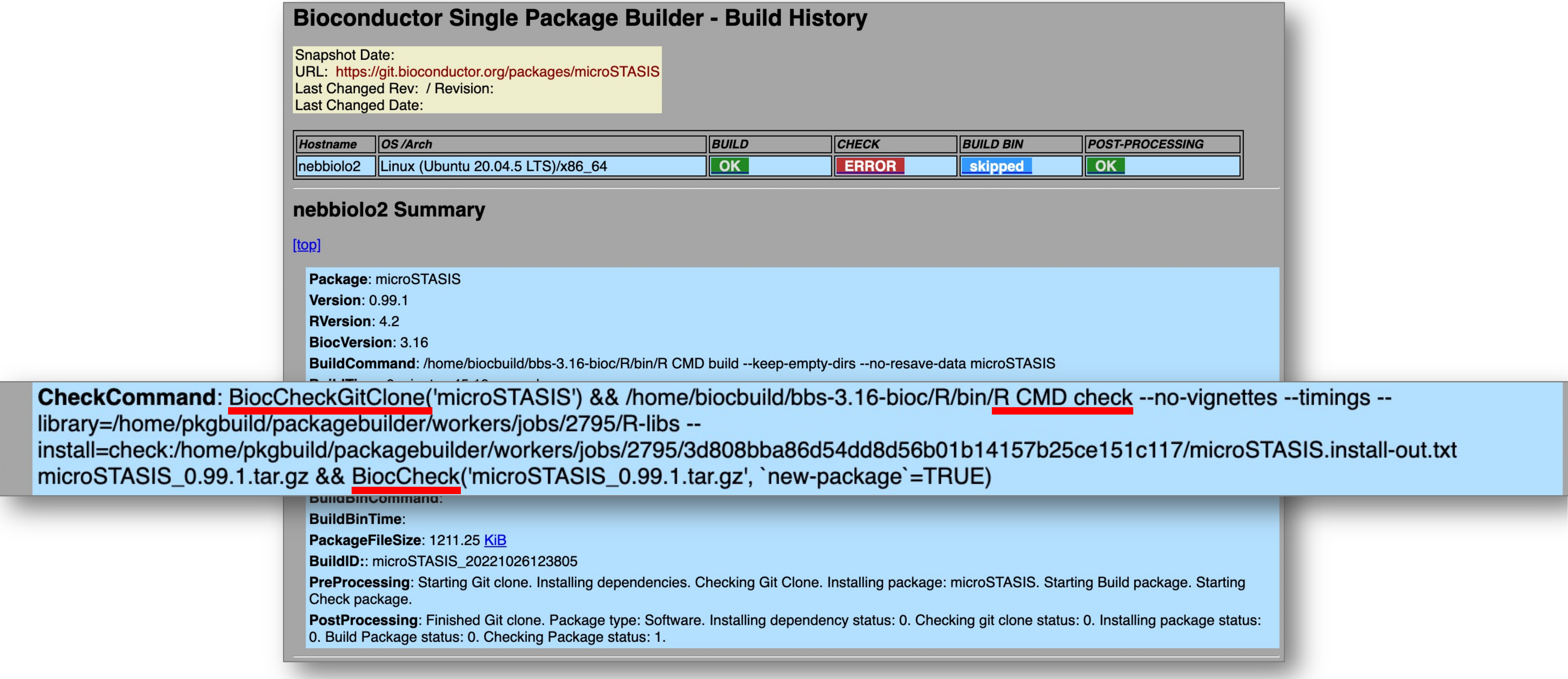


Bioconductor Single Package Builder - Build History

Snapshot Date:
URL: https://git.bioconductor.org/packages/microSTASIS
Last Changed Rev: / Revision:
Last Changed Date:

Hostname	*OS /Arch*	*BUILD*	*CHECK*	*BUILD BIN*	*POST-PROCESSING*
nebbiolo2	Linux (Ubuntu 20.04.5 LTS)/x86_64	OK	ERROR	skipped	OK

nebbiolo2 Summary

[top]

Package: microSTASIS

Version: 0.99.1

RVersion: 4.2

BiocVersion: 3.16

BuildCommand: /home/biocbuild/bbs-3.16-bioc/R/bin/R CMD build --keep-empty-dirs --no-resave-data microSTASIS

CheckCommand: BiocCheckGitClone('microSTASIS') && /home/biocbuild/bbs-3.16-bioc/R/bin/R CMD check --no-vignettes --timings --library=/home/pkgbuild/packagebuilder/workers/jobs/2795/R-libs --install=check:/home/pkgbuild/packagebuilder/workers/jobs/2795/3d808bba86d54dd8d56b01b14157b25ce151c117/microSTASIS.install-out.txt microSTASIS_0.99.1.tar.gz && BiocCheck('microSTASIS_0.99.1.tar.gz', `new-package`=TRUE)

BuildBinCommand:

BuildBinTime:

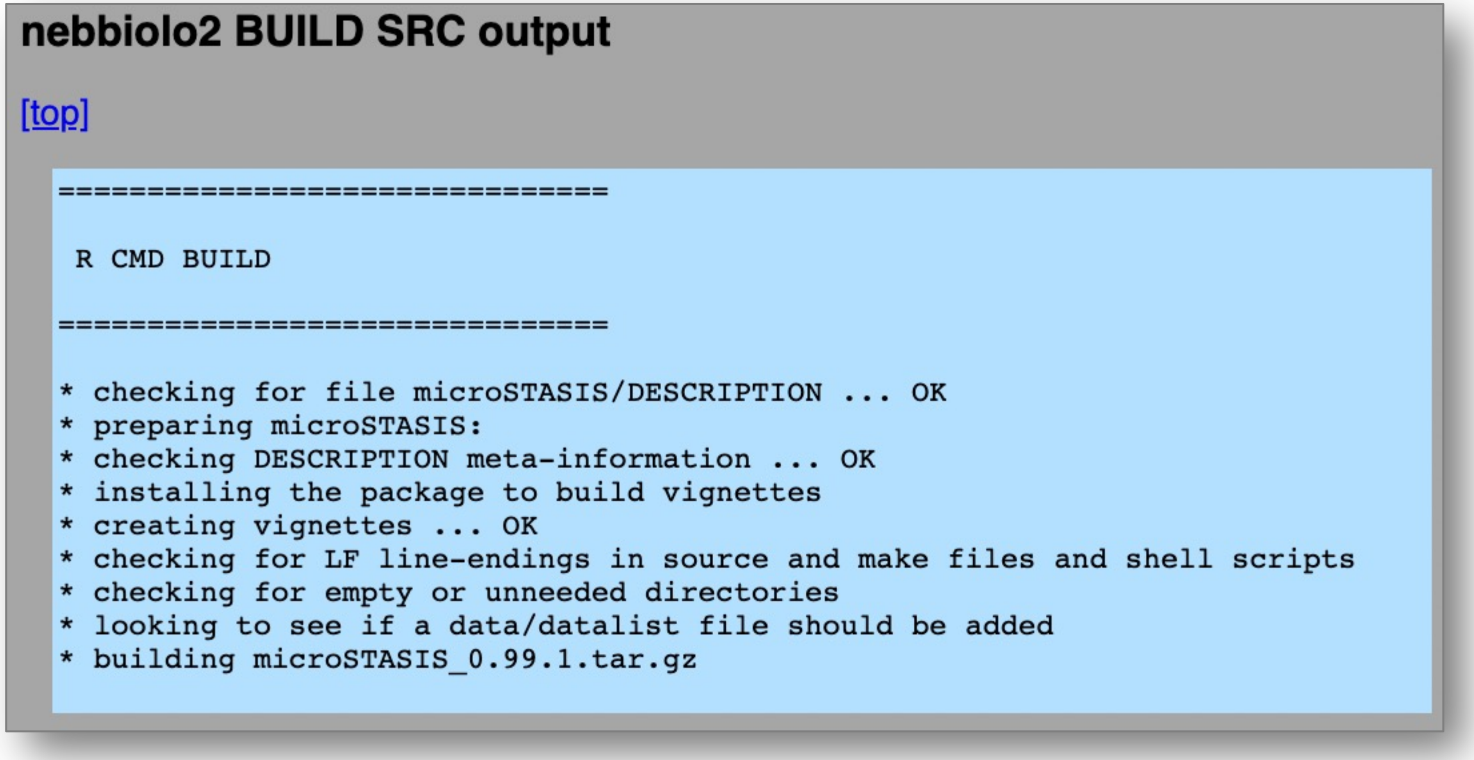
PackageFileSize: 1211.25 KiB

BuildID:: microSTASIS_20221026123805

PreProcessing: Starting Git clone. Installing dependencies. Checking Git Clone. Installing package: microSTASIS. Starting Build package. Starting Check package.

PostProcessing: Finished Git clone. Package type: Software. Installing dependency status: 0. Checking git clone status: 0. Installing package status: 0. Build Package status: 0. Checking Package status: 1.

The most dreaded Bioconductor Build System (BBS)



nebbiolo2 BUILD SRC output

[top]

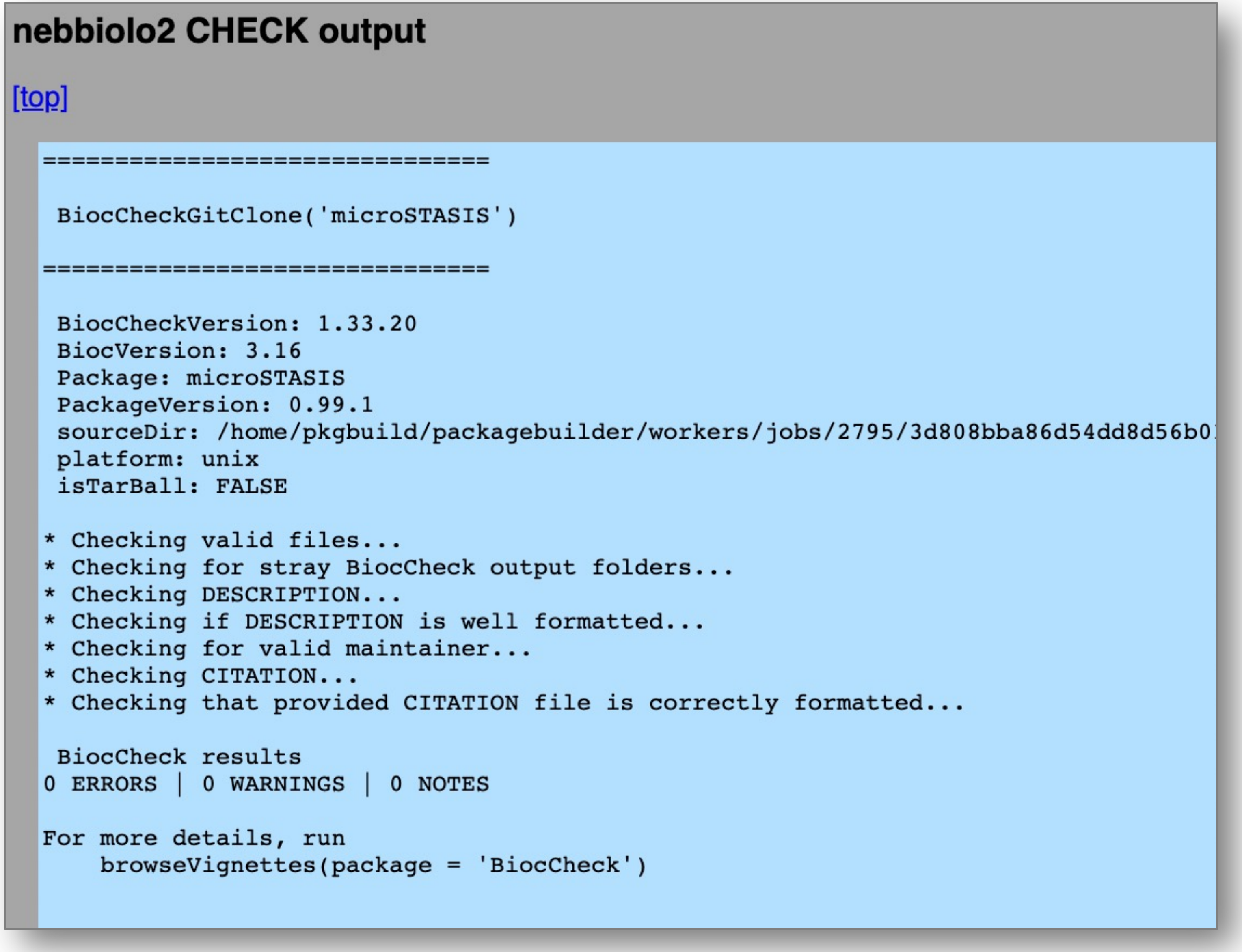
```
===============================

 R CMD BUILD

===============================

* checking for file microSTASIS/DESCRIPTION ... OK
* preparing microSTASIS:
* checking DESCRIPTION meta-information ... OK
* installing the package to build vignettes
* creating vignettes ... OK
* checking for LF line-endings in source and make files and shell scripts
* checking for empty or unneeded directories
* looking to see if a data/datalist file should be added
* building microSTASIS_0.99.1.tar.gz
```

The most dreaded Bioconductor Build System (BBS)



nebbiolo2 CHECK output

[top]

```
===============================

 BiocCheckGitClone('microSTASIS')

===============================

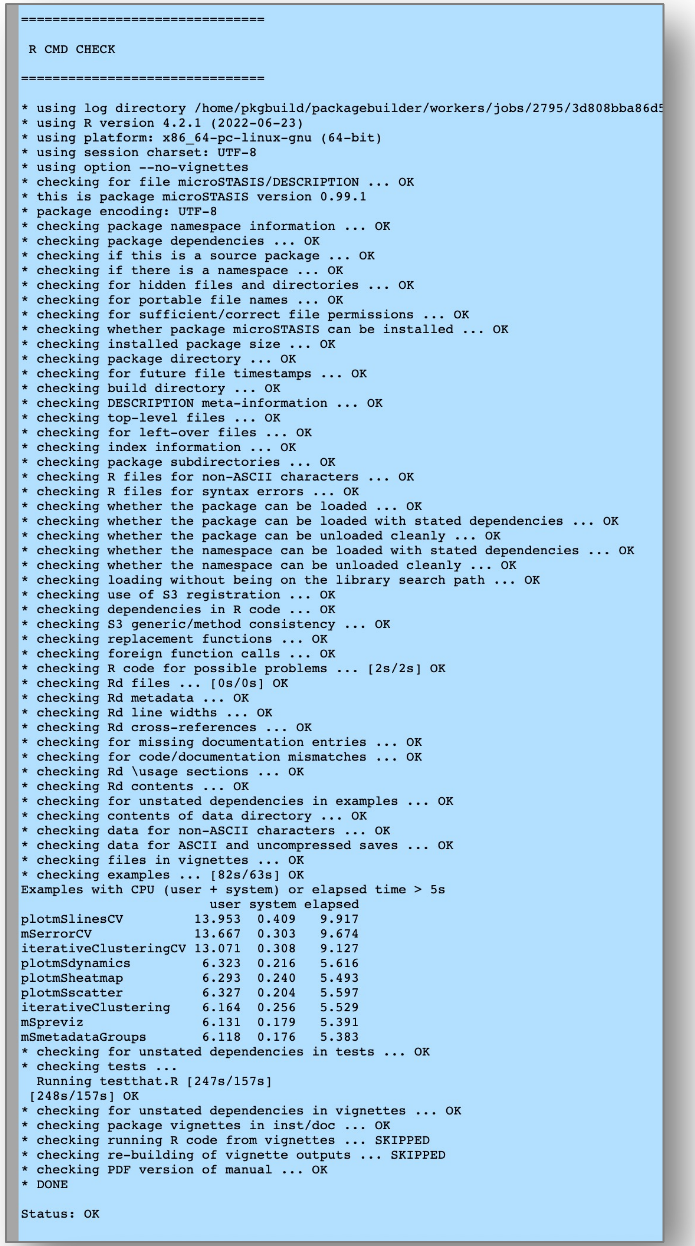
 BiocCheckVersion: 1.33.20
 BiocVersion: 3.16
 Package: microSTASIS
 PackageVersion: 0.99.1
 sourceDir: /home/pkgbuild/packagebuilder/workers/jobs/2795/3d808bba86d54dd8d56b0
 platform: unix
 isTarBall: FALSE

* Checking valid files...
* Checking for stray BiocCheck output folders...
* Checking DESCRIPTION...
* Checking if DESCRIPTION is well formatted...
* Checking for valid maintainer...
* Checking CITATION...
* Checking that provided CITATION file is correctly formatted...

 BiocCheck results
0 ERRORS | 0 WARNINGS | 0 NOTES

For more details, run
    browseVignettes(package = 'BiocCheck')
```

The most dreaded Bioconductor Build System (BBS)



```
===============================

 R CMD CHECK

===============================

* using log directory /home/pkgbuild/packagebuilder/workers/jobs/2795/3d808bba86d5
* using R version 4.2.1 (2022-06-23)
* using platform: x86_64-pc-linux-gnu (64-bit)
* using session charset: UTF-8
* using option --no-vignettes
* checking for file microSTASIS/DESCRIPTION ... OK
* this is package microSTASIS version 0.99.1
* package encoding: UTF-8
* checking package namespace information ... OK
* checking package dependencies ... OK
* checking if this is a source package ... OK
* checking if there is a namespace ... OK
* checking for hidden files and directories ... OK
* checking for portable file names ... OK
* checking for sufficient/correct file permissions ... OK
* checking whether package microSTASIS can be installed ... OK
* checking installed package size ... OK
* checking package directory ... OK
* checking for future file timestamps ... OK
* checking build directory ... OK
* checking DESCRIPTION meta-information ... OK
* checking top-level files ... OK
* checking for left-over files ... OK
* checking index information ... OK
* checking package subdirectories ... OK
* checking R files for non-ASCII characters ... OK
* checking R files for syntax errors ... OK
* checking whether the package can be loaded ... OK
* checking whether the package can be loaded with stated dependencies ... OK
* checking whether the package can be unloaded cleanly ... OK
* checking whether the namespace can be loaded with stated dependencies ... OK
* checking whether the namespace can be unloaded cleanly ... OK
* checking loading without being on the library search path ... OK
* checking use of S3 registration ... OK
* checking dependencies in R code ... OK
* checking S3 generic/method consistency ... OK
* checking replacement functions ... OK
* checking foreign function calls ... OK
* checking R code for possible problems ... [2s/2s] OK
* checking Rd files ... [0s/0s] OK
* checking Rd metadata ... OK
* checking Rd line widths ... OK
* checking Rd cross-references ... OK
* checking for missing documentation entries ... OK
* checking for code/documentation mismatches ... OK
* checking Rd \usage sections ... OK
* checking Rd contents ... OK
* checking for unstated dependencies in examples ... OK
* checking contents of data directory ... OK
* checking data for non-ASCII characters ... OK
* checking data for ASCII and uncompressed saves ... OK
* checking files in vignettes ... OK
* checking examples ... [82s/63s] OK
Examples with CPU (user + system) or elapsed time > 5s
                        user system elapsed
plotmSlinesCV         13.953  0.409   9.917
mSerrorCV             13.667  0.303   9.674
iterativeClusteringCV 13.071  0.308   9.127
plotmSdynamics         6.323  0.216   5.616
plotmSheatmap          6.293  0.240   5.493
plotmSscatter          6.327  0.204   5.597
iterativeClustering    6.164  0.256   5.529
mSpreviz               6.131  0.179   5.391
mSmetadataGroups       6.118  0.176   5.383
* checking for unstated dependencies in tests ... OK
* checking tests ...
  Running testthat.R [247s/157s]
 [248s/157s] OK
* checking for unstated dependencies in vignettes ... OK
* checking package vignettes in inst/doc ... OK
* checking running R code from vignettes ... SKIPPED
* checking re-building of vignette outputs ... SKIPPED
* checking PDF version of manual ... OK
* DONE

Status: OK
```

The most dreaded Bioconductor Build System (BBS)

```
===============================

 BiocCheck('microSTASIS_0.99.1.tar.gz')

===============================

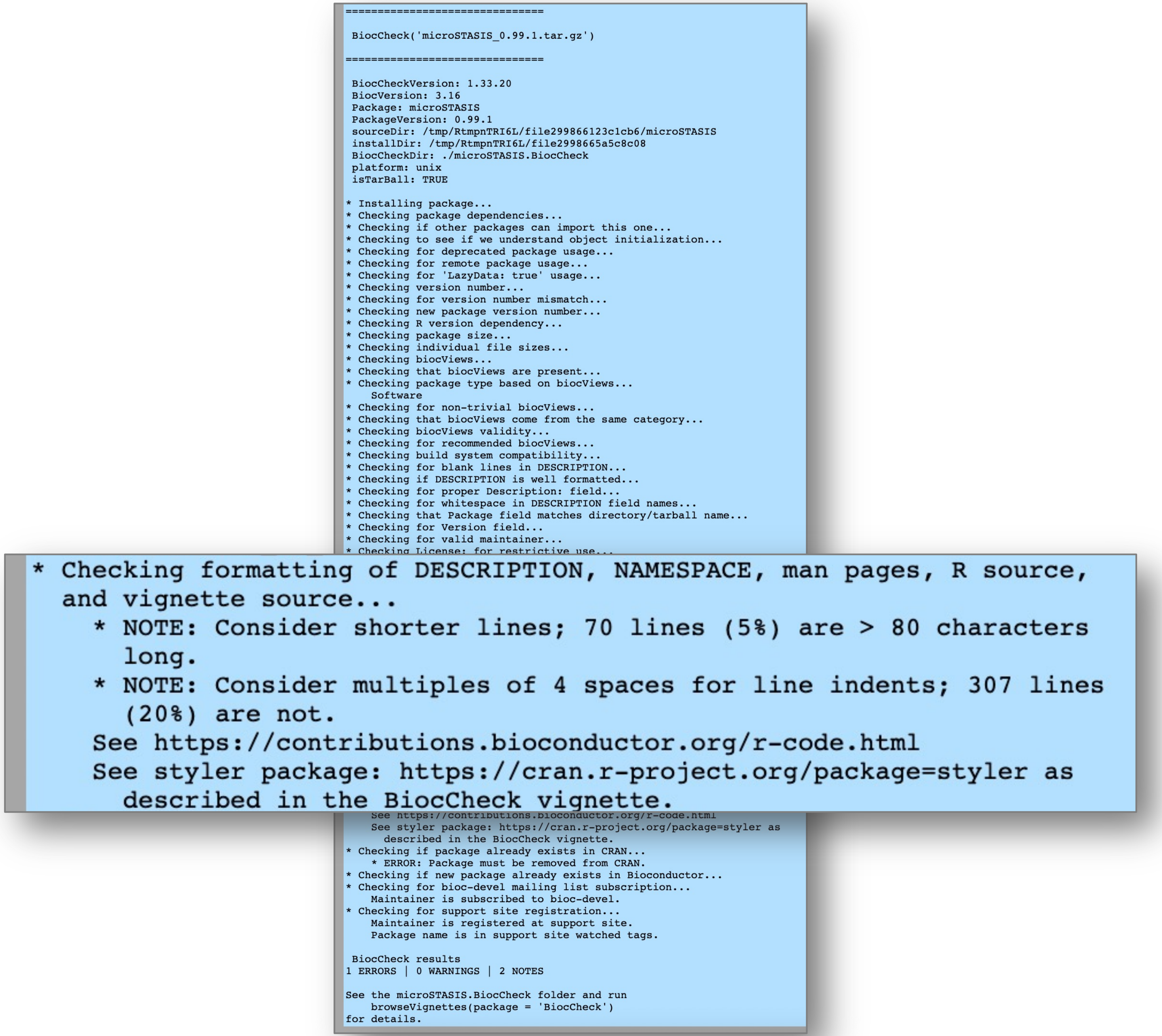
 BiocCheckVersion: 1.33.20
 BiocVersion: 3.16
 Package: microSTASIS
 PackageVersion: 0.99.1
 sourceDir: /tmp/RtmpnTRI6L/file299866123c1cb6/microSTASIS
 installDir: /tmp/RtmpnTRI6L/file2998665a5c8c08
 BiocCheckDir: ./microSTASIS.BiocCheck
 platform: unix
 isTarBall: TRUE

* Installing package...
* Checking package dependencies...
* Checking if other packages can import this one...
* Checking to see if we understand object initialization...
* Checking for deprecated package usage...
* Checking for remote package usage...
* Checking for 'LazyData: true' usage...
* Checking version number...
* Checking for version number mismatch...
* Checking new package version number...
* Checking R version dependency...
* Checking package size...
* Checking individual file sizes...
* Checking biocViews...
* Checking that biocViews are present...
* Checking package type based on biocViews...
    Software
* Checking for non-trivial biocViews...
* Checking that biocViews come from the same category...
* Checking biocViews validity...
* Checking for recommended biocViews...
* Checking build system compatibility...
* Checking for blank lines in DESCRIPTION...
* Checking if DESCRIPTION is well formatted...
* Checking for proper Description: field...
* Checking for whitespace in DESCRIPTION field names...
* Checking that Package field matches directory/tarball name...
* Checking for Version field...
* Checking for valid maintainer...
* Checking License: for restrictive use...
* Checking for pinned package versions...
* Checking DESCRIPTION/NAMESPACE consistency...
* Checking .Rbuildignore...
* Checking for stray BiocCheck output folders...
* Checking vignette directory...
* Checking whether vignette is built with 'R CMD build'...
* Checking package installation calls in R code...
* Checking for library/require of microSTASIS...
* Checking coding practice...
* Checking parsed R code in R directory, examples, vignettes...
* Checking function lengths...
* Checking man page documentation...
* Checking package NEWS...
* Checking unit tests...
* Checking skip_on_bioc() in tests...
* Checking formatting of DESCRIPTION, NAMESPACE, man pages, R source,
  and vignette source...
    * NOTE: Consider shorter lines; 70 lines (5%) are > 80 characters
      long.
    * NOTE: Consider multiples of 4 spaces for line indents; 307 lines
      (20%) are not.
    See https://contributions.bioconductor.org/r-code.html
    See styler package: https://cran.r-project.org/package=styler as
      described in the BiocCheck vignette.
* Checking if package already exists in CRAN...
    * ERROR: Package must be removed from CRAN.
* Checking if new package already exists in Bioconductor...
* Checking for bioc-devel mailing list subscription...
    Maintainer is subscribed to bioc-devel.
* Checking for support site registration...
    Maintainer is registered at support site.
    Package name is in support site watched tags.

 BiocCheck results
1 ERRORS | 0 WARNINGS | 2 NOTES

See the microSTASIS.BiocCheck folder and run
    browseVignettes(package = 'BiocCheck')
for details.
```

The most dreaded Bioconductor Build System (BBS)



```
===============================

 BiocCheck('microSTASIS_0.99.1.tar.gz')

===============================

 BiocCheckVersion: 1.33.20
 BiocVersion: 3.16
 Package: microSTASIS
 PackageVersion: 0.99.1
 sourceDir: /tmp/RtmpnTRI6L/file299866123c1cb6/microSTASIS
 installDir: /tmp/RtmpnTRI6L/file2998665a5c8c08
 BiocCheckDir: ./microSTASIS.BiocCheck
 platform: unix
 isTarBall: TRUE

* Installing package...
* Checking package dependencies...
* Checking if other packages can import this one...
* Checking to see if we understand object initialization...
* Checking for deprecated package usage...
* Checking for remote package usage...
* Checking for 'LazyData: true' usage...
* Checking version number...
* Checking for version number mismatch...
* Checking new package version number...
* Checking R version dependency...
* Checking package size...
* Checking individual file sizes...
* Checking biocViews...
* Checking that biocViews are present...
* Checking package type based on biocViews...
    Software
* Checking for non-trivial biocViews...
* Checking that biocViews come from the same category...
* Checking biocViews validity...
* Checking for recommended biocViews...
* Checking build system compatibility...
* Checking for blank lines in DESCRIPTION...
* Checking if DESCRIPTION is well formatted...
* Checking for proper Description: field...
* Checking for whitespace in DESCRIPTION field names...
* Checking that Package field matches directory/tarball name...
* Checking for Version field...
* Checking for valid maintainer...
* Checking License: for restrictive use...
```

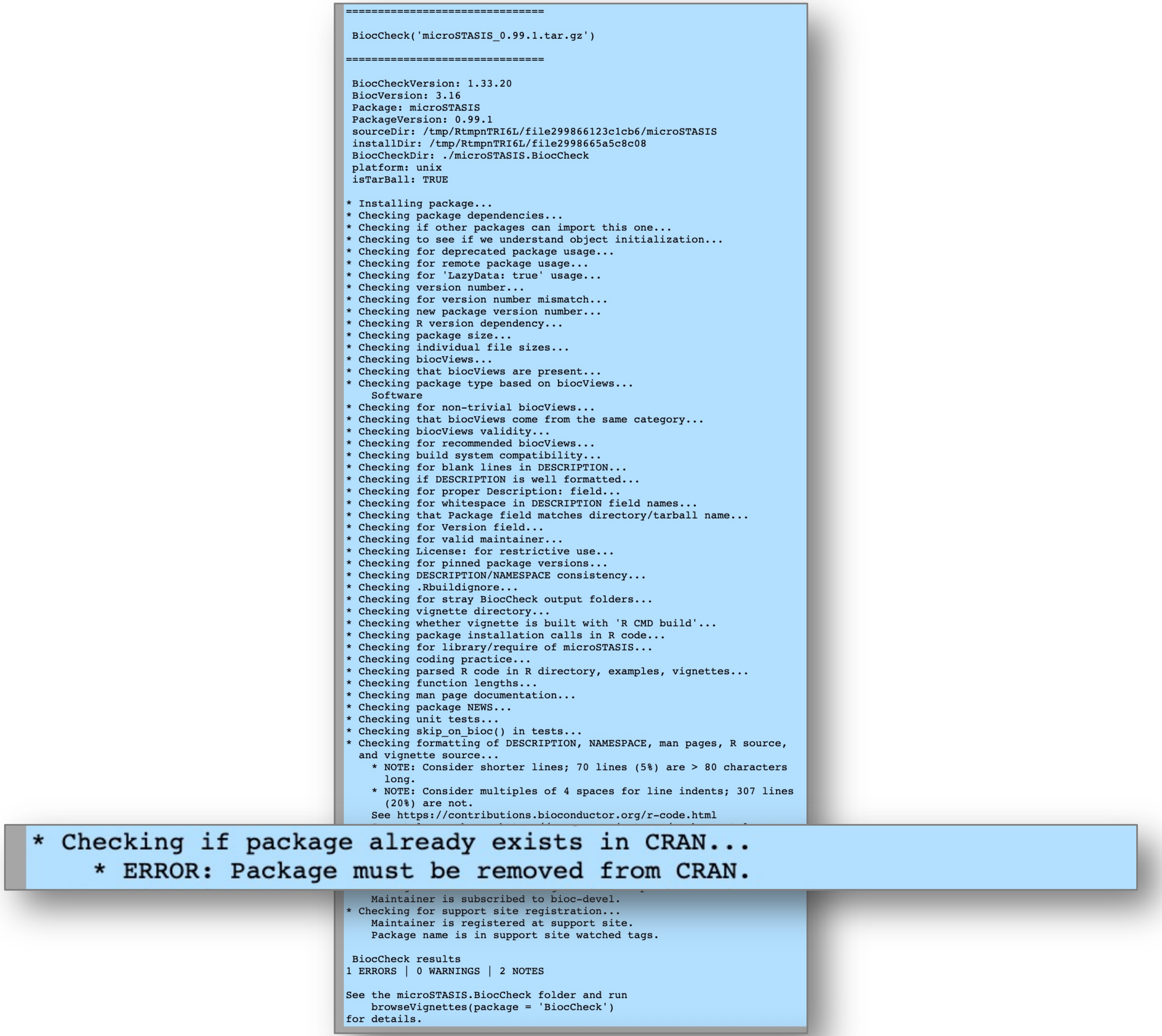
```
* Checking formatting of DESCRIPTION, NAMESPACE, man pages, R source,
  and vignette source...
    * NOTE: Consider shorter lines; 70 lines (5%) are > 80 characters
      long.
    * NOTE: Consider multiples of 4 spaces for line indents; 307 lines
      (20%) are not.
    See https://contributions.bioconductor.org/r-code.html
    See styler package: https://cran.r-project.org/package=styler as
      described in the BiocCheck vignette.
```

```
* Checking if package already exists in CRAN...
    * ERROR: Package must be removed from CRAN.
* Checking if new package already exists in Bioconductor...
* Checking for bioc-devel mailing list subscription...
    Maintainer is subscribed to bioc-devel.
* Checking for support site registration...
    Maintainer is registered at support site.
    Package name is in support site watched tags.

 BiocCheck results
1 ERRORS | 0 WARNINGS | 2 NOTES

See the microSTASIS.BiocCheck folder and run
    browseVignettes(package = 'BiocCheck')
for details.
```

The most dreaded Bioconductor Build System (BBS)



```
===============================

 BiocCheck('microSTASIS_0.99.1.tar.gz')

===============================

 BiocCheckVersion: 1.33.20
 BiocVersion: 3.16
 Package: microSTASIS
 PackageVersion: 0.99.1
 sourceDir: /tmp/RtmpnTRI6L/file299866123c1cb6/microSTASIS
 installDir: /tmp/RtmpnTRI6L/file2998665a5c8c08
 BiocCheckDir: ./microSTASIS.BiocCheck
 platform: unix
 isTarBall: TRUE

* Installing package...
* Checking package dependencies...
* Checking if other packages can import this one...
* Checking to see if we understand object initialization...
* Checking for deprecated package usage...
* Checking for remote package usage...
* Checking for 'LazyData: true' usage...
* Checking version number...
* Checking for version number mismatch...
* Checking new package version number...
* Checking R version dependency...
* Checking package size...
* Checking individual file sizes...
* Checking biocViews...
* Checking that biocViews are present...
* Checking package type based on biocViews...
    Software
* Checking for non-trivial biocViews...
* Checking that biocViews come from the same category...
* Checking biocViews validity...
* Checking for recommended biocViews...
* Checking build system compatibility...
* Checking for blank lines in DESCRIPTION...
* Checking if DESCRIPTION is well formatted...
* Checking for proper Description: field...
* Checking for whitespace in DESCRIPTION field names...
* Checking that Package field matches directory/tarball name...
* Checking for Version field...
* Checking for valid maintainer...
* Checking License: for restrictive use...
* Checking for pinned package versions...
* Checking DESCRIPTION/NAMESPACE consistency...
* Checking .Rbuildignore...
* Checking for stray BiocCheck output folders...
* Checking vignette directory...
* Checking whether vignette is built with 'R CMD build'...
* Checking package installation calls in R code...
* Checking for library/require of microSTASIS...
* Checking coding practice...
* Checking parsed R code in R directory, examples, vignettes...
* Checking function lengths...
* Checking man page documentation...
* Checking package NEWS...
* Checking unit tests...
* Checking skip_on_bioc() in tests...
* Checking formatting of DESCRIPTION, NAMESPACE, man pages, R source,
  and vignette source...
    * NOTE: Consider shorter lines; 70 lines (5%) are > 80 characters
      long.
    * NOTE: Consider multiples of 4 spaces for line indents; 307 lines
      (20%) are not.
    See https://contributions.bioconductor.org/r-code.html
```

```
* Checking if package already exists in CRAN...
    * ERROR: Package must be removed from CRAN.
```

```
    Maintainer is subscribed to bioc-devel.
* Checking for support site registration...
    Maintainer is registered at support site.
    Package name is in support site watched tags.

 BiocCheck results
1 ERRORS | 0 WARNINGS | 2 NOTES

See the microSTASIS.BiocCheck folder and run
    browseVignettes(package = 'BiocCheck')
for details.
```

Moving to (pre-)review process

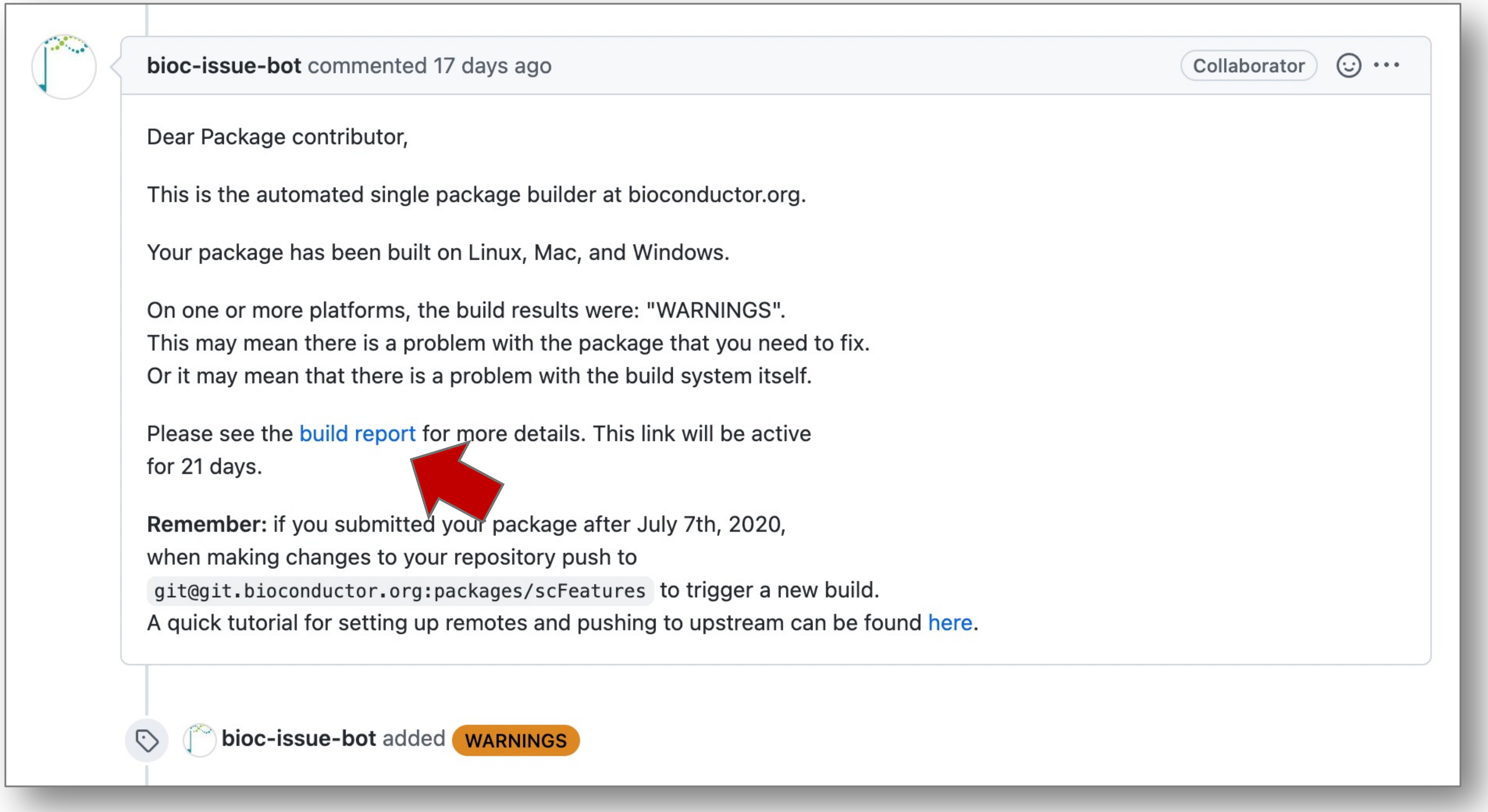
3. Fix errors!

4. Fix errors!

5. Fix errors!

Fixing errors/warnings

a. Check the build reports.



bioc-issue-bot commented 17 days ago

Dear Package contributor,

This is the automated single package builder at bioconductor.org.

Your package has been built on Linux, Mac, and Windows.

On one or more platforms, the build results were: "WARNINGS".
This may mean there is a problem with the package that you need to fix.
Or it may mean that there is a problem with the build system itself.

Please see the build report for more details. This link will be active for 21 days.

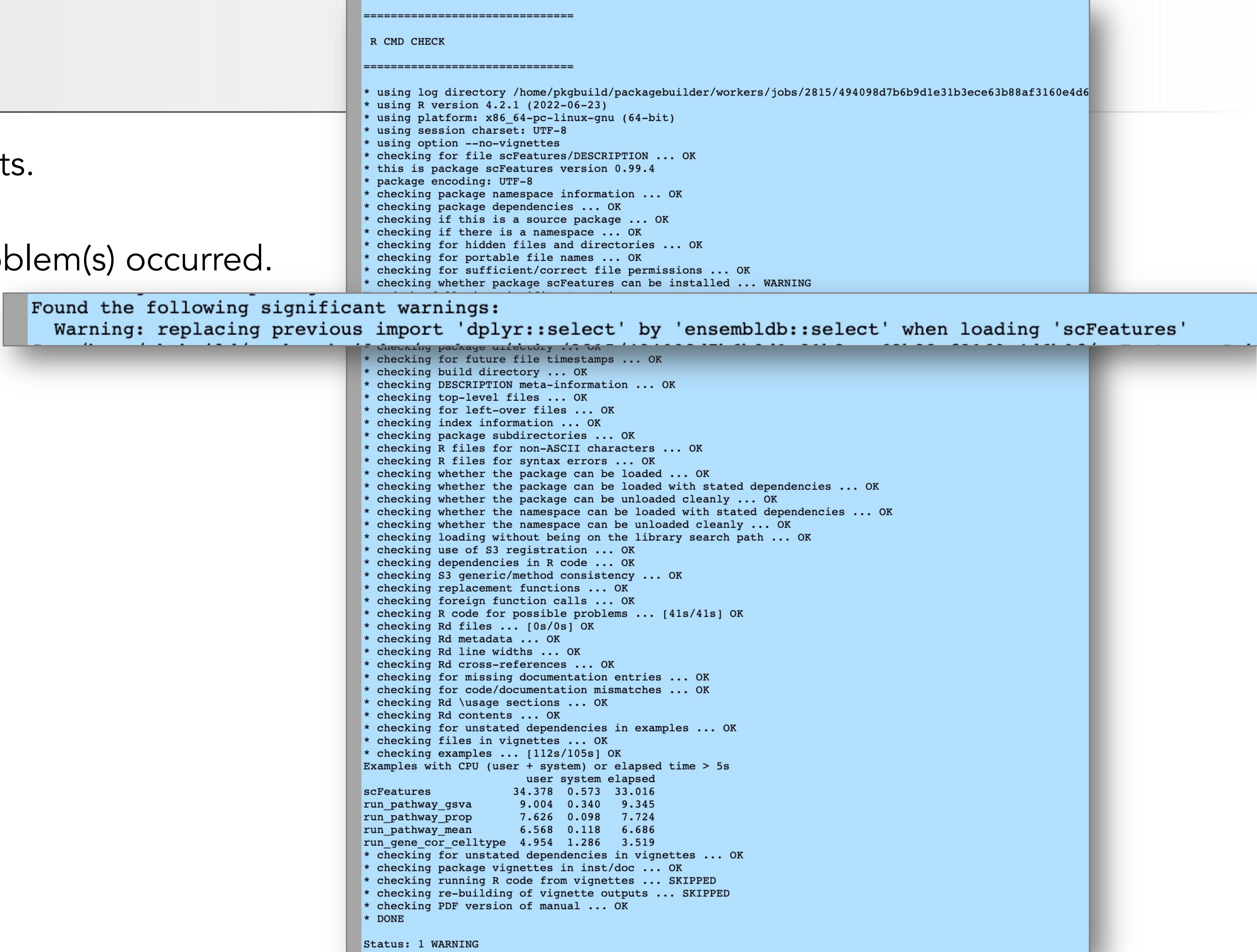
Remember: if you submitted your package after July 7th, 2020, when making changes to your repository push to `git@git.bioconductor.org:packages/scFeatures` to trigger a new build.
A quick tutorial for setting up remotes and pushing to upstream can be found here.

bioc-issue-bot added WARNINGS

Fixing errors/warnings

a. Check the build reports.

b. Identify where the problem(s) occurred.



```
===============================

 R CMD CHECK

===============================

* using log directory /home/pkgbuild/packagebuilder/workers/jobs/2815/494098d7b6b9d1e31b3ece63b88af3160e4d6
* using R version 4.2.1 (2022-06-23)
* using platform: x86_64-pc-linux-gnu (64-bit)
* using session charset: UTF-8
* using option --no-vignettes
* checking for file scFeatures/DESCRIPTION ... OK
* this is package scFeatures version 0.99.4
* package encoding: UTF-8
* checking package namespace information ... OK
* checking package dependencies ... OK
* checking if this is a source package ... OK
* checking if there is a namespace ... OK
* checking for hidden files and directories ... OK
* checking for portable file names ... OK
* checking for sufficient/correct file permissions ... OK
* checking whether package scFeatures can be installed ... WARNING
```

```
Found the following significant warnings:
  Warning: replacing previous import 'dplyr::select' by 'ensembldb::select' when loading 'scFeatures'
```

```
* checking for future file timestamps ... OK
* checking build directory ... OK
* checking DESCRIPTION meta-information ... OK
* checking top-level files ... OK
* checking for left-over files ... OK
* checking index information ... OK
* checking package subdirectories ... OK
* checking R files for non-ASCII characters ... OK
* checking R files for syntax errors ... OK
* checking whether the package can be loaded ... OK
* checking whether the package can be loaded with stated dependencies ... OK
* checking whether the package can be unloaded cleanly ... OK
* checking whether the namespace can be loaded with stated dependencies ... OK
* checking whether the namespace can be unloaded cleanly ... OK
* checking loading without being on the library search path ... OK
* checking use of S3 registration ... OK
* checking dependencies in R code ... OK
* checking S3 generic/method consistency ... OK
* checking replacement functions ... OK
* checking foreign function calls ... OK
* checking R code for possible problems ... [41s/41s] OK
* checking Rd files ... [0s/0s] OK
* checking Rd metadata ... OK
* checking Rd line widths ... OK
* checking Rd cross-references ... OK
* checking for missing documentation entries ... OK
* checking for code/documentation mismatches ... OK
* checking Rd \usage sections ... OK
* checking Rd contents ... OK
* checking for unstated dependencies in examples ... OK
* checking files in vignettes ... OK
* checking examples ... [112s/105s] OK
Examples with CPU (user + system) or elapsed time > 5s
                        user system elapsed
scFeatures            34.378  0.573  33.016
run_pathway_gsva       9.004  0.340   9.345
run_pathway_prop       7.626  0.098   7.724
run_pathway_mean       6.568  0.118   6.686
run_gene_cor_celltype  4.954  1.286   3.519
* checking for unstated dependencies in vignettes ... OK
* checking package vignettes in inst/doc ... OK
* checking running R code from vignettes ... SKIPPED
* checking re-building of vignette outputs ... SKIPPED
* checking PDF version of manual ... OK
* DONE

Status: 1 WARNING
```

Fixing errors/warnings

a. Check the build reports.

b. Identify where the problem(s) occurred.

c. Optional: ask Bioconductor people!!

Fixing errors/warnings

a. Check the build reports.

b. Identify where the problem(s) occurred.

c. Optional: ask Bioconductor people!!

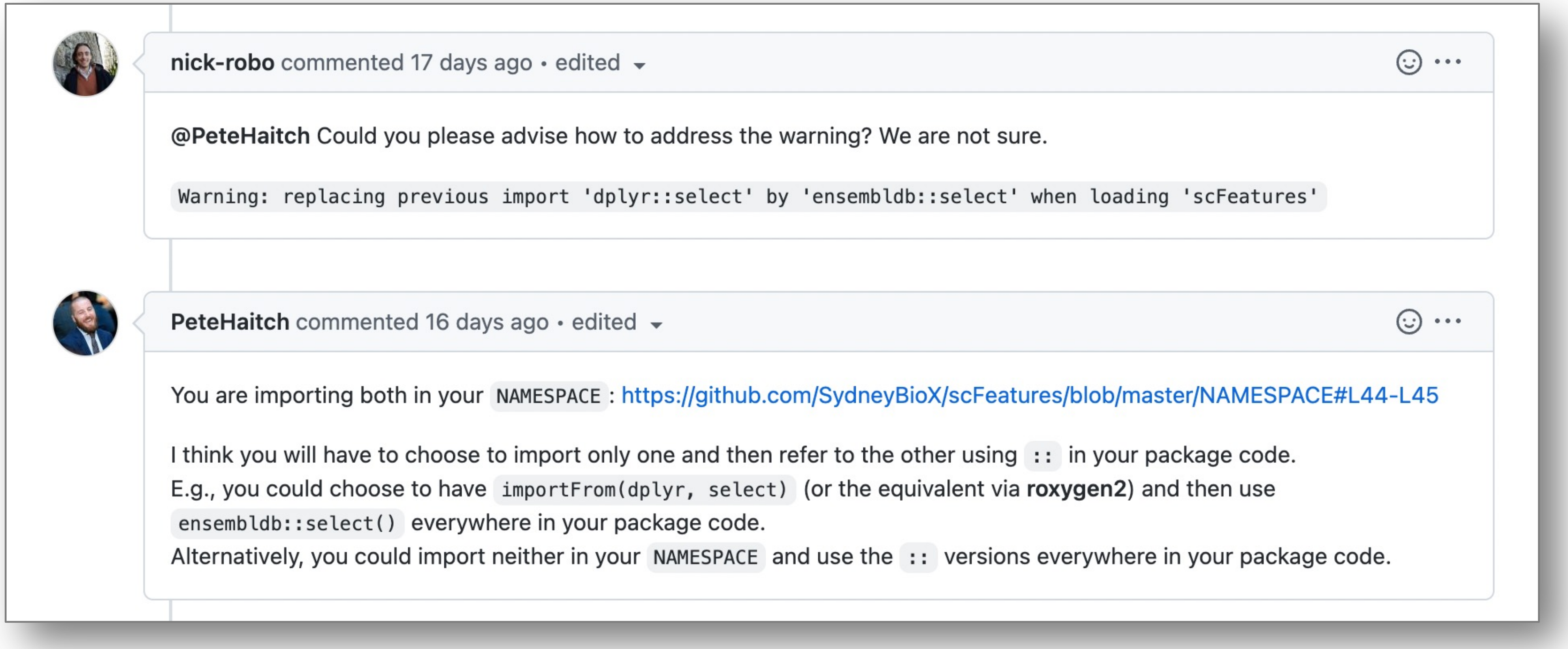
   - Please don’t: ask directly in the issue…
   - Please do: ask on bioc-devel mailing list!

Fixing errors/warnings

a. Check the build reports.

b. Identify where the problem(s) occurred.

c. Optional: ask Bioconductor people!!



nick-robo commented 17 days ago • edited

@PeteHaitch Could you please advise how to address the warning? We are not sure.

```
Warning: replacing previous import 'dplyr::select' by 'ensembldb::select' when loading 'scFeatures'
```

PeteHaitch commented 16 days ago • edited

You are importing both in your `NAMESPACE` : https://github.com/SydneyBioX/scFeatures/blob/master/NAMESPACE#L44-L45

I think you will have to choose to import only one and then refer to the other using `::` in your package code.
E.g., you could choose to have `importFrom(dplyr, select)` (or the equivalent via **roxygen2**) and then use `ensembldb::select()` everywhere in your package code.
Alternatively, you could import neither in your `NAMESPACE` and use the `::` versions everywhere in your package code.

Fixing errors/warnings

a. Check the build reports.

b. Identify where the problem(s) occurred.

c. Optional: ask Bioconductor people!!

d. Attempt to fix your errors

   - Change your code locally

   - Check locally

Fixing errors/warnings

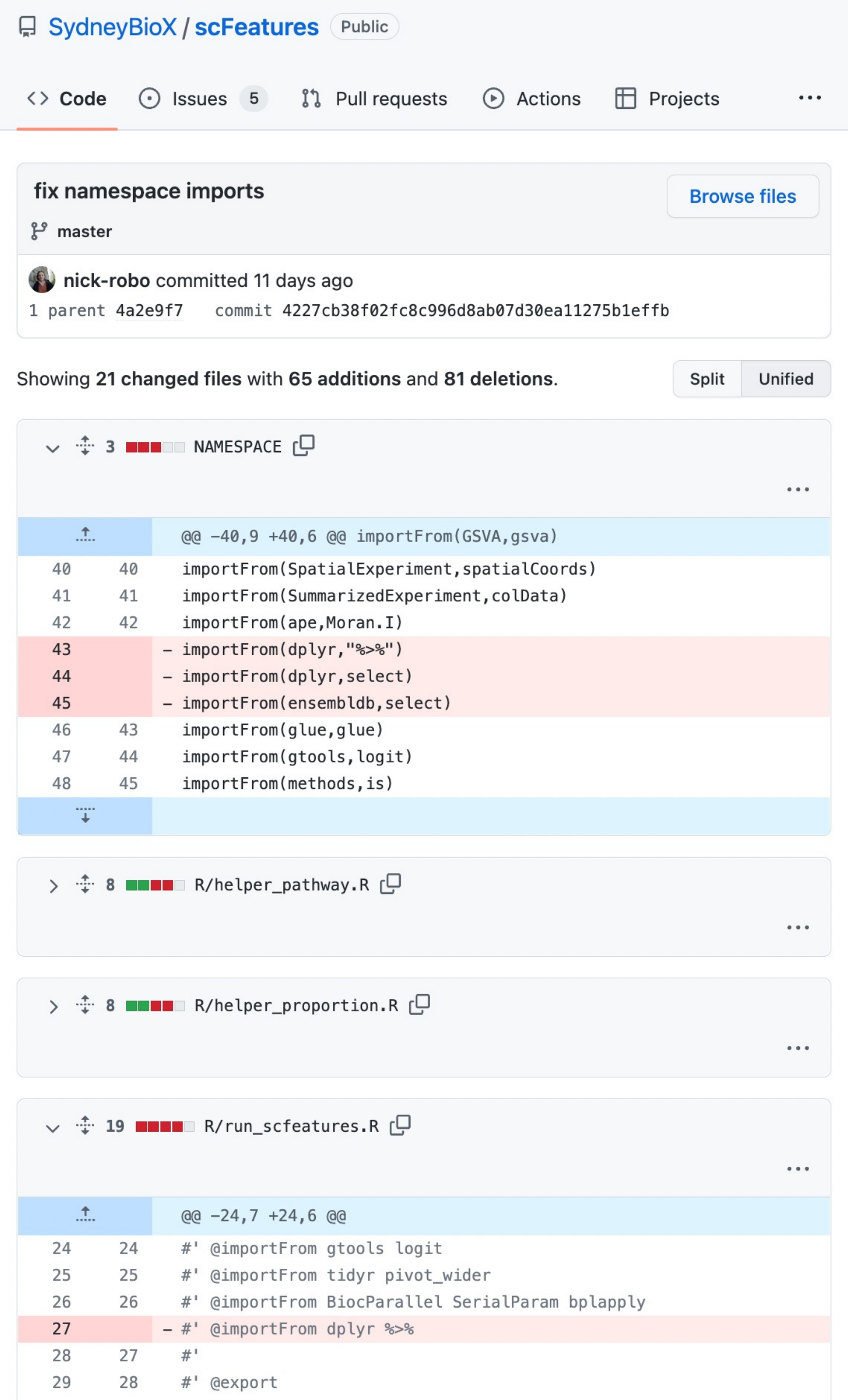
a. Check the build reports.

b. Identify where the problem(s) occurred.

c. Optional: ask Bioconductor people!!

d. Attempt to fix your errors

  - Change your code locally
  - Check locally
  - Push to <u>**your own**</u> GitHub repo



fix namespace imports

master

nick-robo committed 11 days ago

1 parent 4a2e9f7 commit 4227cb38f02fc8c996d8ab07d30ea11275b1effb

Showing **21 changed files** with **65 additions** and **81 deletions**.

3 NAMESPACE

```
@@ -40,9 +40,6 @@ importFrom(GSVA,gsva)
  importFrom(SpatialExperiment,spatialCoords)
  importFrom(SummarizedExperiment,colData)
  importFrom(ape,Moran.I)
- importFrom(dplyr,"%>%")
- importFrom(dplyr,select)
- importFrom(ensembldb,select)
  importFrom(glue,glue)
  importFrom(gtools,logit)
  importFrom(methods,is)
```

8 R/helper_pathway.R

8 R/helper_proportion.R

19 R/run_scfeatures.R

```
@@ -24,7 +24,6 @@
  #' @importFrom gtools logit
  #' @importFrom tidyr pivot_wider
  #' @importFrom BiocParallel SerialParam bplapply
- #' @importFrom dplyr %>%
  #'
  #' @export
```

Fixing errors/warnings

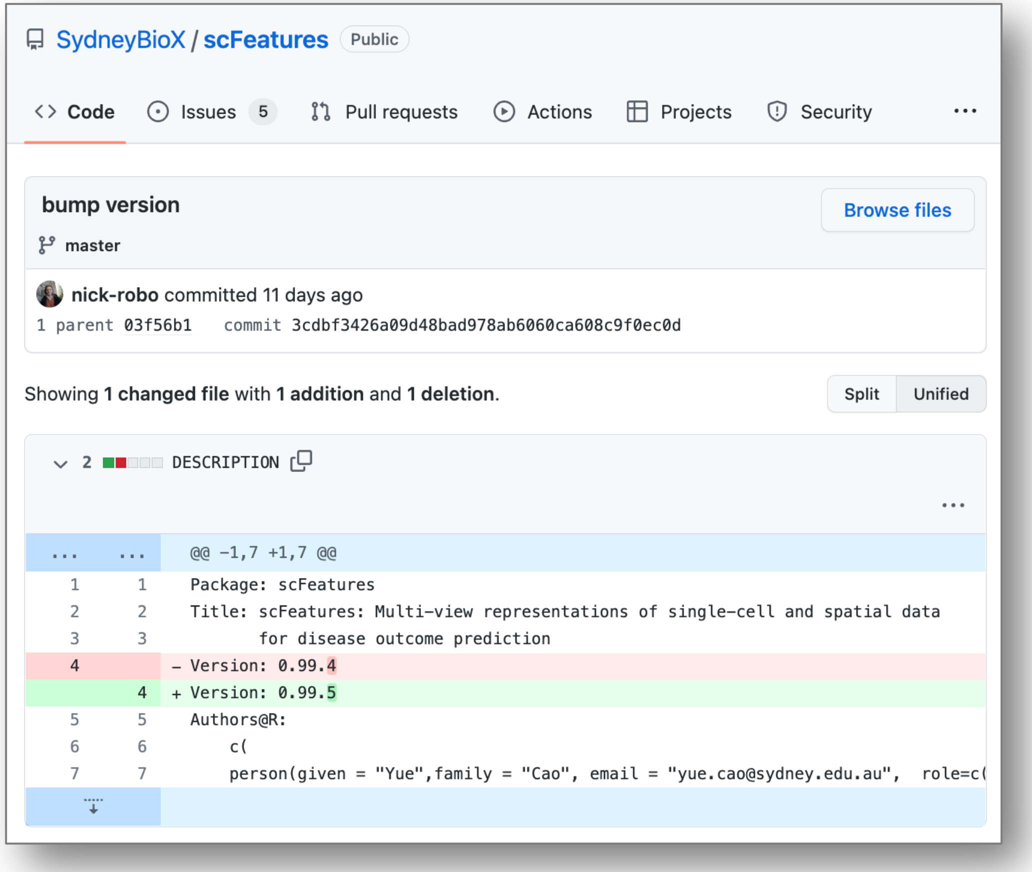
a. Check the build reports.

b. Identify where the problem(s) occurred.

c. Optional: ask Bioconductor people!!

d. Attempt to fix your errors

  - Change your code locally
  - Check locally
  - Push to **your own** GitHub repo
  - Bump package version!



bump version

master

nick-robo committed 11 days ago

1 parent 03f56b1 commit 3cdbf3426a09d48bad978ab6060ca608c9f0ec0d

Showing **1 changed file** with **1 addition** and **1 deletion**.

2 DESCRIPTION

```
@@ -1,7 +1,7 @@
  Package: scFeatures
  Title: scFeatures: Multi-view representations of single-cell and spatial data
         for disease outcome prediction
- Version: 0.99.4
+ Version: 0.99.5
  Authors@R:
      c(
      person(given = "Yue",family = "Cao", email = "yue.cao@sydney.edu.au",  role=c(
```

Fixing errors/warnings

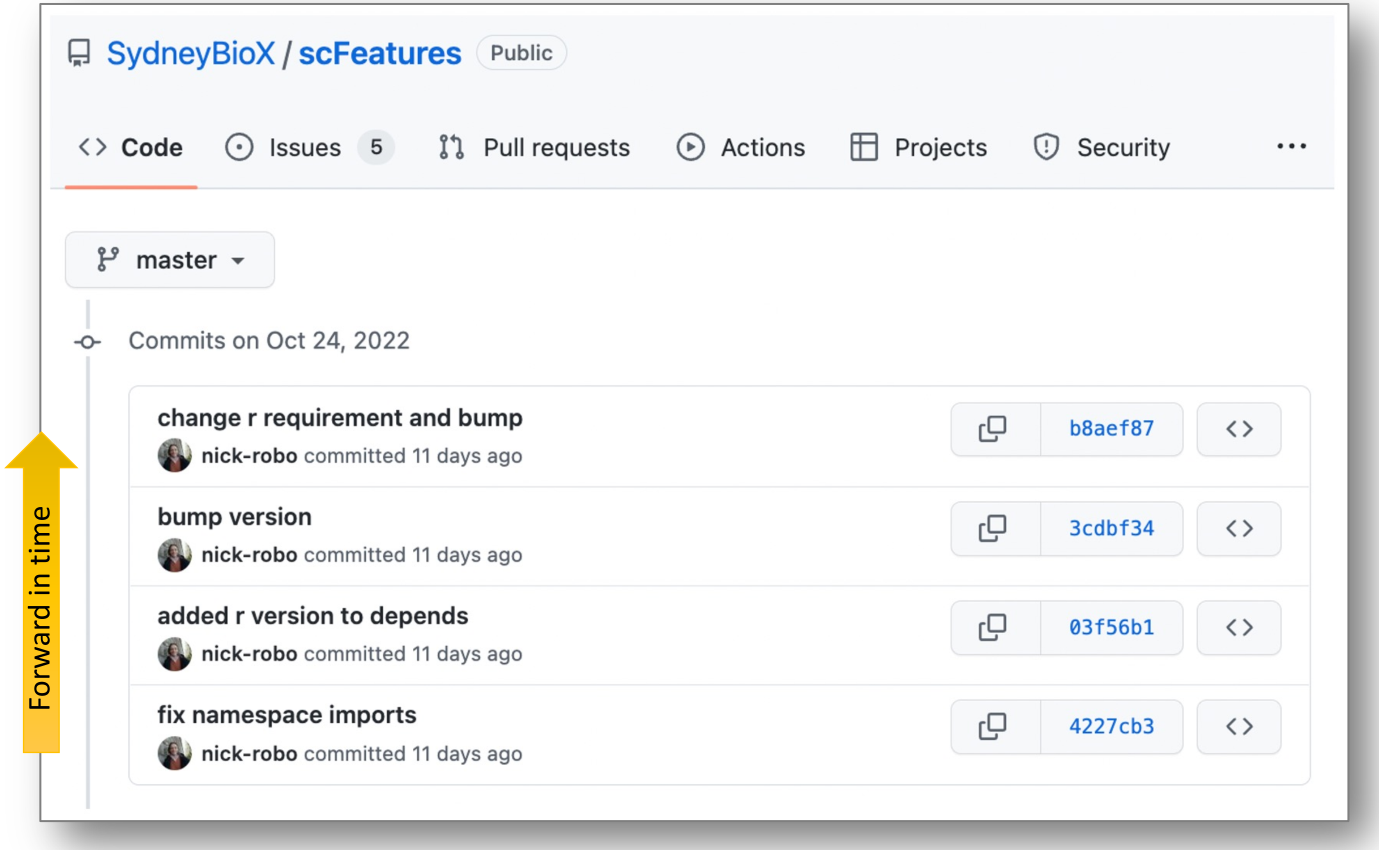
a. Check the build reports.

b. Identify where the problem(s) occurred.

c. Optional: ask Bioconductor people!!

d. Attempt to fix your errors

  - Change your code locally
  - Check locally
  - Push to <u>**your own**</u> GitHub repo
  - Bump package version!



SydneyBioX / **scFeatures** Public

Commits on Oct 24, 2022

change r requirement and bump
nick-robo committed 11 days ago b8aef87

bump version
nick-robo committed 11 days ago 3cdbf34

added r version to depends
nick-robo committed 11 days ago 03f56b1

fix namespace imports
nick-robo committed 11 days ago 4227cb3

Forward in time

Fixing errors/warnings

a. Check the build reports.

b. Identify where the problem(s) occurred.

c. Optional: ask Bioconductor people!!

d. Attempt to fix your errors
    - Change your code locally
    - Check locally
    - Push to <u>your own</u> GitHub repo
    - Bump package version!
    - Push to Bioc upstream branch!!!!

```
## Add Bioconductor upstream remote
> git remote add upstream
git@git.bioconductor.org:packages/<YOUR-REPOSITORY-NAME>.git

## Commit changes
> git add <files changed>
> git commit -m "<informative commit message>"

## Bump package version
> git add DESCRIPTION
> git commit -m ”bump to 0.99.4"

## Push to BioC upstream remote and your own remote
> git push
> git push upstream master
```

Fixing errors/warnings

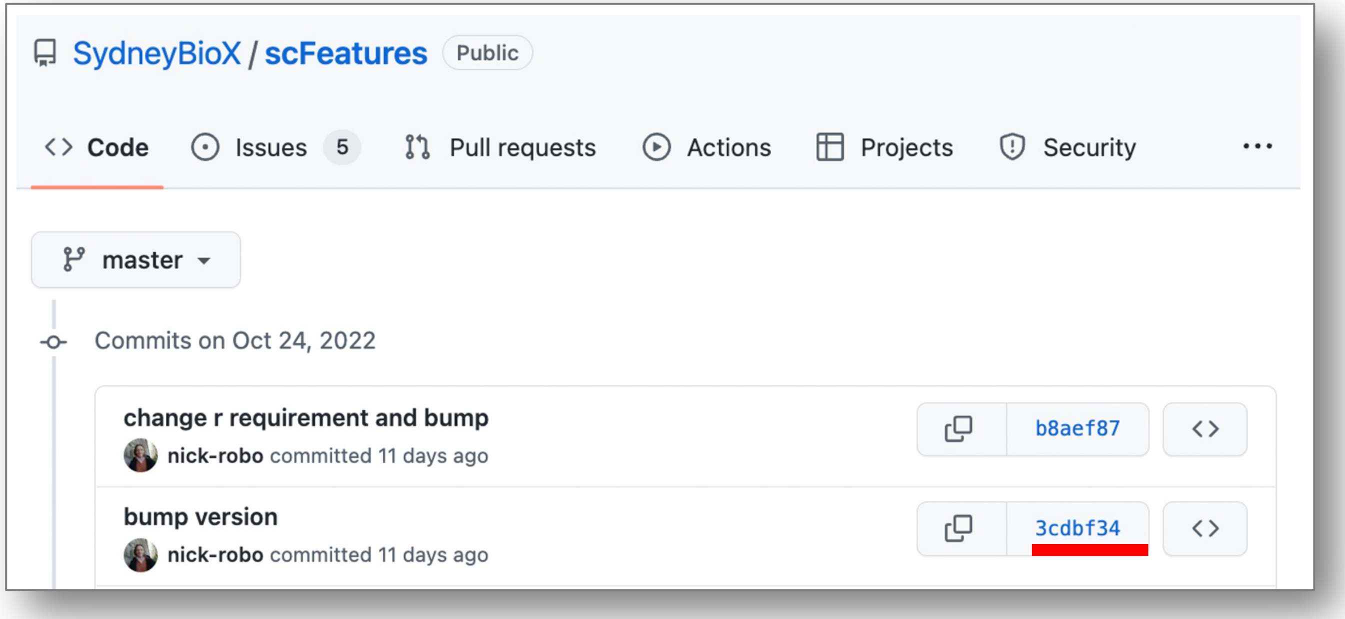
a. Check the build reports.

b. Identify where the problem(s) occurred.

c. Optional: ask Bioconductor people!!

d. Attempt to fix your errors

e. Version bumping will trigger a new Single Package Builder run



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nick-robo committed 11 days ago
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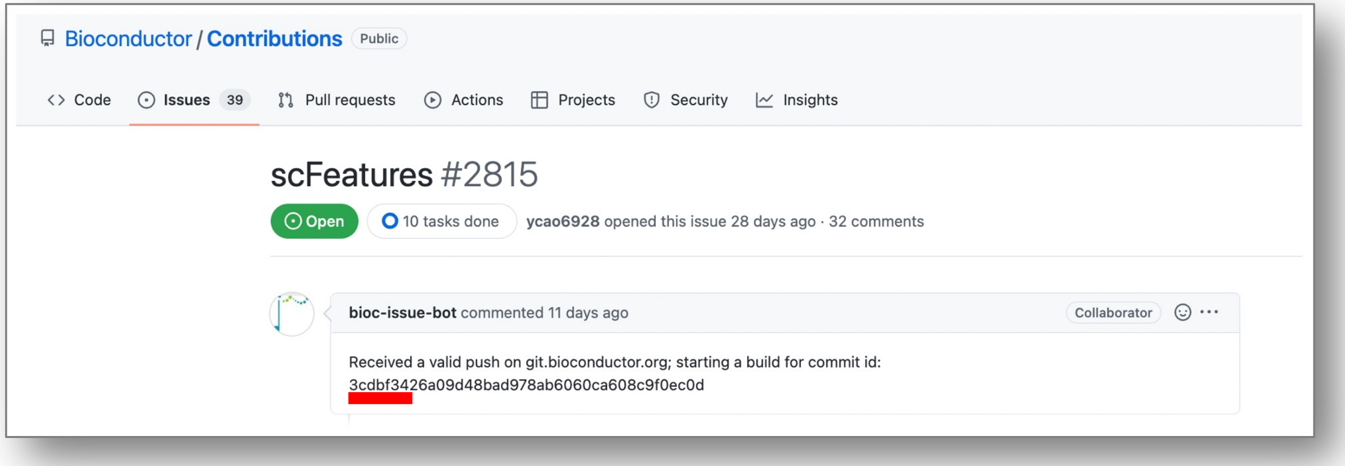

scFeatures #2815

Open · 10 tasks done · **ycao6928** opened this issue 28 days ago · 32 comments

bioc-issue-bot commented 11 days ago

Received a valid push on git.bioconductor.org; starting a build for commit id:
3cdbf3426a09d48bad978ab6060ca608c9f0ec0d

Fixing errors/warnings

a. Check the build reports.

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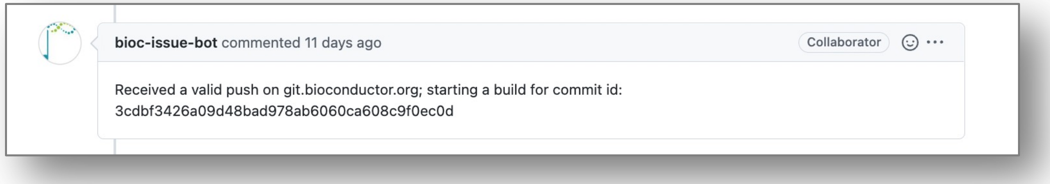

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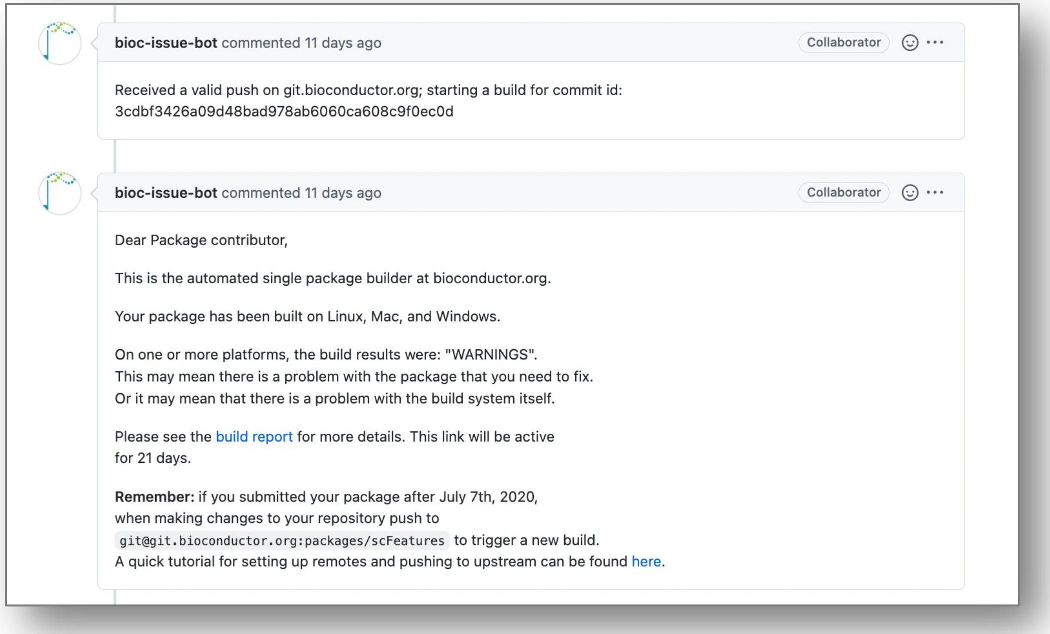

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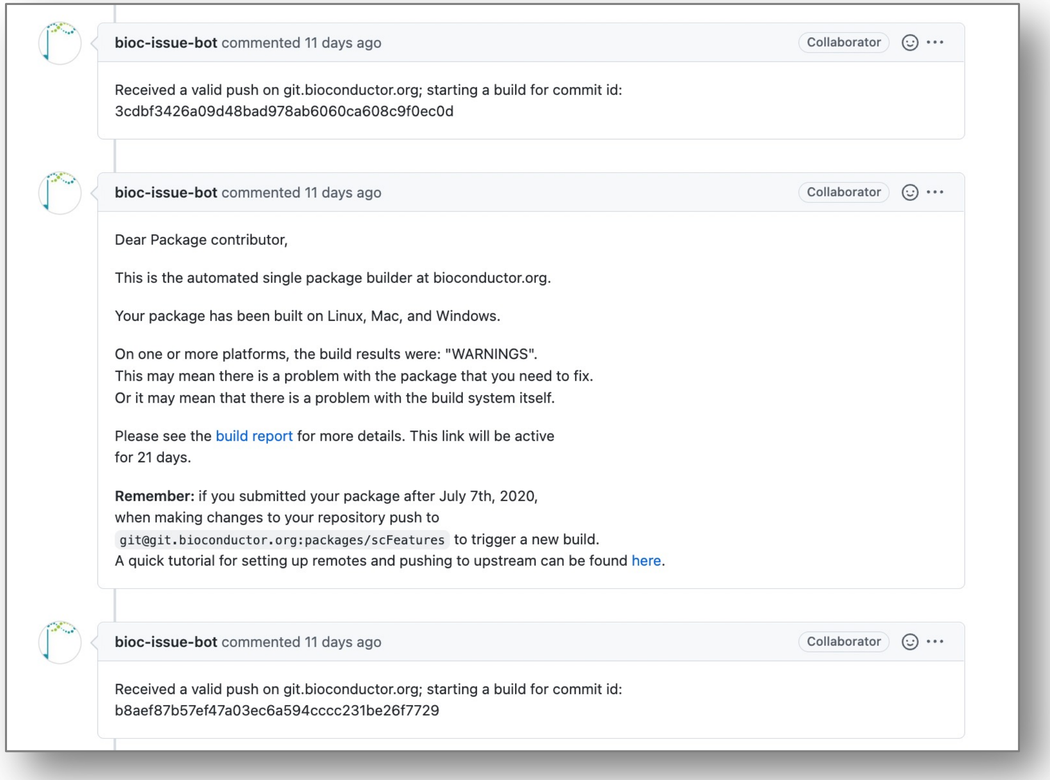
f. Repeat…



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bioc-issue-bot commented 11 days ago

Received a valid push on git.bioconductor.org; starting a build for commit id:
b8aef87b57ef47a03ec6a594cccc231be26f7729

Fixing errors/warnings

a. Check the build reports.

b. Identify where the problem(s) occurred.

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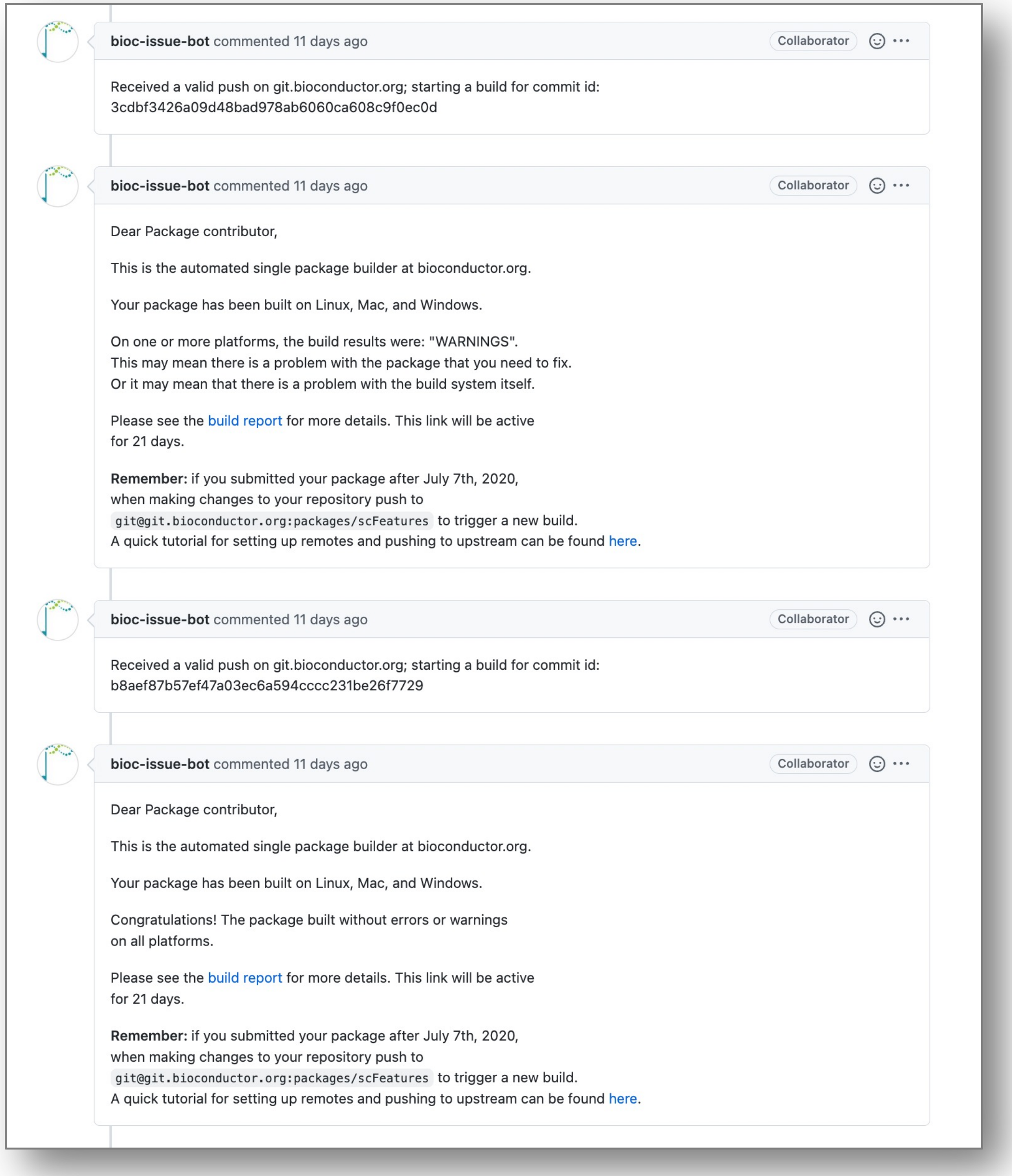
e. Version bumping will trigger a new Single Package Builder run

f. Repeat…



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Dear Package contributor,

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on all platforms.

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a. Check the build reports.

b. Identify where the problem(s) occurred.

c. Optional: ask Bioconductor people!!

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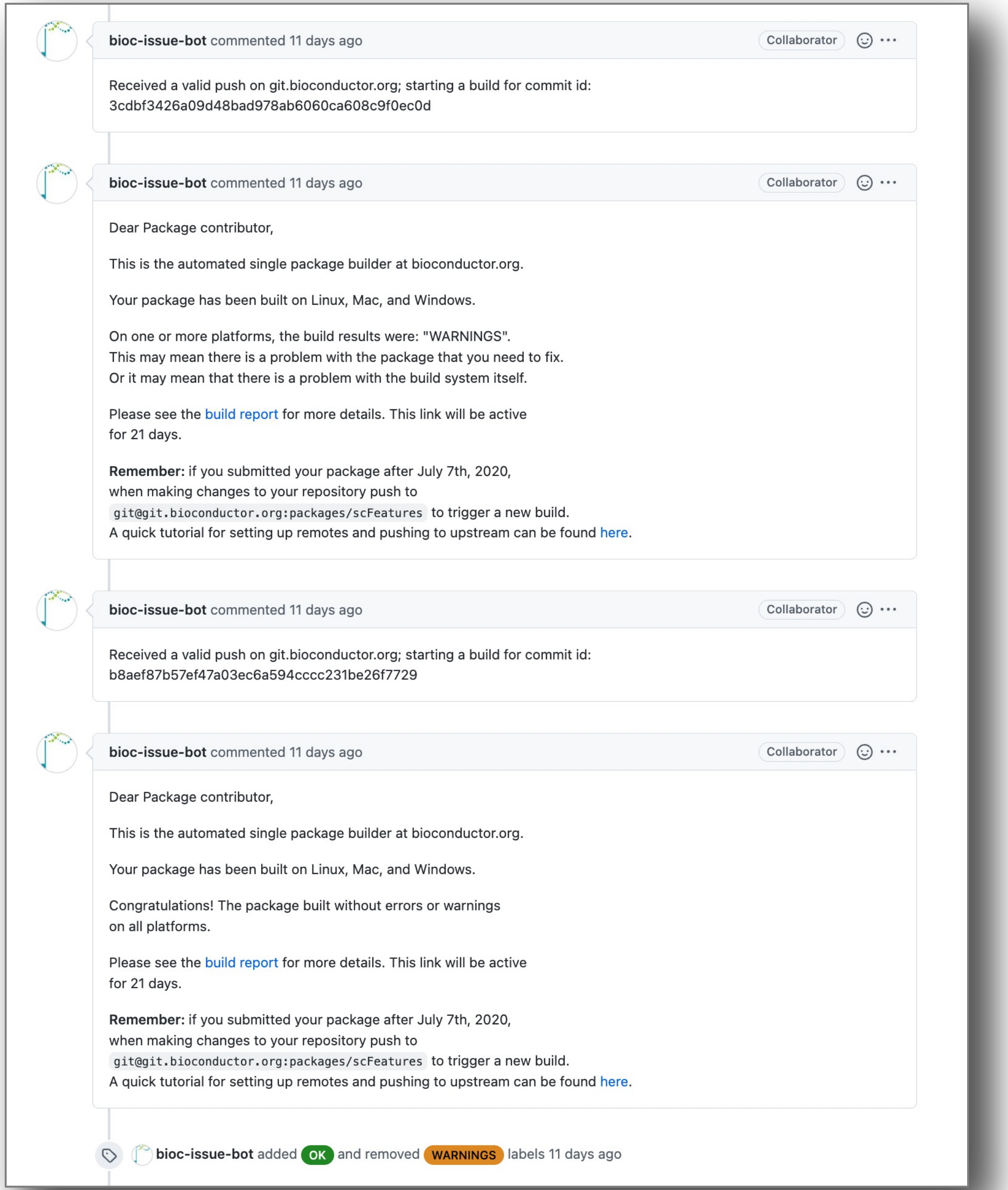
e. Version bumping will trigger a new Single Package Builder run

f. Repeat…

g. Hurray 🎉🥳🎊



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bioc-issue-bot added OK and removed WARNINGS labels 11 days ago

Fixing errors/warnings

a. Check the build reports.

b. Identify where the problem(s) occurred.

c. Optional: ask Bioconductor people!!

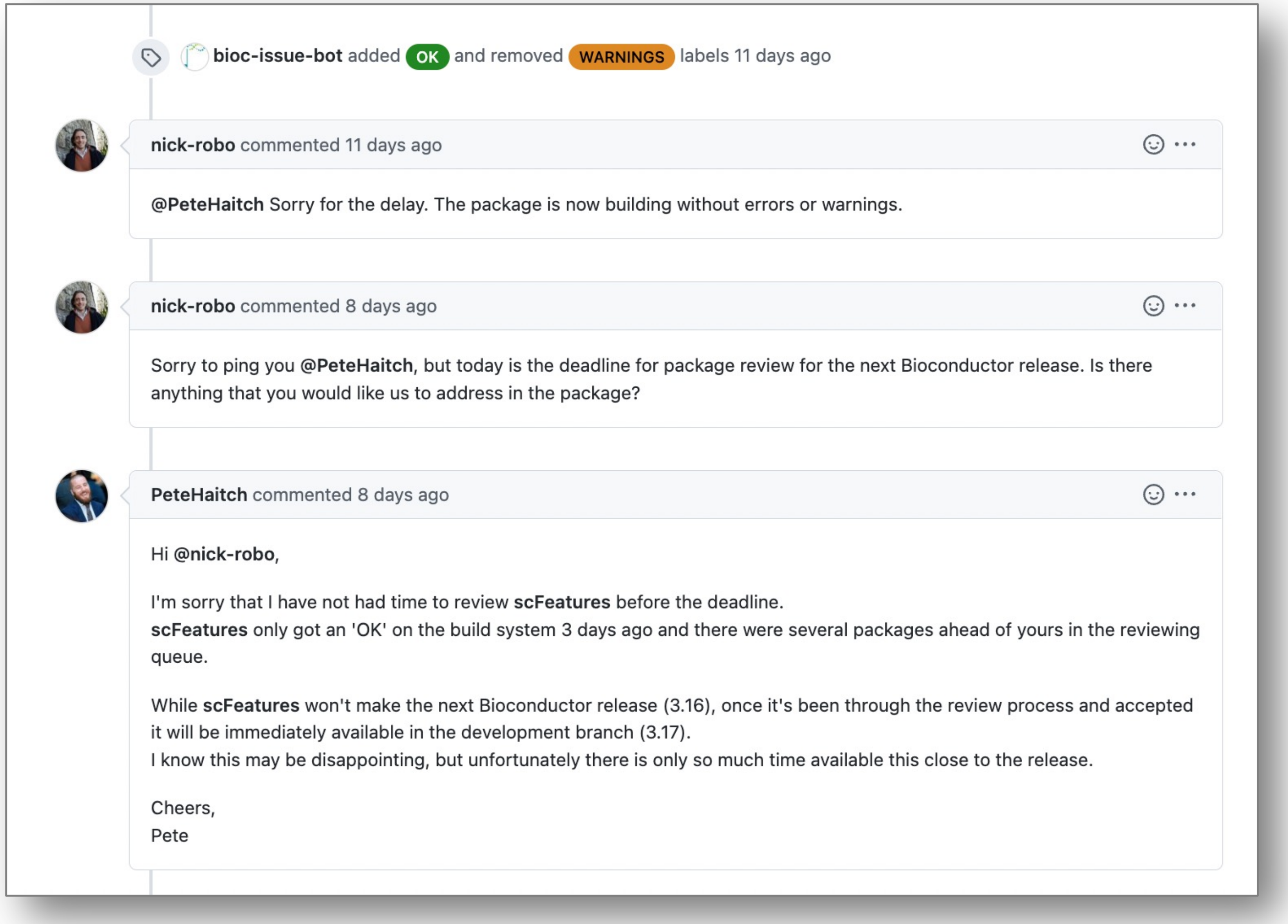
d. Attempt to fix your errors

e. Version bumping will trigger a new Single Package Builder run

f. Repeat…

g. Hurray 🎉🥳🎊

h. Well not so fast…



bioc-issue-bot added OK and removed WARNINGS labels 11 days ago

nick-robo commented 11 days ago

@PeteHaitch Sorry for the delay. The package is now building without errors or warnings.

nick-robo commented 8 days ago

Sorry to ping you **@PeteHaitch**, but today is the deadline for package review for the next Bioconductor release. Is there anything that you would like us to address in the package?

PeteHaitch commented 8 days ago

Hi **@nick-robo**,

I'm sorry that I have not had time to review **scFeatures** before the deadline.
scFeatures only got an 'OK' on the build system 3 days ago and there were several packages ahead of yours in the reviewing queue.

While **scFeatures** won't make the next Bioconductor release (3.16), once it's been through the review process and accepted it will be immediately available in the development branch (3.17).
I know this may be disappointing, but unfortunately there is only so much time available this close to the release.

Cheers,
Pete

Reviewer’s comments

6. Addressing reviewer’s comments

Review

Key: ❗ Required ⚠ Recommended ● Optional ? Question

General package development

DESCRIPTION file

The NEWS file

The CITATION file

Documentation

Vignette

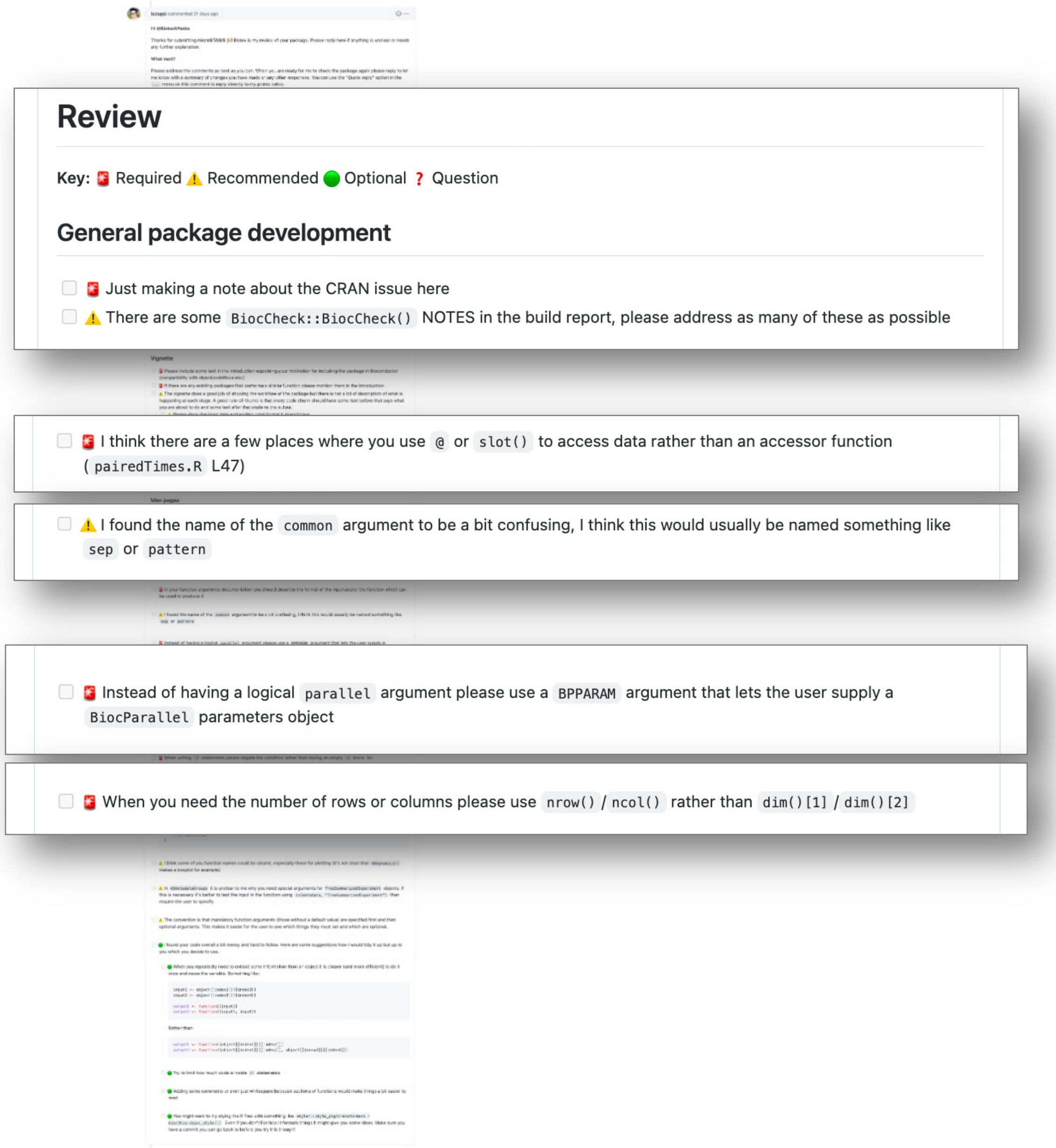
Man pages

Code

R

Reviewer's comments

6. Addressing reviewer's comments



Review

Key: 🟥 Required ⚠️ Recommended 🟢 Optional ❓ Question

General package development

- ☐ 🟥 Just making a note about the CRAN issue here
- ☐ ⚠️ There are some `BiocCheck::BiocCheck()` NOTES in the build report, please address as many of these as possible

- ☐ 🟥 I think there are a few places where you use `@` or `slot()` to access data rather than an accessor function (`pairedTimes.R` L47)

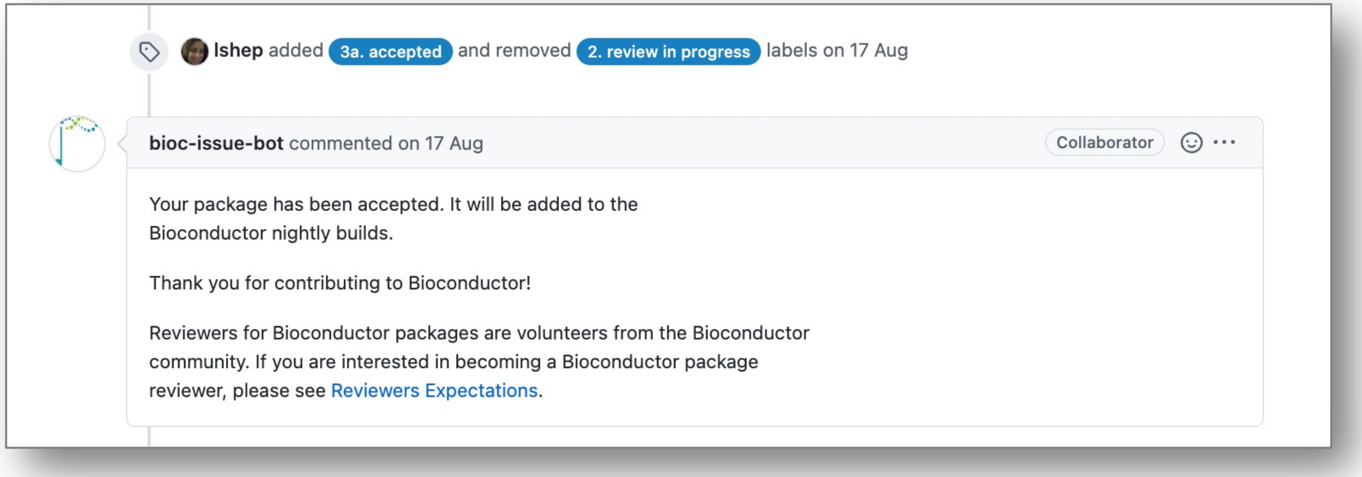
- ☐ ⚠️ I found the name of the `common` argument to be a bit confusing, I think this would usually be named something like `sep` or `pattern`

- ☐ 🟥 Instead of having a logical `parallel` argument please use a `BPPARAM` argument that lets the user supply a `BiocParallel` parameters object

- ☐ 🟥 When you need the number of rows or columns please use `nrow()` / `ncol()` rather than `dim()[1]` / `dim()[2]`

Reviewer's comments

6. Addressing reviewer's comments



bioc-issue-bot commented on 17 Aug

Your package has been accepted. It will be added to the Bioconductor nightly builds.

Thank you for contributing to Bioconductor!

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Reviewer’s comments

As a general principle, reviews are largely unfair/unhomogenized across reviewers. Sounds familiar?

Review

General package development

DESCRIPTION file

The NEWS file

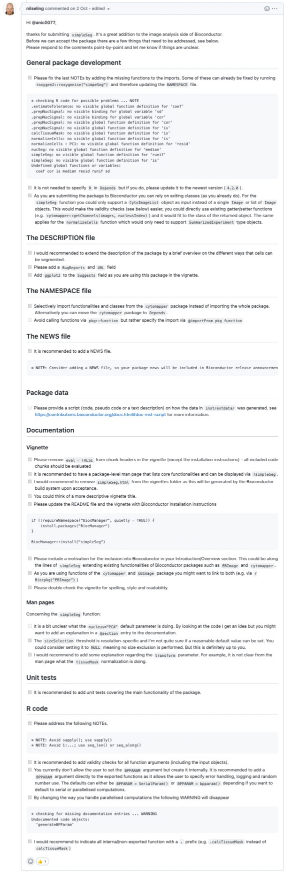
The CITATION file

Documentation

Vignette

Man pages

Code



nilseling commented on 2 Oct • edited

Hi **@anic0077**,

thanks for submitting `simpleSeg`. It's a great addition to the image analysis side of Bioconductor.
Before we can accept the package there are a few things that need to be addressed, see below.
Please respond to the comments point-by-point and let me know if things are unclear.

General package development

- ☑ Please fix the last NOTEs by adding the missing functions to the imports. Some of these can already be fixed by running `roxygen2::roxygenise("simpeSeg")` and therefore updating the `NAMESPACE` file.

```
* checking R code for possible problems ... NOTE
.estimateTolerance: no visible global function definition for ‘coef’
.prepNucSignal: no visible binding for global variable ‘sd’
.prepNucSignal: no visible binding for global variable ‘cor’
.prepNucSignal: no visible global function definition for ‘cor’
.prepNucSignal: no visible global function definition for ‘is’
calcTissueMask: no visible global function definition for ‘is’
normalizeCells: no visible global function definition for ‘is’
normalizeCells : PC1: no visible global function definition for ‘resid’
nucSeg: no visible global function definition for ‘median’
simpleSeg: no visible global function definition for ‘runif’
simpleSeg: no visible global function definition for ‘is’
Undefined global functions or variables:
  coef cor is median resid runif sd
```

- ☑ It is not needed to specify `R` in `Depends` but if you do, please update it to the newest version (`4.2.0`).
- ☑ As you are submitting the package to Bioconductor you can rely on exiting classes (as you already do). For the `simpleSeg` function you could only support a `CytoImageList` object as input instead of a single `Image` or list of `Image` objects. This would make the validity checks (see below) easier, you could directly use existing getter/setter functions (e.g. `cytomapper::getChannels(images, nucleusIndex)`) and it would fit to the class of the returned object. The same applies for the `normalizeCells` function which would only need to support `SummarizedExperiment` type objects.

The DESCRIPTION file

- ☑ I would recommended to extend the description of the package by a brief overview on the different ways that cells can be segmented.
- ☑ Please add a `BugReports` and `URL` field
- ☑ Add `ggplot2` to the `Suggests` field as you are using this package in the vignette.

The NAMESPACE file

- ☑ Selectively import functionalities and classes from the `cytomapper` package instead of importing the whole package. Alternatively you can move the `cytomapper` package to `Depends`.
- ☐ Avoid calling functions via `pkg::function` but rather specify the import via `@importFrom pkg function`

The NEWS file

- ☑ It is recommended to add a NEWS file.

```
* NOTE: Consider adding a NEWS file, so your package news will be included in Bioconductor release announcemen
```

Package data

- ☐ Please provide a script (code, pseudo code or a text description) on how the data in `inst/extdata/` was generated. see https://contributions.bioconductor.org/docs.html#doc-inst-script for more information.

Documentation

Vignette

- ☑ Please remove `eval = FALSE` from chunk headers in the vignette (except the installation instructions) - all included code chunks should be evaluated
- ☑ It is recommended to have a package-level man page that lists core functionalities and can be displayed via `?simpleSeg`.
- ☑ I would recommend to remove `simpleSeg.html` from the vignettes folder as this will be generated by the Bioconductor build system upon acceptance.
- ☑ You could think of a more descriptive vignette title.
- ☑ Please update the README file and the vignette with Bioconductor installation instructions

```
if (!requireNamespace("BiocManager", quietly = TRUE)) {
    install.packages("BiocManager")
}

BiocManager::install("simpleSeg")
```

- ☑ Please include a motivation for the inclusion into Biocodunctor in your Introduction/Overview section. This could be along the lines of `simpleSeg` extending existing functionalities of Bioconductor packages such as `EBImage` and `cytomapper`.
- ☑ As you are using functions of the `cytomapper` and `EBImage` package you might want to link to both (e.g. via `r Biocpkg("EBImage")`)
- ☑ Please double check the vignette for spelling, style and readability.

Man pages

Concerning the `simpleSeg` function:

- ☐ It is a bit unclear what the `nucleus="PCA"` default parameter is doing. By looking at the code I get an idea but you might want to add an explanation in a `@section` entry to the documentation.
- ☑ The `sizeSelection` threshold is resolution-specific and I'm not quite sure if a reasonable default value can be set. You could consider setting it to `NULL` meaning no size exclusion is performed. But this is definitely up to you.
- ☑ I would recommend to add some explanation regarding the `transform` parameter. For example, it is not clear from the man page what the `tissueMask` normalization is doing.

Unit tests

- ☑ It is recommended to add unit tests covering the main functionality of the package.

R code

- ☑ Please address the following NOTEs.

```
* NOTE: Avoid sapply(); use vapply()
* NOTE: Avoid 1:...; use seq_len() or seq_along()
```

- ☑ It is recommended to add validity checks for all function arguments (including the input objects).
- ☑ You currently don't allow the user to set the `BPPARAM` argument but create it internally. It is recommended to add a `BPPARAM` argument directly to the exported functions as it allows the user to specify error handling, logging and random number use. The defaults can either be `BPPARAM = SerialParam()` or `BPPARAM = bpparam()` depending if you want to default to serial or parallelised computations.
- ☑ By changing the way you handle parallelised computations the following WARNING will disappear

```
* checking for missing documentation entries ... WARNING
Undocumented code objects:
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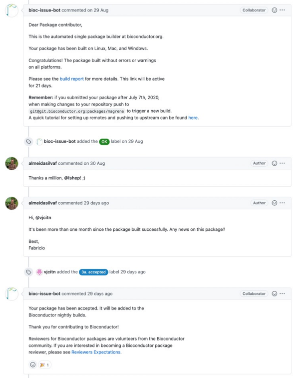
- ☑ I would recommend to indicate all internal/non-exported function with a `.` prefix (e.g. `.calcTissueMask` instead of `calcTissueMask`)

👍 1



bioc-issue-bot commented on 29 Aug

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on all platforms.

Please see the build report for more details. This link will be active
for 21 days.

Remember: if you submitted your package after July 7th, 2020,
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`git@git.bioconductor.org:packages/magrene` to trigger a new build.
A quick tutorial for setting up remotes and pushing to upstream can be found here.

bioc-issue-bot added the OK label on 29 Aug

almeidasilvaf commented on 30 Aug

Thanks a million, **@lshep**! ;)

almeidasilvaf commented 29 days ago

Hi, **@vjcitn**

It's been more than one month since the package built successfully. Any news on this package?

Best,
Fabricio

vjcitn added the 3a. accepted label 29 days ago

bioc-issue-bot commented 29 days ago

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🎉 1

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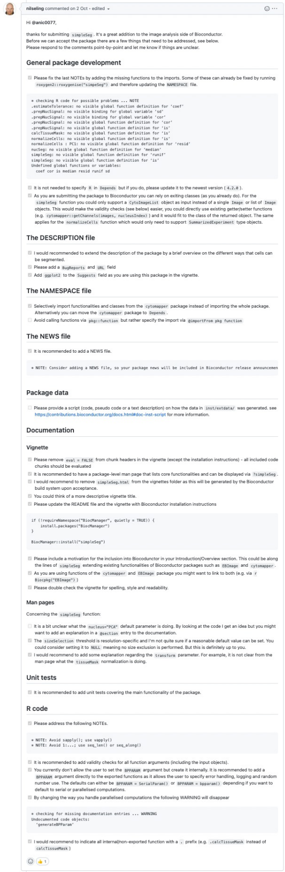

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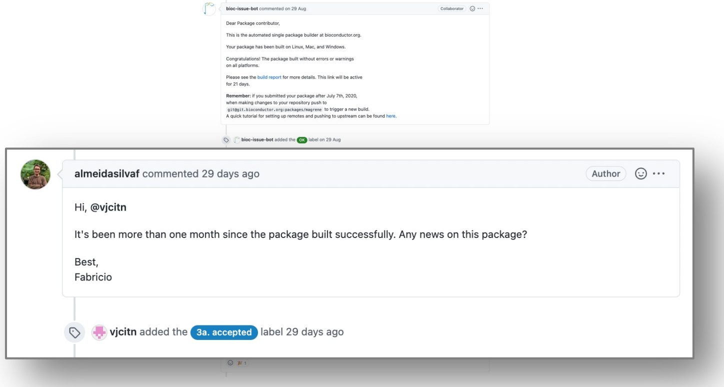

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It's been more than one month since the package built successfully. Any news on this package?

Best,
Fabricio

vjcitn added the 3a. accepted label 29 days ago

Maintaining package

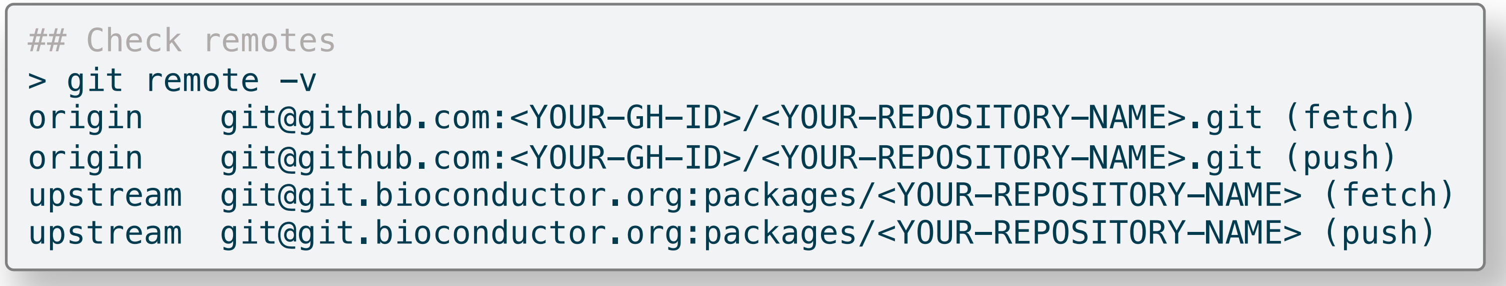
Once your package is accepted, you will have to maintain it, e.g. to fix bugs/implement new functionalities.

Full instructions: https://contributions.bioconductor.org/git-version-control.html

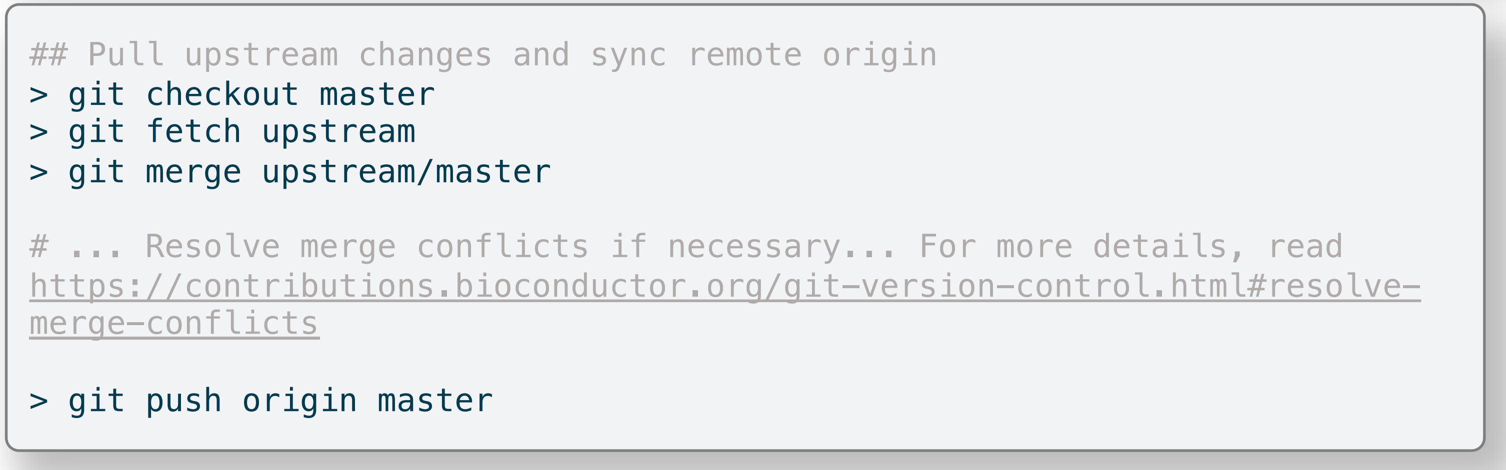
Maintaining package

Maintaining a Bioconductor package will require to:

1. Pull upstream changes (**There will be some!!! Don't mess that up!**)



```
## Check remotes
> git remote -v
origin    git@github.com:<YOUR-GH-ID>/<YOUR-REPOSITORY-NAME>.git (fetch)
origin    git@github.com:<YOUR-GH-ID>/<YOUR-REPOSITORY-NAME>.git (push)
upstream  git@git.bioconductor.org:packages/<YOUR-REPOSITORY-NAME> (fetch)
upstream  git@git.bioconductor.org:packages/<YOUR-REPOSITORY-NAME> (push)
```



```
## Pull upstream changes and sync remote origin
> git checkout master
> git fetch upstream
> git merge upstream/master

# ... Resolve merge conflicts if necessary... For more details, read
https://contributions.bioconductor.org/git-version-control.html#resolve-
merge-conflicts

> git push origin master
```

Maintaining package

Maintaining a Bioconductor package will require to:

1. Pull upstream changes (**There will be some!!! Don’t mess that up!**)
2. Commit changes to local master and push to remote origin & upstream (i.e. your GH and Bioconductor)

```
## Commit changes
> git checkout master
> git add <name of file changed>
> git commit -m "My informative commit message describing the change"

## Bump package version
> git add DESCRIPTION
> git commit -m ”bump to 1.0.1"

## Push your local commits to the remote origin (your GitHub)
> git push origin master

## Push your local commits to the remote upstream (Bioconductor)
> git push upstream master
```

Maintaining package

Maintaining a Bioconductor package will require to:

1. Pull upstream changes (**There will be some!!! Don't mess that up!**)
2. Commit changes to local master and push to remote origin & upstream (i.e. your GH and Bioconductor)
3. If you intend to work a new functionalities, it's recommended to do it in a separate local branch.

```
## Create new local branch and work there
> git checkout -b <NEW-FUNC-BRANCH>
# ...multiple rounds of edit, add, commit

## Merge with local master branch
> git checkout master
> git merge <NEW-FUNC-BRANCH>

## Bump package version
> git add DESCRIPTION
> git commit -m ”bump to 1.0.1"

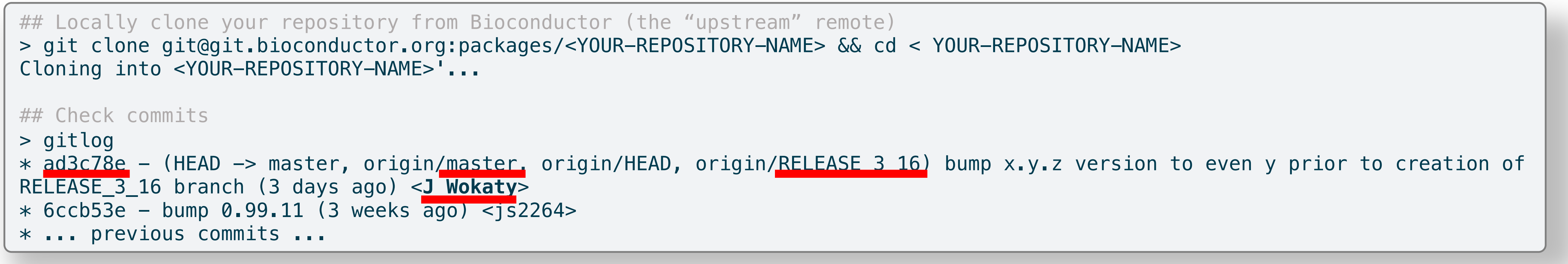
## Push your local commits to the remote origin (your GitHub)
> git push origin master

## Push your local commits to the remote upstream (Bioconductor)
> git push upstream master
```

Updating your origin after each Bioconductor release

At each Bioconductor release, a Bioconductor core member will:

1. Create a new branch for your package, in upstream remote (RELEASE_<#>)



```
## Locally clone your repository from Bioconductor (the “upstream” remote)
> git clone git@git.bioconductor.org:packages/<YOUR-REPOSITORY-NAME> && cd < YOUR-REPOSITORY-NAME>
Cloning into <YOUR-REPOSITORY-NAME>'...

## Check commits
> gitlog
* ad3c78e - (HEAD -> master, origin/master, origin/HEAD, origin/RELEASE_3_16) bump x.y.z version to even y prior to creation of
RELEASE_3_16 branch (3 days ago) <J Wokaty>
* 6ccb53e - bump 0.99.11 (3 weeks ago) <js2264>
* ... previous commits ...
```

Updating your origin after each Bioconductor release

At each Bioconductor release, a Bioconductor core member will:

1. Create a new branch for your package, in upstream remote (RELEASE_<#>)
2. Update your package version (DESCRIPTION file) in this branch

```
## Check last commit
> git show
commit ad3c78e02c0b0210508ab3499a78f51e1fbdfcf0 (origin/RELEASE_3_16)
Author: J Wokaty <jennifer.wokaty@sph.cuny.edu>
Date:   Tue Nov 1 11:27:34 2022 -0400

    bump x.y.z version to even y prior to creation of RELEASE_3_16 branch

diff --git a/DESCRIPTION b/DESCRIPTION
index a9710ef..bda26ca 100644
--- a/DESCRIPTION
+++ b/DESCRIPTION
@@ -1,6 +1,6 @@
-Version: 0.99.11
+Version: 1.0.0
```

Updating your origin after each Bioconductor release

You must keep your local (and origin) repos in sync!

```
## Fetch changes from all remote branches (BioC upstream and your origin)
> git fetch --all

## Make sure you are working in master
> git checkout master

## Merge changes from BioC upstream and your origin
> git merge upstream/master
> git merge origin/master

# ... Resolve merge conflicts if any...

## Push your local commits to the remote origin (your GitHub) and remote upstream (Bioconductor)
> git push upstream master
> git push origin master
```

Updating your origin after each Bioconductor release

Don’t forget to do that for the release branch as well.

```
## Fetch changes from all remote branches (BioC upstream and your origin)
> git fetch --all

## Make sure you are working in master
> git checkout RELEASE_<#>

## Merge changes from BioC upstream and your origin
> git merge upstream/RELEASE_<#>
> git merge origin/RELEASE_<#>

# ... Resolve merge conflicts if any...

## Push your local commits to the remote origin (your GitHub) and remote upstream (Bioconductor)
> git push upstream RELEASE_<#>
> git push origin RELEASE_<#>
```