

GitHub issues and pull requests

Contributing to a BIGslu R package

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Contents


Overview	1
1. GitHub issues	1
1.1: Create an issue	2
1.2: Create an issue list	2
1.3: Have an issue conversation	3
2. GitHub branches and forks	3
2.1: Create a branch (owner)	4
2.2: Create a fork (non-owner)	4
2.3: Working within a branch/fork	5
3. GitHub pull request	5
3.1: Create a pull request	5
3.2: Link to original issue	7
3.3: Code review	8
3.4: Merge pull request with main	9
4. Cleaning up	10

Overview

This document takes you through contributing to one of BIGslu’s R packages on GitHub. In the process, you will be introduced to GitHub issues, branches, forks, and pull requests. This tutorial assumes a working knowledge of git and GitHub similar to what is covered in our [GitHub tutorial](#). (coming soon)

1. GitHub issues

An issue is a note posted to a GitHub repo letting the owner know that there is a problem or need within that repo. They can relate to anything, and owners often use color-coded tags to group similar types of issues. For example, in the `kimma` package repository, there are a number of open issues. A common type is a **bug** which details an error or warning with something in the repo. There are also requests for new functions or features (**enhancement**) and for new or edits of help pages, vignettes, etc (**documentation**). Tags can be customized by the repo owner so you will see others across GitHub.








BIGslu / kimma
Public

Watch 0
Star 0
Fork 0

<> Code
Issues 6
Pull requests
Discussions
Actions
Projects
Wiki
Security
...


Filters

Labels 9
Milestones 0
New issue

<input type="checkbox"/>	6 Open ✓ 2 Closed	Author	Label	Projects	Milestones	Assignee	Sort
<input type="checkbox"/>	 Improve summarise_ outputs enhancement #8 opened 6 days ago by kdiillmcfarland 2 tasks						
<input type="checkbox"/>	 foreach connection errors bug #7 opened 6 days ago by kdiillmcfarland						
<input type="checkbox"/>	 Fill in missing kinship enhancement #6 opened on Oct 14 by kdiillmcfarland						
<input type="checkbox"/>	 Mac foreach warning bug #5 opened on Sep 9 by kdiillmcfarland						
<input type="checkbox"/>	 Vignette documentation help wanted #4 opened on Sep 9 by kdiillmcfarland						
<input type="checkbox"/>	 Add kmFit isSingular warning enhancement good first issue help wanted #3 opened on Aug 11 by kdiillmcfarland						

1.1: Create an issue

If you notice something wrong in a repo or have an idea for a change/addition, you can make a new issue with the green button in the upper right. In BIGslu, you can then choose a template that best describes the issue you'd like to create. If none of the templates apply, you can create a blank issue to fill out using the link at the bottom.



Bug report
 Report a bug, error, or warning
 Get started

Feature request
 Suggest an idea for this project
 Get started

Don't see your issue here? [Open a blank issue.](#)
Edit templates

1.2: Create an issue list

Sometimes you'll have multiple errors or ideas for a repo. In this case, you can create one issue with the entire list of ideas by selecting "Open a blank issue" and using the checklist - [] markdown formatting. Then, when someone wants to address one, they can quickly convert it to its own separate issue by hovering over the list and selecting the blue circle for that line.

Improve summarise_ outputs #8

[Edit](#)[New issue](#)[Open](#)

2 tasks

kdillmcfarland opened this issue 6 days ago · 0 comments



kdillmcfarland commented 6 days ago

Member

...

Open convert to issue

- ☐ Don't drop variables in summary table if row is all NA (no significant genes)
- ☐ Improve variable names to explicitly ID variable name and level of variable

Assignees

No one—assign yourself

Labels

enhancement

1.3: Have an issue conversation

Once an issue is posted, it has its own page where others can ask questions or continue to build on the idea. Often there will be a lot of back-and-forth in this conversation before anyone is ready to make changes to the code as we clarify what is being asked and debate the best ways to accomplish it. Posting issues and contributing to open issue conversations is a great way to help BIGslu without writing any code!

In this tutorial, we will tackle the following issue on a fit warning in `kimma::kmFit()`. This example uses our “feature request” template and contains a little bit of conversation between myself and a colleague.

Add kmFit isSingular warning #3

[Edit](#)[New issue](#)[Open](#)

kdillmcfarland opened this issue on Aug 11 · 1 comment



kdillmcfarland commented on Aug 11 · edited

Member

...

Is your feature request related to a problem? Please describe.

Currently, `kmFit` prints a "boundary (singular) fit: see `?isSingular`" warning to the console for each gene that cannot be fit.

Describe the solution you'd like

It would be helpful to collapse these into a single warning like

X of Y genes could not be fit due to boundary (singular) fit. See `?isSingular`

Describe alternatives you've considered

NA



kdillmcfarland added [enhancement](#) [good first issue](#) [help wanted](#) labels on Aug 11



basilinb commented yesterday

Member

...

Suggest we save the list of failed genes to the result object



1

Assignees

No one—assign yourself

Labels

enhancement

good first issue

help wanted

Projects

None yet

Milestone

No milestone

Linked pull requests

Successfully merging a pull request may close this issue.

None yet

Notifications

Customize

Unsubscribe

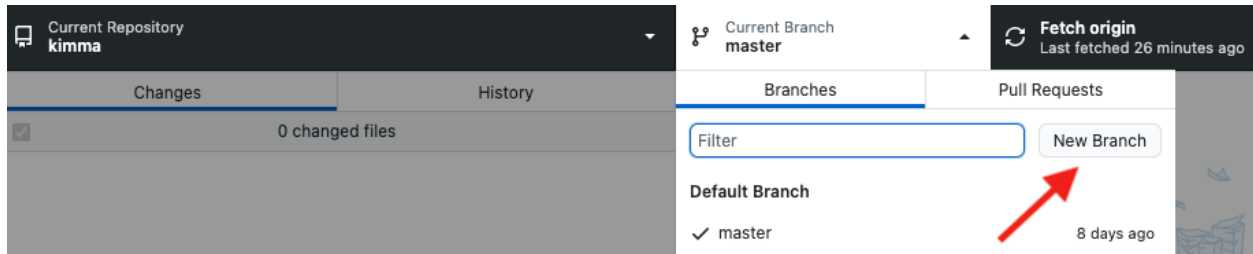
2. GitHub branches and forks

If you're not the owner of a repo, you can't simply make changes and push them to GitHub. And even if you are the owner, it's best to separate your experimental changes from the main version that others are using.

To do this, we create a separate branch to house changes. This branch is later merged with the main branch to create a harmonious single version for everyone.

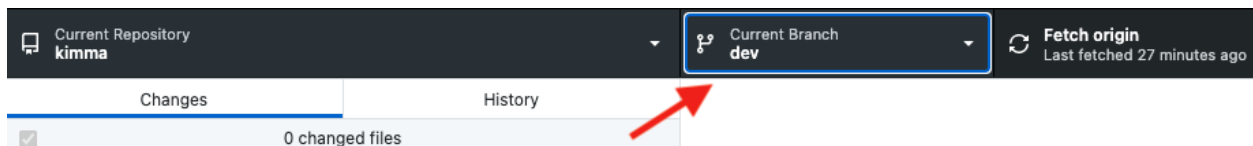
2.1: Create a branch (owner)

I prefer to work in a GitHub GUI, though these steps can also be accomplished in the command line. In GitHub Desktop, I create a new branch like so.



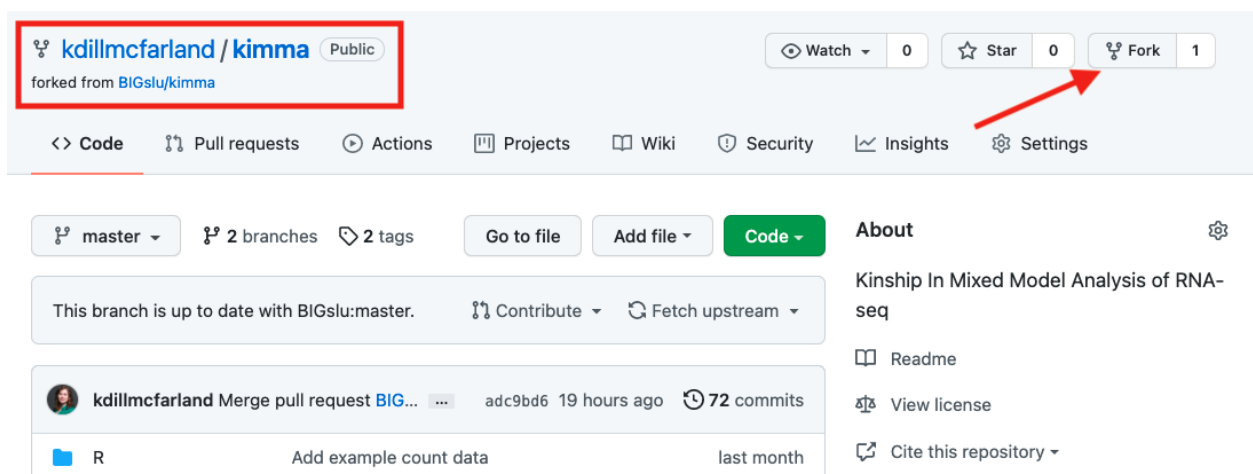
Every branch must have its own unique name. I generally name the branch where I work on GitHub issues **dev** for development. This branch can be used to address multiple issues in the future so don't feel like you need to name it anything specific to the issue you're currently addressing.

Creating the branch will automatically move you into that branch in the GUI. You can move between branches under this menu.



2.2: Create a fork (non-owner)

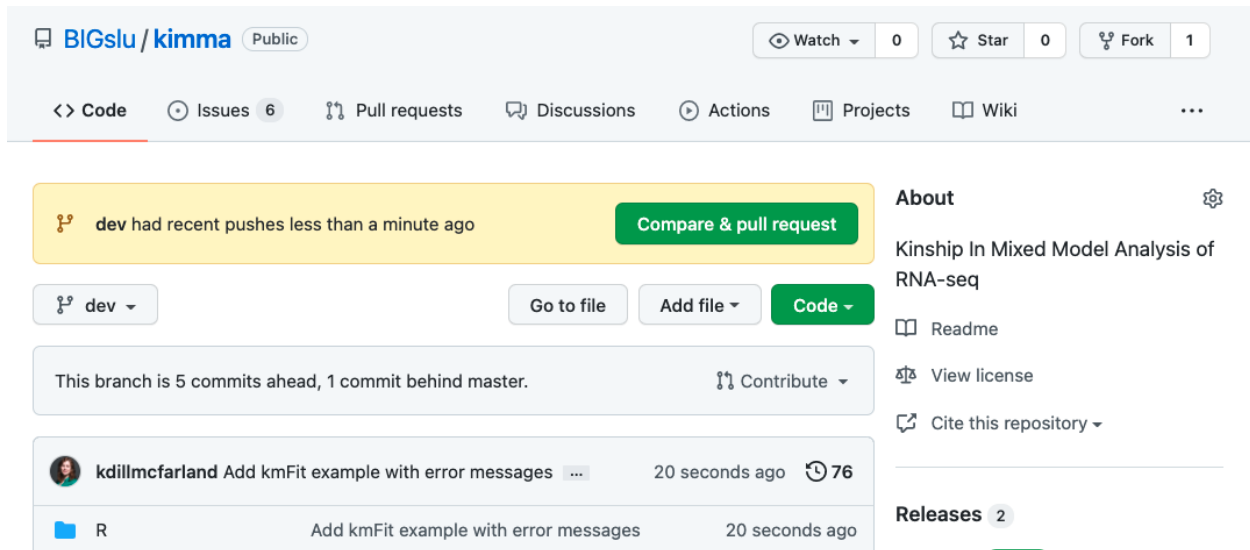
The above works because I have write privileges to the repo. You will likely not have these privileges so you will need to create a fork instead by using the Fork button in the upper right on the original repo page. A GitHub fork is a copy of the repo (like a branch) but it is housed in your account instead of the original account. In the red box below, notice that this fork of **kimma** is in my account (**kdillmcfarland**) but still linked to the original repo under **BIGslu**.



2.3: Working within a branch/fork

Whether you are in a branch or a fork, you can now make changes to the repo without impacting the main branch that everyone else uses. Here, I've made a number of changes in my branch to accomplish the goals in the GitHub issue. I've also added and committed these changes to the `dev` branch with git.

Now looking at the branch on GitHub, we can see a message that the branch is 5 commits ahead of the main (also called master) branch. This means my changes are only available on the `dev` branch.



You may spend a couple hours to even months working on a branch/fork! Whenever you've completed and tested your changes, it's time to merge it with the main so everyone can benefit from your work.

3. GitHub pull request

A pull request asks the owner of the repo to review your branch/fork and merge those changes with the main. Like an issue, this opens up a conversation where collaboration can take place.

3.1: Create a pull request


In the last screenshot, you'll see a Compare & pull request button. Since GitHub noticed that the `dev` branch is ahead of the main, it automatically points you to the next step. You can also create a request under the Pull requests tab at the top. Make sure that the to <- from branches in grey are correct for merging your branch with the main. If you're working in a fork, select the blue compare across forks link first.

Once you've initiated the request, you will see our template where you should provide an informative title and purpose. Later, we will link this request to the GitHub issue, so you don't need to write exhaustive notes here. You can leave the tests unchecked or pre-mark those you've completed with an `x`.

Open a pull request










Create a new pull request by comparing changes across two branches. If you need to, you can also [compare across forks](#).

base: master ← compare: dev ✓ **Able to merge.** These branches can be automatically merged.



Add fit warning output to kmFit

Write Preview


H B I         

****Describe the purpose of these changes****
A clear and concise description of what the bug or feature request this pull request addresses. Link to a current GitHub issue if available.


****Tests****
Verify that you have completed the following tests by checking the appropriate box. All tests must pass prior to merging with the main branch.


R packages


- ☐ All code contains sufficient commenting
- ☐ `check()` completes with no errors or warnings
- ☐ If the output is changed and is used as example data in another BIGslu package, these changes do not disrupt the other package's workflow. This can be done but running


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


Create pull request


Reviewers 
No reviews

Assignees 
No one—assign yourself

Labels 
None yet

Projects 
None yet

Milestone 
No milestone

Linked issues 
Use [Closing keywords](#) in the description to automatically close issues

Once submitted, the pull request contains the form, summary of commits on the `dev` branch, and an auto-merge check. This check let's us know if there are any conflicts with simply merging the `dev` changes with the main branch as is. Here, we have no conflicts since the main branch has not changed since I started `dev`. Resolving merge conflicts is outside the scope of this tutorial.

6

Add fit warning output to kmFit #10

Edit <> Code

 Open kdillmcfarland wants to merge 5 commits into `master` from `dev`

Conversation 0

Commits 5

Checks 0

Files changed 4

+121 -44



kdillmcfarland commented now

Member

Describe the purpose of these changes

Modifies completion message to include total number of failed genes. Saves failed gene names and error messages to `_error` data frames in result list object.

Tests

Verify that you have completed the following tests by checking the appropriate box. All tests must pass prior to merging with the main branch.

R packages

- ☒ All code contains sufficient commenting
- ☒ `check()` completes with no errors or warnings
- ☐ If the output is changed and is used as example data in another BIGslu package, these changes do not disrupt the other package's workflow. This can be done but running `check()` within the other package with your changes from this packages loaded by `load_all()`

 kdillmcfarland added 5 commits 40 minutes ago

-  Update Renv versions 20935dc
-  Add error capture functions and merge output with results e535646
-  Update completion message to include # failed cda6edb
-  Format kmFit results with error messages 49f510f
-  Add kmFit example with error messages 4ffeb4c

Reviewers

No reviews

Still in progress? Convert to draft

Assignees

No one—assign yourself

Labels

None yet

Projects

None yet

Milestone

No milestone


Linked issues

Successfully merging this pull request may close these issues.

None yet

Notifications

Customize

 Unsubscribe

You're receiving notifications because you authored the thread.

1 participant



 Lock conversation

Add more commits by pushing to the `dev` branch on `BIGslu/kimma`.



Continuous integration has not been set up

[GitHub Actions](#) and [several other apps](#) can be used to automatically catch bugs and enforce style.



This branch has no conflicts with the base branch

Merging can be performed automatically.

Merge pull request

You can also [open this in GitHub Desktop](#) or view [command line instructions](#).



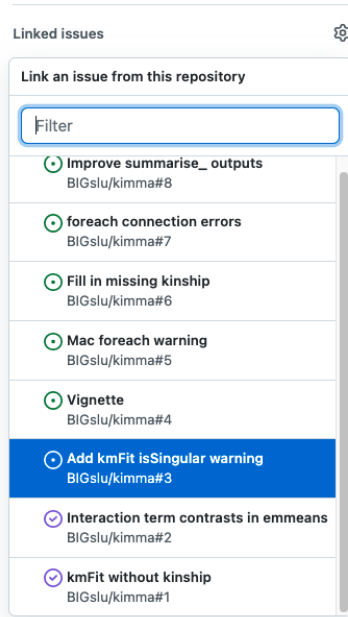
Write Preview

H B I         

Leave a comment

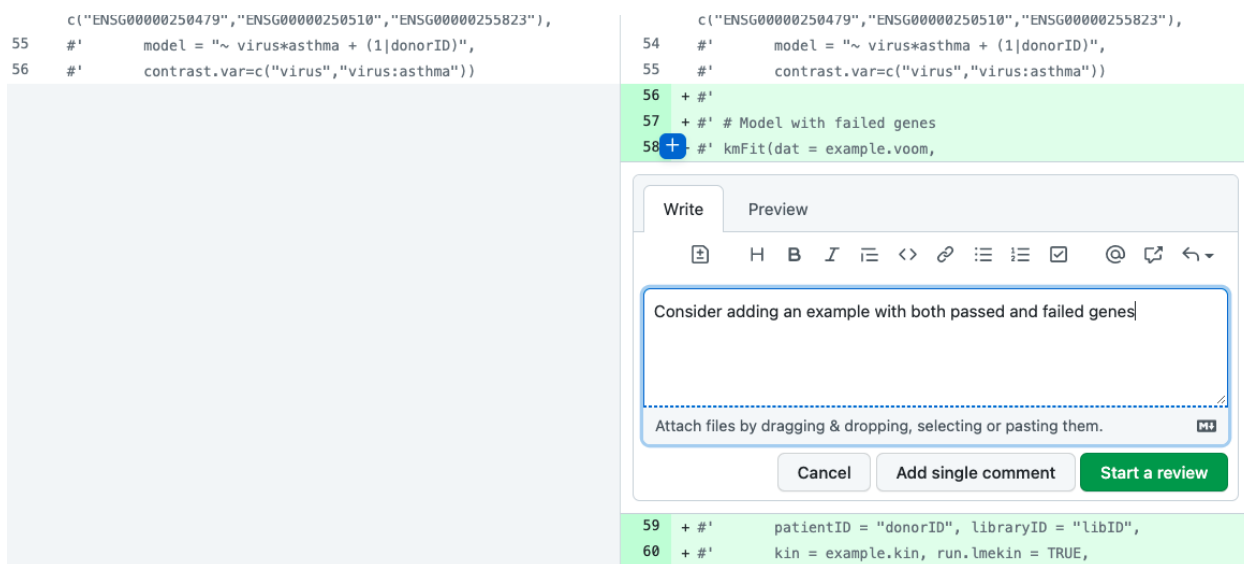
3.2: Link to original issue

On the right-side, select Linked issues and select the appropriate the appropriate issue for this request. This keeps things tidy and will automatically close the issue once the request is completed!




3.3: Code review

Prior to merging your pull request, another member of BIGslu must review it. GitHub has a lot of features to facilitate this collaboration. The main request page is a conversation space like the original issue. You can also go to the Commits or Files change tabs to see the line-by-line changes made to the code. This space also has conversational features seen when you hover over the code and select the blue +.




Once complete, the reviewer will either initiate the merge or (more likely) provide comments for you to address. These are summarized on the main request page.

 **kdillmcfarland** reviewed 2 minutes ago [View changes](#)


kdillmcfarland left a comment Member Author

Additional example needed

```
R/kmFit.R
...    @@ -54,6 +53,13 @@
54    53    #'    subset.genes = c("ENSG00000250479","ENSG0000025051")
55    54    #'    model = "~ virus*asthma + (1|donorID)",
56    55    #'    contrast.var=c("virus","virus:asthma")
56    + #'
57    + #' # Model with failed genes
58    + #' kmFit(dat = example.voom,
```

 **kdillmcfarland** 2 minutes ago Member Author

Consider adding an example with both passed and failed genes

 Reply...



[Resolve conversation](#)



3.4: Merge pull request with main


Once everyone is happy with the edits, the repo owner will merge the pull request. This places all the `dev` changes to the main branch.

Merged Add fit warning output to kmFit #10
kdillmcfarland merged 6 commits into `master` from `dev` [now](#)

[Resolve conversation](#)

  Update kmFit examples 7a0e7a5


  **kdillmcfarland** merged commit `54adb1` into `master` [now](#) [Revert](#)




 **Pull request successfully merged and closed**
You're all set—the `dev` branch can be safely deleted. [Delete branch](#)

Because they are linked, this also closes the associated issue.

Add kmFit isSingular warning #3

 Closed kdimlmcFarland opened this issue on Aug 11 · 1 comment





kdimlmcFarland commented on Aug 11 · edited Member  


Is your feature request related to a problem? Please describe.
Currently, kmFit prints a "boundary (singular) fit: see ?isSingular" warning to the console for each gene that cannot be fit.



Describe the solution you'd like
It would be helpful to collapse these into a single warning like
`X of Y genes could not be fit due to boundary (singular) fit. See ?isSingular`

Describe alternatives you've considered
NA






 **kdimlmcFarland** added enhancement good first issue help wanted labels on Aug 11




basilnb commented yesterdayMember  


Suggest we save the list of failed genes to the result object


  1



 **kdimlmcFarland** linked a pull request that will close this issue 22 minutes ago

Add fit warning output to kmFit #103 tasksMerged



 **kdimlmcFarland** closed this in [#10](#) 32 seconds ago

See the full pull request history at <https://github.com/BIGslu/kimma/pull/10>

4. Cleaning up

If you don't plan to make regular contributions to a repo, it's best to delete your `dev` branch or fork. This keeps things from getting cluttered. However, if you're a regular contributor, you can use the branch/fork again for future issues. See the live workshop where I use this same branch to tackle another `kimma` issue. https://www.youtube.com/playlist?list=PL_Oo8UFoIb03x3g4iVTgY1yMkXO7nqKK-