

Project #02 – sPlot Open - Edit the manuscript using GitHub



Version 1.0, 22.10.2020

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This short tutorial describes how to contribute edits to the manuscript - **sPlot open - An environmentally-balanced, open-access, global dataset of vegetation plots**.

Preparing manuscripts with hundreds of coauthors is challenging, time-consuming, and often, frustrating. Sharing word files per email is clearly inefficient and leads to versioning problems. Using Google docs is slightly better, but often results in unreadable manuscripts clogged with comments, where it is difficult to keep track of the different points of view in a transparent manner. Furthermore, Google docs do not handle references, which is obviously inconvenient.

To overcome these problems, we decide to test an alternative workflow, i.e., 'Manubot' - <https://manubot.org/>

In a nutshell, the manuscript is created and maintained similarly to programming code, whose versions (=edits) are handled using Git – the popular version control software ([an introduction here](#)). The code is stored in an online repository (<https://github.com/>), and each user can access it and suggest changes. Suggested changes are then revised by the manuscript maintainer (fmsabatini in this case) and, if accepted, implemented in the manuscript. Each time a change is done, a hidden workflow (i.e., Manubot) will **render** the code-like manuscript into a pdf file, as well as an html webpage. An additional benefit of using Github is that co-authors can discuss problems and ideas in dedicated forum threads, called **issues**.

This workflow is clearly different from what most people are used to, so it requires a bit of adaptability, and a **github account**.

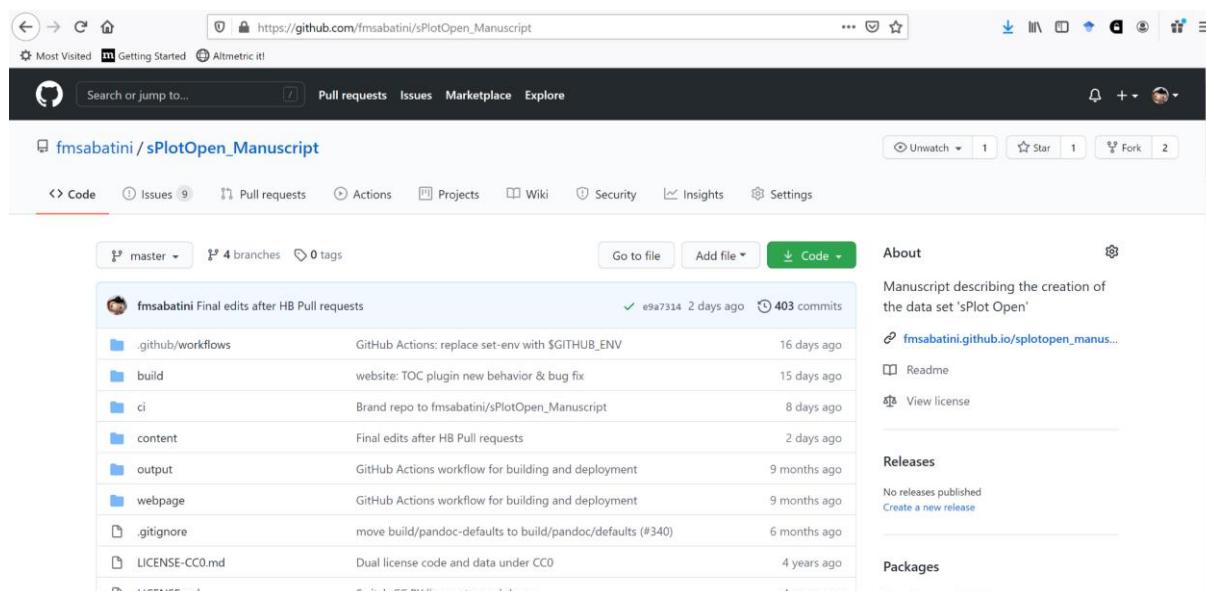
In this document, we describe:

- 1) *How to access the manuscript*
- 2) *How to contribute edits using GitHub's browser interface*
- 3) *Editing personal and affiliation information*
- 4) *How to open issues, suggest ideas and discuss problems*

1. How to access the manuscript

The manuscript is maintained on GitHub at:

https://github.com/fmsabatini/sPlotOpen_Manuscript



The automatically rendered versions of the manuscript are at the link below:

Webpage: https://fmsabatini.github.io/sPlotOpen_Manuscript/

PDF: https://github.com/fmsabatini/sPlotOpen_Manuscript/raw/gh-pages/manuscript.pdf

The source files, i.e., the files containing the actual manuscript are in the [‘content’ subfolder](#) of the `fmsabatini/sPlotOpen_manuscript` project and are numbered. These are .md files, i.e., simple text files which are formatted using [Markdown](#).

The metadata of the paper, including title, authors and their affiliations, is contained in the file [content/metadata.yaml](#).

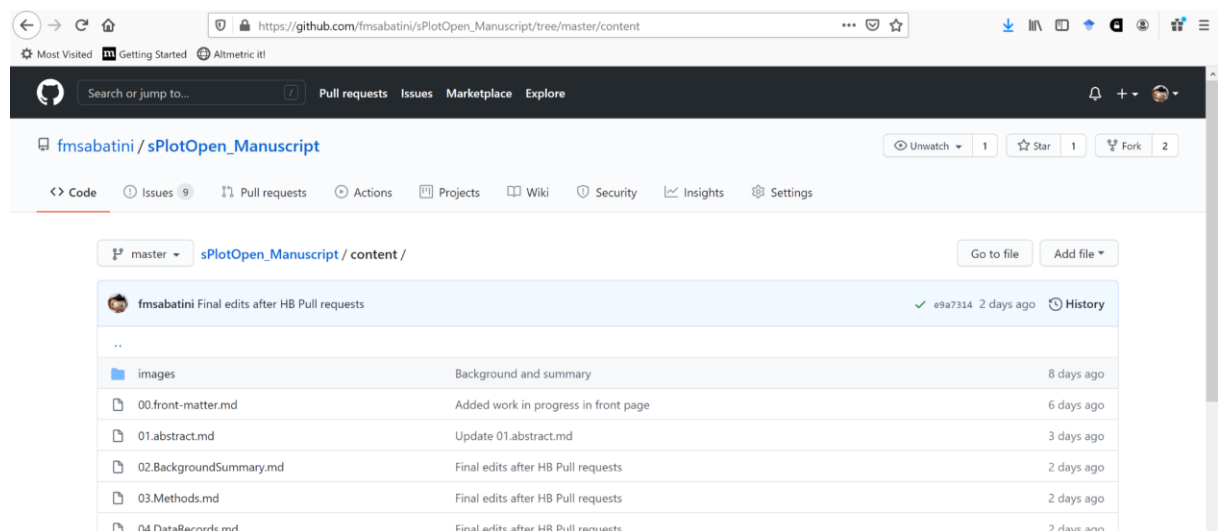
2. How to contribute edits using GitHub browser interface

There a short video on how to contribute edits with Manubot: <https://manubot.org/docs/getting-started.html>



Below a walkthrough.

- 1) Log-in to Github [create an account first, if needed]
- 2) Open the project page - https://github.com/fmsabatini/sPlotOpen_Manuscript
- 3) Click on the '[content](#)' subfolder, and open the file that you wish to change, e.g., 02.BackgroundSummary.md



sPlot – The Global Vegetation Database

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[illegible]

<https://github.com/fmsabatini/sPlotOpen> Manuscript/blob/master/USAGE.md

@doi:

6) Enter a commit message and, if desired, a comment. Click on Commit changes

```

34 assemblages (@doi:10.1111/ivs.12710).
35 Established in 2013, sPlot currently contains more than 1.9 million vegetation plots, and is fully integrated with the TRY database (@https://doi.org/10.1111/ecb.14904), from
36 which it derives information on plant functional traits.
37 The sPlot database is increasingly being used to study continental- to global-scale vegetation patterns, such as the relative contribution of regional vs. local factors on the
38 global patterns of fern richness (@doi:10.1111/1365-1376), the mechanisms underlying the spread and abundance of native vs. invasive tree species (@doi:10.1111/ecb.13927), and
39 worldwide trait-environment relationships in plant communities (@doi:10.1038/s41559-018-0699-8).
40 Here, we provide an open-access data set composed of 91,031 plots, which is representative of the environmental space covered by the sPlot database.
41 Plots stem from 183 databases, and span across 115 countries (Figure (@fig:Figure1)).
42 This resampled dataset (sPlot Open - hereafter) is composed of:
43 (1) plot-level information, including metadata and basic vegetation structure descriptors;
44 (2) the species composition of each vegetation plot, including species cover or abundance information when available; and
45 (3) community-level functional diversity indices derived from the TRY database (@https://doi.org/10.1111/ecb.14904).
46 [Global map of sPlot Open (n = 91,031) and spatial distribution of vegetation plot density per hexagonal cell with a spatial resolution of approximately 70,000 km². Map
47 projection is Eckert IV.] (images/figure1.png) (@fig:Figure1)

```

Commit changes

Mentioned other important databases

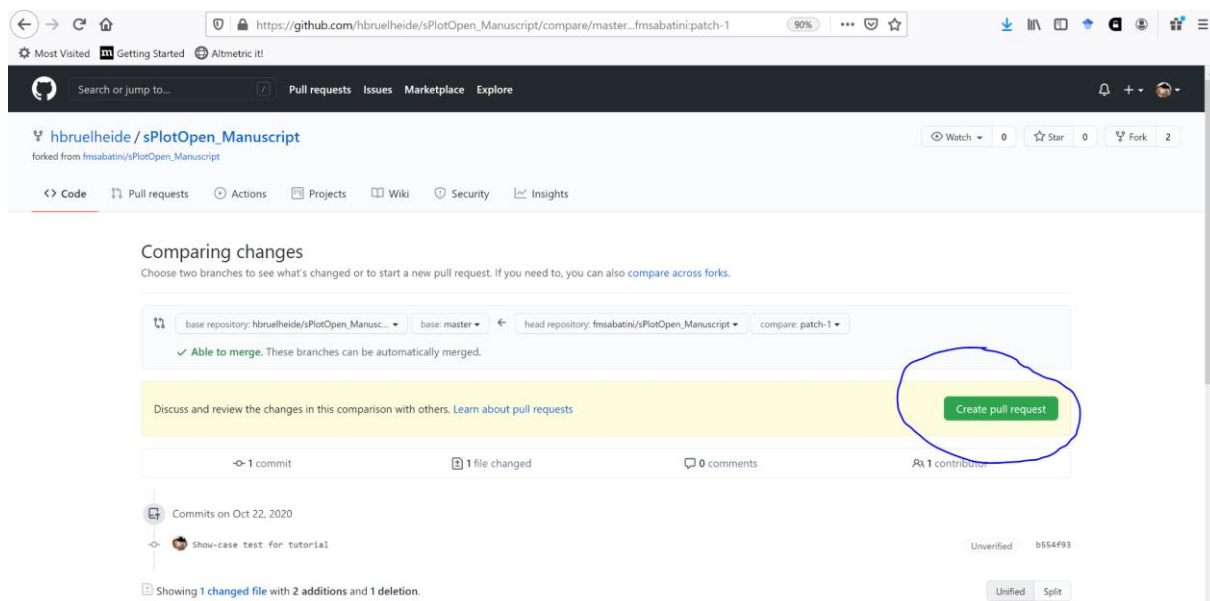
I edited the third paragraph to mention [GBIF](#), GIFT and other important databases

☒ Commit directly to the `master` branch.

☐ Create a new branch for this commit and start a pull request. [Learn more about pull requests.](#)

[Commit changes](#) [Cancel](#)

7) Once done, you need to Create a [Pull request](#) – to let the maintainer know about changes you've made. Once a pull request is opened, there will be the possibility to discuss and review the potential changes.



https://github.com/hbruelheide/sPlotOpen_Manuscript/compare/master...fmsabatin:patch-1

hbruelheide / sPlotOpen_Manuscript

forked from fmsabatin/sPlotOpen_Manuscript

Comparing changes

Choose two branches to see what's changed or to start a new pull request. If you need to, you can also [compare across forks](#).

base repository: hbruelheide/sPlotOpen_Manuscript base: master head repository: fmsabatin/sPlotOpen_Manuscript compare: patch-1

✓ Able to merge. These branches can be automatically merged.

Discuss and review the changes in this comparison with others. [Learn about pull requests](#)

[Create pull request](#)

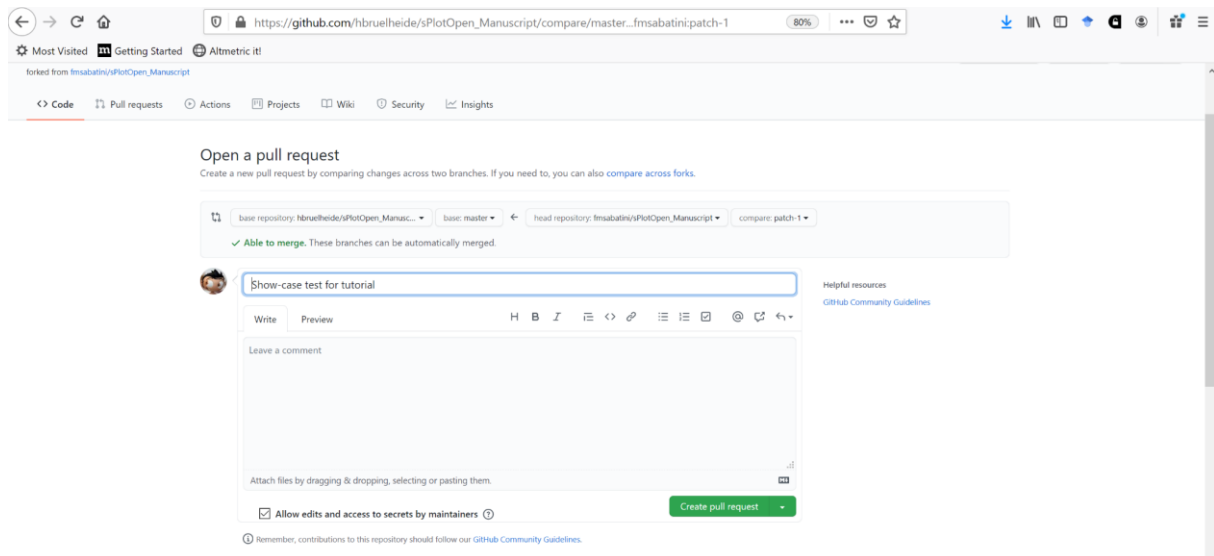
1 commit 1 file changed 0 comments 1 contribution

Commits on Oct 22, 2020

Show case test for tutorial

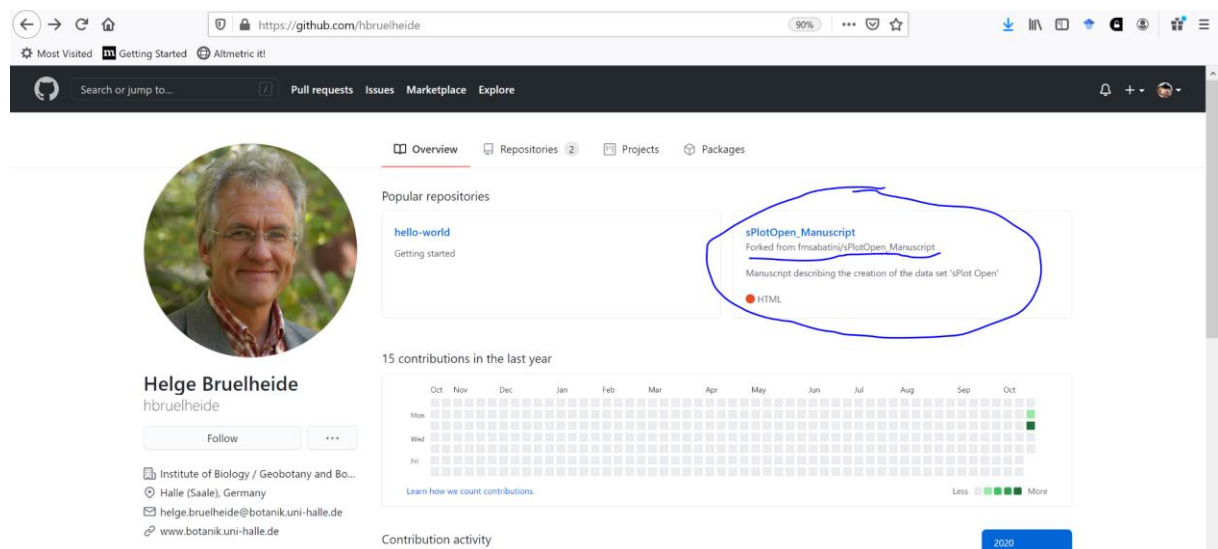
Showing 1 changed file with 2 additions and 1 deletion.

- 8) Enter a message and create pull request. Additional information can be inserted in the comment field.



- 9) Repeat steps 3-8 to implement changes to the other files.
- 10) Wait for the maintainer to receive the Pull Request. The maintainer might ask additional changes before accepting the Pull Request. All changes will remain documented.

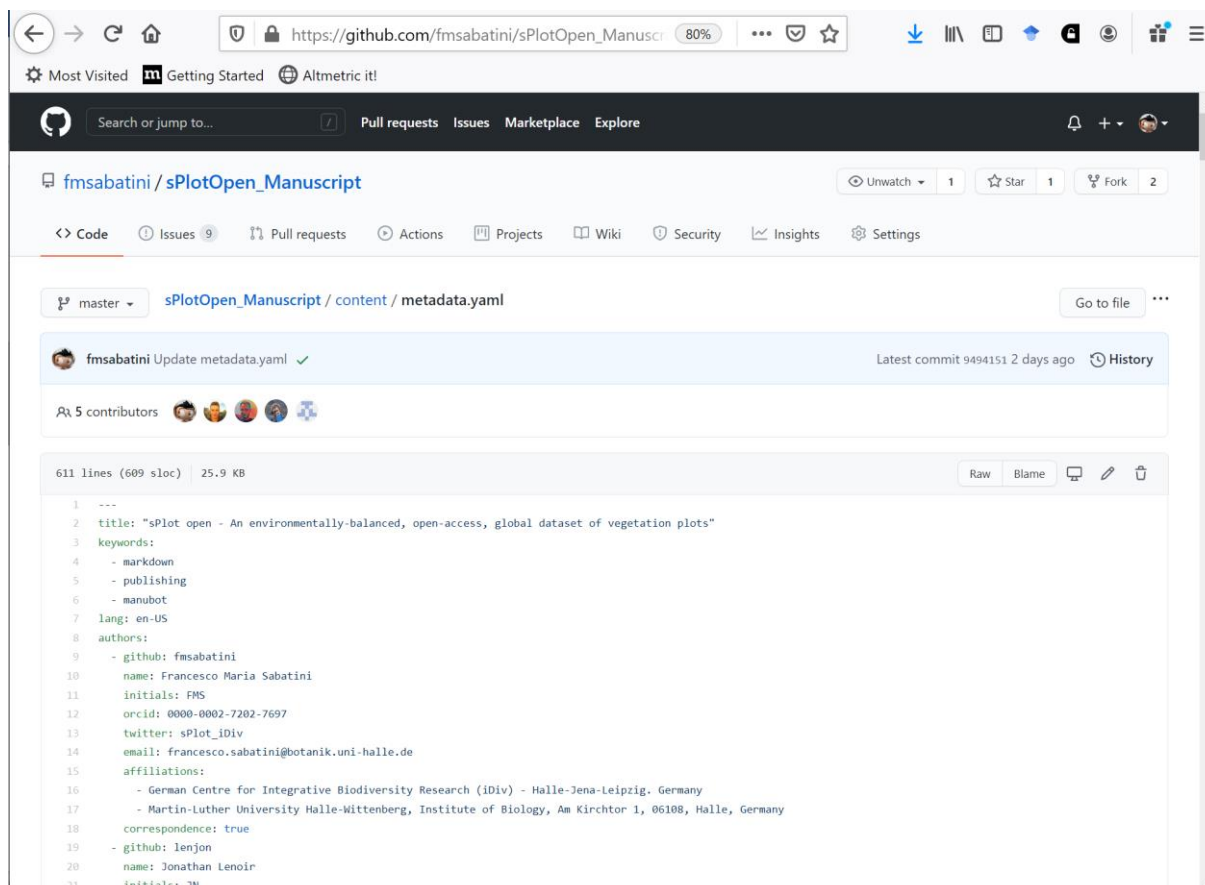
Please note that the maintainer (fmsabatini) is the only person that can implement changes to the source code. By committing changes, Github will automatically produce a forked copy of the project, which will be stored in your personal Github page. This forked copy is just a snapshot of the main (=upstream) project, and will not track its changes. For instance hbruelheide forked the fmsabatini/sPlotOpen_Manuscript project, thus creating the hbruelheide/sPlotOpen_Manuscript forked copy.



If you prefer, you can also work on your forked copy of the project. This can be convenient, because you can make changes to multiple files, and then create a single pull request. Please keep in mind, however, that forked copies of the project will slowly become out-dated while the upstream (=main) project develops. This youtube video (<https://youtu.be/YhwBgYPfoVE>) explains how to update your forked copy to match the upstream project from the browser interface of Github. Please, keep this in mind if you contribute edits days\weeks after you forked the project.

3. Editing personal and affiliation information

Author information is stored in the file [content/metadata.yaml](#)



```

1 ---
2 title: "sPlot open - An environmentally-balanced, open-access, global dataset of vegetation plots"
3 keywords:
4   - markdown
5   - publishing
6   - manubot
7 lang: en-US
8 authors:
9   - github: fmsabatini
10     name: Francesco Maria Sabatini
11     initials: FMS
12     orcid: 0000-0002-7202-7697
13     twitter: sPlot_iDiv
14     email: francesco.sabatini@botanik.uni-halle.de
15 affiliations:
16   - German Centre for Integrative Biodiversity Research (iDiv) - Halle-Jena-Leipzig, Germany
17   - Martin-Luther University Halle-Wittenberg, Institute of Biology, Am Kirchtor 1, 06108, Halle, Germany
18 correspondence: true
19 - github: lenjon
20   name: Jonathan Lenoir
21   initials: JN
  
```

We produce this file programmatically using sPlot's member affiliation information we have in our archive. **PLEASE, DO NOT MANUALLY EDIT THIS PAGE.** Rather let us know of any changes in your affiliation or contact information, so that we can keep our archive up-to-date. The changes in the archive will then be mirrored in the metadata page.

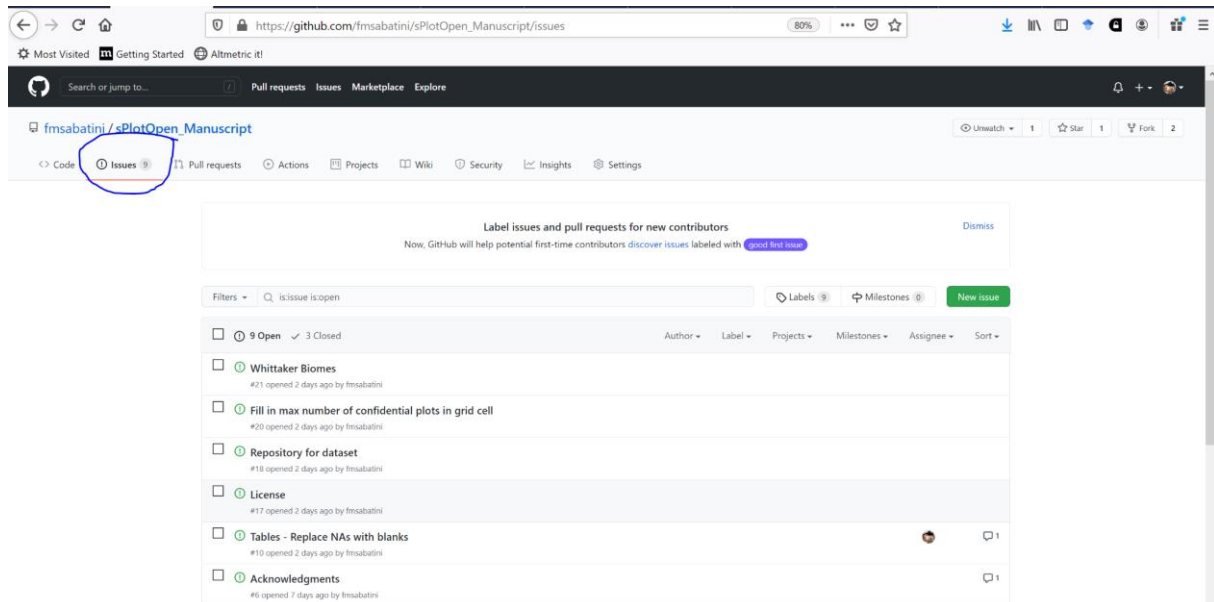
In case you wish to update your affiliation information, please use this online form

UPDATE AFFILIATION:

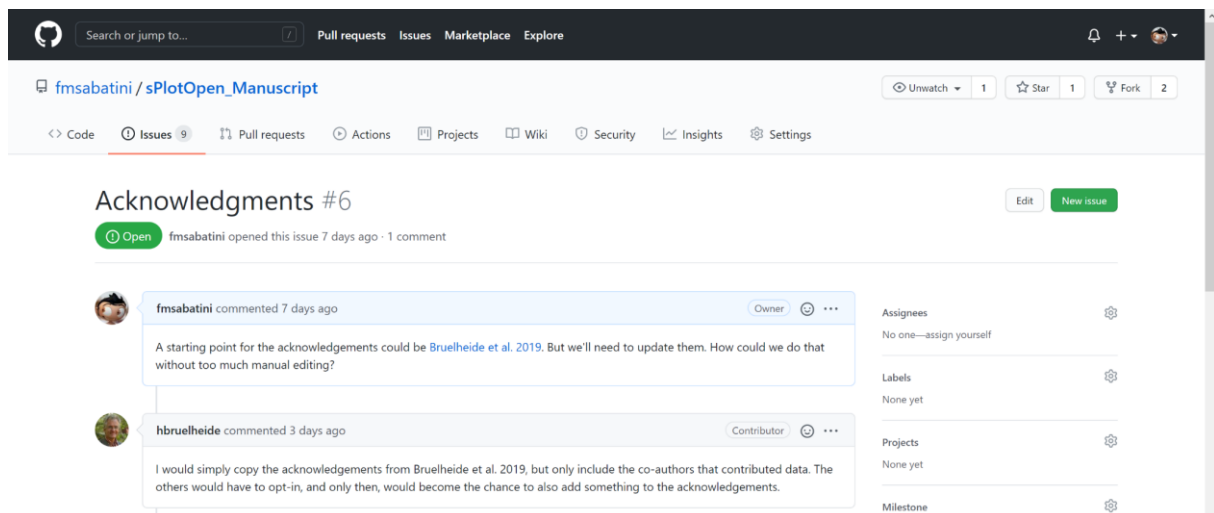
<https://docs.google.com/forms/d/e/1FAIpQLScMP85xd9OERFHyHJXlvCOjbmcGQEPcqT2YCcYmU49iX-HfUQ/viewform>

4. How to open issues, suggest ideas and discuss problems

One of the most useful features of GitHub is how it handles discussions among project contributors.

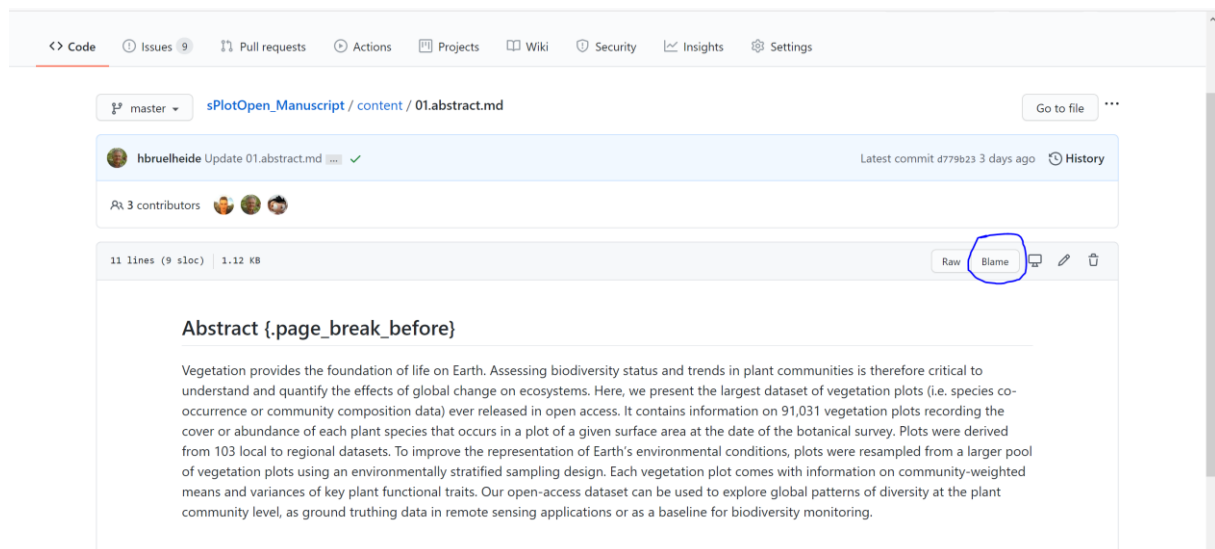


Everybody can **open a new issue**, which can be used as a forum for discussion, or to assign tasks. Feel free to explore the existing (and closed!) issues, to see if the argument is already under discussion somewhere else.



Issues can also be **linked to specific sentences** of the manuscript, by referring to the sentence line number.

To do so, just open the source code of the specific section, e.g., the abstract, and click the ‘**Blame**’ button.



By clicking on the desired row number(s), you can see that the URL of the page will change automatically. By copy-pasting this url into an issue, you can easily make explicit the sentence that you refer to.

