

# Ten Simple Rules for Taking Advantage of GitHub in Bioinformatics

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## Introduction

Bioinformatics is a broad discipline in which the common denominator is the need to produce and/or use software that can be applied to biological data in different contexts. To enable and ensure the reproducibility of scientific claims, it is essential that the scientific publication, the corresponding datasets and the data analysis are made publicly available [1,2]. All software used for the analysis should be either carefully documented (e.g. for commercial software) or, better, openly shared and directly accessible to others [3,4]. The rise of openly available software and source code, and concomitant collaborative development is facilitated by the existence of several code repository services such as SourceForge (<http://sourceforge.net/>), Bitbucket (<https://bitbucket.org/>) and GitHub (<https://github.com/>), among others. These resources are also essential for collaborative software projects, since they enable the organisation and sharing of programming tasks between different remote contributors. Here, we introduce the main features of GitHub, a popular web-based platform which offers a free and integrated environment for hosting the source code, documentation and web page for open source projects. GitHub also offers paid plans for private repositories. GitHub relies, at its core, on the well-known and open source version control system git, designed and developed by Linus Torvalds for the development of the Linux kernel. One reason for GitHub's success is that it offers more than a simple source code hosting service. It provides developers with a dynamic and collaborative environment, often coined as social coding platform, with the ability to review, comment and discuss code [5].

Some of our recommendations outlined below are applicable to other hosting services. However our main aim here is to highlight specific GitHub features. We provide a set of recommendations to take full advantage of GitHub's features to

manage small and large bioinformatics projects and increase their profile and visibility. These rules have been ordered to reflect a typical development process: learning git and GitHub basics, use branches, label and tag code, track the project using issues, etc.

## Rule 1. Structure your projects: users, organisations, repositories and teams

Open source projects on GitHub are visible to everyone, but write permissions, i.e. the possibility to directly modify the content, need to explicitly be granted. On the other hand, everyone with a GitHub account can fork any public project and start developing in one's own fork. This forking is the basis of social coding. It allows anyone to develop and test novel features into existing code and offers the possibility to merge novel features back the into the main project, thereby becoming a contributor. Structuring your projects allows to manage permissions and restrict access at different levels: users, teams and organisations. Users are the keystone of GitHub, as for any other social network. Every user has a profile listing their GitHub projects and activities, which can be populated optionally with personal information including name, e-mail address, image and webpage. To stay up to date with the activity of other users one can *follow* their accounts. Collaboration can be achieved by simply adding a trusted *Collaborator* and thereby granting write access. However, development in large projects is usually done by teams of people, within a larger organisation. GitHub organisations are a great way to manage team-based access permissions for the individual projects of institutes, research labs, and large open source projects that need multiple owners and administrators (Fig. 1). We recommend that you (as an individual researcher) make your profile visible to other users and display all the projects and organisations you are working in, including a list of the latest activities on the site (Fig. 1). Finally, repositories (the shortened term is *repo*) are versioned directories or dedicated storage spaces for your software projects, which can be included inside an organisation or can belong to particular users. Users can usually keep code, text files, images and small data files inside a repo. And while many users store programs and code projects, there is nothing preventing users from keeping text documents such as analysis reports and manuscripts (see for example the repository for this manuscript at <https://github.com/ypriverol/github-paper>), or other file types in your projects. Note that until recently, GitHub was lacking support for storing large files (>100 MB), a issue that has been recently addressed by the GitHub large file storage.

**Figure 1.** The structure of a GitHub-based project illustrating project structure and interactions with the community.

## Rule 2. Learn Git and embrace its power

The cornerstone of GitHub is the distributed version control system git. Every change, from fixing a typo to a complete redesign of the software is controlled by versions, so called revisions. While beginners may consider the learning curve of Git steep, many introductory and detailed tutorials are available. A revision can be considered as a *snapshot* (version) of a file system. Git is remarkably effective in archiving the complete history of a project (all revisions) by, amongst other things, storing only the differences among them. To create a new revision, the set of changes introduced (e.g. new, deleted or modified files) are committed to the repository. Following the rule: "commit often, as most as you can, perfection later", one can keep track of the

development in small incremental changes. At any time it is possible to go back to a previous version. In larger projects, multiple users contribute to the same repository.

### Rule 3. Use branches

Concurrent development including commits to the same repository can be organised using several common approaches. The most common way is to use git *branches* to separate different lines of development. Active development is often performed on a development branch and stable versions e.g. those used for a software release, are kept in a master branch. In practice, developers work on one or several features or improvements. To keep commits of the different features logically separated, distinct branches are typically used. Later, when development is complete and none of the tests fail (see Rule 6) new features can be merged back into the development line or master branch. During such a development, the original branch might continuously be developed and other features might be merged into the master branch. Nevertheless, one can always pull the currently up-to date master branch into one fork, always enabling to react or adapt to the changes in the code. In projects involving more than one contributor, everyone wants to be sure that the contributions of others increase the quality and move the project forward. *Forking* a repository and providing *pull requests* constitute an easy way for collaboration inside and over organisations boundaries. A user that forks a repository creates a copy under their GitHub account. Modifications like a branch with new features or bug fixes can conveniently be provided to the forked (upstream) repository by opening a pull request. Once it is opened for review and discussion, it usually results in additional insights and in an increased code quality. Once a pull request gets accepted, typically it gets merged into the development branch.

### Rule 4. Use tags and semantic version numbering

Tags offer the possibility to label versions during the development process, tracking its progress. Version numbering should follow semantic versioning in the form X.Y.Z, with X being the major, Y the minor and Z the patch version of the release, including possible meta information, as described in <http://semver.org/>. Correct labelling allows developers and users to easily recover older versions, compare them, or simply use them to reproduce results described in publications (see Rule 8). This approach will also help defining a coherent software publication strategy (see Rule 6).

### Rule 5. The code must always be ready to use: continuously integrate

The first rule of software development is that the code needs to be ready to use as soon as possible [6], remain so during development, and should be well-documented and tested. In 2005, Martin Fowler defined the basic principles for continuous integration in software development [7]. These principles have become the main reference for best practices in continuous integration, providing the framework needed to deploy software, and in some way also data. Every repository, script, mathematical model, and function should contain a set of self-automated tests. A source code may run, but that does not mean it is doing the right thing. The simple use of those self-automated tests is to detect possible bugs introduced by new features, or changes in the code or dependencies, but also to detect wrong results, the so called *logic errors*, where the source code produces a different result compared to what one intended it to do. Then, continuous integration provides the way of automatically run all of these

tests in the repository by checking data and software dependencies. Continuous integration can be done automatically on GitHub (See Rule 6).

## Rule 6: Automate for better code quality

GitHub offers different types of hooks that are executed after each push to a repository, making easier to follow the basic principles of continuous integration. The GitHub web hooks allows third-party platforms to access and interact with a GitHub repository and thus to automate post-processing tasks. Such tasks demonstrate to the community that a project follows rigorous software engineering processes, often associated with high quality development. It also shows that is currently working and has documentation that reflects the current code. We suggest that all these three tasks become part of your project. Firstly, continuous integration can be achieved by *Travis* (<https://travis-ci.org>), a hosted continued integration platform that is free for all open source projects. Travis builds and tests the source code using a plethora of options such as different platforms and interpreter versions. Furthermore it offers notifications which allow your team and contributors to know if the new changes work, and prevent the introduction of errors in the code, making the repo always ready to use. Secondly, in addition to successful completion of the tests, one can also demonstrate that they cover the existing code base sufficiently. For this task, the integration of *Codecov* is recommended (<https://codecov.io>). Thirdly, one might consider to automatically update the documentation upon code modification. This implies that your projects provide comprehensive documentation so others can understand, and contribute back to them. For Python or C/C++ code, automatic documentation generation can be done using sphinx (<http://sphinx-doc.org/>) and subsequently integrated into GitHub using “Read the Docs” (<https://readthedocs.org/>). All of these platforms will create reports and badges (also called shields) for the projects that can be included on your GitHub page, thereby making your projects easily identifiable as high quality and well-maintained.

## Rule 7. Use and maintain your GitHub issue trackers

GitHub *issues* are a great way to keep track of bugs, tasks, and enhancements. Classical issue trackers are primarily intended to be used as bug trackers. In contrast, GitHub issues follow a different philosophy: each tracker has its own section in every repository, and can be used to trace bugs, new ideas, and enhancements, by using a powerful but optional tagging system for each issue. Its main focus is put in promoting collaboration, providing context by using cross-references, and an excellent text formatting for each issue: (i) a title and description, (ii) colour-coded labels help to categorise and filter issues, (iii) milestones act as a container for issues, (iv) one assignee responsible for working on the issue, and (v) comments that allow anyone with access to the repository to provide feedback. Another aspect is its simplicity. For instance, it does not require to fill lengthy forms including every piece of information that might be valuable to reproduce the bug. It only requires to give the title and provide some optional text. If the developer needs more information, they can simply request it in a comment. GitHub issues are then more dynamic and pose a lower barrier for users to report bugs and request features. A well-organised and tagged issue tracker will help upcoming contributors and users to understand a project more deeply.

## Rule 8. Make your code easily citable, and cite source code!

In research, it is a good practice to ensure permanent and unambiguous identifiers for citable items like articles, datasets, or biological entities such as proteins, genes and

metabolites, among others. Digital Object Identifiers (DOIs) have been used for many years as unique and unambiguous identifiers for enabling the citation of scientific publications. More recently, a trend has started to produce DOIs for other types of scientific outputs such as datasets [8] or training materials (for example [9]). The main motivation behind this is to give scientists a better credit for their work [10], enabling at the same time a better way to cite and track it. A common issue with software is that it normally evolves at a different speed than what is published in the scientific literature. In fact, it is common to find software having novel features and functionalities that were not described in the original publication. GitHub now enables the use of DOIs to cite the code deposited, using the data archiving tool Zenodo (<https://zenodo.org/>). The procedure is simple (see <https://guides.github.com/activities/citable-code/>) and, by default, Zenodo takes an archive of a repository each time a new release is created in GitHub. However, before Zenodo can issue a DOI, metadata needs to be provided about the archived repository. Once the DOI has been assigned, apart from using it in your CV, you can add it to literature information resources such as Europe PubMed Central [11]. As already mentioned in the introduction, reproducibility of scientific claims should be enabled by providing openly the software, the datasets and the process leading to interpretable results that are used in a particular study. One should always highlight as much as possible in publications that the code is freely available in, for example, GitHub, together with any other relevant piece of information that may have been deposited. In our experience, this openness substantially increases your chances of getting the paper accepted for publication. On one hand, journal editors and reviewers have the opportunity to reproduce your findings during the manuscript review process, increasing the confidence of your results. On the other hand, once the paper is published, your work can be reproduced by any member of the scientific community, which can increase citations and foster opportunities for further discussion and collaboration. Also one must have in mind that the availability of a public repository with the source code does not make the software open source *per se*, as it needs to have an appropriate license (<http://opensource.org/licenses/>).

## Rule 9. Promote your projects in the scientific community - create a web page and more

Additional steps can be done to boost the visibility of a organisation. For example, GitHub *Pages* are simple landing webpages that GitHub hosts for free without the need for a server or database. GitHub users can create and host blog websites, help pages, manuals, tutorials and websites related to specific projects. *Pages* comes with a powerful static site generator called Jekyll (<https://jekyllrb.com>) that can be integrated with other platforms such as Bootstrap (<http://getbootstrap.com/>) or Disqus (<https://disqus.com/>), to support and moderate comments. In addition, GitHub also provides mechanisms for real-time communication called Gitter (<http://gitter.im>). Gitter is a GitHub-based chat tool (in limited beta at the time of writing) which enables developers and users to share aspects of their work. Gitter inherits the shape of the social groups operating around GitHub repositories, organisations, and issues. It relies on the identity within GitHub, creating IRC (Internet Relay Chat)-like chat rooms for public and private repositories. From within a Gitter chat, members can reference issues, comments, or pull-requests. A different service is Gist (<https://gist.github.com>), which represents a unique way to share *code snippets*, single files, parts of files, or full applications. Gist can be generated in two different ways: public *gists*, that can be browsed and searched, and secret gists that are not provided through *Discover* (<https://gist.github.com/discover>). One of the

main features of Gist is the possibility to embed code snippets in other applications, enabling users to embed gists in any text field that supports JavaScript.

## Rule 10. Check periodically existing open source projects

One of the main tasks of scientists is to actively follow the developments in their field. Analogously, scientific programmers need to revise publicly available (e.g. open source) projects and code that can be interesting for their research. Therefore, you should try to learn as much as possible from your peers and keep up-to-date with all the developments of relevant projects. GitHub enables this functionality by *following* other GitHub users (also mentioned in Rule 1) or *watching* the activity of projects, which is a common feature in many social media platforms. Take advantage of it as much as possible!

## Conclusions

If you are interested and have not used GitHub so far, we recommend you to get started as soon as possible. As in any other topic, a learning curve is required for beginners. However, we anticipate the reward will be worth your effort.

## Disclaimer

The authors have no affiliation with GitHub, nor any commercial entity mentioned in this article. The views described here reflect our own without any input from any third party organisation.

## References

1. Goodman A, Pepe A, Blocker AW, Borgman CL, Cranmer K, Crosas M, et al. Ten simple rules for the care and feeding of scientific data. PLoS Comput Biol. 2014 Apr;10(4):e1003542.
2. Perez-Riverol Y, Alpi E, Wang R, Hermjakob H, Vizcaíno JA. Making proteomics data accessible and reusable: current state of proteomics databases and repositories. Proteomics. 2015 Mar;15(5-6):930–49.
3. Osborne JM, Bernabeu MO, Bruna M, Calderhead B, Cooper J, Dalchau N, et al. Ten simple rules for effective computational research. PLoS Comput Biol. 2014 Mar;10(3):e1003506.
4. Vihinen M. No more hidden solutions in bioinformatics. Nature. 2015 May;521(7552):261.
5. Dabbish L, Stuart C, Tsay J, Herbsleb J. Social Coding in GitHub: Transparency and Collaboration in an Open Software Repository. In: Proceedings of the ACM 2012 Conference on Computer Supported Cooperative Work. CSCW '12. New York, NY, USA: ACM; 2012. p. 1277–1286. Available from: <http://doi.acm.org/10.1145/2145204.2145396>.
6. Leprevost FV, Barbosa VC, Francisco EL, Perez-Riverol Y, Carvalho PC. On best practices in the development of bioinformatics software. Front Genet. 2014;5:199.
7. Fowler M. Continuous Integration; 2006. Accessed: 2015-12-09. <http://www.martinfowler.com/articles/continuousIntegration.html>.

8. Vizcaíno JA, Deutsch EW, Wang R, Csordas A, Reisinger F, Ríos D, et al. ProteomeXchange provides globally coordinated proteomics data submission and dissemination. *Nat Biotechnol.* 2014 Mar;32(3):223–6.
9. Ahmadi A, Aiello-Lammens M, Ainsley J, Allen J, Alsheikh-Hussain A, Banaszkiewicz P, et al.. *Software Carpentry: Programming with R*; 2015. Available from: <http://dx.doi.org/10.5281/zenodo.27353>.
10. Credit where credit is overdue. *Nat Biotechnol.* 2009 Jul;27(7):579.
11. Europe PMC Consortium. Europe PMC: a full-text literature database for the life sciences and platform for innovation. *Nucleic Acids Res.* 2015 Jan;43(Database issue):D1042–8.