Not just for programmers: A friendly guide on the versatility/benefits of GitHub for accelerating collaborative research in Ecology and Evolution

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Abstract

Researchers in ecology and evolutionary biology are increasingly dependent on computational code to conduct scientific research. With the growing role of data science in ecology and evolutionary biology (EEB), the use of efficient methods to collaborate, share, and reproduce code has become fundamental. GitHub is an online, cloud-based service that can help researchers to track, organize, discuss, share, and collaborate on software and code. Despite these benefits, the use of GitHub by EEB researchers is not widespread due to the lack of domain-specific information and guidelines. To help EEB researchers adopt useful features from GitHub in their own workflows, we review thirteen practical ways to use the platform. We outline features ranging from low to high technical difficulty: storing code, managing projects, coding collaboratively, conducting peer review, and writing a manuscript. Given that members of a research team may have different technical skills and responsibilities, we describe how the optimal use of GitHub features may vary among members of a research collaboration. As more ecologists and evolutionary biologists establish their workflows using GitHub, the faster our collective scientific progress, and the more our fields can be at the forefront of pushing the boundaries of collaborative, transparent, and open research.

Introduction

Most scientists, including ecologists and evolutionary biologists, are increasingly dependent on computational tools in their research [see 1]. Researchers now write and use code as part of their scientific workflow to perform a wide-variety of tasks ranging from data management, data analysis, study replication, to the application and the development of tools for hypothesis testing. This code-dependent workflow imposes steep requirements towards an efficient, well-documented process in the publication and collaboration of maintainable scientific code [2]. To facilitate this process, scientists have been increasingly borrowing and adopting tools from information system technology, such as cloud-based services for documentation and version control (*e.g.* from the Google Suite (with Docs, Sheets and Drive), the Microsoft Suite (with Word, Excel and OneDrive), and GitHub, [3]). However, most researchers lack exposure to adequate software development practices and are required to dedicate valuable time and effort to self-teach the use of research-facilitating tools, and thus may find practical barriers when applying adequate standards to maintain their scientific code [1,4,5]. Here, we review and discuss one of the most used web-based platforms for computational version control and collaboration, GitHub, and provide researchers in ecology and evolutionary biology (EEB) with practical workflows aimed at facilitating their scientific code and management process.

With over 73 million registered users, GitHub is the most common web-platform used for collaborating on computer code [6]. GitHub builds on the Git version control system [7], providing a simplified but powerful web interface that allows users to participate in projects, contribute code, report and discuss software bugs, discover existing code and data, as well as publish new code. Through version control, users have a detailed, chronological record on the files and directories stored in their repositories [8]. This workflow raises a strong and clear advantage over receiving, processing and sending files back-and-forth, a process that can easily become challenging and time-consuming in projects extending in time and in the number of collaborators [9]. Through the combination of version control management and the network- and collaboration-based features, GitHub can broadly facilitate openly available source code alongside concomitant collaborative development [10].

Git is the version control system that enables all the collaborative tools available on GitHub. Although the understanding of basic concepts of Git (such as commit, push, pull, checkout; see Box 1) is necessary, the GitHub web-based platform and its integrated development environments (such as the GitHub Desktop) allow users to manage their repositories without using more technical command-line sessions. We do not focus on Git in this paper, but we recommend users explore the many resources providing detailed information on Git, such as journal articles [10,11], video tutorials, and books [12].

The expansive user-community and the numerous resources providing pedagogical instruction material on how to use GitHub streamlined its widespread use [13]. Nevertheless, although multiple articles have encouraged researchers in EEB to adopt GitHub as part of their research process [3,14], its use is still not widespread. First-time users from domains without formal training in information technology may face steep learning curves because GitHub and its features have been centered on collaboration for software development in information systems [15]. Moreover, domain-specific perspectives and resources providing tractable examples and practical guidance for researchers in ecology and evolution on GitHub are scarce (but see [13,16]). An increased availability of data and code management standards – of which GitHub is one increasingly important component – make research more reproducible and collaborative [17]. More importantly, a widespread, common adoption of GitHub for collaborating on a variety of research tasks can ultimately enable EEB researchers to spend less time on creating novel processes for collaboration and more time on their scientific research [18].

This manuscript is the result of an academic hackathon held during the 2021 conference for the Society for Open, Reliable, and Transparent Ecology and Evolutionary Biology (SORTEE) [19]. We convened a group of ~30 EEB researchers with varying levels of familiarity with using GitHub as part of their research projects to showcase and discuss how existing features can contribute to the documentation and collaboration in EEB research. During the hackathon, we identified the need for a formal discussion on how EEB researchers can benefit from GitHub and its features to make their research more collaborative and transparent. Here, we outline thirteen practical ways that EEB researchers can use GitHub features for more collaborative, transparent, and reproducible science. We also provide critical perspectives on features that could be improved and catered towards research development.

Box 1

Glossary
repository: A collection of files (e.g. a directory) tracked by git. Commonly shortened to "repo". Repositories are managed by an owner and can be listed as "public" where the repository will be visible to all GitHub users or "private" where the repository is visible only to added team members.
commit: Commits are like snapshots in the development of a project. In Git, versions of files and directories are uniquely identified as "commits", allowing one to identify and track modifications line-by-line. Commits can include changes in multiple files and must include a brief commit message describing the changes made. A typical workflow is to make some related changes in files, make a commit (e.g. "generate and include fig1 in results"), and after several commits **push** those commits to the remote GitHub **repository**.
clone: Cloning a **repository** is a way of making a local copy (i.e. on your computer) of a GitHub **repository**. If you have access to **push** to a **repository**, this can be a first step to contributing to a project.
branch: Development branches can be created at any point in time and work on each branch can continue independently.This is useful for testing out new ideas (both code and text) which may or may not eventually get integrated into the main branch of the project. Branches can also be used to isolate contributions of multiple contributors. Each person working on their own branch eliminates problems that arise when conflicting edits are pushed to the same remote branch. Changes in a development branch can be **merged** into the main branch via **pull requests**. Branches can only be made by those who are given access to the project **repository**.
fork: A fork is a copy of a **repository** hosted on GitHub. If a repository is public, then anyone can make a fork. Even if they do not have access to push to the original repository, they can make a fork and edit it independently. Forks are linked to the original GitHub repository and "upstream" changes (those in the original repository) can be **merged** to keep the fork up to date with the original project. Changes made in the fork can be integrated into the original project via **pull requests**.
push/pull: When **commits** are made in a project locally, they must be synced with the remote GitHub repository by "**pushing**" them. Changes on a GitHub repository can then be "**pulled**" to keep your local version of the project up-to-date.
pull request: A pull request is a request that the owner(s) of a GitHub repository integrate changes you've made on either a **branch** in the repository or in your own **fork**. When you initiate a pull request, you must provide a description of what changes are made. Some automated tests may be run and review may be required before integrating your changes into the main **branch**.
merge: Combining **commits** from two different branches together into one **branch**
Release: At any point a release can be made on GitHub to mark a significant milestone in the progression of a repository. While this GitHub feature is designed with releases of new versions of software in mind (e.g., v1.0.0), it can also be used to create a snapshot of a repository at significant stages like submission, revision, and acceptance of an associated manuscript.

GitHub in EcoEvo Examples

Storing and archiving version-controlled data

Many researchers often start their use of GitHub to backup their working code and data to a remote server (Just push and pull, see Box [box:box-1-definitions?], from their own repo). This saves the user time from backing up code on their own portable devices, such as hard drives. This also offers some peace of mind, as this information is retrievable even if one's laptop ends up at the bottom of a lake. Thus, an additional benefit of this 'cloud' storage is that one's GitHub repository can be accessed by any machine with internet access, allowing the user to be more mobile if they wish to both work from home and the office from different computers. Each time a user pushes changes to their repository, GitHub tracks what these changes are and stores this history. This feature allows for version control, such that users can re-visit previous versions code. Version control is particularly useful if a mistake has been made where a user has unknowingly overwritten or deleted information that would otherwise be irretrievable without GitHub having saved that information.

Although common, data (as opposed to code) storage on GitHub is actually discouraged as the platform is explicitly about sharing code. Commits (see Box [box:box-1-definitions?]) greater than 50 MB receive a warning and there is a hard block on commits larger than 100 MB (https://docs.github.com/en/repositories/working-with-files/managing-large-files/about-large-files-on-github). Large datasets therefore may not be able to pushed up to GitHub repositories. Data greater than 50 MB can be stored in any one of many data repositories that can be integrated or linked with GitHub (e.g. osf.io) or one can make use of large file storage from GitHub (https://git-lfs.github.com/; which may have some costs associated with it).

An even easier way to start using GitHub is for the archival of cleaned code and data (less than 50 MB in size), often accompanying preprinting, manuscript submission, or manuscript acceptance. Many users prefer to host a separate, cleaned repository that they make public when they complete a paper, while keeping the original folders as either a private GitHub repository, or on another cloud storage service such as OneDrive, Dropbox, etc. One benefit of using GitHub for this service is that it can integrate with a website called Zenodo, a free, long-term data archiving service funded by CERN [20] for datasets up to 50 GB. After linking your GitHub account to Zenodo and turning on archiving, any time a release is made, a snapshot of the entire repository is archived in Zenodo with a versioned, citable DOI (see 'Making code citable' below for more information). DOIs for data and code are increasingly being required by journals for paper acceptance (e.g., Journal of Applied Ecology), and Zenodo provides a free alternative to other fee-based hosting services (such as Dryad).

Virtual lab notebook

Lab notebooks have been indispensible tools for keeping track of research methods and laboratory policies [21]. Digital lab notebooks, stored in the cloud, provide clear benefits given the ease with which documents can be shared with new employees and updated as policy changes or experimental methods are modified [22]. Increasingly, researchers are leveraging GitHub's underlying version control to keep and share digital lab notebooks [3]. At a minimum, commit statements can provide a record of daily changes made to any code stored on GitHub [9].
GitHub issues can be used to track and prioritize lab objectives and goals, as well as tracking any status updates. Some EEB labs have even turned their lab notebooks into shareable websites [23,24] as a centralized location for all lab resources.

Educational materials

GitHub supports a broad set of mechanisms for hosting educational materials. The entire process of running a course, workshop, or even just a lecture, can all be done openly on GitHub. For example, organizing a course could be broken down into: 1) developing the material (i.e., slides, examples, relevant readings, labs, etc.), 2) hosting the course on some online platform for students to access, 3)

delivering the content, 4) accepting student work submissions and 5) returning graded material. While there are other purpose-built platforms for this, GitHub provides a free, open-source alernative.

GitHub's open nature allows colleagues to see, review and offer feedback on your process. Making presentations can be done through most major high-level programming languages such as R, with `RMarkdown` [25], Python, with `python-ppt` [26]), and Julia, with `Remark.jl` [27]. Since all these programs work via code bases, they can be version-controlled through git and GitHub. Once content is made, hosting a course website can be done through GitHub Pages, and there are lots of templates available (e.g., see [28]). This way, not only can the course content be available to enrolled students, but also to a global pool of learners and teachers interested in the course material. Content can then be delivered via the course website, and/or a GitHub organization with, for example, template repositories for assignments. Student submissions are perhaps the most challenging component, but for assignments submitted as code files (i.e., `.R` & `.Rmd` as two of the most common) and/or `.pdf` files, GitHub has a new tool in development - GitHub classroom [29] - where instructors can host private assignments, and even build custom autograding tests.

While most instructors can feasibly only incorporate some of these tools to deliver their content to students, it is still valuable to do so and to encourage students to begin learning about version control through interacting with git/GitHub, however minimally, through the course.
Especially if a central tenet of a given course or educational unit is to introduce or give students experience to version control and the tools that working professionals in EEB use, then adopting a few of these tools can be a great way to do so.

Project management

GitHub can be a powerful tool for team-based project management, allowing collaborators to share feedback, brainstorm ideas, and troubleshoot problems (Figure 1). The "Issues" feature of GitHub allows for discrete tasks and sub-tasks to be identified, assigned to team members, and categorized with custom labels. The new GitHub "Discussion" feature serves as a message board for conversation. Scripts, commit messages, and pull requests can be linked directly to issues and discussions, providing a clear record of project workflow. The use of GitHub for all project-related conversation and planning, rather than e-mail or messaging tools, makes it easier to keep track of progress throughout the lifespan of a project. This is because unlike emails and messages which can get lost as more new tasks arise, GitHub issues exist until they are intentionally closed by repository administrators. Fortunately, it is not essential for all team members to have proficiency in git or programming, as users can interact with Issues and Discussions via web browser or e-mail (e-mail responses still get tracked as comments on the focal GitHub issue). For larger projects with many team members and tens or hundreds of GitHub issues to sort through, project management software like ZenHub, can help prioritize issues and pull requests. ZenHub's web interface includes a GitHub Issue visualizer where users can organize issues into high priority or backlogged tasks as well as link issues togther when they are related to a shared project goal or milestone. GitHub is currently beta testing a similar project management feature called GitHub Projects [30]. GitHub can also be integrated with other project management software such as Slack.

Building website

It is now common for many scientists to have personal, project, or lab websites (hereafter, personal websites) to share and promote their work. There are many options for creating and hosting websites. Some sites are built through a point-and-click user interface that requires no coding experience, but these services tend to have monthly or annual fees (e.g., Wix, Squarespace, Wordpress). GitHub Pages [31] allows users with a GitHub account to easily create a website, hosted by GitHub, from one of their many website templates [3]. It is also possible to fork any public website hosted on GitHub in order to

use it as a template. When creating a website with GitHub Pages, all content is stored in a GitHub repository, the content is written in markdown (e.g., [32]), and a website is automatically rendered in HTML from the markdown documents (e.g., [33/]). Aside from free hosting services, another benefit is that GitHub pages are autogenerated, meaning that when content is modified in the associated GitHub repository, the website instantly updates [8]. Though the templates are useful for quickly starting up a new website, users are able to fully customize their Pages websites (for technical details of customizing GitHub Pages site see [34]). We emphasize that despite the many benefits of using GitHub pages (free hosting, templates, customization), this avenue for creating a website will be more time intensive than the out of the box platforms mentioned above and requires consideration of tradeoffs offered by website creation services. For more advance GitHub users, Jekyll [35] and Hugo [36] are both "static website generators", which also include template libraries for websites that can be hosted freely via GitHub pages. Both of these tools require some additional learning because they are deployed via the computer's terminal or command line, still they are a great resource for creating free, eye-catching websites.

Making code citable

GitHub makes it easy to store and share a variety of data files in the cloud. If a repository is made "public" the URL to the repository can be shared freely with others. However, for a variety of reasons (e.g., privately owned company, ability to make repositories private, accounts can be deleted at will) GitHub is not considered a long-term data or code repository like Zenodo and Figshare [3,10]. Also, unlike the long-term repositories, GitHub does not issue Digital Object Identifiers (DOIs) for content uploaded to their servers. DOIs are persistent and unique alpha-numeric IDs assigned to research products like papers, code, and data. DOIs allows tracking and citing research products. For this reason, scientists who share code and data through GitHub are strongly encouraged to also submit GitHub repository content to a long-term data archive [37]. Fortunately, both long-term repositories mentioned above (Zenodo and Figshare) have integrations with GitHub which facilitates archiving a snapshot of all repository content with the click of a button.

Linking one's GitHub repository with Zenodo, etc. to achieve a DOI helps work become findable, gives proper attribution, and that can ensure long-term stability [38]. Thus, when researchers wish to include data and code with their publications, they ought to reference a DOI from a long-term storage site, rather than a URL from GitHub (which can change or be deleted). Additionally, referencing a DOI for data and code is preferable to submitting these as supplementary materials to the journal, as supplementary materials are more difficult to find and reuse (i.e. often not centralized and searchable in a database) and not necessarily permanent (as most journals offer no guarantee of long-term storage).

Many researchers believe that their code is not useful because their analysis is context-specific and not designed for re-use like software. However, there are many reasons to share data and code beyond re-use. Even if code is rough, it shows the exact steps taken to conduct an analysis, and therefore provides the most detailed look into how to reproduce a given analysis [39]. This is important in light of the reproducibility crisis [40] and will become increasingly important to the collective scientific enterprise as advances in computing power and accessibility unlock the ability to conduct 'big data' meta research with data that has already been collected by others. Failing to include data and code with our publications leaves future scientists with many fewer resources from which to understand the world.

An important aspect of making your code citable and reusable is adding an appropriate licence. Code without a licence is (by default) actually provided more protection from reuse than code with an open licence meaning that the openness of your science could be compremised. The standard GitHub licensing options are best suited for software, so depending on how you want your code to be used you can choose one of the other license options. For example, if your code is intended only for your

specific analysis, consider a Creative Commons License. If you wish to receive attribution for any reuse of your code, consider a CC BY 4.0 license. If you have built an app, tool, package, or other product that you would like others to use and would like attribution for any reuse of your code, consider the GNU General Public License v3. This license also prohibits the re-user from making their re-used version private. To help navigate through the potential licenses available to you and their attributes the Choose a License [41/] website can offer further guidance.

Collaborative (code) editing and asynchronous working

From its inception, one of the primary uses of GitHub has been for collaborative coding. We acknowledge that there are important differences between the average software developer and EEB researcher using GitHub, and that not all GitHub collaboration features are optimal for research purposes. However, core features of git like forking and branching can allow for simultaneous coding on different versions of the same research project, and alternative versions can be easily discussed and resolved with GitHub. Researchers can easily stay abreast of progress made by other collaborators without the need for meetings or emails. Collaborative project work can also be clearly split among team members, giving them the flexibility to contribute when it best fits their schedule. The version control [42] features also allow users to make progress and changes without worrying about irreparably writing over someone else's work. While a complete review of these features is beyond the scope of our paper, there are many free resources for learning how to use these collaborative features of GitHub [43]. (e.g. https://docs.github.com/en/pull-requests/collaborating-with-pull-requests/incorporating-changes-from-a-pull-request/merging-a-pull-request) It is often best to develop comfort with features like pull requests and merges on "practice" repositories with colleagues before integrating these tools fully into a collaborative workflow.

GitHub can also facilitate interactions between research advisors and advisees, providing a platform for students or other trainees to share in-progress code, and flag specific challenges or questions for their supervisors or mentors. Periodic code review can also help advisors to identify errors early in the process, and inform further training and mentorship to fill gaps in skills.

Of course, EEB researchers can use GitHub for accelerating research collaborations beyond working on computer code. Recently, a community-led data standardization effort supported by the ESS-DIVE data repository took place on GitHub [37] and involved dozens of scientists across the U.S. Department of Energy National Labs. The researchers leveraged GitHub to version control and share data formatting instructions and templates with the broader community of environmental scientists (e.g., ESS-DIVE's GitHub Community Space, [44]). In this effort, teams of environmental scientists, software developers, and informatics specialists worked asynchronously across many time zones to create, edit, and received community input on their proposed data standardization guidelines (Crystal-Ornelas et al. in review).

Recently, asynchronous communication tools have become essential for workplace productivity, especially given the growing role of remote work. With GitHub, researchers can seamlessly access and contribute to data and code regardless of disparities in schedules or location. However, the benefits of asynchronous work can also extend far beyond the "work from home" model. Improving remote collaboration can encourage the exchange of ideas among researchers at different institutions and in different countries, which can serve to improve the quality of the research itself. Researchers can work directly with experts from all over the world, who have access to the same data and code as they do.

Writing manuscript

Beyond supporting collaboration at the level of code, GitHub can even be used for collaborative writing of manuscripts. Writing a manuscript in GitHub and storing it with associated data and code all in the same repository increases scientific reproducibility because files associated with a manuscript can be found in one place. Co-authors can contribute new text to a manuscript or suggest revisions through GitHub's robust pull request feature which provides a sentence-by-sentence view of all proposed changes. Further, authors can make use of the Discussions tab to suggest relevant papers to be cited, and can raise issues during the writing process that can be assigned to collaborators.

While GitHub is not considered as user-friendly for manuscript development as conventional word processors [9], it has been substantially improved with recent tools. Manuscripts can be written on GitHub with Mardown which is a simple, easy to learn markup language that helps users format and stylize plain text documents. Add-ons like HackMD [45], can enable real-time collaboration like Google Docs for individual Markdown documents. We used HackMD early in the process of writing this manuscript to generate an outline. Many tools exist for extending Markdown and Pandoc to add formatting features necessary for scietnific writing like in-text citations and figure and table cross references.

We wrote this manuscript using Manubot, a collaborative manuscript platform that uses Markdown for writing and GitHub for storing and tracking changes to a manuscript over time [46]. Manubot uses a GitHub Actions-based typesetting system to compile individual Markdown files stored in a GitHub repository into a single LaTeX document, which can be displayed in Word, HTML, or PDF formats. The resulting manuscript can also be compiled using a journal's .tex template to match their formatting requirements. Since this tool reruns the entire manuscript compilation process with any change to the underlying repository, it can also accomodate continuous integration of code updates into figures and tables with additional GitHub Actions (as we have done in this manuscript). Manubot also allows for straightforward citation management based on URLs or DOIs. Manubot is being used for an increasing number of manuscripts (see examples in [47]).

Since Manubot works on documents in a distributed format, it can be difficult to edit manuscripts for overall flow with only this tool. We employed hypothes.is [48] to write comments on the HTML manuscript document produced by Manubot, which we then addressed by committing changes to the underlying Markdown files via pull requests. Other authors can reply to the comments to indicate agreement or disagreement, and to note when changes have been made. Other tools can also be used for version control of scientific manuscripts including R Markdown via the bookdown package [49/], jupyter notebooks [50] and a relatively new tool, Quarto [51].

Peer-Review

Peer review of research software by rOpenSci (https://ropensci.org/software-review/) and of research software and associated manuscripts by the Journal of Open Source Software (https://joss.readthedocs.io/en/latest/submitting.html) requires that submitted work is hosted on GitHub and their review processes make use of GitHub issues. rOpenSci's efforts have resulted in many well-used R packages for ecology research including rfishbase [52] and taxize [53].

GitHub can also be used as a hub for reviewers and authors during the peer review process of an ordinary research manuscript. If the code associated with a manuscript is made available at the time of submission (e.g. via a link to a GitHub repository in a Data Availability Statement), peer-reviewers may be able to offer more helpful suggestions on written methods and may even make comments on the code itself, potentially catching bugs or errors before publication . GitHub issues can also be used to organize and discuss reviewer suggestions and to assign them to co-authors (See example in [54, =is%3Aissue+label%3A%22reviewer+comment%22+]. When reviewer comments are posted as separate issues, authors can comment on the issues to discuss possible changes and assign

themselves to indicate which comments they intend to handle. Co-authors can then integrate their edits and responses to reviewers using pull requests.

Open science discussion

Research papers are condensed outputs that hide the underlying intellectual and computational workflows, including the treatment of the raw data and analytical steps. Granting readers access to code and other documentation of the analysis allows them to retrace and comprehend analytical decisions. GitHub provides a platform to access all aspects of the project, using citable DOIs, rather than just the final manuscript. While often thought of as storage for data and code, GitHub repositories can also be used to publish a time-stamped preregistration of research plans and hypotheses.

GitHub is a tool for managing and sharing components of any research project, that can help accelerate progress towards Open Science goals [55], from developing the analysis through to publication and ensuring reproducibility. Conventional research practices typically rely on one or two people running and checking the data analyses, while most coauthors (and readers of the subsequent publication) see only the final results and a verbal description of the analytical steps. In the developmental stages, collaborators can directly see the code for the analysis, manipulate and explore the data themselves, and check for errors. Cynically, there is also more insurance against nefarious colleagues that may be tempted to distort results [56]. Collaborators are better positioned to discover questionable findings if they have full and transparent access to the project.

This transparency can similarly be extended beyond coauthors to the entire scientific community. Publishing the data and reproducible workflows along with the manuscript allows any reader to review the analysis and reproduce the experiment [57]. Supplying code for (novel) methods that are proposed or used also reduces barriers to knowledge and can greatly improve the ability of others to build on existing work, resulting in greater proliferation and accessibility for a broader audience. GitHub even provides a useful Discussions Forum [58] that aids the direct communication with repository owners, as well as the GitHub Community [59/] forum for more general questions and sharing of expertise.

If the methods and analyses used are fully available during the peer-review process, they can be as critically evaluated as the rest of the manuscript. However, fear of being scooped feeds into cultural reluctance to do science openly due to worries of intellectual property. A solution would be to allow sharing a private link with a citable DOI for peer review, and update the DOI post-acceptance or post-publication. Updating DOIs is currently yet a missing feature of GitHub, but implemented in other open-access repositories such as Zenodo, which was developed under the European OpenAIRE program and is being hosted by CERN. Alternatively, GitHub users can to keep their data and code repository private until publication, and then make it public.

Project continuity

The development of research software continues to be on the rise, and with that comes the need to consider the continuity of the research software. This is particularly relevant for software developed for relatively short-term research projects, such as projects developed by graduate students or postdoctoral fellows [60]. Often with these projects, once the research contract expires, the research software upkeep tends to fall off as the researchers move on to new projects. Additionally, if the research software is kept on only the researcher's hard drive, it becomes increasingly difficult to access the software and code for future uses.

When the project owner is finished with the project, or their contract expires, there generally should be a handover period of this software in order for the next cohort of researchers to reuse what was already developed [9,60]. GitHub facilitates project continuity among research software and research code by providing tools that make this handover period easier. As we have already mentioned, using Git for code in Ecology and Evolution can allow for a “paper trail” of sorts to be created for the research software, thus allowing for future owners of the code access to the entire history of the project [14]. Additionally, GitHub allows for repositories and organizations to have designated Code Owners [61]; these code owners can change through time allowing for the transition of research software from one cohort of researchers to the next [38]. There are also multiple means by which to archive package version information with GitHub. Most simply, package versions can be included in README files. More sophisticated recording options include adding an enviornment.yml and/or an environment.txt file, or using tools such as Packrat [62/] to store all packages in the repository itself. This ensures that as packages continue to develop with new syntax, code will still run as it did when it was developed.

Within EEB projects, tasks are often divided among contributors taking various roles (see CRediT taxonomy [63/]). The creation of project repositories is commonly the purview of those involved in the software, formal analysis, and/or visualization components of the project through their roles as code writers. However, the structural components of a typical GitHub repository and the derived EEB-specific templates can provide functional ways for other non-code writers to be engaged in aspects of repository design in a way that improves institutional memory and facilitates project continuity. Non-code writers can offer many contributions to repository design and development, and their active involvement can both aid authors ability to act as guarantors of the project, and the clarity and reproducibility of the project for future users. In Figure 2, we highlight several elements of good repository structure, and the various ways that contributors may interact with them.

GitHub Organizations

Whether experiments are done in a wetlab, data are gathered in a field site, or analyses are run in a shared office, even conceptually distinct projects are often carried out in a common physical space. GitHub Organizations offer a shared virtual space that allows a team to work in different repositories, while remaining tied together under a larger figurehead, such as a laboratory, a department, an organization, or a large project involving several teams. Organizations are well-suited to ensure larger projects with many steps or moving parts are constrained to one virtual space, where outputs and sub-projects can be easily accessed and located without relying on any one individual. Because the repositories are grouped in one virtual space, members can reference and contribute to each other’s work without necessarily being part of the same repository, broadening the accessibility and longevity of code and writing contributions.

Contributors can be assembled into teams within an organization, which allows administrators to assign roles and tasks to groups of people. Whereas access to repositories is usually assigned to individual contributors, Organizations facilitate the management of access permissions by allowing each team to be granted access to certain repositories, and not to others. This ensures that more sensitive repositories remain as restricted as needed, while repositories with greater general interest can be easily accessible to many members at once.

As an example, GitHub Organizations are particularly well-suited to house documents and projects within a laboratory, such as research compendia, codes of conduct, protocols, training documents, and other such documents that evolve collaboratively over time and are relevant to many colleagues. In this way, students or teams can have full ownership of repositories within an organization, while ensuring that these materials stay accessible to the laboratory after people have moved on (or upgraded their computers). This application extends to research centres, which may include several distinct projects that remain linked under a given institution, such as the German Centre for

Integrative Biodiversity Research (iDiv)[64]. Of course, the utility of this tool goes beyond laboratories - they are useful to structure the organization, presentation, and outcomes of working groups such as the hackathon which inspired this paper (SORTEE-Github-Hackathon [65] by keeping track of all materials as ideas develop and take shape in one virtual space. Organizations are also convenient for hosting a set of related learning materials such as a set of lectures or workshops, such as the Québec Centre for Biodiversity Science R Workshop Series (QCBSRworkshops, [66]) or the University of Edinburgh's Coding Club (Coding Club, [67]), which may be updated by an ever-evolving group of contributors over time.

Utilizing GitHub organizations as a research group or even for a handful of individuals working on a group of projects can be incredibly useful for all involved. GitHub organizations are relatively easy to set up, and especially easy to manage as membership to the organization changes through time. Not only is it a useful way to store repositories of lab-related research products, but it's also incredibly helpful for storing "living documents" that may be edited frequently, and may be linked to a lab website (that could also be generated via a repository that lives within the organization!). The use of the "Teams" feature can allow certain groups to have varying levels of access to repos in the organization with a select group having push access to some repos but not others. This can manifest in a group working on some common dataset(s) (e.g. some genetic data) to have push access to the handful of repositories used for processing sequence data, while another group of students/researchers may have push access to an entirely different set of repos. The organization structure also allows for easy tracking of issues, projects, and discussions related to the research group, and provides PIs/group leads an easy birds-eye view of the progress going on across multiple projects.

Additionally, organizations provide a convenient location for students to archive the code for their projects, for use/reference by future students in the research group, thus providing a type of knowledge communication that may not exist otherwise. Indeed, providing new students with access to the organization and ideally a template repository for lab projects can soften the burden on those new to the software, in that it provides them with examples to work off of, and an online location to ask for help from their labmates and/or advisors through tools like projects, discussions, and issues.

Discussion

The promise of GitHub for EEB researchers

There have been many calls for researchers outside of the software development community to join the 73 million GitHub users for their collaborative research [3,37,68]. This call comes in light of both the continual shift toward open-science and increasing computational and data requirements in EEB. Until now, resources and practical guidance specifically focused on using GitHub within the EEB community have been dispersed in blog posts and video tutorials (Box [**box:box-2?**]). We felt these resources have been extremely useful for us to learn to use GitHub in our own work, and that a collation of the main ideas into one medium, while adding on our personal perspectives, would be of use in the EEB community.

In this paper, we describe 13 tractable ways that EEB researchers can leverage GitHub to enable more transparent and collaborative research (Figure 2). Many of the examples are specifically meant for first-time GitHub users and can likely be adopted with just several hours of practice (storing data, creating virtual notebooks, making code citable). For example, storing code and data and making it citable generally just involve creating a repository on GitHub, pushing code to the repository, and then going through the necessary steps (e.g., connecting a GitHub repository with Zenodo; see below) for creating a DOI for the repository. These actions are often covered in any introduction to GitHub tutorial and take little overhead to implement. On the other hand, some other examples we describe

may require a greater time commitment, but have the potential to make EEB research more open, accessible, and collaborative than ever before. For example, managing full research projects or research labs on GitHub will require careful thought as to how to delegate tasks such as reviewing pull requests or creating issues, as well as thought as to how modular to make the research project or research lab (i.e., which repository will be used for what, and how many repositories are needed). Additionally, collaboratively writing a paper using GitHub, as we have done here, will involve a learning curve for co-authors less familiar with the intricacies of GitHub, and also require overhead to set up the repository using GitHub actions. Despite the many potential applications of GitHub to EEB research, we acknowledge that there will still be many times when researchers might look to other platforms for research collaboration.

When to look to other platforms for collaboration

Though we see GitHub as a useful tool for collaboration in EEB, we describe two use cases where, to our knowledge, GitHub's features still fall short of the type of highly collaborative work emblematic of EEB research. First, real-time collaborative editing (e.g., as on a shared Google Doc or a Word document stored on Dropbox) is not possible on GitHub. There are now websites outside of the GitHub ecosystem that are built on top of the GitHub architecture that allow real-time collaborative editing (e.g., hackMD or replit). We used HackMD at two key points in writing our manuscript when real-time co-writing was essential: when taking meeting notes and writing the outline of our paper. Second, we looked to other software when working on figures and tables. Creating tables and figures on GitHub using markdown or other scripting languages is possible, we found that it was not practical at the early brainstorming stages. We needed to rapidly iterate on figure and table design, share feedback through comments, and merge/reorder ideas when necessary. For these reasons, we used Google Slides for working on figures and Google Sheets for working on tables. As our figures and tables moved towards more finalized forms, some co-authors chose to create the tables and figures using R and Markdown which could then be tracked using the same version control system as the rest of manuscript.

Why aren't more EEB researchers using GitHub?

Though GitHub has been available as a platform for more than a decade, its uptake among EEB researchers, especially as a tool for collaboration, has been slow. Here we discuss four potential barriers to GitHub use in EEB.

First, there may be a hesitation to use GitHub due to the somewhat steep learning curve to using the platform combined with limited instruction available through traditional university courses. Even we, a group of highly motivated researchers who write code as part of our research, experienced a substantial learning curve. When GitHub is taught within an EEB context, it is usually accompanying coursework in topics such as statistical programming, and some students may find it overwhelming to juggle learning git alongside scripting languages, statistical theory, and file system navigation, especially when many may also be new to using command-line interfaces in general. Instructors likewise may confuse the expected digital literacy of younger students with computational fluency, even when modern technology increasingly abstracts many relevant concepts through search optimization and preponderant IDEs (Integrated Development Environments).

Second, while many EEB researchers take advantage of GitHub for individual use, collaborative use may lag due to how researchers traditionally divide labor within projects. Despite broad utility, GitHub remains a tool predominantly used by computer scientists and software developers, and EEB researchers may take the view that GitHub is a platform that only needs to be used by individuals writing code, and may silo those aspects of projects to a single individual. Those assumptions may obscure the utility of GitHub for tasks other than traditional data analysis and software development,

or how GitHub can facilitate the integration of code with non-coding aspects of projects through the practice of repository design. However, we emphasize that there are opportunities for collaboration using GitHub by researchers of all skill levels or time constraints (Table 1); for example, project stakeholders can provide a list of use-cases or highlight important conceptual components of a project using the issues or discussions functionality of GitHub.

A third barrier may comes from general reluctance to share data and code publicly, or technical and logistical issues related to storing and sharing large data files and lack of integration with other research platforms. The default public nature of GitHub usage can add additional pressure to students and scientists learning to use the platform. We also note that large file storage is discouraged (and limited) on GitHub but add-ons do exist (e.g. [69]/) that permit data storage, and increasing integration between platforms (e.g. [70]) allows data to be stored away from GitHub and linked dynamically. We suspect a major additional barrier to EEB researchers is a distinct lack of GitHub help documents for non-English researchers in ecology and evolution, meaning that EEB researchers potentially miss the opportunity to fully understand the importance of version control as well as the other benefits of GitHub.

Lastly, GitHub has both free and paid plans. When projects get highly collaborative they may have to pay for additional GitHub support. The acquisition of GitHub by Microsoft has led to some concerns over the future of free plans and several biodiversity data managers have begun to switch to Open Source Git services (e.g. Bitbucket and GitLab). At this point however, there is little practical difference for EEB researchers between the paid and free GitHub plans (paying gives easier access to technical support for example for very large projects which are not typical for our fields).

Box 2

10 Tips for getting started in GitHub
1. **Check for an existing solution to your problem** The GitHub Help webpage [71] contains extensive and detailed documents with helpful screenshots. It is a good starting point for handling an issue, and has troubleshooting tips for specific problems. Alternatively, consider Tweeting your issue. There is a large community of GitHub users around the world who have likely faced analogous problems and may be able to provide quick solutions. Third, try to follow blogs e.g. [72], Twitter accounts or YouTube channels that regularly post practical solutions about common GitHub issues.
2. **Consider taking free courses** such as those from Software Carpentries [73] and sharing these courses with your lab members or colleagues.
3. **Take the advantage of GitHub as an asynchronous working tool for team-based projects** See the repository for this paper [74] as an example of a collaborative manuscript that includes discussions, issues, and a website via GitHub.
4. **The GitHub Learning Lab[75]** allows you to learn GitHub basics through short projects and tasks, and allows you to get feedback from their Learning Lab bot.
5. **Check out the following markdown cheatsheet [76]** so that you can write clear metadata README files for your repositories.
6. **The Jenny Bryan universe of GitHub material** provides a thorough and accessible introduction for a multitude of research-related uses for GitHub, and includes a book [77], statistics course [78] and academic article [8].
7. **Don't be afraid of trial and error** One of the best ways to learn GitHub is the trial and error method. Learning from your own mistakes can be the better way to master your GitHub abilities. In any case, GitHub has the advantage of making it easy to go back to any steps that you desire via version controlling if you make mistakes.
8. **If you are an educator, include lectures on reproducibility and tools for creating reproducible workflows in your curricula**. Some graduate programs now include coursework on course Rmarkdown and GitHub. Getting students started with these tools earlier will prevent the resistance that comes from working with a less reproducible workflow for a longer period of time.

10 Tips for getting started in GitHub
9. **Try to begin committing with GUI (Graphical user interface) tools** like GitHub Desktop [79], git-gui [80], RStudio [81], Visual Studio Code [82], Atom [83], GitKraken [84] tools instead of CLI (Command line interface) tools such as Terminal or Console for more advanced features.
10. **Get help deciphering GitHub Notifications.** Try using tools like Octobox [85] to disentangle and manage multiple notifications from distinct GitHub projects.

Conclusion

We provide 13 practical ways that Ecologists and Evolutionary Biologists can incorporate GitHub into their research workflows.
GitHub is still an emerging platform for many working in EEB, and so we include definitions (Box 1) and key user groups (Figure 1) that can help researchers prioritize which GitHub skills to learn first. Some GitHub uses are highly collaborative (e.g., open science discussion and collaborative code editing) while others are focused on individual actions (e.g., storing code/data, building a website). Regardless of the degree of collaboration, GitHub use in Ecology and Evolution has the potential to make the field more open and transparent than ever before.
Our paper provides the most comprehensive review of how EEB researchers can use GitHub to date, and we encourage EEB researchers at any career stage studying any topic to try GitHub as a platform for sharing and collaboration.

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Code and data availability

The source code and data for this manuscript are available at https://github.com/SORTEE-Github-Hackathon/manuscript.

Figures

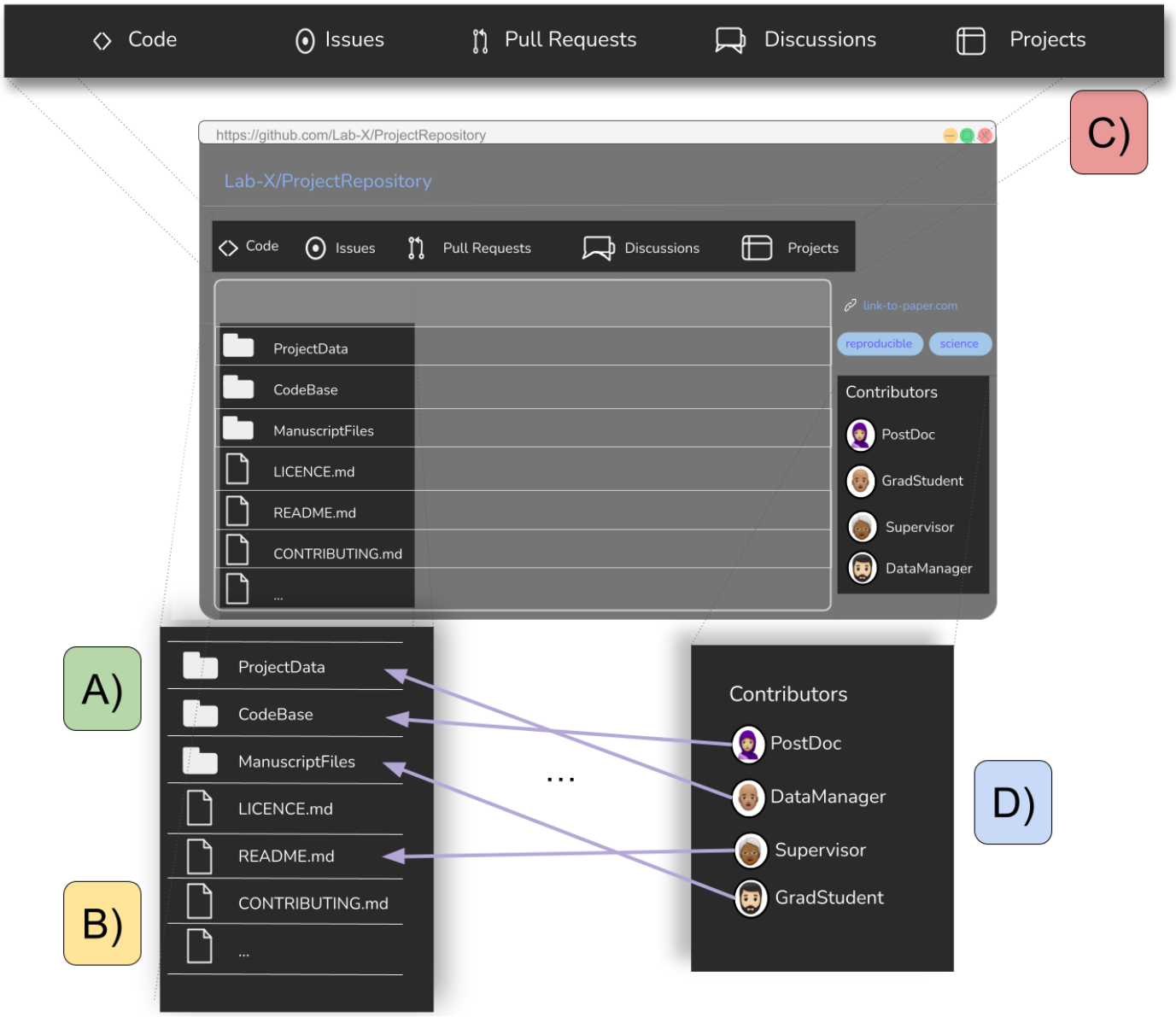

Figure 1: An overview of the features of a GitHub repository. A) Multi-faceted components allow for code writing, small data storage, manuscript writing, and project management to all be done in one place. B) Issues, Pull Requests, Discussions, and Projects allow for team members to ask for feedback, suggest fixes, discuss related ideas, and keep track of all the moving parts of a project. C) All collaborators on a project can be a part of a single repository, with varying push privileges and responsibilities. D) CONTRIBUTING.md, LICENCE.md, & README.md files can allow new team members or others wanting to use materials to understand the project components and learn how they can engage with the project and existing team members.

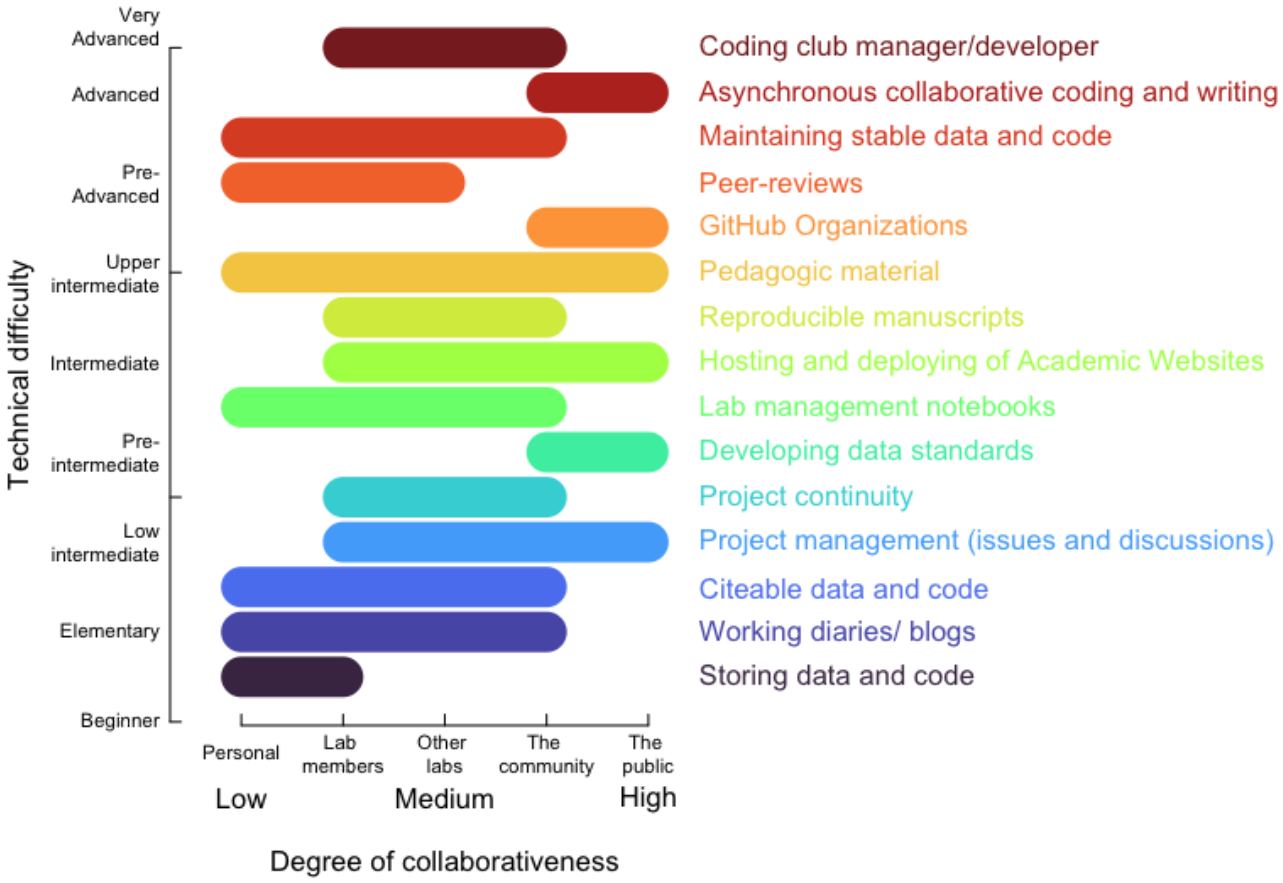

Figure 2: A summary of ways GitHub can be used showing technical difficulty and degree of collaborativity for each. Activities higher on the vertiucal axis require usage knowledge of more GitHub features than activities lower on the axis. On the horizontal axis, each activity spans a region representing who is potentially involved with or benefits from each activity. For example, storing data and code mainly benefits individual researchers or members of a lab group while making data and code citable and reproducible benefit other labs and the larger community as well. Independently of a users knowledge level of GitHub features, there are ways to use GitHub that allow tapping unto one of the most salient benefits of the platform: facilitating and enhancing collaboration.

Tables

Table 1: A non-exhaustive collection of ideas for how various GitHub features could be utilized for a research project. Here we have categorized contributors/collaborators into five roles. A Project Manager owns the GitHub repository for a project, and leads the academic project (e.g., lead author of a manuscript). A co-author contributes to writing and other aspects of research, but may have limited or no experience with programming, git, and/or GitHub. A code contributor writes or edits analysis code for the project. A code reviewer could be a project collaborator or a peer reviewer who reviews project code. They are familiar with coding, but not necessarily with git or GitHub (but they are willing to learn). Finally, community members could be other researchers or non-researchers interested in reproducing results, re-using code or data, or communicating with researchers involved in the project. These roles are not mutually exclusive—a co-author could also be e code contributor and code reviewer, for example. For definitions of the GitHub features, see Box 1.

Role	GitHub repo	README	Issue	Discussion	Pull Request	Fork	GitHub Pages

Role	GitHub repo	README	Issue	Discussion	Pull Request	Fork	GitHub Pages
Project manager	Set contributor permissions, share code of conduct	Project descritption, citation, DOIs	Assign tasks to collaborators	Discuss project directions and goals	Approve and incorporate edits to code and/or writing		Share up-to-date reports, figures, or draft manuscript
Co-author	Edit Markdown text or add files		Propose changes involving code (e.g. analyses, figures)	Discuss proposed changes to manuscript			
Code contributor			Suggest code changes		Contribute changes to code, initiate code review		Contribute to project website
Code reviewer	Find all code related to a project		Highlight specific lines of code and make suggestions		Review or recommended changes in code		
Community			Suggest additional features and report bugs	Ask questions about data and code		Create a linked, editable copy of the repository	View project website

Table 2: a comparison of technologies...

Guild	Software	Version control	Backup (cloud)	Passive collaboration	Active real-time collaboration	Free $	Permanent (DOI)	Storage limits	GitHub Integration

Multi-tool	GitHub	yes	yes	yes	NA	Broadly limited free version. Advanced features are provided for free to students and education professionals.	A DOI can only be obtained when integrating to other services that can mint DOI (e.g. Zenodo, OSF).	100MB per file, 500MB per private repo (2GB for paid accounts). 100GB for public repos. Larger files (up to 2GB) can be attached to releases	NA
Multi-tool	OSF	yes	yes	yes	yes	yes	yes	25GB for private projects, up to 5GB per file, plus partner add-ons, 50GB for public projects	yes
Long-term (public) data repositories	PANGAEA	yes	yes	yes	NA	yes	yes	10 GB free	NA
Long-term (public) data repositories	Zenodo	afterpublished	afterpublished	NA	NA	yes	yes	50 GB per dataset	yes
Long-term (public) data repositories	Dryad	afterpublished	afterpublished	NA	NA	some journals cover cost	yes	300 GB per publication	Can link to individual files (not entire repo); not really integrated
Long-term (public) data repositories	Figshare	yes	yes	yes	NA	yes	yes	20 GB free, up to 5 TB	yes

Temporary (personal) drive storage	Google Drive	yes	yes	yes	yes	limited free version & paid	NA	15GB free, up to 100GB with Google One	yes
Temporary (personal) drive storage	Box	limited	yes	?	?	NA	NA	Unlimited total size for subscription	yes
Temporary (personal) drive storage	DropBox	limited	yes	yes	yes	limited free version & paid	NA	2GB free	yes
Temporary (personal) drive storage	OneDrive and the Office Suite	yes	yes	yes	yes	limited free version & paid	NA	5 GB free, up to 1TB paid	yes
Collaborative code/text editors	Overleaf (online latex editor)	yes	yes	yes	NA	NA	NA	1MB for individual .tex, 50MB for individual files, unlimited project size	yes
Collaborative code/text editors	JupyterNotebook	yes	?	yes	with Colab	yes	NA	via Binder: no hard limit, but suggests no files >100MB, can also store on GitHub or Google Colab	yes
Collaborative code/text editors	HackMD	yes	yes	yes	yes	yes	NA	3 documents free, private invitee limits	yes

References

1. **How do scientists develop and use scientific software?**
Jo Erskine Hannay, Carolyn MacLeod, Janice Singer, Hans Petter Langtangen, Dietmar Pfahl, Greg Wilson
2009 ICSE Workshop on Software Engineering for Computational Science and Engineering (2009-05) https://doi.org/bw966x
DOI: 10.1109/secse.2009.5069155

2. **Challenge to scientists: does your ten-year-old code still run?**
Jeffrey M Perkel
Nature (2020-08-24) https://doi.org/gg89cr
DOI: 10.1038/d41586-020-02462-7 · PMID: 32839567

3. **Democratic databases: science on GitHub**
Jeffrey Perkel
Nature (2016-10-03) https://doi.org/gdz6dq
DOI: 10.1038/538127a · PMID: 27708327

4. **A survey of the practice of computational science**
Prakash Prabhu, Yun Zhang, Soumyadeep Ghosh, David I August, Jialu Huang, Stephen Beard, Hanjun Kim, Taewook Oh, Thomas B Jablin, Nick P Johnson, … David Walker
State of the Practice Reports on - SC '11 (2011) https://doi.org/bdpsrp
DOI: 10.1145/2063348.2063374

5. **Best Practices for Scientific Computing**
Greg Wilson, DA Aruliah, CTitus Brown, Neil P Chue Hong, Matt Davis, Richard T Guy, Steven HD Haddock, Kathryn D Huff, Ian M Mitchell, Mark D Plumbley, … Paul Wilson
PLoS Biology (2014-01-07) https://doi.org/qtt
DOI: 10.1371/journal.pbio.1001745 · PMID: 24415924 · PMCID: PMC3886731

6. **Build software better, together**
GitHub
https://github.com

7. **Pro Git**
Scott Chacon
Apress (2014)
ISBN: 9781484200773

8. **Excuse Me, Do You Have a Moment to Talk About Version Control?**
Jennifer Bryan
The American Statistician (2018-01-02) https://doi.org/gdhzdp
DOI: 10.1080/00031305.2017.1399928

9. **Git can facilitate greater reproducibility and increased transparency in science**
Karthik Ram
Source Code for Biology and Medicine (2013-02-28) https://doi.org/krv
DOI: 10.1186/1751-0473-8-7 · PMID: 23448176 · PMCID: PMC3639880

10. **Ten Simple Rules for Taking Advantage of Git and GitHub**
Yasset Perez-Riverol, Laurent Gatto, Rui Wang, Timo Sachsenberg, Julian Uszkoreit, Felipe da Veiga Leprevost, Christian Fufezan, Tobias Ternent, Stephen J Eglen, Daniel S Katz, … Juan Antonio Vizcaíno

PLOS Computational Biology (2016-07-14) https://doi.org/gbrb39
DOI: 10.1371/journal.pcbi.1004947 · PMID: 27415786 · PMCID: PMC4945047

11. **A Quick Introduction to Version Control with Git and GitHub**
John D Blischak, Emily R Davenport, Greg Wilson
PLOS Computational Biology (2016-01-19) https://doi.org/gbqsnf
DOI: 10.1371/journal.pcbi.1004668 · PMID: 26785377 · PMCID: PMC4718703

12. **Let's Git started | Happy Git and GitHub for the useR**
Jenny Bryan Hester the STAT 545 TAs, Jim
https://happygitwithr.com/

13. **Coding Club: A Positive Peer-Learning Community** https://ourcodingclub.github.io/

14. **Our path to better science in less time using open data science tools**
Julia SStewart Lowndes, Benjamin D Best, Courtney Scarborough, Jamie C Afflerbach, Melanie R Frazier, Casey C O'Hara, Ning Jiang, Benjamin S Halpern
Nature Ecology & Evolution (2017-05-23) https://doi.org/gc4jb3
DOI: 10.1038/s41559-017-0160 · PMID: 28812630

15. **Social network of software development at GitHub**
William Leibzon
2016 IEEE/ACM International Conference on Advances in Social Networks Analysis and Mining (ASONAM) (2016-08) https://doi.org/gph5qt
DOI: 10.1109/asonam.2016.7752419

16. **Openscapes** //

17. **A Beginner's Guide to Conducting Reproducible Research**
Jesse M Alston, Jessica A Rick
The Bulletin of the Ecological Society of America (2021-01-15) https://doi.org/gk5v4p
DOI: 10.1002/bes2.1801

18. **Foundational Practices of Research Data Management**
Kristin Briney, Heather Coates, Abigail Goben
Research Ideas and Outcomes (2020-07-27) https://doi.org/ghssbk
DOI: 10.3897/rio.6.e56508

19. **SORTEE**
SORTEE
SORTEE https://www.sortee.org/

20. **Zenodo - Research. Shared.** https://www.zenodo.org/

21. **Electronic lab notebooks: can they replace paper?**
Samantha Kanza, Cerys Willoughby, Nicholas Gibbins, Richard Whitby, Jeremy Graham Frey, Jana Erjavec, Klemen Zupančič, Matjaž Hren, Katarina Kovač
Journal of Cheminformatics (2017-05-24) https://doi.org/gfz287
DOI: 10.1186/s13321-017-0221-3 · PMID: 29086051 · PMCID: PMC5443717

22. **Ten Simple Rules for a Computational Biologist's Laboratory Notebook**
Santiago Schnell
PLOS Computational Biology (2015-09-10) https://doi.org/gf5fnr
DOI: 10.1371/journal.pcbi.1004385 · PMID: 26356732 · PMCID: PMC4565690

23. **Welcome! | lab-book.knit** https://scheuerell-lab.github.io/lab-book/

24. **GitHub - HuckleyLab/how_we_work: Lab best practices and policies to conduct open, reproducible, and inspiring science that is efficient and fun**
GitHub
https://github.com/HuckleyLab/how_we_work

25. **R Markdown: the definitive guide**
Yihui Xie, JJ Allaire, Garrett Grolemund
CRC Press, Taylor and Francis Group (2019)
ISBN: 9780429782961

26. **python-pptx — python-pptx 0.6.21 documentation** https://python-pptx.readthedocs.io/en/latest/index.html

27. **Remark.jl**
Dan Segal (dan@seg.al)
Julia Packages https://juliapackages.com/p/remark

28. **Build software better, together**
GitHub
https://github.com

29. **GitHub Classroom** https://classroom.github.com/

30. **About projects (beta)**
GitHub Docs
https://ghdocs-prod.azurewebsites.net/en/issues/trying-out-the-new-projects-experience/about-projects

31. **GitHub Pages**
GitHub Pages
https://pages.github.com/

32. **GitHub - SORTEE-Github-Hackathon/main-website: This is the home of the main website for hackathon information, then later for collaborative writing.**
GitHub
https://github.com/SORTEE-Github-Hackathon/main-website

33. **Introduction** https://sortee-github-hackathon.github.io/

34. **Building tools with GitHub: customize your workflow**
Chris Dawson
O'Reilly (2016)
ISBN: 9781491933503

35. **Jekyll • Simple, blog-aware, static sites**
Jekyll • Simple, blog-aware, static sites
https://jekyllrb.com/

36. **The world's fastest framework for building websites** https://gohugo.io/

37. **A Guide to Using GitHub for Developing and Versioning Data Standards and Reporting Formats**
Robert Crystal-Ornelas, Charuleka Varadharajan, Ben Bond-Lamberty, Kristin Boye, Madison Burrus, Shreyas Cholia, Michael Crow, Joan Damerow, Ranjeet Devarakonda, Kim S Ely, … Deborah A Agarwal
Earth and Space Science (2021-08) https://doi.org/gmbs9c

DOI: 10.1029/2021ea001797

38. **The Tao of open science for ecology**
Stephanie E Hampton, Sean S Anderson, Sarah C Bagby, Corinna Gries, Xueying Han, Edmund M Hart, Matthew B Jones, WChristopher Lenhardt, Andrew MacDonald, William K Michener, … Naupaka Zimmerman
Ecosphere (2015-07) https://doi.org/gdj5w6
DOI: 10.1890/es14-00402.1

39. **Elevating The Status of Code in Ecology**
KAS Mislan, Jeffrey M Heer, Ethan P White
Trends in Ecology & Evolution (2016-01) https://doi.org/gg43mk
DOI: 10.1016/j.tree.2015.11.006 · PMID: 26704455

40. **1,500 scientists lift the lid on reproducibility**
Monya Baker
Nature (2016-05-25) https://doi.org/gdgzjx
DOI: 10.1038/533452a · PMID: 27225100

41. **Non-Software Licenses**
Choose a License
https://choosealicense.com/non-software/

42. **Not just for programmers: A friendly guide on the versatility/benefits of GitHub for accelerating collaborative research in Ecology and Evolution**
Dylan GE Gomes, Cole B Brookson, Robert Crystal-Ornelas, Ali Guncan, Brandon PM Edwards, Kaitlyn M Gaynor, Vivienne Foroughirad, Katherine Hébert, Emma J Hudgins, Saeed Shafiei Sabet, … Helen Weierbach
Manubot (2022-05-12) https://SORTEE-Github-Hackathon.github.io/manuscript/

43. **Barely sufficient practices in scientific computing**
Graham Lee, Sebastian Bacon, Ian Bush, Laura Fortunato, David Gavaghan, Thibault Lestang, Caroline Morton, Martin Robinson, Philippe Rocca-Serra, Susanna-Assunta Sansone, Helena Webb
Patterns (2021-02) https://doi.org/gjpcb6
DOI: 10.1016/j.patter.2021.100206 · PMID: 33659915 · PMCID: PMC7892476

44. **ESS-DIVE Community Space**
GitHub
https://github.com/ess-dive-community

45. **HackMD - Collaborative Markdown Knowledge Base**
HackMD
https://hackmd.io

46. **Open collaborative writing with Manubot**
Daniel S Himmelstein, Vincent Rubinetti, David R Slochower, Dongbo Hu, Venkat S Malladi, Casey S Greene, Anthony Gitter
PLOS Computational Biology (2019-06-24) https://journals.plos.org/ploscompbiol/article?id=10.1371/journal.pcbi.1007128
DOI: 10.1371/journal.pcbi.1007128

47. **Manubot Catalog** https://manubot.org

48. **Home**
dwhly

Hypothesis https://web.hypothes.is/

49. **Home | Bookdown** https://bookdown.org/home/

50. **Creating an executable paper is a journey through Open Science**
Jana Lasser
Communications Physics (2020-08-19) https://doi.org/gg89zd
DOI: 10.1038/s42005-020-00403-4

51. **Quarto** https://quarto.org/

52. **rfishbase: exploring, manipulating and visualizing FishBase data from R**
C Boettiger, DT Lang, PC Wainwright
Journal of Fish Biology (2012-11) https://doi.org/gh5x27
DOI: 10.1111/j.1095-8649.2012.03464.x · PMID: 23130696

53. **taxize: taxonomic search and retrieval in R**
Scott A Chamberlain, Eduard Szöcs
F1000Research (2013-10-28) https://doi.org/ggdskx
DOI: 10.12688/f1000research.2-191.v2 · PMID: 24555091 · PMCID: PMC3901538

54. **Issues · BrunaLab/HeliconiaDemography**
GitHub
https://github.com/BrunaLab/HeliconiaDemography

55. **The Open Knowledge Foundation: Open Data Means Better Science**
Jennifer C Molloy
PLoS Biology (2011-12-06) https://doi.org/g3b
DOI: 10.1371/journal.pbio.1001195 · PMID: 22162946 · PMCID: PMC3232214

56. **#PruittData and the Ethics of Data in Science**
Professor Lee BKass January 18, 2022 2:51 Pm
Ecology for the Masses (2020-02-04) https://ecologyforthemasses.com/2020/02/04/pruittdata-and-the-ethics-of-data-in-science/

57. **Low availability of code in ecology: A call for urgent action**
Antica Culina, Ilona van den Berg, Simon Evans, Alfredo Sánchez-Tójar
PLOS Biology (2020-07-28) https://doi.org/gg6rgf
DOI: 10.1371/journal.pbio.3000763 · PMID: 32722681 · PMCID: PMC7386629

58. **GitHub Discussions Documentation**
GitHub Docs
https://ghdocs-prod.azurewebsites.net/en/discussions

59. **GitHub Community**
GitHub Community
https://github.community/

60. **Sustainable Research Software Hand-Over**
J Fehr, C Himpe, S Rave, J Saak
Journal of Open Research Software (2021-04-30) https://doi.org/g4n4
DOI: 10.5334/jors.307

61. **About code owners**
GitHub Docs

https://ghdocs-prod.azurewebsites.net/en/repositories/managing-your-repositorys-settings-and-features/customizing-your-repository/about-code-owners

62. **Packrat: Reproducible package management for R** https://rstudio.github.io/packrat/

63. **CRediT - Contributor Roles Taxonomy**
CASRAI
https://casrai.org/credit/

64. **German Centre for Integrative Biodiversity Research (iDiv)**
GitHub
https://github.com/idiv-biodiversity

65. **SORTEE Hackathon #4: Promoting the use of Github in Ecology and Evolution**
GitHub
https://github.com/SORTEE-Github-Hackathon

66. **QCBS R Workshop Series / Série d'ateliers R du CSBQ**
GitHub
https://github.com/QCBSRworkshops

67. **Coding Club**
GitHub
https://github.com/ourcodingclub

68. **A collaborative GIS programming course using GitHub Classroom**
Berk Anbaroğlu
Transactions in GIS (2021-07-21) https://doi.org/gp44fx
DOI: 10.1111/tgis.12810

69. **Git Large File Storage**
Git Large File Storage
https://git-lfs.github.com/

70. **Connect GitHub to a Project - OSF Support** https://help.osf.io/article/211-connect-github-to-a-project

71. **GitHub.com Help Documentation**
GitHub Docs
https://ghdocs-prod.azurewebsites.net/en

72. **The GitHub Blog**
The GitHub Blog
https://github.blog/

73. **swcarpentry/git-novice: Software Carpentry: Version Control with Git, June 2019**
Madicken Munk, Katherine Koziar, Katrin Leinweber, Raniere Silva, François Michonneau, Rich McCue, Nima Hejazi, Simon Waldman, Rémi Emonet, Rayna Michelle Harris, … Wolmar Nyberg Åkerström
Zenodo (2019-07-01) https://doi.org/gp44fz
DOI: 10.5281/zenodo.3264950

74. **GitHub - SORTEE-Github-Hackathon/manuscript: This repository implements an automated system to write our collaborative manuscript, while tracking changes and contributions.**
GitHub

https://github.com/SORTEE-Github-Hackathon/manuscript

75. **GitHub Learning Lab**
GitHub Learning Lab
https://lab.github.com/

76. **Basic Syntax | Markdown Guide** https://www.markdownguide.org/basic-syntax/

77. **Let's Git started | Happy Git and GitHub for the useR**
Jenny Bryan Hester the STAT 545 TAs, Jim
https://happygitwithr.com/

78. **STAT 545**
Jenny Bryan, The STAT 545 TAs
https://stat545.com/

79. **GitHub Desktop**
GitHub Desktop
https://desktop.github.com/

80. **Git - git-gui Documentation** https://git-scm.com/docs/git-gui

81. **RStudio | Open source & professional software for data science teams**
https://www.rstudio.com/

82. **Visual Studio Code - Code Editing. Redefined** https://code.visualstudio.com/

83. **A hackable text editor for the 21st Century**
Atom
https://atom.io/

84. **GitKraken Legendary Git Tools | GitKraken** https://www.gitkraken.com

85. **Octobox**
Octobox
https://octobox.io/