

In the [Knight Lab](#) we produce the highest-quality software tools & packages, analytical techniques and pipelines, and the most reproducible scientific results for the microbiome. For more information visit the full list of [software types and their workflows](#) and the current [Knight Lab list of software projects](#).

All [Software types and their workflows](#) should have the following components:

- The code/IPython-Jupyter-notebook/scripts should be publicly available either in your own GitHub repository or under the biocore organization. Normally, we prefer to move repositories to biocore once they reach an [alpha](#) (a bit more developed) state, as many prototypes end up as learning exercises.
 - Alpha: code has to be tested and should have enough documentation so people/users can install and follow up tutorial. Basically, your code should be at this stage just before the first time you are using it in a publication.
- Any new functionality should have tests, following the [test-driven development methodology](#).
- All code should be documented and generated in an easily readable format. For python you should follow <https://www.python.org/dev/peps/pep-0008/>. Note that these guidelines are for python but similar principles apply to most programming languages. If you are adding a formula explanation to your documentation, make sure that it matches the code; this should help understanding both sections and avoid future problems. For example, with Emperor which relies on both Python and JavaScript, we follow PEP-8 and Google's JS coding guidelines (automatically checked with [gjslint](#), additionally documentation can be built with [jsdoc](#)), more information about this can be found [here](#). For Python + SQL, we put together some rules that are not following any official standard but we are following in our code:
<https://github.com/biocore/qiita/blob/master/CONTRIBUTING.md#sql-coding-guidelines>
- The repository should have a README.md explaining the goals of the files in the repository, and with basic install and execution information.
- All new code (excluding notebooks or shell scripts for automation) should have their tests run automatically every time a new pull request is generated via [Travis CI](#). If the codebase is python, you should always run flake8. The travis generated banner should be added to the README.md
- The repo should run coveralls (excluding notebooks or shell scripts for automation). The coveralls-generated banner should be added to the README.md
- We recommend small, incremental pull requests to facilitate revision and merge. Normally large changes can be made in smaller PRs against their own branch. Some guidelines can be found in the [CONTRIBUTING.md Qiita file](#).
- Each PR should have at least one reviewer, do not merge your own code. The PR creator and the first reviewer will decide if more reviewers are needed.
- Notebook general standards in github:
 - They should only be used for:
 - Benchmarks
 - Exemplifying analysis and pipelines

- All repos should contain the executed ipython notebooks (ipynb)
- For an example see [this repository](#).
- Evaluate the use of mybinder: <http://mybinder.org/>
- If the collaborator wants private analyses perhaps using: <https://bitbucket.org/>. This should be a case by case decision.
- Knightlab analyses repository: <https://github.com/knightlab-analyses>

Thanks for maintaining the high quality of our codebase -- it will save us all a lot of time in the long run, and help guarantee that our scientific results are correct!