XBrainMap Documentation

Release 0.1.0

Argonne National Laboratory

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Overview

1.1 Motivations

Complete maps of brains detailing how the billions of neurons in a brain connect with each other (connectomics) are now emerging as a valuable tool in neuroscience. Such maps will provide insight into the ways in which brains store and process information at low energies as well as reveal how brains vary from each other as well as in development, aging, and disease.

1.2 Objectives

This and that...

1.3 Features

- Registration of x-ray micrographs

- Reconstruction of full mouse brain microstructure

- Segmentation of neurons and blood vessels

- High-performace and automated data processing workflows

History

This section contains project history.

Roadmap

Progress Notes.

Software

Related software, and sister projects.

Tutorials

Tutorials.

Development

This section explains the basics for developers who are contributing to the XBrainMap project.

Contents:

6.1 Cloning the repository

The project is maintained on GitHub, which is a version control and a collaboration platform for software developers. To start first register on GitHub and fork the XBrainMap repository by clicking the **Fork** button in the header of the XBrainMap repository:
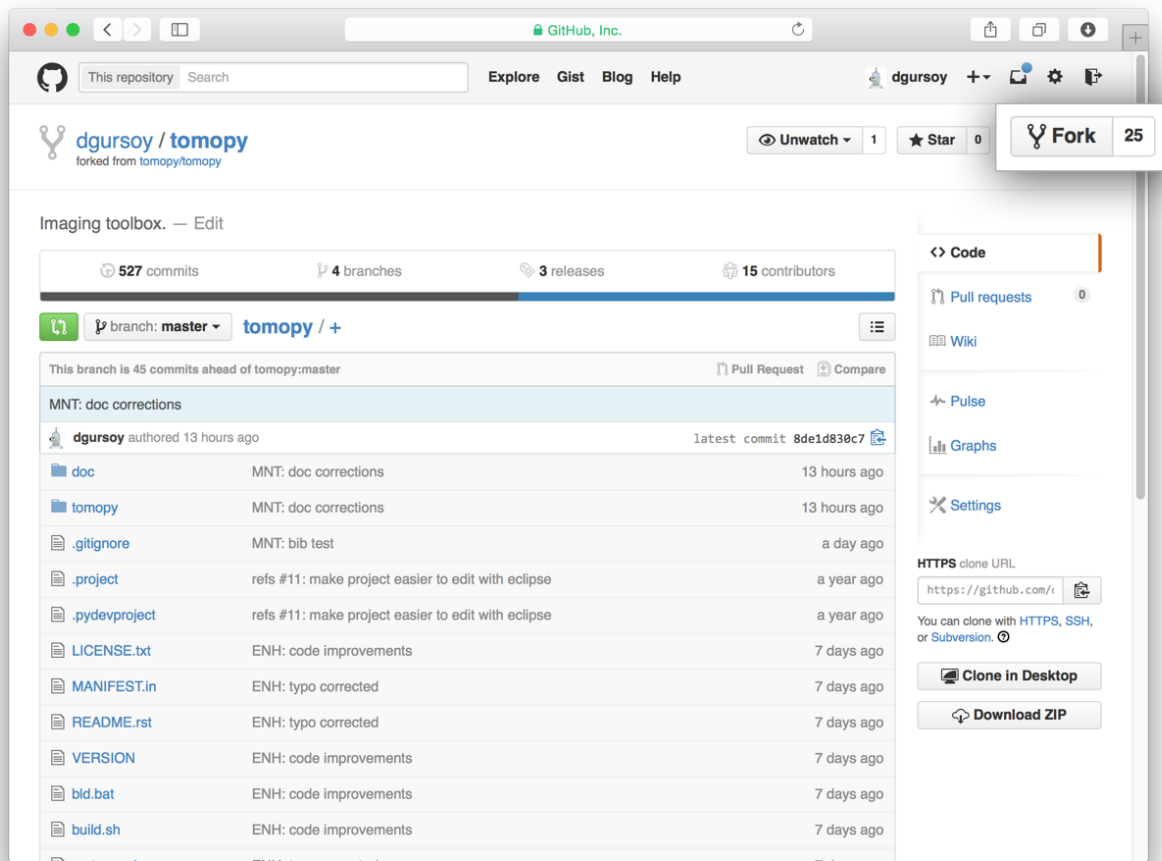
This successfully creates a copy of the project in your personal GitHub space. The next thing you want to do is to clone it to your local machine. You can do this by clicking the **Clone in Desktop** button in the bottom of the right hand side bar:
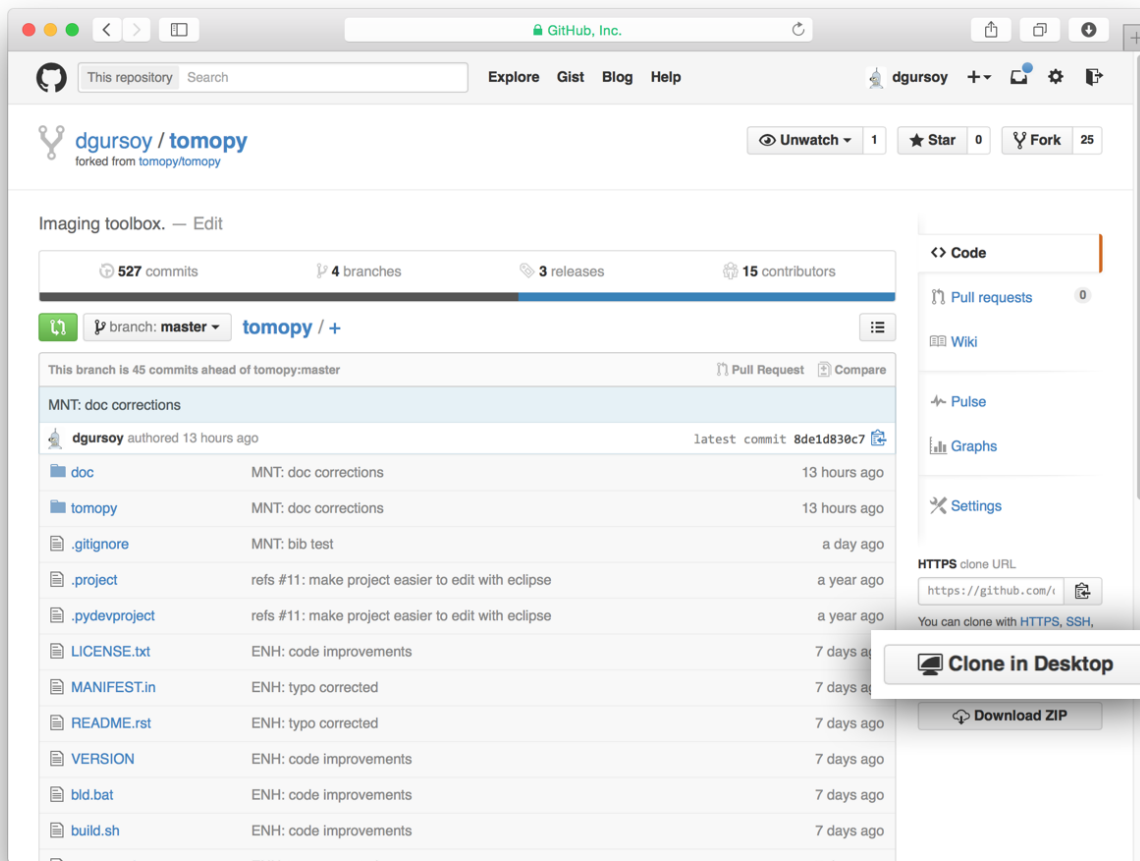
This will launch the GitHub desktop application (available for both Mac and Win) and ask you where you want to save it. Select a location in your computer and feel comfortable with making modifications in the code.

6.2 Coding conventions

We try to keep a consistent and readable code. So, please keep in mind the following style and syntax guidance before you start coding.

First of all the code should be well documented, easy to understand, and integrate well into the rest of the project. For example, when you are writing a new function always describe the purpose and the parameters:

```
def my_awesome_func(a, b):
    """
    Adds two numbers.

    Parameters
    ----------
    a : scalar (float)
        First number to add

    b : scalar (float)
        Second number to add

    Returns
```

```
    -------
output : scalar (float)
    Added value
"""
return a+b
```

## 6.3 Package versioning

We follow the X.Y.Z (Major.Minor.Patch) semantic for package versioning. The version should be updated before each pull request accordingly. The patch number is incremented for minor changes and bug fixes which do not change the software's API. The minor version is incremented for releases which add new, but backward-compatible, API features, and the major version is incremented for API changes which are not backward-compatible. For example, software which relies on version 2.1.5 of an API is compatible with version 2.2.3, but not necessarily with 3.2.4.

6.4 Commiting changes

After making some changes in the code, you may want to take a *snapshot* of the edits you made. That's when you make a *commit*. To do this, launch the GitHub desktop application and it should provide you all the changes in your code since your last commit. Write a brief *Summary* and *Description* about the changes you made and click the **Commit** button:
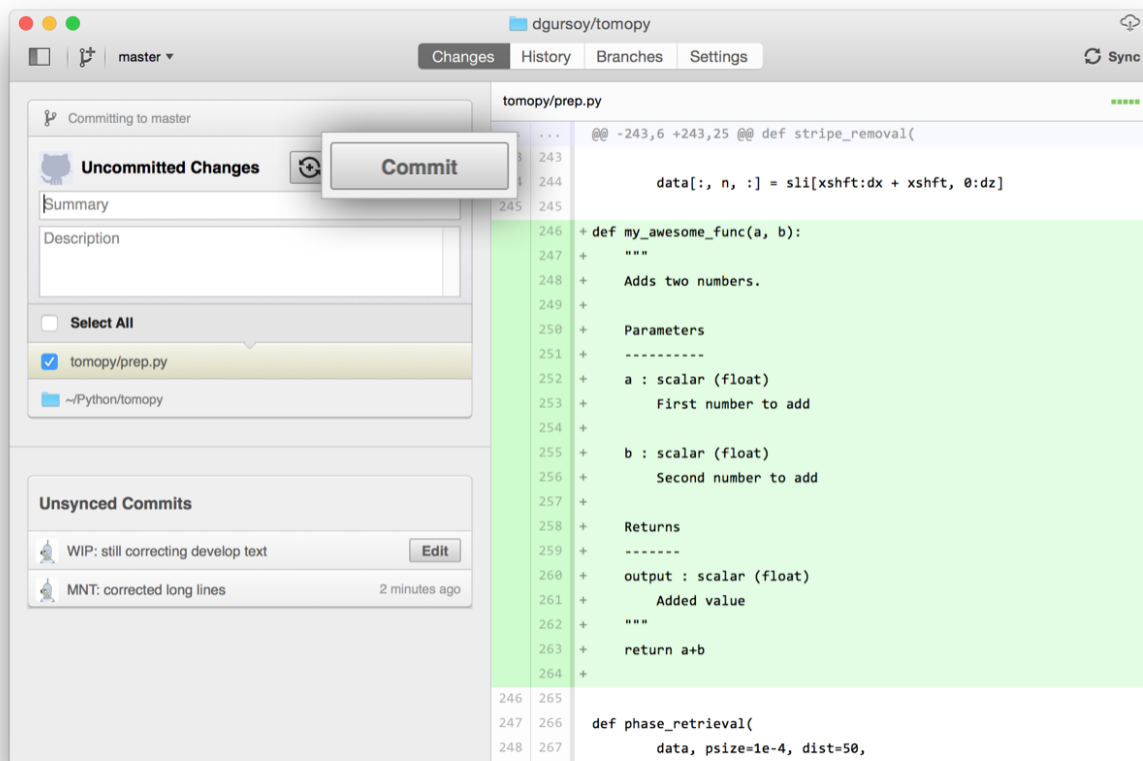

You can continue to make changes, add modules, write your own functions, and take more *Commit snapshots* of your code writing process.

6.5 Contributing back

Once you feel that the functionality you added would benefit the community, then you should consider contributing back to the XbrainMap project. For this, go to your online GitHub repository of the project and click on the *green* button to compare, review and create a pull request.
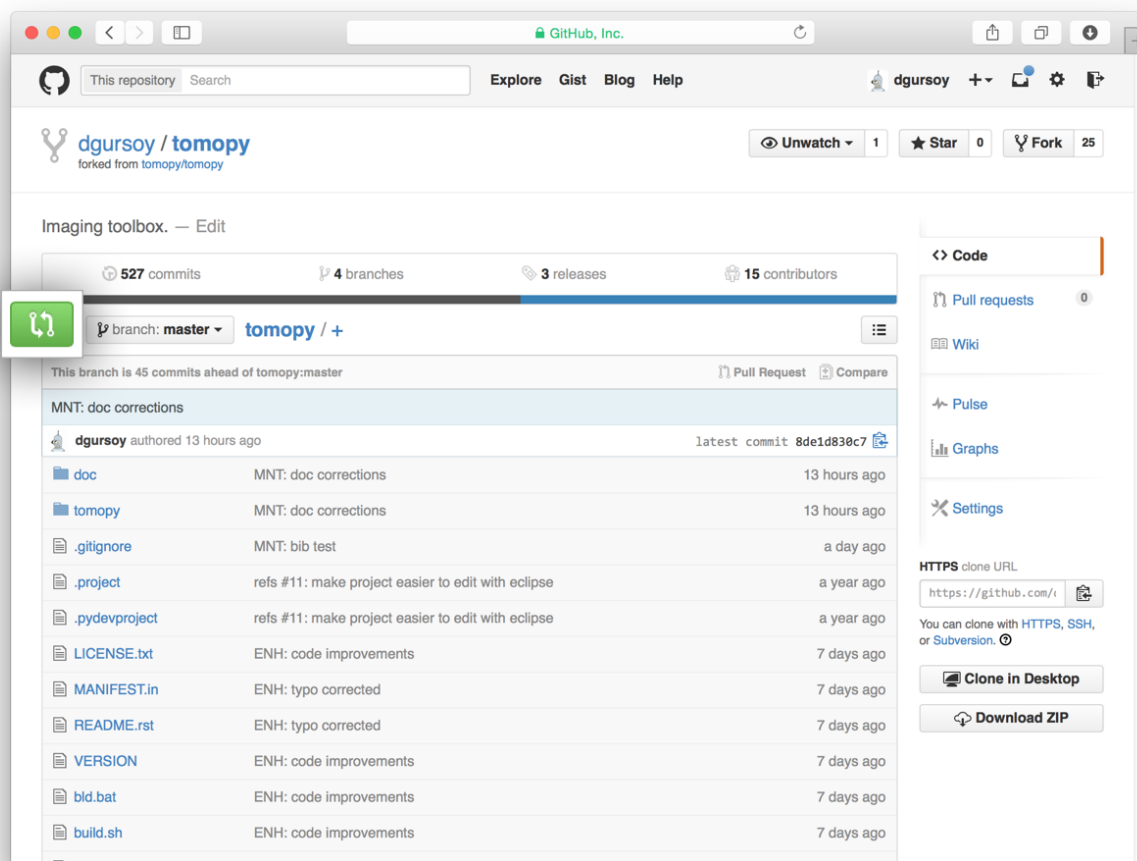
After clicking on this button, you are presented with a review page where you can get a high-level overview of what exactly has changed between your forked branch and the original XBrainMap repository. When you're ready to submit your pull request, click **Create pull request**:
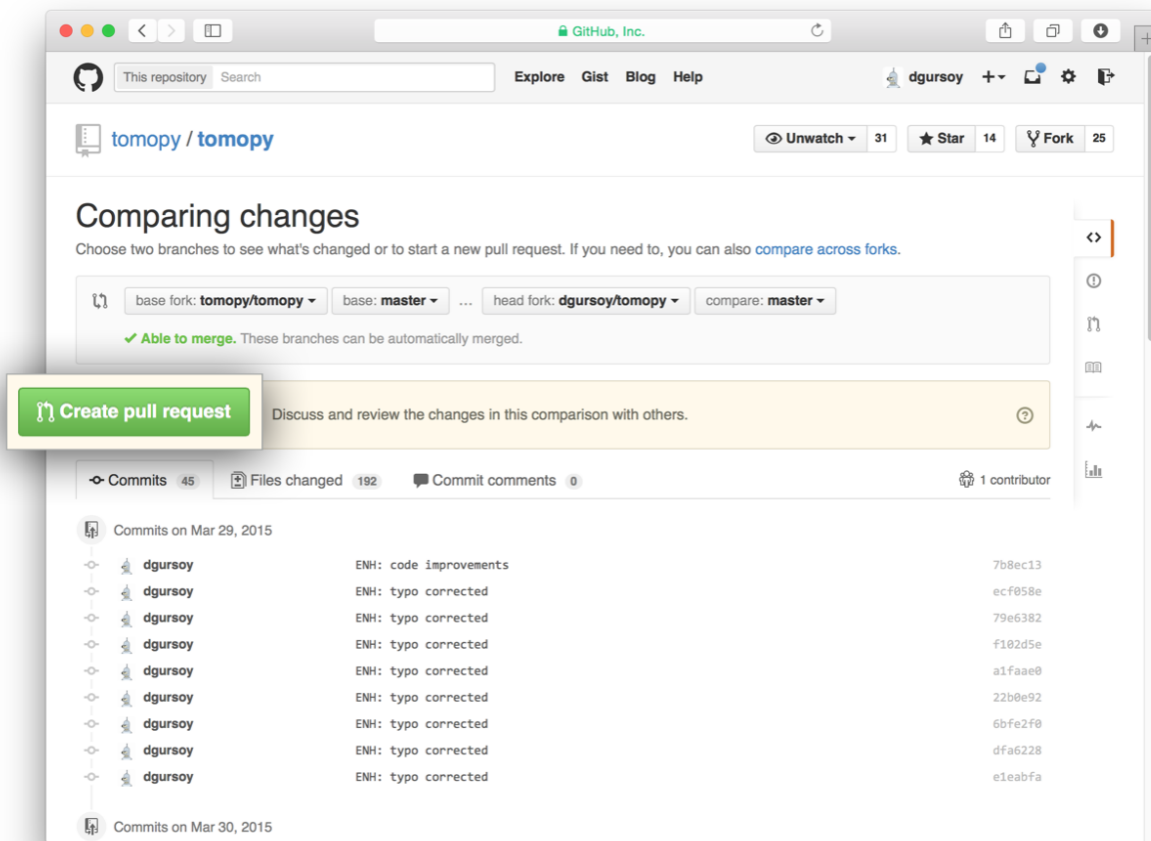
Clicking on **Create pull request** sends you to a discussion page, where you can enter a title and optional description. It's important to provide as much useful information and a rationale for why you're making this Pull Request in the first place.

When you're ready typing out your heartfelt argument, click on **Send pull request**. You're done!

Credits

7.1 Project Team

- Vincent De Andrade (@vdeandrade)
- Francesco De Carlo (@decarlof)
- Eva Dyer (@evadyer)
- Doga Gursoy (@dgursoy)
- Chris Jacobsen (@altaskier)
- Bobby Kasthuri
- Konrad Kording (@koerding)
- Mehdi Tondravi (@anlmehdi)
- Rafael Vescovi (@ravescovi)
- Xianghui Xiao (@xianghuix)

7.2 Sponsors

- National Institutes of Health
- U.S. Department of Energy

References

Indices and tables

- genindex
- modindex
- search

[A1] Gürsoy D, De Carlo F, Xiao X, and Jacobsen C. Tomopy: a framework for the analysis of synchrotron tomographic data. *Journal of Synchrotron Radiation*, 21(5):1188–1193, 2014.

[A2] De Carlo F, Gursoy D, Marone F, Rivers M, Parkinson YD, Khan F, Schwarz N, Vine DJ, Vogt S, Gleber SC, Narayanan S, Newville M, Lanzirotti T, Sun Y, Hong YP, and Jacobsen C. Scientific data exchange: a schema for hdf5-based storage of raw and analyzed data. *Journal of Synchrotron Radiation*, 21(6):1224–1230, 2014.