

Using Git for Comp-Neuro

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ABRG Sheffield Internal Seminar

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Find this at: <https://github.com/ABRG-Models/GitTutorial>

Introduction

- ▶ This seminar is about a command-line tool called Git.
- ▶ There's going to be a lot of **text** in these slides (sorry!)
- ▶ I'll give an overview of Git and why it's helpful to use it, then we'll go through some example tasks together.

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You might then have **branches** like **master**, **tryingIdea1**, **PlosCompBio2018** and so on.

Project revisions

- ▶ The ability to branch and tag *really* comes into its own when you have any kind of project with more than one file in it.
- ▶ Without this, you find yourself needing one folder for each version of your project, duplicating files left, right and centre.

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You need a revision control system to automate the process of distributing changes between users of a set of files, and to manage the merging of changes together.

Other revision control systems

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- ▶ SCCS (Source Code Control System)
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- ▶ In 2005 Linus fell out with BitMover Inc., and Git was created to replace it.
- ▶ The name *git* doesn't really mean anything.

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- ▶ And every copy of the **repo** is a backup!

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- ▶ It's now a big business; it was acquired by Microsoft in early June

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- ▶ “It used to work, but now I've broken it and I can't get it back to working again”: Revision control makes it easy to revert to a version of your code which you know will work
- ▶ You can include your paper alongside your model code in a single, public repository
- ▶ Use of Github is a very effective way to share your published models with your peers

The Git Tutorial

The rest of these pages have been put together from material taken from the Software Carpentry project, which emphasises the use of Git.

Head over to:

<http://sebjameswml.github.io/git-novice/>

And start on the lesson “A better kind of Backup”

Compiling libmorphologica

Github webpage:

<https://github.com/ABRG-Models/morphologica>

```
1 # Prerequisites on Linux:
2 sudo apt install build-essential cmake libopencv-dev
   libarmadillo-dev libglu1-mesa-dev libxmu-dev libxi-
   dev
3 # Clone the repository:
4 git clone https://github.com/ABRG-Models/morphologica.
   git
5 # To look at the readme file:
6 cd morphologica
7 less README.md
8 # The cmake-driven build process:
9 mkdir build
10 cd build
11 cmake ..
12 make -j4
13 sudo make install
14 sudo ldconfig
```

Compiling Ermentrout2009

Github webpage:

<https://github.com/ABRG-Models/Ermentrout2009>

This is an example of a model which links to libmorphologica

```
1 git clone git@github.com:ABRG-Models/Ermentrout2009.git
2 cd Ermentrout2009/processes/sim
3 mkdir build
4 cd build
5 cmake ..
6 make
7 cd ../../../../
8 # Run the model:
9 python sim.py
```