



Mouse Model of Autism

Vanessa Valiquette



Illustration by: Katie Carey

Introduction

Nice to meet you

Hello!

I am Vanessa Valiquette

MSc, Integrated Program in Neuroscience, McGill University
Computational Brain Anatomy Lab, Dr. Mallar Chakravarty



Interests:

- Neurodevelopmental trajectories.
- Translation from mouse models to human.

Current work:

- Better understand the impact of litter-effect on neurodevelopment in mouse model studies.



Goals

- Project structure
 - Directory
 - History
- Improve script writing and structure
 - Chunking script by steps
 - Optimize
- Use High Performance Computing (Niagara) to run MAGeT Brain
(**M**ultiple **A**utomatically **G**enerated **T**emplates **B**rain Segmentation Algorithm)
- Navigate the Open data world
 - Get familiar with datasets available



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Project

What's been happening in the past 3 weeks

Data

Brain-CODE platform

- Ontario Brain Institute
- Model for Autism
 - Chromosome 15q11.13 duplication

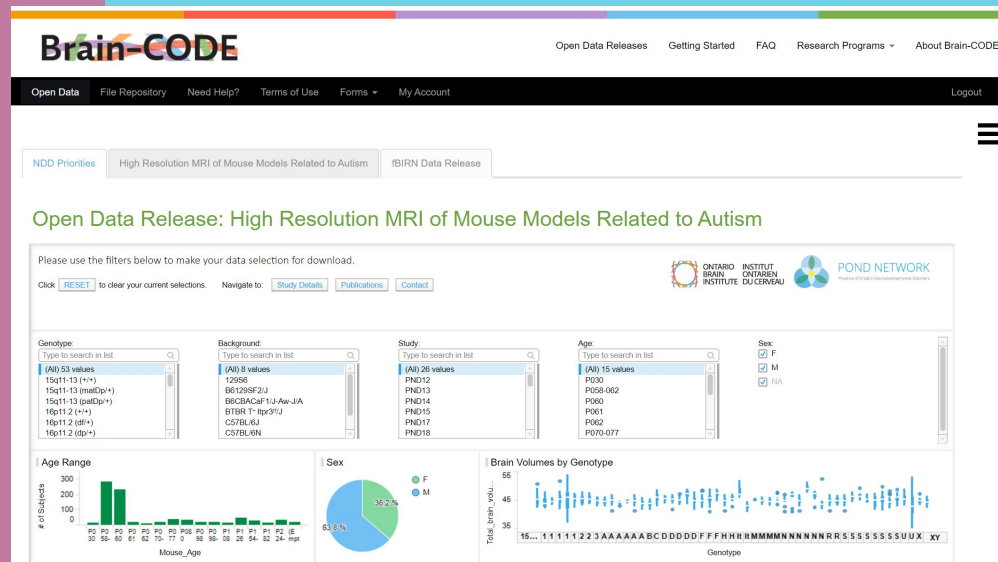
Dataset:

5 scans (.minc) for each or 37 mice

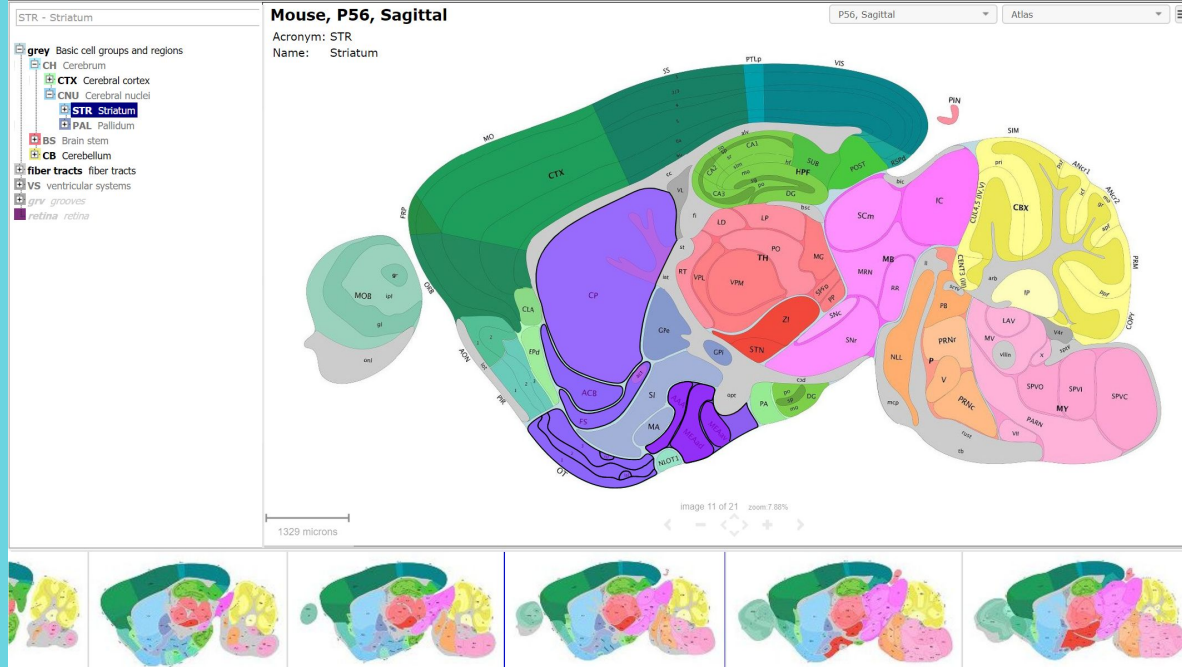
- 1 Raw
- 4 Processed

CSV file

- Descriptive information
- Brain structure volumes



Allen brain atlas



Tools

- ❑ **Cookiecutter**
- ❑ **Git & Github**
- ❑ **Jupyter Notebook**
 - ❑ Plotly
 - ❑ Nibabel
- ❑ **Compute Canada / Niagara**

CookieCutter

Data science cookiecutter
template for projects in
Python



```

├── LICENSE
├── Makefile
├── README.md
├── data
│   ├── external
│   ├── interim
│   ├── processed
│   └── raw
├── docs
├── models
├── notebooks
├── references
├── reports
│   └── figures
├── requirements.txt
├── src
│   ├── __init__.py
│   ├── data
│   │   └── make_dataset.py
│   ├── features
│   │   └── build_features.py
│   ├── models
│   │   ├── predict_model.py
│   │   └── train_model.py
│   └── visualization
│       └── visualize.py
└── tox.ini

```

<- Makefile with commands like `make data` or `make train`
 <- The top-level README for developers using this project.
 <- Data from third party sources.
 <- Intermediate data that has been transformed.
 <- The final, canonical data sets for modeling.
 <- The original, immutable data dump.
 <- A default Sphinx project; see sphinx-doc.org for details
 <- Trained and serialized models, model predictions, or model summaries
 <- Jupyter notebooks. Naming convention is a number (for ordering),
 the creator's initials, and a short `-` delimited description, e.g.
 `1.0-jqp-initial-data-exploration`.
 <- Data dictionaries, manuals, and all other explanatory materials.
 <- Generated analysis as HTML, PDF, LaTeX, etc.
 <- Generated graphics and figures to be used in reporting
 <- The requirements file for reproducing the analysis environment, e.g.
 generated with `pip freeze > requirements.txt`
 <- Source code for use in this project.
 <- Makes src a Python module
 <- Scripts to download or generate data
 <- Scripts to turn raw data into features for modeling
 <- Scripts to train models and then use trained models to make
 predictions
 <- Scripts to create exploratory and results oriented visualizations
 <- tox file with settings for running tox; see tox.testrun.org

Git and Github

1. Forked project from BHS2020 to personal Github
2. Copy to personal machine
3. Added cookiecutter file structure
4. Pushed to personal Github
5. Pull request to BHS2020 project repo

The screenshot shows a GitHub repository page for 'brainhack-school2020 / ValiquetteVanessa_MouseModelAutism_T2W'. The repository has 162 commits, 1 branch, 0 packages, 0 releases, 1 contributor, and a license. The file list includes folders like docs, images, models, notebooks, references, reports, results, src, tools, and files like Deliverable_week3.md, LICENSE, Makefile, README.md, requirements.txt, setup.py, test_environment.py, and tox.ini. The README.md file is selected, showing a preview of a colorful bar chart.

brainhack-school2020 / ValiquetteVanessa_MouseModelAutism_T2W

Watch 1 Star 0 Fork 1

Code Issues 0 Pull requests 0 Actions Projects 0 Wiki Security 0 Insights Settings

Learn how to preprocess and segment Mouse MRI images from an open source dataset [Edit](#)

Manage topics

162 commits 1 branch 0 packages 0 releases 1 contributor View license

Branch: master New pull request Create new file Upload files Find file Clone or download

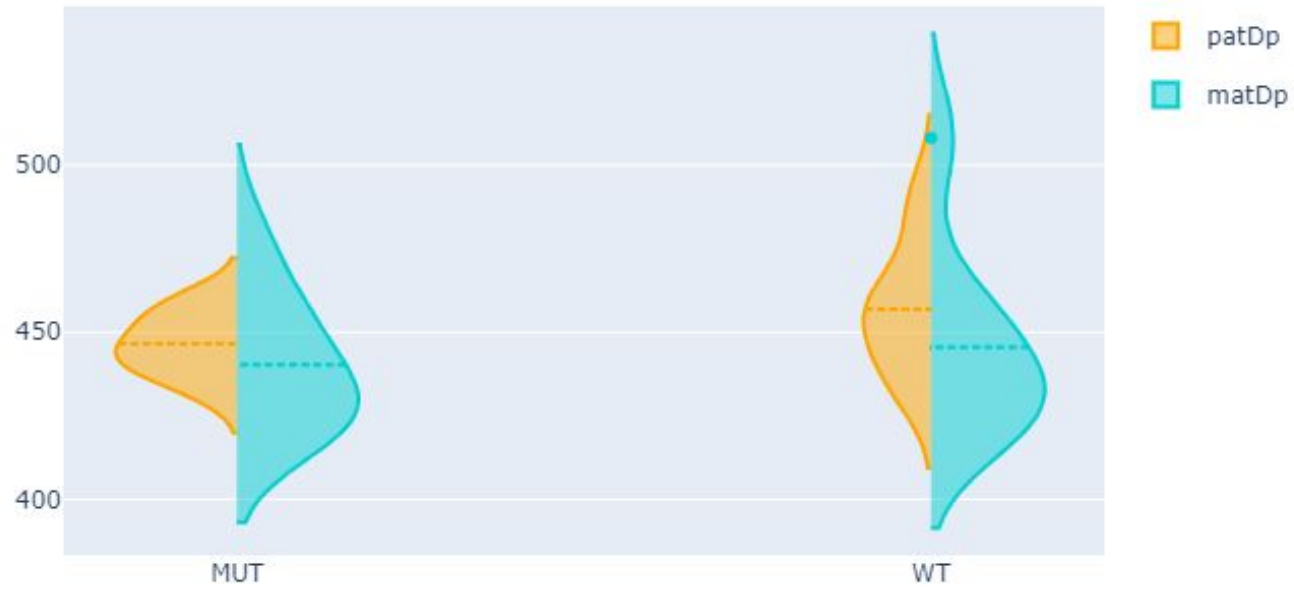
ValiquetteVanessa Update README.md Latest commit 8300467 18 hours ago

docs	Add cookiecutter directory to repo	yesterday
images	Delete MouseModelAutism_KatieCarey_httpswww.spectrumnews.orgfeatureess...	yesterday
models	Add cookiecutter directory to repo	yesterday
notebooks	Upload Plotly and Image Manipulation (Nibabel) jupyter notebooks	yesterday
references	Add cookiecutter directory to repo	yesterday
reports	Add cookiecutter directory to repo	yesterday
results	Delete newplot.png	23 hours ago
src	Add cookiecutter directory to repo	yesterday
tools	Update README.md	18 hours ago
Deliverable_week3.md	Create Deliverable_week3.md	8 days ago
LICENSE	Add cookiecutter directory to repo	yesterday
Makefile	Add cookiecutter directory to repo	yesterday
README.md	Update main picture and link	3 days ago
requirements.txt	Add cookiecutter directory to repo	yesterday
setup.py	Add cookiecutter directory to repo	yesterday
test_environment.py	Add cookiecutter directory to repo	yesterday
tox.ini	Add cookiecutter directory to repo	yesterday

README.md

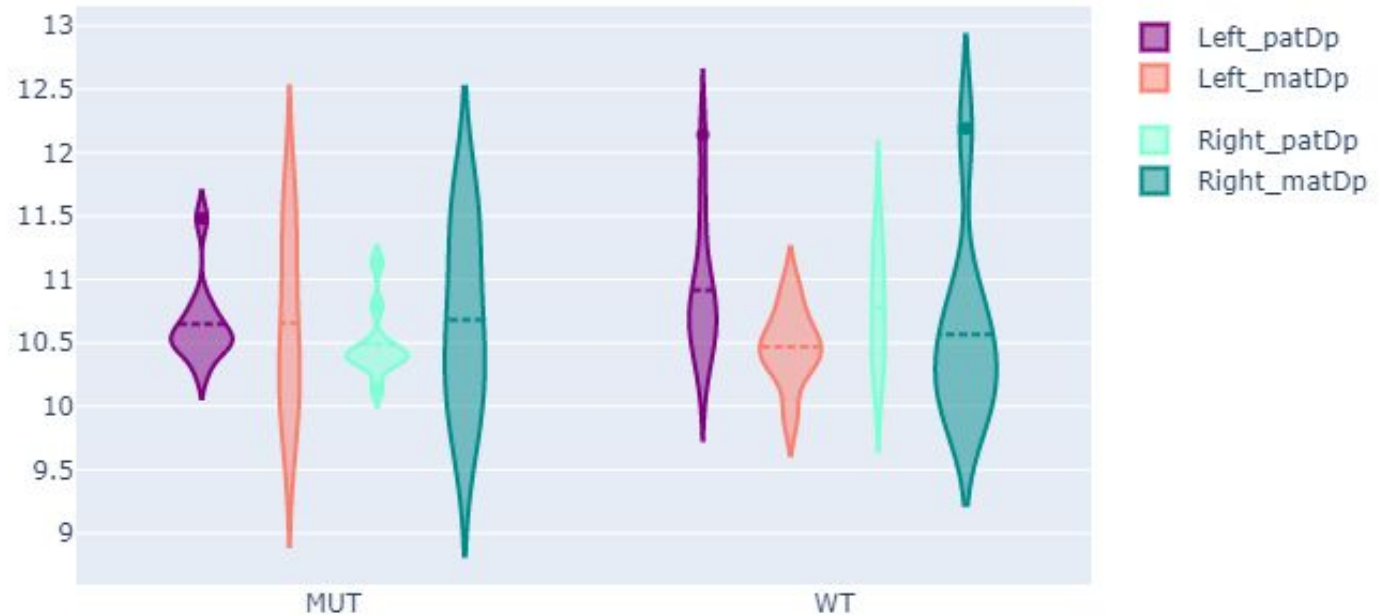
Plotly

Total brain volume

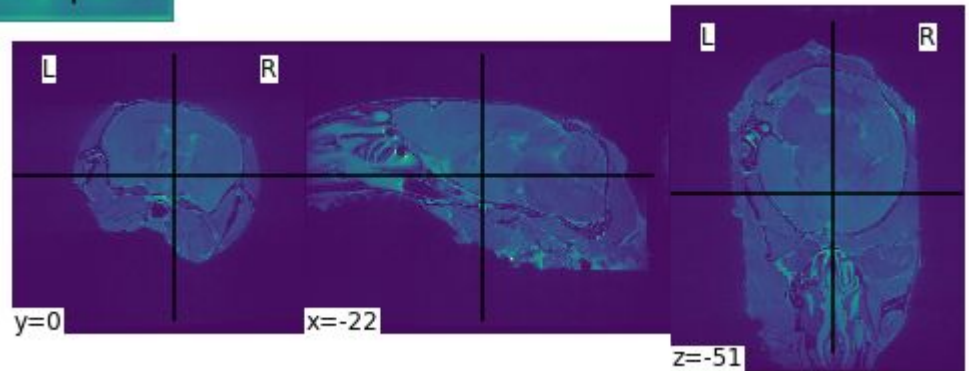
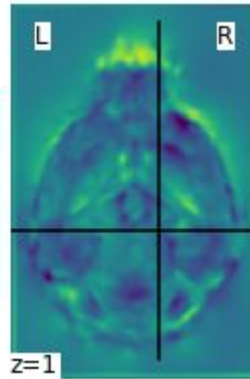
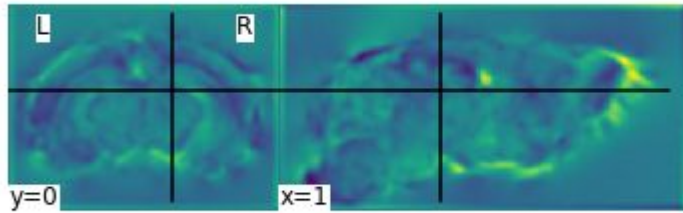


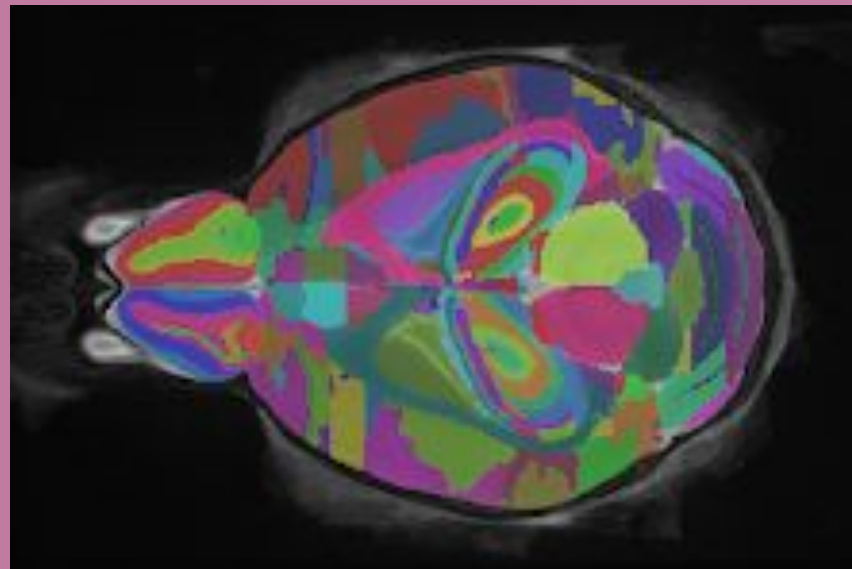
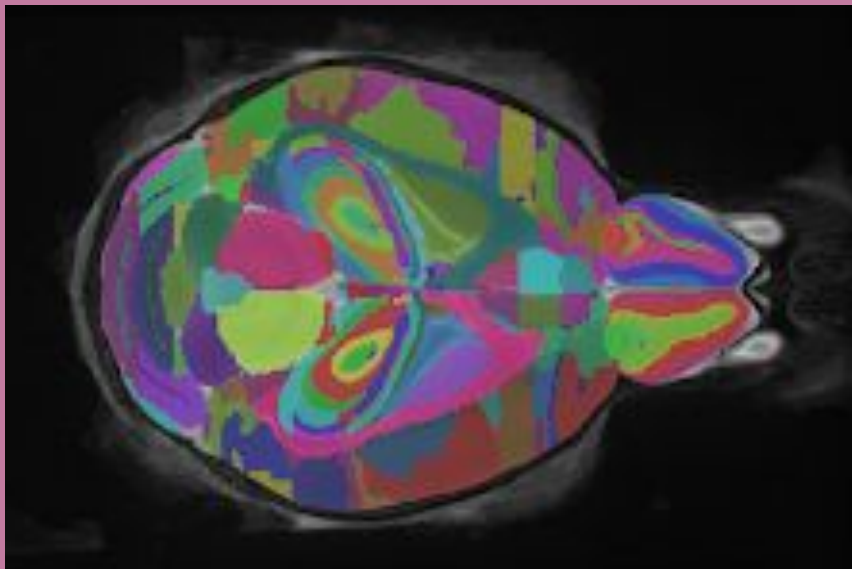
Plotly

Striatum



Nibabel



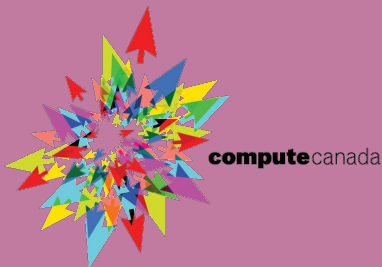


Picture: MAgE T Brain Github wiki

MAGeT Brain

Niagara

- Github cheatsheet
- Setup Niagara's account and files to run MAGeT Brain



README.md

Getting started

Running MAGeT on a high performance computer

Starting on compute canada

1. Create a compute canada and get sponsored by your supervisor.
2. Since the CoBraLab mainly uses Niagara, I will use Niagara for further steps.
3. Login and aim for bigger goals....

Starting with MAGeT

1. [Get modules](#) that you will need to run MAGeT on your compute canada env.
2. Read the [MAGeT documentation](#)
 - 2.1 Load modules
 - 2.2 Clone MAGeT Brain pipeline to your directory
 - 2.3 Create a directory structure that corresponds to the pipeline
 - 2.4 Populate your directory with the corresponding files (atlas, mask, labels, brain files)

Use [Globus](#) or `rsync` to transfer your data to your compute canada directory.

```
rsync -avz /path/to/file username@niagara.compute canada.ca:/path/to/put/file (usually starts with scratch/...)
```

There is atlases provided by the CoBRA Lab or you can find some other ones on the Allen brain Institute wiki.

- [Human Brain](#)
- [Mouse Brain](#)

3. Do a first check run, to make sure everything is setup right

```
mb check
```

4. Run MAGeT for the first time and hope for the best. 🙏

```
mb run
```



Conclusion

What a month...

BrainHack school



I learned

I applied

I consolidated

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Cookiecutter
Git and Github
lecture

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Github projects
Course material

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High performance
computing lecture

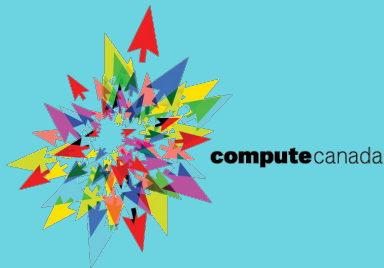
Globus

MAGeT Github wiki

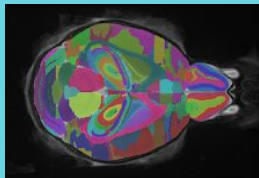
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Brain-CODE
Datasets lecture
Sebastian Urchs



MAGeT Brain



Thank you
BrainHack School!



For PowerPoint and
Google Slides



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or commercial use

