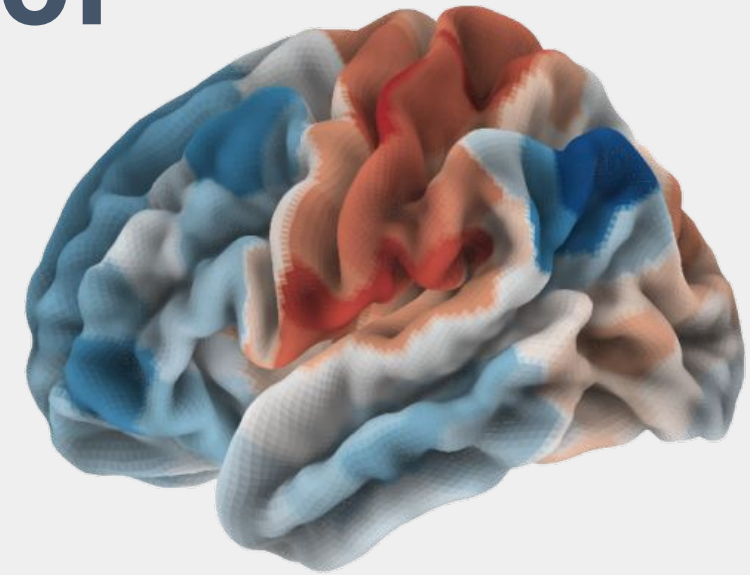
# Fundamentals of fMRI data analysis



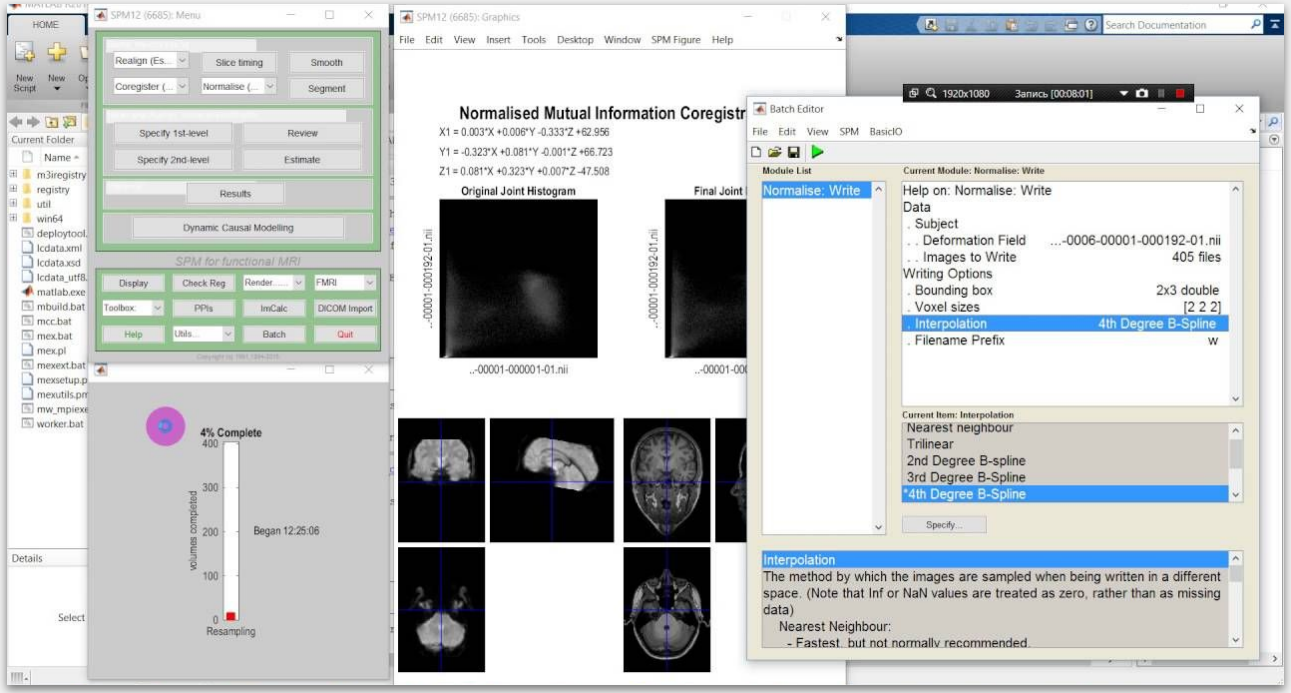
**Karolina Finc**

Centre for Modern Interdisciplinary Technologies

Nicolaus Copernicus University in Toruń

**COURSE #1:** **Reproducible neuroimaging** | 5th October 2020

# My story



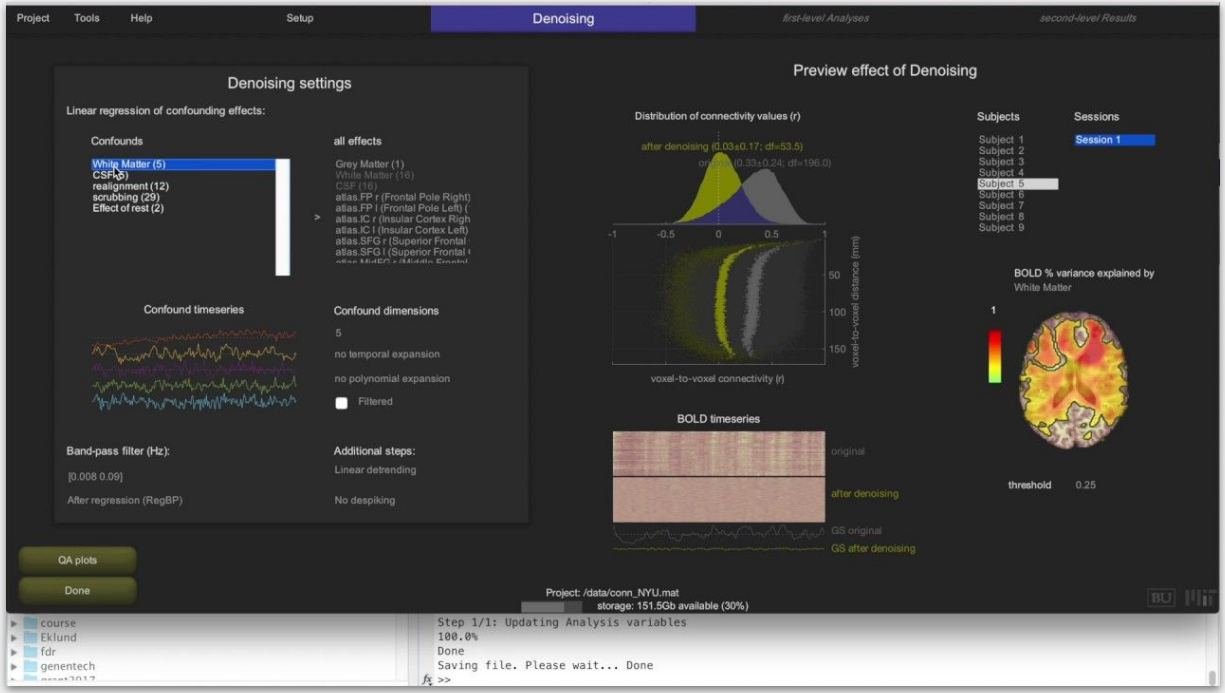

**2014**

Learning brain activity analysis in SPM.

MATLAB

Statistical Parametric Mapping: `https://www.fil.ion.ucl.ac.uk/spm/`

# My story




**2014**

Learning functional connectivity & graph theory analysis in CONN & BCT.

MATLAB

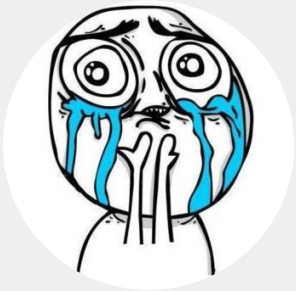
Functional connectivity toolbox: `https://web.conn-toolbox.org/`
Brain Connectivity Toolbox: `https://sites.google.com/site/bctnet/`

# Fast way to scientist's depression

| Processing step | Reason | Options [suboptions] | Number of plausible option |
|---|---|---|---|
| Motion correction | Correct for head motion during scanning | • 'Interpolation' [linear or sinc]<br>• 'Reference volume' [single or mean] | 4 |
| Slice timing correction | Correct for differences in acquisition timing of different slices | 'No', 'before motion correction' or 'after motion correction' | 3 |
| Field map correction | Correct for distortion owing to magnetic susceptibility | 'Yes' or 'no' | 2 |
| Spatial smoothing | Increase SNR for larger activations and ensure assumptions of GRF theory | 'FWHM' [4 mm, 6 mm or 8 mm] | 3 |
| Spatial normalization | Warps an individual brain to match a group template | 'Method' [linear or nonlinear] | 2 |
| High-pass filter | Remove low-frequency nuisance signals from data | 'Frequency cut-off' [100 s or 120 s] | 2 |
| Head motion regressors | Remove remaining signals owing to head motion via statistical model | 'Yes' or 'no' [if yes: 6/12/24 parameters or single time point 'scrubbing' regressors] | 5 |
| Haemodynamic response | Account for delayed nature of haemodynamic response to neuronal activity | • 'Basis function' ['single-gamma' or 'double-gamma']<br>• 'Derivatives' ['none', 'shift' or 'dispersion'] | 6 |
| Temporal autocorrelation model | Model for the temporal autocorrelation inherent in fMRI signals | 'Yes' or 'no' | 2 |
| Multiple-comparison correction | Correct for large number of comparisons across the brain | 'Voxel-based GRF', 'cluster-based GRF', 'FDR' or 'non-parametric' | 4 |
| Total possible workflows | | | 69,120 |

Poldrack et al. (2001), *Nat. Rev. Neurosc.*

- Which software to select?
- Which method to select?
- Which option to select?

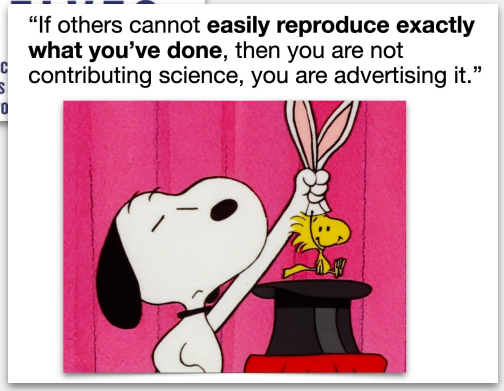


# Fast way to scientist's depression cd.

Many results you've read in papers are false positives and are not reproducible.

**BAD RESEARCH PRACTICES:**

- Not sharing the data
- Not sharing the code
- P-hacking
- HARKing - hypothesis after results are known

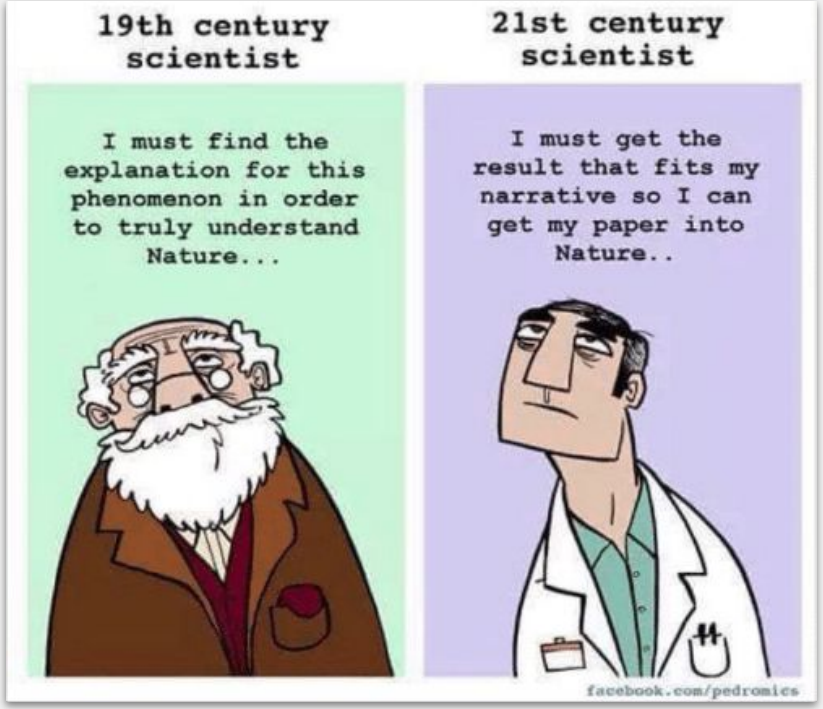



Practical guide to reproducibility

Why?

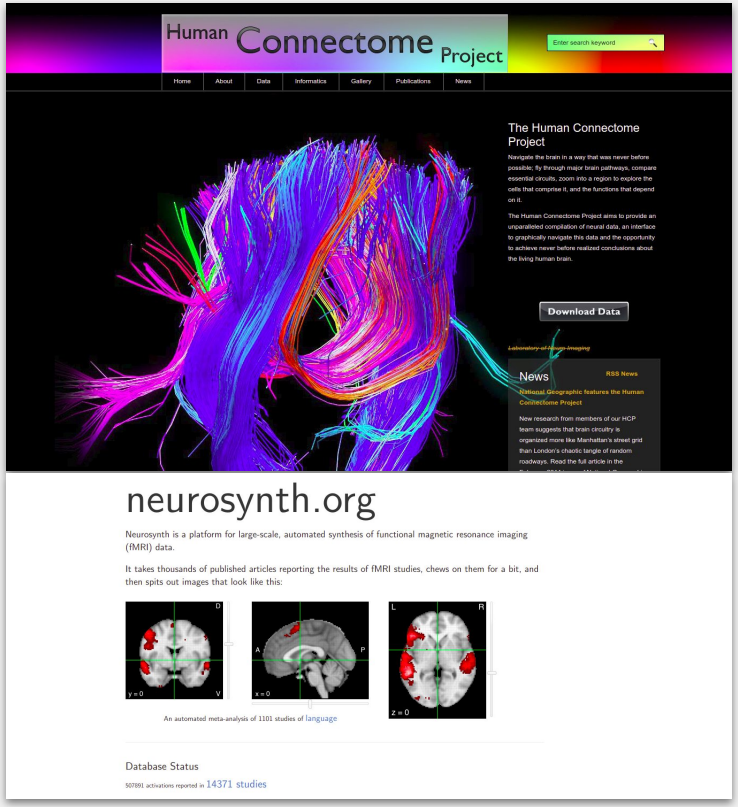
# Incentives

- Significant results are easier to publish
- Journals are not very open to publish replications (what's new in this?)
- fMRI studies are expensive and time consuming (small sample sizes)
- Learning programming takes time and much effort
- Designing a good experiment and stating a good hypothesis takes time
- etc.



# Open science

# Open data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The Human Connectome Project
Navigate the brain in a way that was never before possible: fly through major brain pathways, compare essential circuits, zoom into a region to explore the cells that comprise it, and the functions that depend on it.
The Human Connectome Project aims to provide an unparalleled compilation of neural data, an interface to graphically navigate this data and the opportunity to achieve never before realized conclusions about the living human brain.
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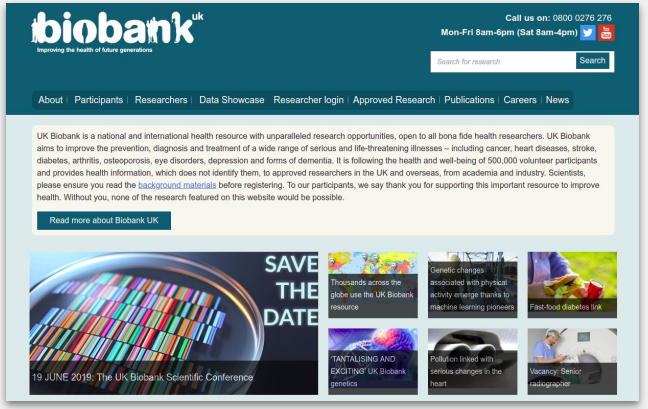
News
RSS News
National Geographic features the Human Connectome Project
New research from members of our HCP team suggests that brain circuitry is organized more like Manhattan's street grid than London's chaotic tangle of random roadways. Read the full article in the
neurosynth.org
Neurosynth is a platform for large-scale, automated synthesis of functional magnetic resonance imaging (fMRI) data.
It takes thousands of published articles reporting the results of fMRI studies, chews on them for a bit, and then spits out images that look like this:
An automated meta-analysis of 1101 studies of language
Database Status
507891 activations reported in 14371 studies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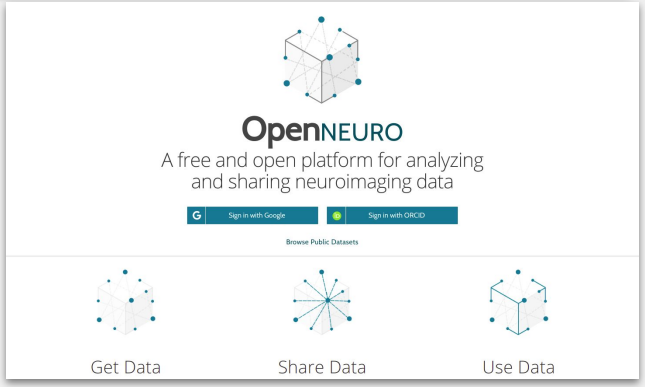
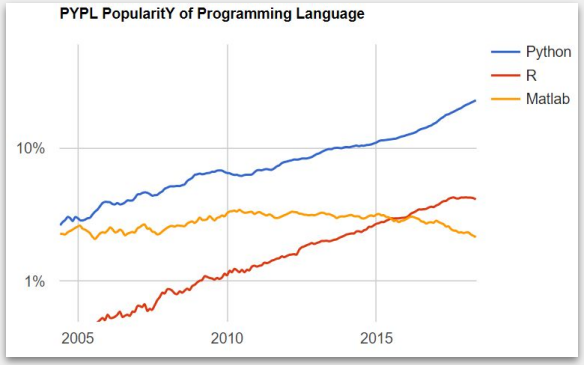
19 JUNE 2019: The UK Biobank Scientific Conference
Thousands across the globe use the UK Biobank resource
Genetic changes associated with physical activity emerge thanks to machine learning pioneers
Fast-food diabetes link
TANTALISING AND EXCITING' UK Biobank genetics
Pollution linked with serious changes in the heart
Vacancy: Senior radiographer


OpenNEURO
A free and open platform for analyzing and sharing neuroimaging data
Sign in with Google
Sign in with ORCID
Browse Public Datasets
Get Data
Share Data
Use Data

# Open source

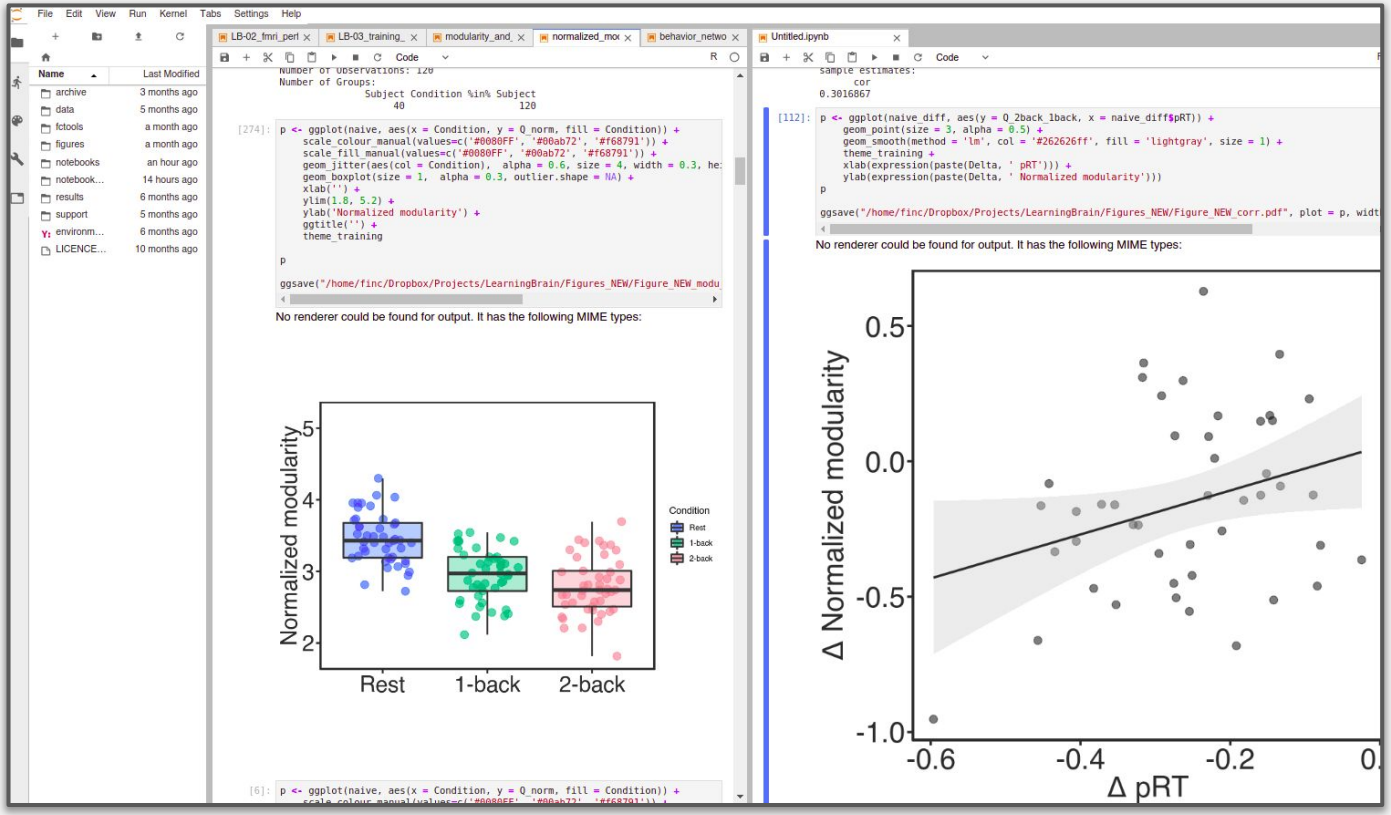
## Open programming languages




## Open source packages

## Code sharing platforms

# Jupyter notebook



# Getting started with Jupyter notebooks

Jupyter = **Ju**(lia) + **pyt**(hon) + e**R**

Goal of Project Jupyter is to "develop open-source software, open-standards, and services for interactive computing across dozens of programming languages".
More: https://en.wikipedia.org/wiki/Project_Jupyter

1. Open terminal
2. Type “jupyter lab”
3. If you don’t have it installed, go to website: https://jupyter.org/try

# Getting started with Git/GitHub

**Git** - version control system that stores multiple versions of your files over time

**GitHub** - provides hosting for software development version control using Git

Example:

https://github.com/kfinc

1. Create an account using academic email! (for PRO access)
2. Install Git on your computer (or check if it's already installed)

GitHub

# What to install?

1. Git
2. Anaconda 3 (Python distribution)

3. FSL (optional)
4. MATLAB (optional)

# Homework

1. **GitHub Classroom**

   fMRI Q&A in Markdown
   Deadline: 18-10-2020

2. **Data Camp Classroom**

   `https://www.datacamp.com/enterprise/advanced-fmri-data-analysis/assignments`

   Introduction to Python
   Deadline: 11-10-2020

   Intermediate Python
   Deadline: 18-10-2020

## Next

# fMRI data manipulation and plotting in Python