

# Programming for Psychologists 2025

Course code: M\_PROPSY

Course coordinator: Matthias Nau

## Welcome to your home assignment!

The following is a step-by-step description of your home assignment constituting 25% of your final grade. If you complete all mandatory steps listed below, your grade for this assignment will be a 9. In addition to the home assignment, you will write an exam (50% of your grade), and complete weekly quizzes (25% of your grade). Finally, there is an optional assignment (Step 5) based on which we may round up your grade. All tools are allowed, but we highly recommend doing it without artificial intelligence. Instead, remember what you have learned, review the course slides and notebooks, and ask Google or fellow students for advice. Consider working together but on separate projects.

**Deadline for completion is December 19th, 6pm. Good luck and have fun!**

## Summary

As part of this assignment, you will write your own version-controlled Python code to visualize fMRI data. The data are publicly available on Neurosynth, a meta-study platform that synthesizes the results of thousands of fMRI studies. Neurosynth hosts brain maps that illustrate the strength of the association between specific brain regions and certain cognitive concepts (e.g., episodic memory; see Figure 1) or clinically relevant terms (e.g., depression). You can choose which term you want to visualize, choose your own adventure! To this aim, you will create a new project from scratch, which includes setting up a conda environment, writing your code, and uploading it to GitHub for version control and for writing and receiving feedback.

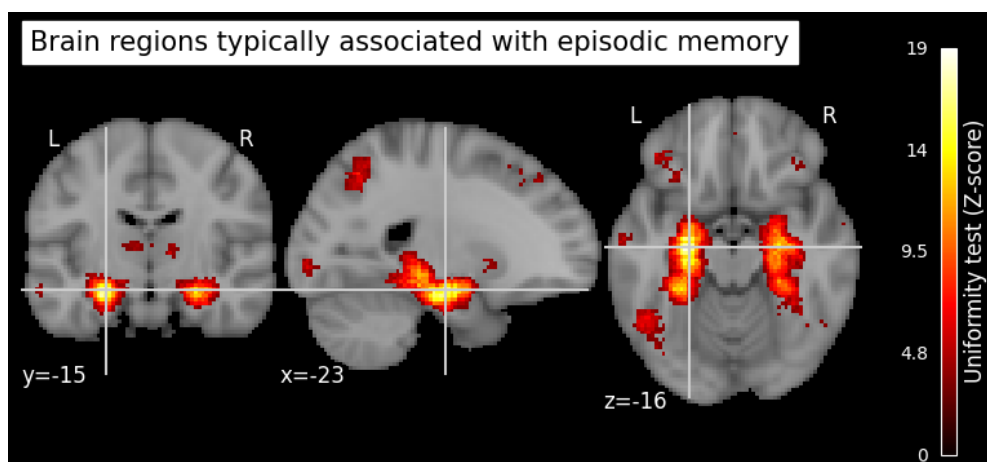


Figure 1. Python visualization example. Which brain regions are associated with episodic memory? This figure highlights voxels (3D pixels of an MRI image) whose activity has been linked to episodic memory in 332 neuroimaging studies. Data were downloaded from Neurosynth.org. XYZ coordinates reflect the 3D position of the crosshair in brain space. The color indicates the strength of association with the concept.

## Overview of steps

### Step 1: Download the data

1. Check out [Neurosynth.org](https://neurosynth.org) and go to the [Meta-Analysis terms](#) (or [click here](#)).
2. In the [Search](#) field, search for your favorite psychological or clinical concept and explore the map you get using the graphical user interface. You will see a **brain image** with a statistical overlay indicating regions typically associated with your chosen concept (See Figure 2).
3. Under [Layers](#), download the following files into a dedicated folder:
  - **Structural MRI data** (called “**anatomical**”):  
A higher resolution MRI scan of the anatomy of the human brain.
  - **Functional data** (called “**uniformity test**”):  
The statistical map associated with your concept. Check out the [FAQ page](#) for more information on what this map shows.

**Expected outcome:** You should now have **2 files in total** (1 functional & 1 anatomical file), stored in a dedicated folder. The files have the extension .nii.gz, which stands for compressed NIFTI format, a standard file type in MRI.

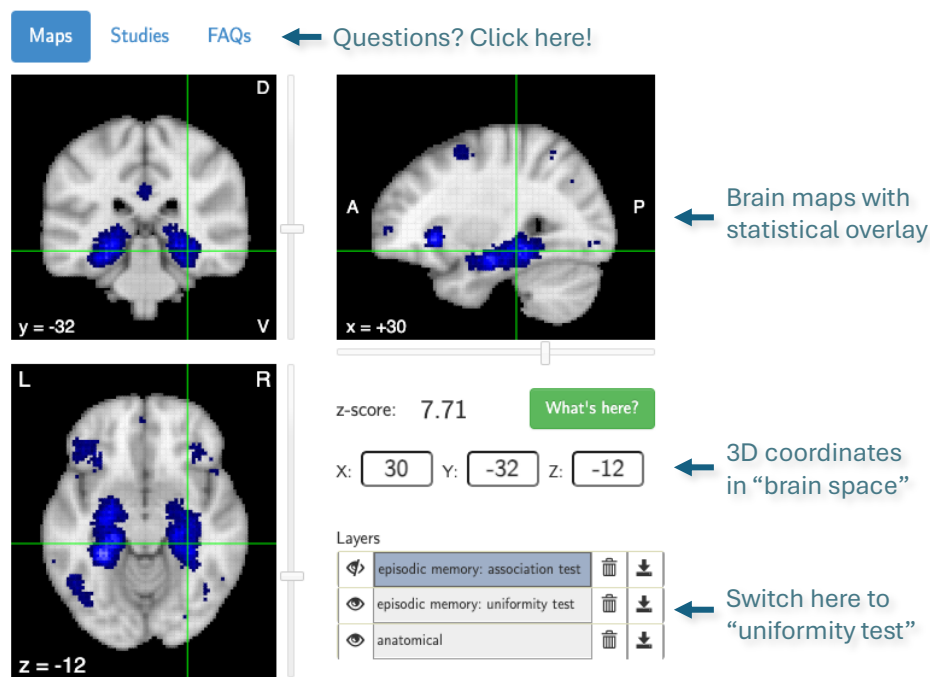


Figure 2: Screenshot of the Neurosynth interface showing uniformity-test results for the term “episodic memory”. This is the same interface you will see when searching for your favorite cognitive concept.

## Step 2: Set up your virtual environment

1. Create a new **Conda environment** with a name of your choosing using the terminal or command prompt (e.g., inside VScode).
2. Inside your conda environment, pip install:
  - **Python 3** (e.g., version 3.12.4)
  - **Nilearn**
  - **Nibabel**
  - **Matplotlib**
  - **Any other package you want or need**

**Expected outcome:** You should now have a conda environment with all required packages that shows up under “Select kernel” in a notebook within VScode.

## Step 3: Write your code

1. Within **VScode**, create a new **Jupyter notebook** (click: File → New File → Jupyter Notebook) and save it together with your MRI data in the same folder.
2. **Write code that locates your MRI data automatically** based on the file extensions and file names. Avoid hardcoding file paths.
3. **Visualize your functional data ontop of the anatomical scan** using nilearn’s **plot\_stat\_map** function. You do not know how to do this yet, but you know how to find out (e.g., [function documentation](#)). This function is all you need to make a figure showing regions with strong association (similar to Figure 1).

### Customize your figures

- **Add a title** indicating which concept term you are visualizing.
  - **Pick a new colormap** (e.g., `cmap="hot"`).
  - **Set the voxel threshold** to 0.1 to exclude values below this level.
  - **Choose cut coordinates** (`cut_coords=(X, Y, Z)`) that best show your functional data. XYZ refers to the 3 spatial dimensions of an MRI scan (see Figure 1).
  - Further customize the figure to your liking (optional).
4. **Plot a histogram of the values in the functional data file.** You will need to load the file (e.g., using [nibabel](#)), select all positive values (`values>0`), and then plot a histogram. This histogram shows the distribution of values in your data.

### Customize your figure

- **Add a title** that describes what you are plotting.
  - **Add axes labels**
  - **Choose colors** that you like.
  - Further customize the figure to your liking (optional).
5. **Add comments** to your code that describe your reasoning briefly.

**Expected outcome:** You should now have 2 figures (1 brain-map figure and the histogram) as well as the code that produced these figures.

#### **Step 4: Upload Your Code to GitHub and write and receive pull requests**

1. **Create a GitHub repository** and upload your completed notebook. Make sure it includes the figures you made.
2. **Submit a pull request** for another student's GitHub repository. The pull request should comment on their code stating something you like about it and something to improve. Feel free to use our Canvas mailing list to find other students to exchange pull requests with.
3. **Upload evidence of the pull request to your repo** in the form of a screenshot of your submitted comments.

**Expected outcome:** You should now have an online GitHub repository that hosts your code and data, as well as a screenshot of your pull request.

#### **Step 5. Optional assignment - Write code documentation.**

1. **Add Markdown cells** to your notebook that provide code documentation. Add Markdown cells that briefly describe what each code cell is doing, similar to the format used in our practical notebooks. In addition, **the first Markdown cell should include:**
  - A project title (yours to choose).
  - Your name.
  - The date the notebook was completed.
  - The links to the Neurosynth pages of your concepts.
2. **Add a Readme file to your GitHub repo** that describes your project. The readme file should include the **same information as your first Markdown cell** in the notebook, **as well as the following:**
  - A 3-sentence description of what the project is about.
  - A table of contents that briefly explains what data you used, which file is the notebook etc.
  - A list of Python packages you used.

**Expected outcome:** Your code and repository should now be well documented.

#### **Submit your assignment before the deadline**

**Send an email** to [m.nau@vu.nl](mailto:m.nau@vu.nl) with [programming home assignment] in the subject that includes the **link to your repo**.

**You've got this! Believe in yourself and take it step-by-step!**