**README**

If you would only like to obtain the behavioral and neural traces:

Thirteen .h5 files are compressed and stored under **file.tar.gz**.

Running the following line of code will extract all the .h5 files:

tar xvzf file.tar.gz

Each .h5 file stores the following information for one animal:

* behavioral traces under the field named “behavior”
* neural traces under the field named “gcamp”
* timestamps under the field named “timing”
* neural ID info under the field named “neuropal\_registration”

Here is the genotype information of the recorded animals in each .h5 file:

| SWF415 | SWF702 |
| --- | --- |
| * no neural identity * both off-food and on-food time points were recorded | * with neural identity * only on-food time points were recorded |
| 2022-01-16-01-data.h5  2022-01-25-01-data.h5  2022-03-17-01-data.h5  2022-03-25-03-data.h5  2022-04-05-01-data.h5  2022-04-12-02-data.h5  2022-05-02-01-data.h5 | 2022-07-26-31-data.h5  2022-07-26-38-data.h5  2022-07-27-31-data.h5  2022-07-27-45-data.h5  2022-08-02-38-data.h5  2022-08-03-31-data.h5 |

If you would only like to regenerate plots from/ modify our analysis:

1. Download all the Julia packages from another Dropbox folder:  
   <https://www.dropbox.com/s/3e5qnzam2xvdf4f/code.zip?dl=0>
2. Download all files from this Dropbox folder:  
   <https://www.dropbox.com/scl/fo/x34yevooev7lynjz3c7i7/h?dl=0&rlkey=ha43xcenkd8f11fn95evgewlw>

Here’s a summary of what each file is for:

| File name | Content | Required for DK\_analysis\_masterscript.ipynb to run? | Required for figure7\_code.ipynb to run? |
| --- | --- | --- | --- |
| **file.tar.gz** | behavioral and neural data of 7 SWF415 animals and 6 SWF702 animals; refer to the last page on how to extract them | Y | Y |
| **DK\_analysis\_masterscript.ipynb** | script for testing each behavior, PC and neuron’s association with NSM activity in a single dataset (exemplified in Fig. 6) | Y | N |
| **figure7\_code.ipynb** | script for generating the panels in Fig. 7 | N | Y |
| **DK\_analysis\_functions.jl** | all functions used in the .ipynb scripts are defined in this file | Y | Y |
| **copy\_kmeans.jl** | a public package for k-means clustering | N | Y |
| **nsm\_analysis\_dict\_swf415\_v3.jld2** | output from DK\_analysis\_masterscript.ipynb for 7 SWF415 animals | N | N  (but you can use figure7\_code.ipynb to visualize the content of this file) |
| **nsm\_analysis\_dict\_swf702\_final.jld2** | output from DK\_analysis\_masterscript.ipynb for 6 SWF702 animals | N | Y |
| **NeuroPAL\_labels\_dict.jld2** | neural identity labels are attached to each roi; each roi can be a registered neuron or a registered autofluorescent blob | N | Y |
| **NSM\_like\_garbage\_library\_fastPiezo.jld2** | synthetic NSM controls for SWF415 datasets acquired in Mar-May 2022 | Y | N |
| **NSM\_like\_garbage\_library\_slowPiezo.jld2** | synthetic NSM controls for SWF415 datasets acquired in Jan 2022 | Y | N |
| **NSM\_like\_garbage\_library\_neuroPAL\_v2.jld2** | synthetic NSM controls for SWF702 datasets | Y | N |
| **5htr\_expression\_dv\_final.csv** | neuron classes that express at least one type of serotonin receptor | N | Y |
| **white\_1986\_whole.json** | public electron microscopy annotations (with pharyngeal neurons) | N | Y |
| **witvliet\_2020\_7.json** | public electron microscopy annotations (without pharyngeal neurons) | N | Y |
| **witvliet\_2020\_8.json** | N | Y |

1. Modify the file paths in the .ipynb script(s) that you would like to run. The two .ipynb scripts work independently. You can find all the lines in each script where you need to modify the file paths by searching “path\_”.
2. Run the .ipynb script(s) to regenerate the statistical results/ plots you see in Figure 6 and Figure 7. The comments in the scripts indicate what the key lists, matrices or statistical tests are for so that you can modify the analysis by changing specific inputs.