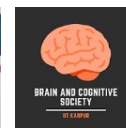**Science and Technology Council, IIT Kanpur**

The Connectome Project
Brain Cognitive Society, April 2020

This Summer Project is carried out under the Brain Cognitive Society, IIT Kanpur during April 2020 - July 2020.

Github - https://github.com/Debu922/BCS_Connectome_Project_2020
(All the code, literature reviews, presentations and documentation can be accessed here)

Objective

- To explore the emerging field of connectomics.
- To learn about the various techniques used in modern Neuroscience.
- To understand how models are being created to interpret the behaviour on the scale of networks within the brain.
- To study and model the circuits that govern the visual and the auditory systems (initial objective)
- To study and model the circuits that govern the olfactory system (current objective)
- To learn how to manage and handle a research project.

Ideation

- Learn the basics of Neuroscience.
- Learn basics of Non-invasive Imaging methods like fMRI, EEG, etc.
- Learn how to navigate through academic literature and find specific works
- Read papers and find paper to replicate.
- Learn the concepts required to create Neural Models.
- Replicate models in chosen paper.
- Create our own models based on data.

Methodology

- Literature Reviews: Understanding the concept of the connectome
- Two layer ANNs: Understanding models of networks
- Presentation: The Insect Visual System
- Presentation: The Human Auditory System
- Flow Chart: Neural Maps and Wiring Diagrams
- Course: Fundamentals of Neuroimaging
- Course: Academic Information Search
- Presentation: The Drosophila Olfactory System
- Course: Learning basics of MATLAB
- Coding: Running simulation of Drosophila Olfactory System

Timeline

Sr. No.	Start Date	End Date	Work
1	24-04-2020	28-04-2020	Literature Review and Two Layer ANN
2	01-05-2020	05-05-2020	The Insect Visual System
3	01-05-2020	05-05-2020	The Human Auditory System
4	10-05-2020	16-05-2020	Neural Maps and Wiring Diagrams
5	02-05-2020	06-05-2020	Fundamentals of Neuroimaging [Coursera]
6	05-05-2020	09-05-2020	Academic Information Seeking [Coursera]
7	12-06-2020	15-06-2020	Contacting Profs

8	18-06-2020	-	Reading Sir's Paper
9	19-06-2020	19-06-2020	The Olfactory System in Drosophila
10	25-06-2020	30-06-2020	Learning MATLAB
11	30-06-2020	15-07-2020	Running simulation of Drosophila Olfactory System
12	10-07-2020	-	Setting up GitHub Repository
13	14-07-2020	17-07-2020	Preparing Project Poster

Auditory System

The Human Auditory System
This looks at the various aspects of sound, its propagation and processing by the human brain, connection with speech and hearing impairments among others.

Olfactory System

The following is for the code contributed at:
https://github.com/Debu922/BCS_Connectome_Project_2020/tree/master/olfactory_system/abhinaya

'Multiple network properties overcome random connectivity to enable stereotypic sensory responses' (Mittal et.al).

This code is an attempt to replicate the first few results of the above paper, especially fig 2.

"We show that stereotypy is a natural consequence of convergence following random connectivity and does not require learning."

Settings for the simulations.

The following are called simultaneously for two individuals A and B.

The neural network considered 50 PNs as the input layer, 2000 KCs as the hidden layer and 1 MBON as the output layer for each individual. The simulation was run for 100 different odors in each individual. PN response vectors varied with the odor but not with the individual, while PN-KC connection matrices varied with the individual but not with the odor. Each network simulation was performed 100 times with different initializations of the random number generator.

Workflow with the DriverLiveScript

- Generate the PN, KC and MBON responses for both the individuals for 100 odors and run the whole simulation 100 times

```
1. function [PN_KC_matrix] = pn_kc_matrix(no_of_PN,no_of_KC,seed)
2. function [KC_MBON_matrix] = kc_mbon_matrix(no_of_KC)
3. function [PN_spikes] = pn_spikes(no_of_PN,seed)
4. function [KC_spikes] = kc_spikes(PN_KC_matrix,PN_spikes)
5. function [MBON_spikes] = mbon_spikes(KC_MBON_matrix,KC_spikes)
```

- Calculate the correlation and PRED stereotypy for the MBON responses - Fig. 2b Also plot Fig 2c. Correlation vs PRED for MBON response

```
6. function [correlation] = correlation(MBON_spikesA,MBON_spikesB)
7. function [stereotypy] = pairstereotypy(response)
8. function [PREDstereotypy] = stereotypy(MBON_spikesA,
   MBON_spikesB)
```

- Calculate the correlation and PRED stereotypy for INDIVIDUAL KC responses - Fig. 2d (top)

```
9. function [KC_correlation] = kc_correlation(kca,kcb)
10.function [KC_indPREDstereotypy] = kc_indpred(kca,kcb)
```

- Calculate the correlation and PRED stereotypy for TOTAL KC responses - Fig. 2d (bottom)

```
11.  function [KC_totcor] = kc_totcor(kca,kcb)
12.function [KCtotalPREDstereotypy] = kc_totpred(kca,kcb)
```

- Plot Fig. 2 using gramm plotting package - Rest of the DriverLiveScript

Figure 2. Results

-Ragha Abhinaya M

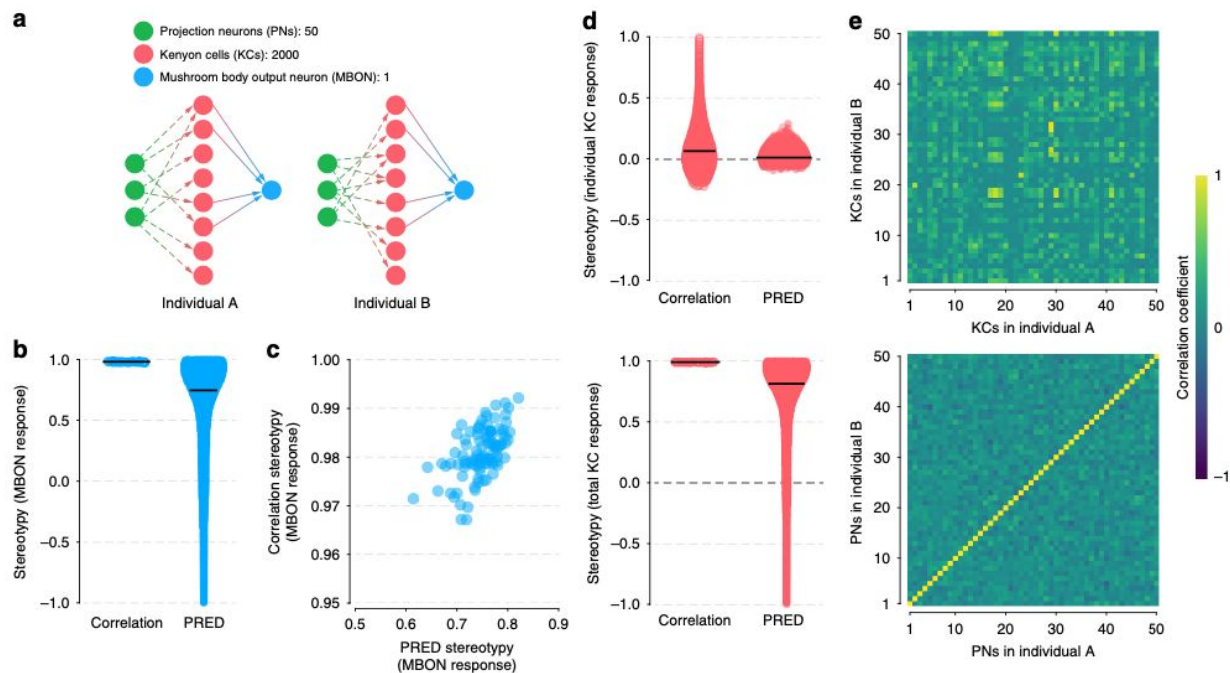Replicating the results of fig2. of from the paper (as shown below). The generated plots follow.

Fig. 2 Stereotypy in model MBONs and KCs. a Schematic representation of the simulated mushroom body networks in two different individuals. Projection neuron (PN, green) to Kenyon cell (KC, pink) connections are random and vary across individuals. The number of KCs connected to the mushroom body output neuron (MBON, blue) was kept same across individuals. **b** Correlation stereotypy and PRED stereotypy in MBON response in a realistic network with random PN-KC connections across individuals; for correlation, $n = 100$ points corresponding to different network iterations with different random seeds; for PRED, $n = 495000$ points (100 iterations × 950 odor pairs from 100 odors). **c** Scatter plot of correlation stereotypy versus PRED stereotypy in MBON response for the same simulations as in (**b**) shows that both metrics behave similarly. The PRED stereotypy is averaged over all 4950 odor pairs within a network iteration ($n = 100$ iterations). **d** (top) Correlation stereotypy and PRED stereotypy in individual KC response for the same simulations as in (**b**). Both metrics confirm the absence of stereotypy in individual KCs, $n = 100537$ KCs that responded to at least one odor in both individuals, out of the 200,000 KCs from 100 network iterations. (bottom) Correlation stereotypy and PRED stereotypy in total KC response for the same simulations as in (**b**); number of data points same as in (**b**). **e** Correlation between the responses of the PNs (bottom) and the KCs (top) in two individuals in a simulation. The correlation is calculated using the 100-length vector (responses to 100 odors) for each pair of PNs (50 in total) or for each pair of KCs among the first 50 KCs (by spatial ordering) that responded to at least one odor in both individuals.
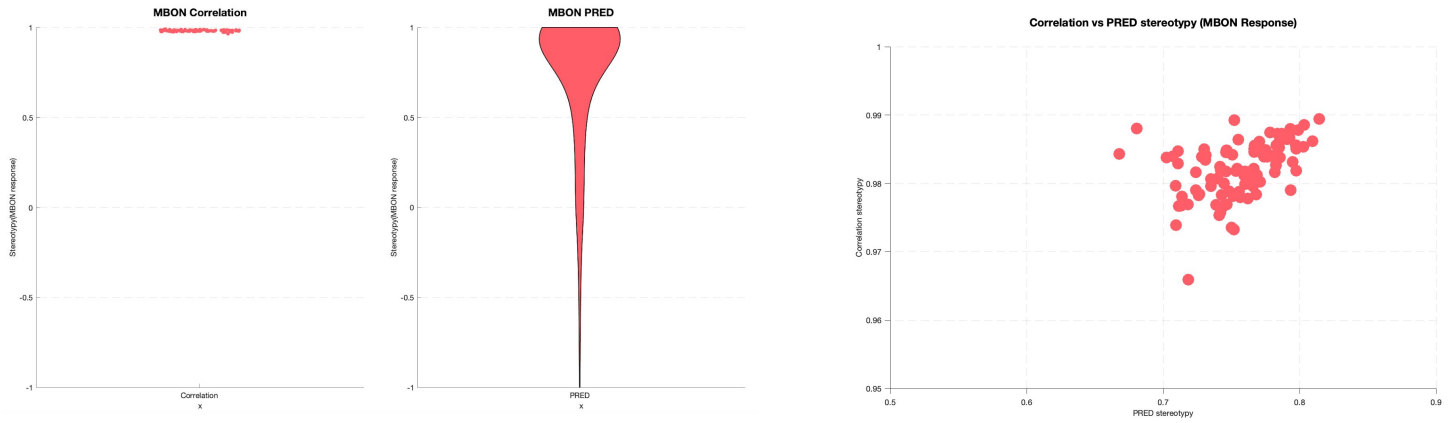
Fig. 2b.(left) Correlation stereotypy and PRED stereotypy in MBON responses of two individuals in a network of random PN KC connections; n=495000 points for PRED and n=100 points for correlation.
Fig. 2c. (right) Scatter plot of correlation stereotypy and PRED stereotypy in MBON responses of two individuals for the same conditions as above; shows the similarity of the metrics.
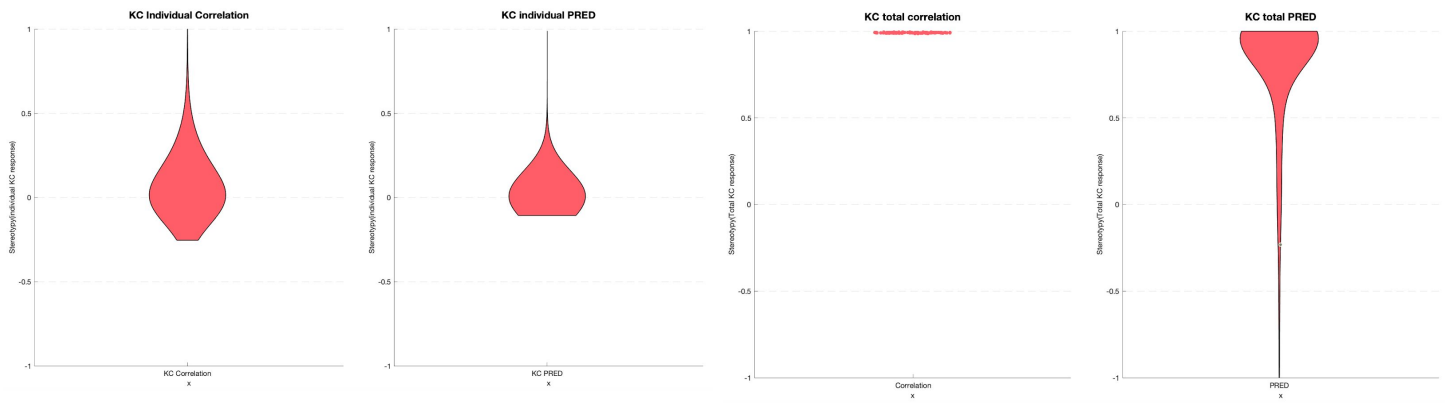

Fig. 2d. (left) Correlation stereotypy and PRED stereotypy in individual KC responses of two individuals for the same conditions as above; both show the absence of stereotypy. (right) Correlation stereotypy and PRED stereotypy in total KC responses; resembles fig. 2b showing that stereotypy exists.
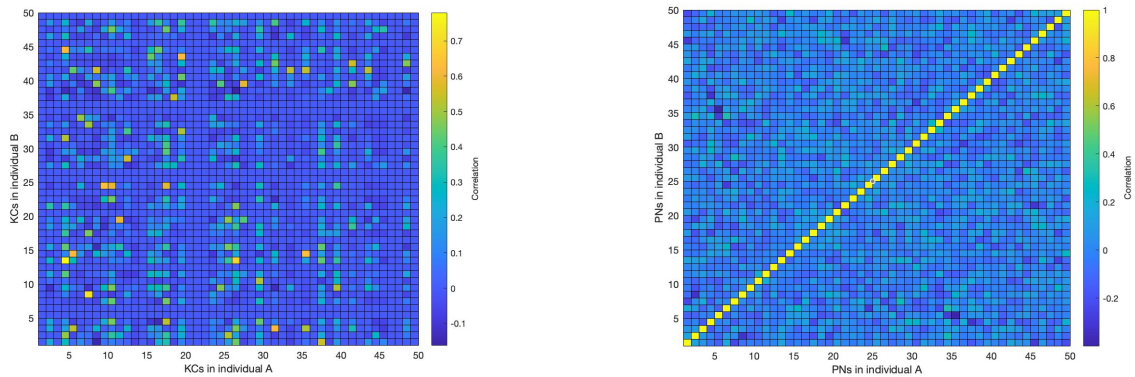

Fig. 2e. Correlation between the responses of KCs (top) and PNs (bottom) in two individuals.

The following is for the code contributed at:
https://github.com/Debu922/BCS_Connectome_Project_2020/tree/master/olfactory_system/debaditya

proto_neurons

- network.m: This is a simple implementation of a neuron network with multiple layers
- neuron.m: This is a simple neuron class generated on based on the principles found in the course: CS231n Convolutional Neural Networks for Visual Recognition
- neuronLayer.m: This is a simple neuron layer class generated on based on the principles found in the course: CS231n Convolutional Neural Networks for Visual Recognition

fig2

- `calculate_sterotypy_KC.m`: This *script* automatically loads the KC data generated by the `sim_script.m` script. It then calculates the total and cell wise stereotypy using the `get_correlation_sterotypy.m` and the `get_PRED_sterotypy.m` functions. It then exports the calculated data in a matlab file. *Note: This function takes a long time to run and requires a lot of free memory. If the system has enough free memory, one may use parfor loops instead of the normal for loops to significantly speed up the calculation.*
- `calculate_sterotypy_MBON.m`: This *script* automatically loads the MBON data generated by the `sim_script.m` script. It then calculates the total stereotypy using the `get_correlation_sterotypy.m` and the `get_PRED_sterotypy.m` functions. It then exports the calculated data in a matlab file.
- `calculate_sterotypy_PN.m`: This *script* automatically loads the KC data generated by the `sim_script.m` script. It then calculates the total and cell wise stereotypy using the `get_correlation_sterotypy.m` and the `get_PRED_sterotypy.m` functions. It then exports the calculated data in matlab files. *Note: This function takes a long time to run and requires a lot of free memory. If the system has enough free memory, one may use parfor loops instead of the normal for loops to significantly speed up the calculation.*
- `get_correlation_sterotypy.m`: This *function* takes in the spiking data as a parameter and outputs the correlation between pairs of individuals.

- `get_PRED_sterotypy.m:` This *function* takes in the spiking data as a parameter and outputs the PRED values between pairs of individuals for all possible combinations of the odor.
- `plot_correlation_img.m:` This *function* plots the correlation pcolour map for a given layer response for a pair of individuals.
- `plot_sterotypy_scatter.m:` This *function* plots the scatter plot comparing the PRED stereotypy to the correlation stereotypy.
- `plot_sterotypy_violin.m:` This *function* plots the violin plot for the PRED stereotypy and the correlation stereotypy.
- `run_simulation.m:` This *function* takes in simulation parameters, generates PN responses to a specific odor seed, generates the connection matrices (masks) for each layer, and returns the masks and the spiking data for each layer.
- `sim_script.m:` This *script* contains the simulation parameters and calls in succession the `run_simulation.m` with appropriate seeds to produce the spiking data. The data is compiled into matrices and saved in a matlab file.

Note: The above documentation for the olfactory system is for two example codes which essentially do the same simulations

The Visual System

Visual System and Recognition Skills of the Bumblebee

The presentation covers topics ranging from the simplistic cognitive model of a bee's vision, including shape, color and pattern recognition to processing and decision making in relation to visual cues.

References:

- Insect Bio-inspired Neural Network Provides New Evidence on How Simple Feature Detectors Can Enable Complex Visual Generalization and Stimulus Location Invariance in the Miniature Brain of Honeybees (Roper et., al. 2017).
- Bumblebees distinguish floral scent patterns, and can transfer these to corresponding visual patterns (Lawson et., al. 2018).

Impact

On a expansive and huge scale, developing a functional human connectome will be the next big thing in the medical industry, diagnosing various diseases, behavioural and mental and in the (data) analysis of the plethora of data our brains collect every waking and sleeping second - a complete new way to look at neuroscience. It would also help us predict certain aspects of human behaviour as well as understand the pathology behind certain psychological disorders

This project that we are attempting will also have a rich educational and social impact, plainly as it encourages more people (ourselves primarily) who are looking to understand brains, how we use them and the fascination associated with them.

People

- Yatin Azad *(Mentor)*
- Debaditya Bhattacharya
- Ragha Abhinaya M
- Bhuvan N
- Kunal Singh
- Vatsal Karwa

Resources

- Work Report
- Gramm Plotting Package
- Multiple network properties overcome random connectivity to enable stereotypic sensory responses
- The Structural Connectome of the Human Brain in Agenesis of the Corpus Callosum
- Mid-Term Evaluation Presentation

Online Courses/Tutorials

- Fundamental Neuroscience of Neuroimaging, John Hopkins University
- Academic Information Seeking
- Getting started with MATLAB
- CS231n: Convolutional Neural Networks for Visual Recognition