### Project Title:

Seed-based Functional Connectivity Analysis of Hippocampal Network of Patients Suffering from Major Depressive Disorder

Supervisors: Alaka Acharya, Kishori Kunwar

Entry number 1: Week 1 (Oct 1 - Oct 7 2021)

- 15 healthy controls (diagnosis 0) and 15 depressed patients (diagnosis 2) were manually selected by just eye balling the data sheet included in the data acquired from the SRBPS public repo.
- Majorly depressed patients were labeled with a BDI (Beck Depression Index) greater than 30. So patients having BDI > 30 were only selected.
- The data sheet contained data of subjects from various different site, data was selected from only one specific site, HUH to be specific. The reason behind this was to make sure that the images that we will be working on were acquired from the same MRI scanner.
- This ensured consistency of image data.
- Trying to acquire data of people from a certain age group was a fail because there were not just enough data of the majorly depressed patients (BDI > 30). So we had to settle with subjects of age group 20 to 50.
- Nonetheless, once we had the subjects decided, two statistical tests were performed:
  - 1. Chi-square test
  - 2. t-test
- Chi-square test was performed to check the goodness of fit between healthy and depressed subjects based on sex and t-test was performed to check the goodness of fit based on age.

Comments:	First	${\rm done}$	by	Namrata	Tamang	and	then	${\rm followed}$	by	$\operatorname{rest}$	of	the	group
members													

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Entry number 2: Week 2 (Oct 17 - Oct 23 2021)

- Created a shell script (BASH) to separate data from the participates info data sheet included in the repo.
- The script converted the .xlsx file into a csv and then awk was used to perform data separation. Once the data had been separated awk was used to perform necessary statistical tests.
- The script had the following dependencies:
  - 1. Python
  - 2. SciPy Module
  - 3. Libreoffice
  - 4. AWK

Comments: Nikin Baidar

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Entry number 3: Week 3 (Oct 24 - Oct 30 2021)

- Familiarization with Linux Shell environment.
- Learned the basics of BASH.
  - 1. Basics of Linux file system
  - 2. Navigation commands
  - 3. Creating, Deleting and Working with files and directories.
  - 4. Path and Environment Variables
- Basics of Linux package management repositories and software installation from the terminal (Windows Subsystem for Linux).
- Successful Installation of MRIcron from NITRC's official website on Windows 10\*.

Comments: All group members.

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<sup>\*</sup>Our full Linux system setup is not complete yet.

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Entry number EntryNumber: Week 4 (Nov 7 - Nov 13 2021)

- The patient data acquired from the SRBPS repository was in DICOM format.
- The rsfmri data of patients needed to be converted to nifiti format for further processing.
- A shell script was created to add the the nifti extension i.e. ".nii" to 143 rsfMR image data of 15 HC as well as 15 MDD patients. These script did not have any dependency.

Comments: Scripted by Nikin Baidar. Run by all the group members on a WSL.

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### Project Title:

Seed-based Functional Connectivity Analysis of Hippocampal Network of Patients Suffering from Major Depressive Disorder

Supervisors: Alaka Acharya, Kishori Kunwar

Entry number 5: Week 5 (Nov 8 - Nov 14 2021)

- Conversion of 3D rs-fMR image data into 4D image data using MRIcron.
- dcm2niigui program was used to convert 3D nifiti images to 4D image data. 143 3D image data of 30 subjects were combined to form a single 4D image.

**Comments:** Each group member was assigned with 4 subjects, 2 HCs and 2 MDD patients. So each member will be working with at least 4 subjects. Conversion of remaining 2 image data is also done.

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### **Project Title:**

Seed-based Functional Connectivity Analysis of Hippocampal Network of Patients Suffering from Major Depressive Disorder

Supervisors: Alaka Acharya, Kishori Kunwar

Entry number 6: Week 6 (Nov 15 - Nov 21 2021)

- Script Revision
- Prep-1-allocateSegbatch.sh was changed as necessary.
- Two files seg\_job.m and seg.m were copied in the same directory as the t1 and rsfmri image data.
- Segbatch was allocated to each inidviudal subject. i.e. the number in the seg\_job.m file was changed to concerned subject ids.

**Comments:** Script revision and study is being done by all group memebers. Prep-1 was done by Nikin Baidar.

**Remarks:** We are all a bit confused about how most functions implemented in these scripts work. Further study is being done.

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