System requirements:

1. 8GB RAM or more
2. QuadCore or higher Processor
3. At least 50GB of Disk space (preferably SSD)
4. Operating Systems:
    a. Windows 10 or higher (64-bit)
    b. Ubuntu 20.04 or higher (LTS versions only)
    c. Mac OS 13.5.1 (22G90)

System Setup

Windows users:

1. Download the graphical interface of Anaconda from the following website: https://www.anaconda.com/download and install it. Make sure you check the following advanced options while installing:
    a. Add anaconda to my PATH environment variable
    b. Register Anaconda as my default Python 3.7
2. Open **Anaconda Prompt** in the Administrative mode
3. Type the command
   `conda`
   (You should see details of Anaconda. If not, you have not downloaded it correctly).
4. Now type each of these commands, one by one.

```
pip install torch torchvision torchaudio
pip install opencv-python
pip install tqdm
pip install pandas
pip install matplotlib
```

   (Resolve any errors, if they occur.)
5. Now run the given python program using the command:

```
python test_installation.py
```

(You should get the message: Congratulations! You have installed all the required libraries for the Workshop Day 2)

Ubuntu users:

1. Open terminal. Browse to the folder in which you have downloaded the "test_installation.py" program using the `cd` command.
2. Type in the following commands to install miniconda. Skip this step if you already have miniconda or anaconda installed in your system.

```
mkdir -p ~/miniconda3
wget
https://repo.anaconda.com/miniconda/Miniconda3-latest-Linux-x86_
64.sh -O ~/miniconda3/miniconda.sh
bash ~/miniconda3/miniconda.sh -b -u -p ~/miniconda3
rm -rf ~/miniconda3/miniconda.sh
~/miniconda3/bin/conda init bash
~/miniconda3/bin/conda init zsh
```

3. Create a new conda environment with all the libraries required for this session.

```
conda env create -f env_brain_tumor.yml
conda activate env_brain_tumor
```

4. Now run the given python program using the command:

```
python test_installation.py
```

You should get the message: *"Congratulations! You have installed all the required libraries for the Workshop Day 2."*

Mac Intel users:

1. Open terminal. Browse to the folder in which you have downloaded the "test_installation.py" program using the `cd` command.
2. Type in the following commands to install miniconda. Skip this step if you already have either miniconda or anaconda installed in your system.

```
mkdir -p ~/miniconda3
```

```
wget
https://repo.anaconda.com/miniconda/Miniconda3-latest-MacOSX-x86
_64.sh -O ~/miniconda3/miniconda.sh
bash ~/miniconda3/miniconda.sh -b -u -p ~/miniconda3
rm -rf ~/miniconda3/miniconda.sh
~/miniconda3/bin/conda init bash
~/miniconda3/bin/conda init zsh
```

3. Create a new conda environment with all the libraries required for this session.

```
conda env create -f env_brain_tumor.yml
conda activate env_brain_tumor
```

4. Now run the given python program using the command:

```
python test_installation.py
```

You should get the message: *"Congratulations! You have installed all the required libraries for the Workshop Day 2."*

Mac M1/M2 users:

1. Open terminal. Browse to the folder in which you have downloaded the "test_installation.py" program using the `cd` command.
2. Type in the following commands to install miniconda. Skip this step if you already have either miniconda or anaconda installed in your system.

```
mkdir -p ~/miniconda3
wget
https://repo.anaconda.com/miniconda/Miniconda3-latest-MacOSX-arm
64.sh -O ~/miniconda3/miniconda.sh
bash ~/miniconda3/miniconda.sh -b -u -p ~/miniconda3
rm -rf ~/miniconda3/miniconda.sh
~/miniconda3/bin/conda init bash
~/miniconda3/bin/conda init zsh
```

3. Create a new conda environment with all the libraries required for this session.

```
conda env create -f env_brain_tumor.yml
conda activate env_brain_tumor
```

4. Now run the given python program using the command:

```
python test_installation.py
```

You should get the message: *"Congratulations! You have installed all the required libraries for the Workshop Day 2."*

Additional prerequisites:

1. This folder contains files named `setup_script.ipynb` and `brain-tumour-mri.zip` . Upload both these files to your google drive.
2. From your google drive, right-click and open the `setup_script.ipynb` with Google Colaboratory. This should open up google colab.
3. On google colab, go to *Runtime → Run all*. This should execute all cells in the ipython notebook. Make sure that the data loading part runs smoothly without errors. You might be asked to grant permission to google colab to access contents from your google drive.