User Manual For Analysis Of Disease Associated Genes

- STEP 1:- Install Anaconda Navigator.
- STEP 2:- Open Anaconda Navigator .
- STEP 3:- Go to Anaconda Navigator Side Menu and click on Environments.
- STEP 4:- Search for NLTK in search bar.
- STEP 5:- Click on Install.
- STEP 6:- Similarly do it for Bio Python.
- STEP 7:- After unzipping the files, you will find a folder with different disease names and ipynb files, and you can also add any abstracts of your choice to designated disease folders.
- STEP 8:- You can run our code with Colab also, you first need to log in to your google account, then go to this link https://colab.research.google.com. Without installing Anaconda.
- STEP 9:- Click on Launch Jupyter Notebook in Anaconda Navigator.
- STEP 10:- You will be redirected to a web interface where you have to select the extracted project folder and navigate to any disease named ipynb file of your choice.
- STEP 11:- Click on Run for each code snippet and finally you will get the result followed by the analysis graphs .