

MICE PROTEIN

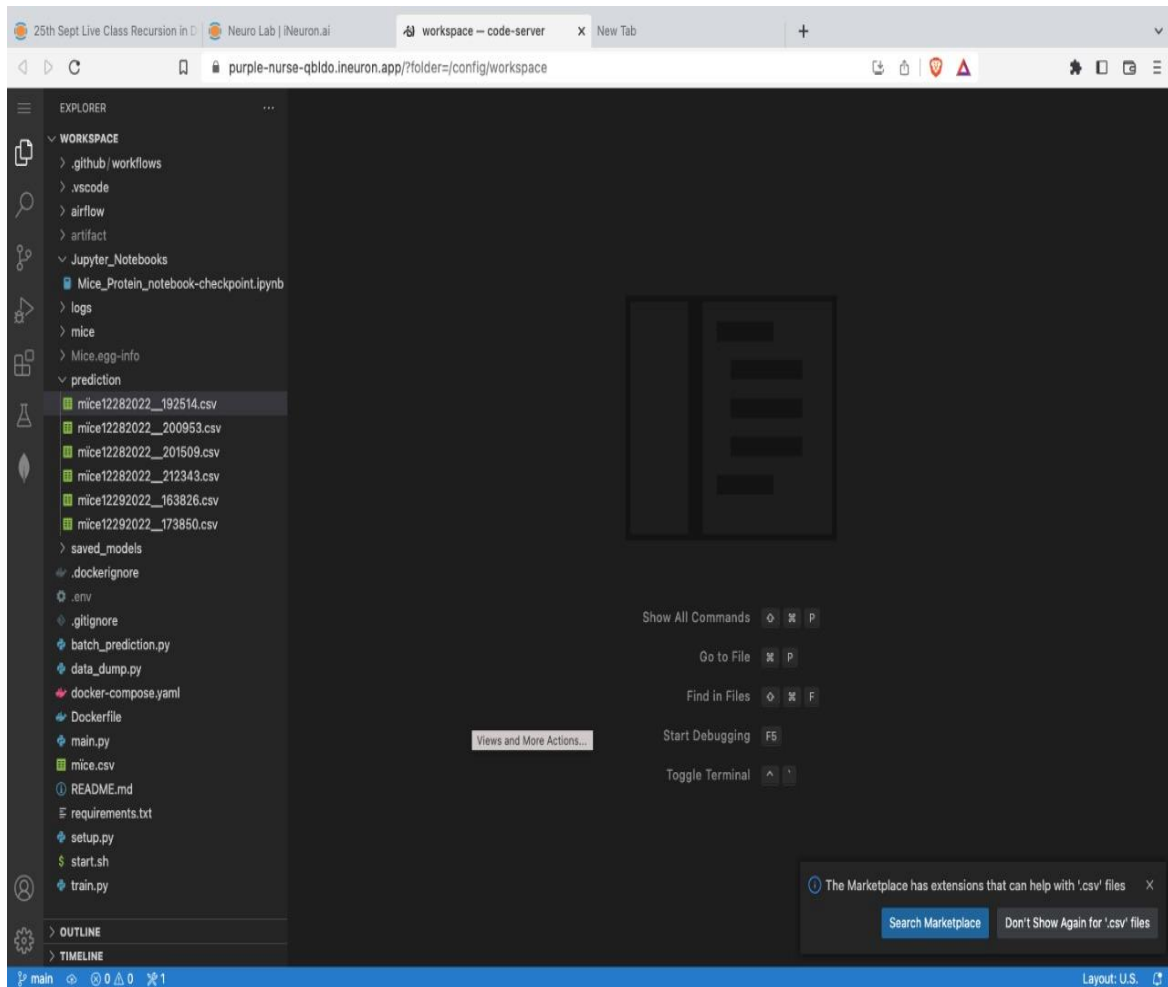
WIREFRAME DOCUMENTATION

D. JAGANNATH

The mice protein expression dataset was created to study the effect of learning between normal and trisomic mice or mice with Down Syndrome (DS). Wire Frame for is not created due too many of features . This project has 83 features divided into two types control mice and trisomic mice. So, when we start prediction it automatically created a file in prediction folder . It will store the prediction data into file in csv format

The process will happen as shown below.

1. Prediction data will store into files in prediction folder as shown below.



2. Within the file prediction data will be shown in csv format as shown below.

The screenshot shows a Jupyter Notebook environment with the following details:

- Explorer Panel:** Lists files in the workspace, including `.github/workflows`, `.vscode`, `airflow`, `artifact`, `Jupyter_Notebooks`, `Mice_Protein_notebook-checkpoint1.ipynb`, `logs`, `mice`, `Mice.egg-info`, `prediction`, `mice12282022_192514.csv` (selected), `mice12282022_200953.csv`, `mice12282022_201509.csv`, `mice12282022_212343.csv`, `mice12292022_163826.csv`, `mice12292022_173850.csv`, `saved_models`, `.dockerignore`, `.gitignore`, `batch_prediction.py`, `data_dump.py`, `docker-compose.yaml`, `Dockerfile`, `main.py`, `mice.csv`, `README.md`, `requirements.txt`, `setup.py`, `start.sh`, and `train.py`.
- Main Editor:** Displays the content of `mice12282022_192514.csv`. The data is a large table of numerical values, with each row representing a data point. The values are comma-separated and include many zeros, suggesting a binary or categorical nature for some features.
- Status Bar:** Shows the current file encoding as UTF-8, line feed (LF) characters, and a plain text layout.