## **User Help**

## **Description of the operating environment of the system**

Train and test the model:

1. Go to the link [RSNA-MICCAI Brain Tumor Radiogenomic Classification | Kaggle](https://www.kaggle.com/competitions/rsna-miccai-brain-tumor-radiogenomic-classification/data) and download the training data.
2. Create a google account.
3. Upload the data to google drive.
4. Go to google colab.
5. Upload the file densenet.ipynb or inception v3.ipynb.
6. Update the path to the labels ****
7. Update the path to the data and specify the filter type**A screenshot of a computer

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8. Choose your model hyperparameters (dropout and learning rate)**Text

   Description automatically generated**
9. Choose the batch size and epochs, change the path of the saved weights**Graphical user interface

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10. Press runtime and then run all

Run the gui:

1. open and run the Tumor\_predict.py
2. load dcm format mri scan using the load button
3. press predict