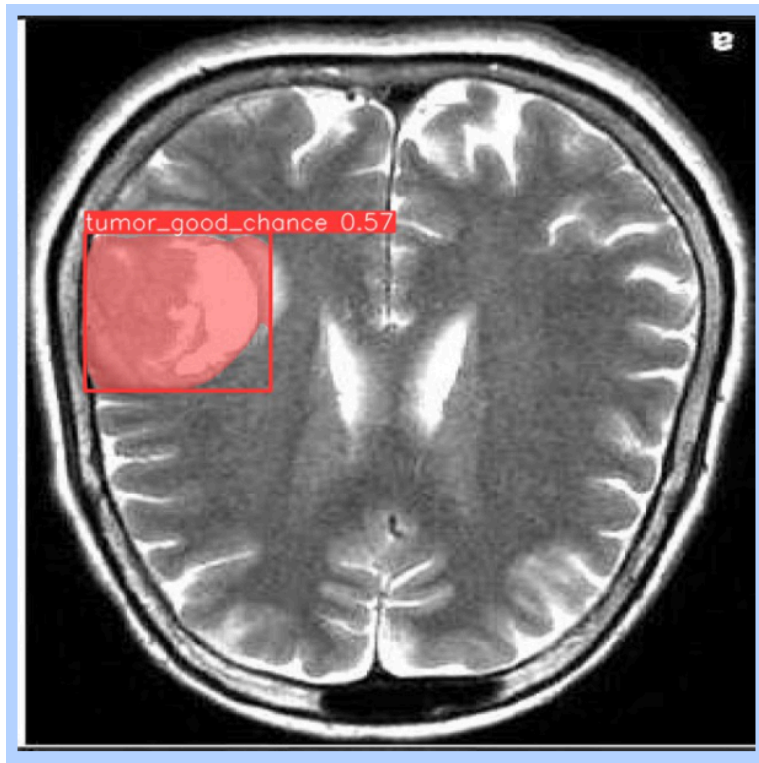# User Guide for Brain Tumor Prediction Tool

Disclaimer:
This was not created by medical professionals and is not intended to be used in place of medical practices. This is merely a tool to help researchers, patients, and doctors see how computer vision could be used for brain tumor detection and to provide resources on brain tumors.

## Step 1:
Clone the project repo:
git clone https://github.com/tchiang0/data_515_brain_tumor_computer_vision.git

## Step 2:
Open a terminal and cd into the project:

cd data_515_brain_tumor_computer_vision

## Step 3:
Create a conda environment with the required packages with the following command:
*Note this may take a couple minutes to install the packages

conda env create -f environment.yml

```
(base) holde@EllieLaptop:/mnt/c/Users/holde/Documents/Data 515/data_515_brain_tumor_computer_vision$ conda env create -f
 environment.yml
Channels:
 - defaults
Platform: linux-64
Collecting package metadata (repodata.json): done
Solving environment: done

Downloading and Extracting Packages:

Preparing transaction: done
Verifying transaction: done
Executing transaction: done
Installing pip dependencies: \ |
```

## Step 4:
Activate the environment with the following command:

conda activate project_env

You should now see the project_env as your environment name in the terminal

```
(base) holde@EllieLaptop:/mnt/c/Users/holde/Documents/Data 515/data_515_brain_tumor_computer_vision$ conda activate proj
ect_env
(project_env) holde@EllieLaptop:/mnt/c/Users/holde/Documents/Data 515/data_515_brain_tumor_computer_vision$
```

## Step 5:
cd into the main project directory, data_515_brain_tumor_computer_vision:

cd data_515_brain_tumor_computer_vision

## Step 6:

Run the following command from inside the data_515_brain_tumor_computer_vision folder to launch the tool:

python -m streamlit run ui_demo/Brain_Tumor_Information.py

Click the URL that pops up to launch the tool site in your browser:

```
(project_env) holde@EllieLaptop:/mnt/c/Users/holde/Documents/Data 515/data_515_brain_tumor_computer_vision/data_515_brai
n_tumor_computer_vision$ python -m streamlit run ui_demo/Brain_Tumor_Information.py

  You can now view your Streamlit app in your browser.

  Local URL: http://localhost:8501
  Network URL: http://172.21.38.196:8501
```

## Step 7:

You should now be at the landing page of our tool site. This page will give you background information on brain tumors. At the bottom of the page you will find links to additional information.
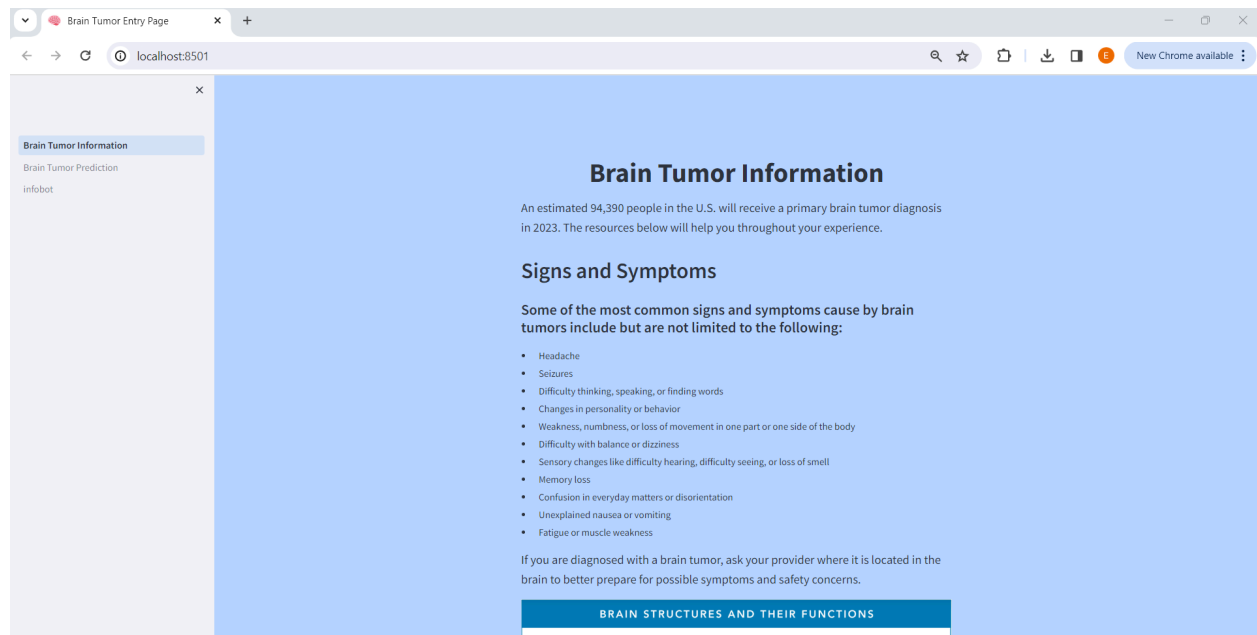
On the right hand side you will see a navigation column where you can click the name of the page you wish to navigate to.

Brain Tumor Information: Background information on brain tumors and links to additional resources

Brain Tumor Prediction: Our brain tumor prediction tool that reads in an image of the brain from a CT scan and returns the predicted probability of a brain tumor.

infobot: This is an interactive way to navigate the website and learn more about brain tumor resources.
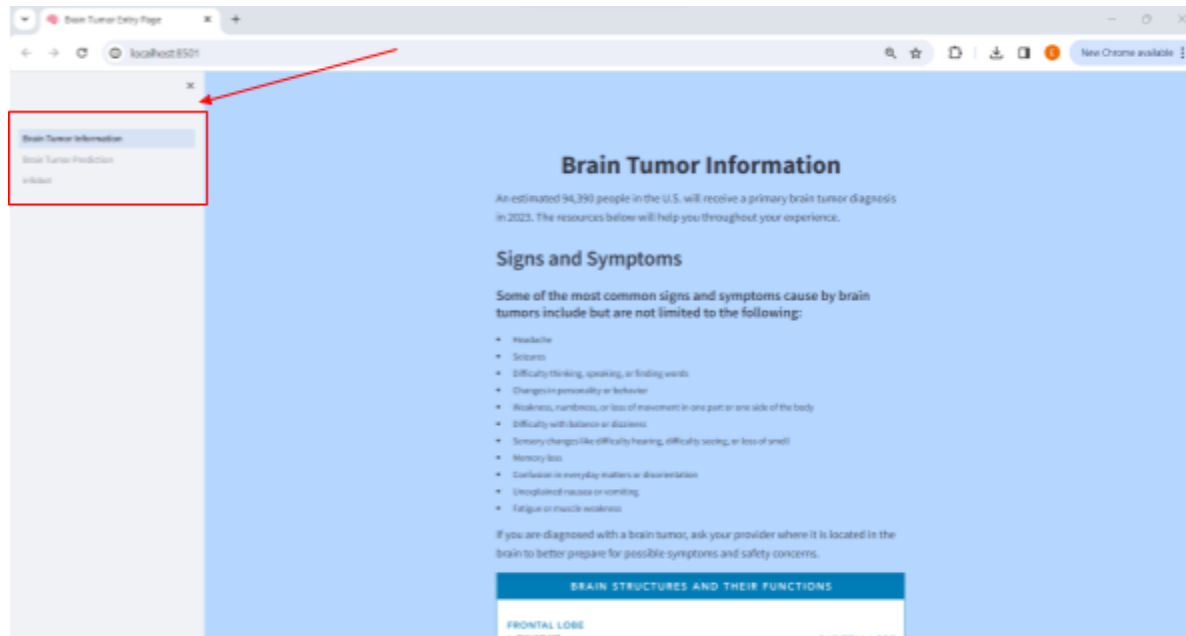
## Step 8:

Click the "Brain Tumor Prediction" tab in the navigation column to navigate to the Brain Tumor Prediction tool. Use the image uploader to select an image of the brain from a CT scan from your computer by clicking "Browse files". The image must be in the format '.jpg', '.jpeg', '.png', '.tiff', '.tif'.
Additionally, in the "examples: directory of the project there is a folder named "example_brain_scans" with 5 sample brain scans for users to test the tool with.
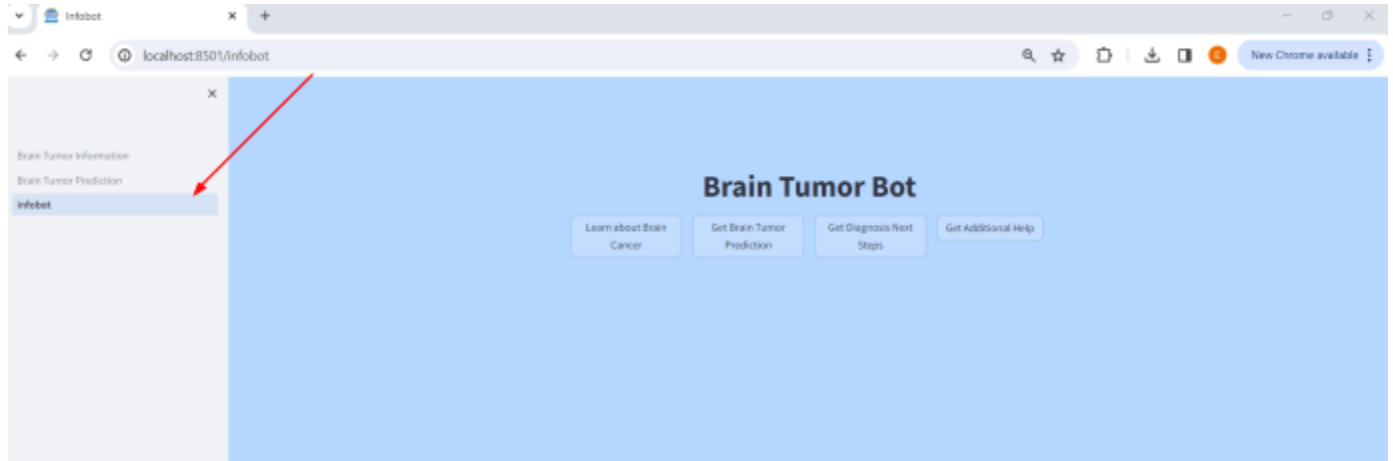
Once uploaded, the tool will return your scanned image with a label of the predicted probability of tumor and the area of the tumor highlighted.
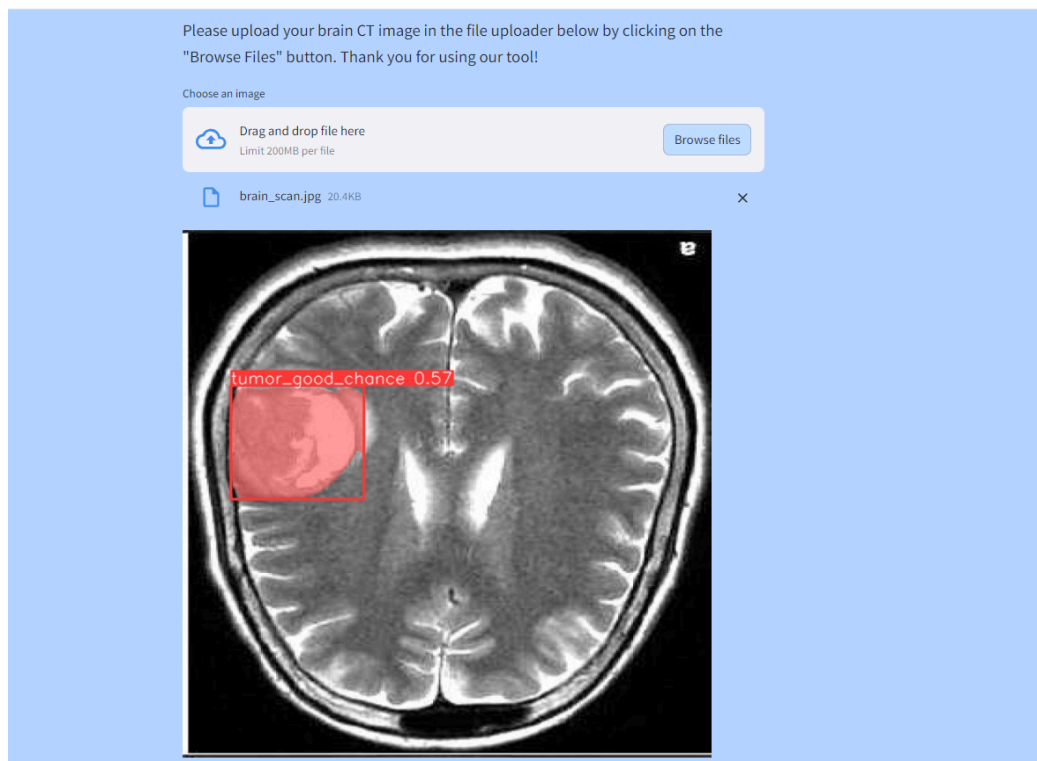
## Step 9:

Click the "infobot" tab in the navigation column to navigate to the infobot page. This page allows you to navigate the tool site in an interactive way.
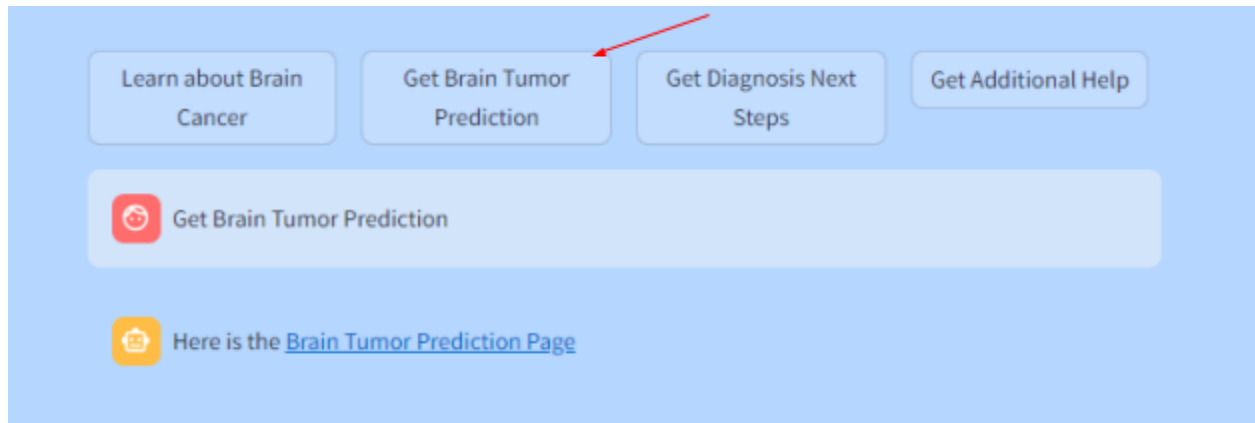


There are 4 buttons that you can click to explore the website.
To learn more about brain cancer click "Learn about Brain Cancer". This will provide you a link to the Brain Tumor Information (landing page) and provide other resources.
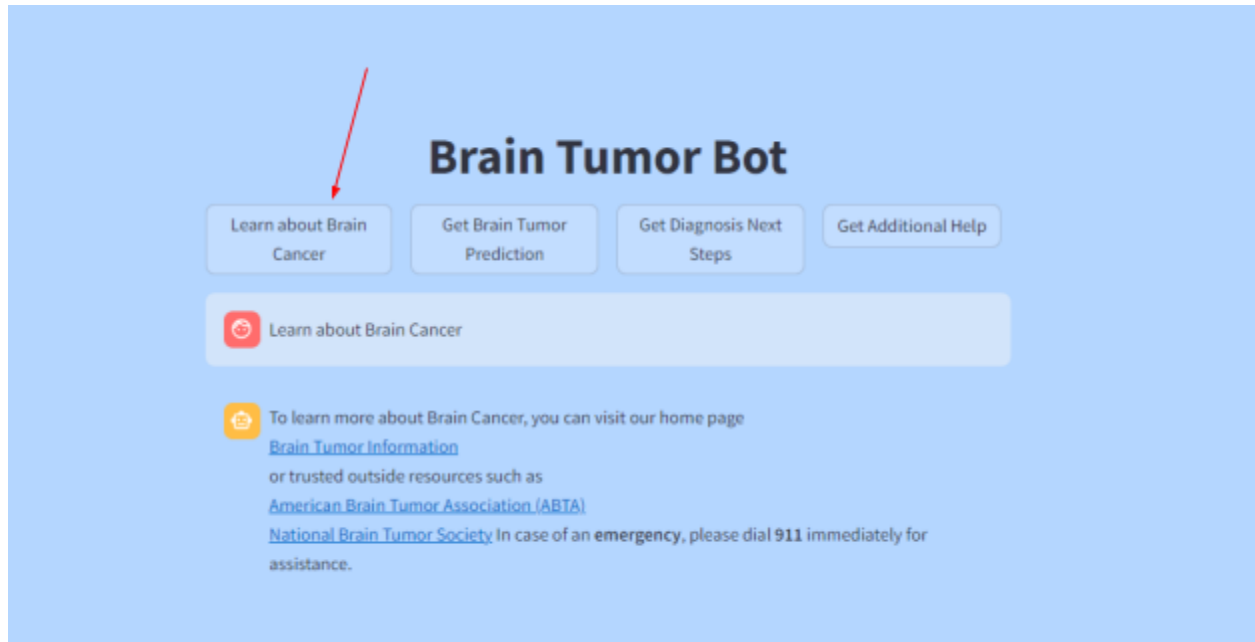


To use the brain tumor prediction tool click "Get Brain Tumor Prediction". This will provide you a link to the "Brain Tumor Prediction" page.

To learn more about diagnosis next steps for someone who was recently diagnosed with a brain tumor or believes they may have one click "Get Diagnosis Next Steps". This will give you information.
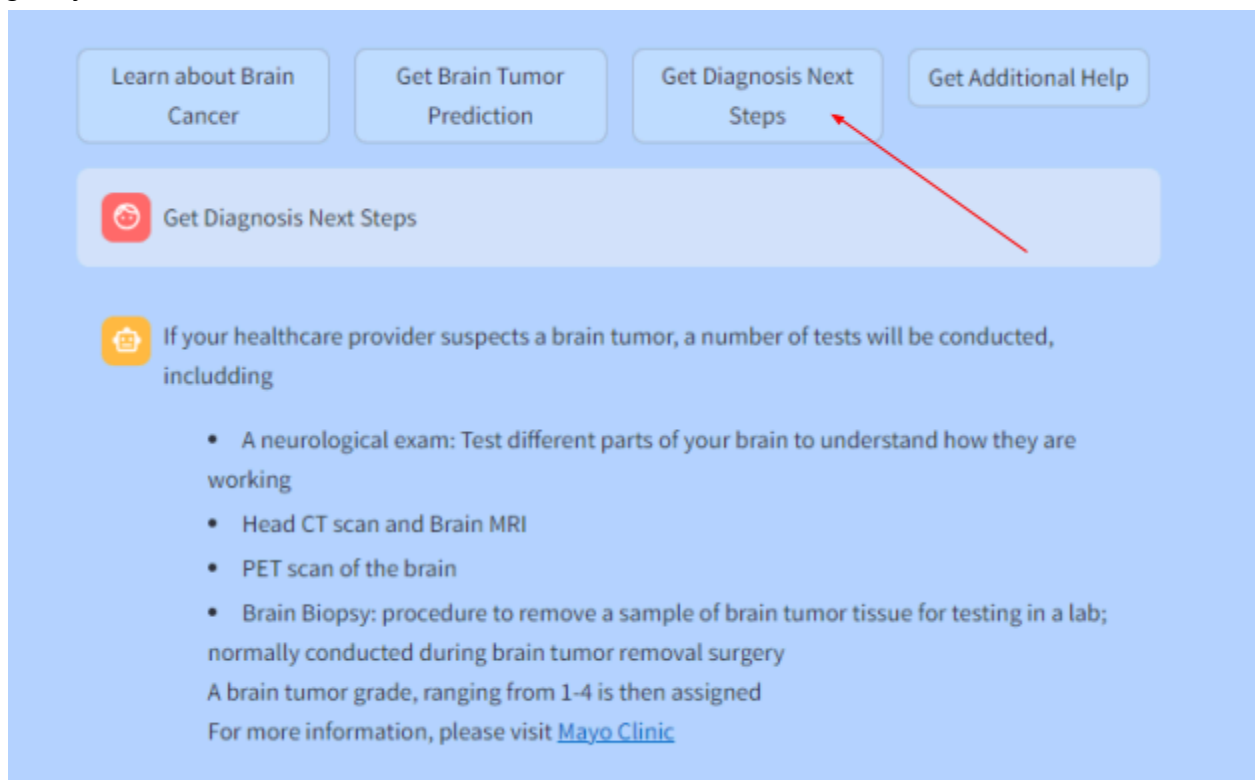
For any additional help click "Get Additional Help" to be provided with additional resources.
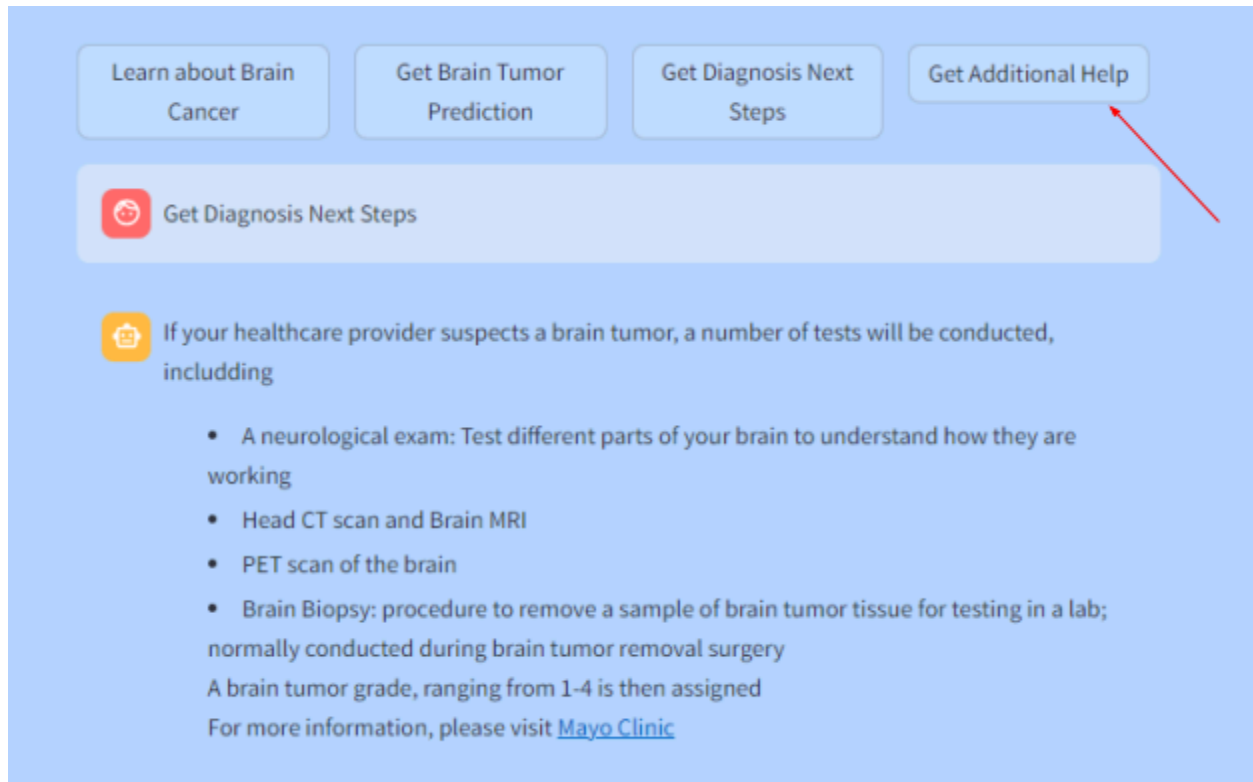


## Step 10:

Once you are done using the tool, click ^C in the terminal to kill the streamlit site. Then you can deactivate the conda environment and remove it if you would like:

conda deactivate

conda remove --name project_env --all

Troubleshooting:
If you are getting an error on the prediction page follow these steps:

^C to kill the streamlit app

Then run the two following commands separately

pip install opencv-python

pip install ultralytics

This will either install these packages or tell you that the requirements are met. Now run the app again using the command:

python -m streamlit run ui_demo/Brain_Tumor_Information.py

If you are still getting an error on the prediction page, specifically an Import error for ImportError: libGL.so.1 follow these commands:

*Note: This will prompt you to sign in and is installing libgl1 with administrator privileges, only proceed if this is okay with you

^C to kill the streamlit app

sudo apt-get update

sudo apt-get install libgl1

To run without a conda environment and with pip, clone the git repository, and run the command:
        Pip install -r requirements.txt

Then follow steps above for running the tool