



GLIOGRADE: Using 3D Convolutional Neural Networks to Type and Grade Gliomas within Human MRI Scans

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Background

Gliomas are the most common of cancerous tumor in the brain.

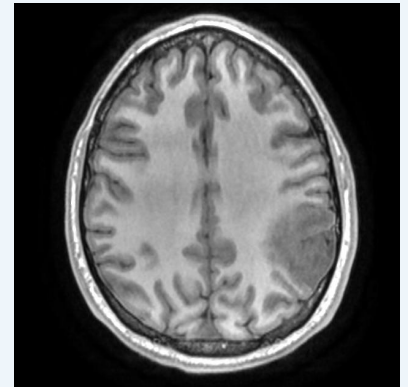
- 6.0 per 100,000 individuals in the US [1]

There are many **types of Glioma**:

- Astrocytoma
 - IDH wild type
 - IDH mutant
- Glioblastoma
- Oligodendroglioma

There are three **grades of Gliomas**:

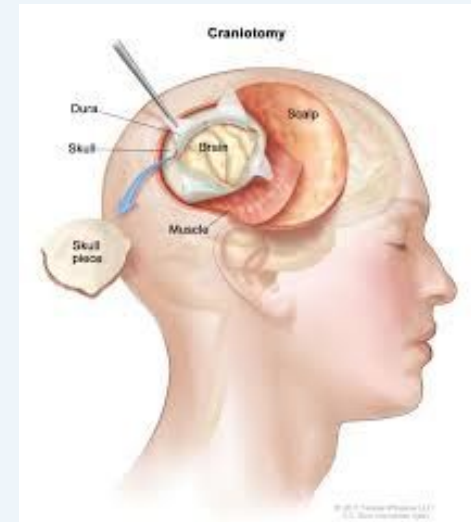
- 2, 3, 4
- Increases depending on the severity



Problem

To diagnose gliomas in humans:

- Invasive:
 - Taking slices of the patient's brain
 - “stereotactic biopsy may not always be useful or necessary in the management of brain tumor patients” [6]
- Non-Invasive:
 - Taking an MRI



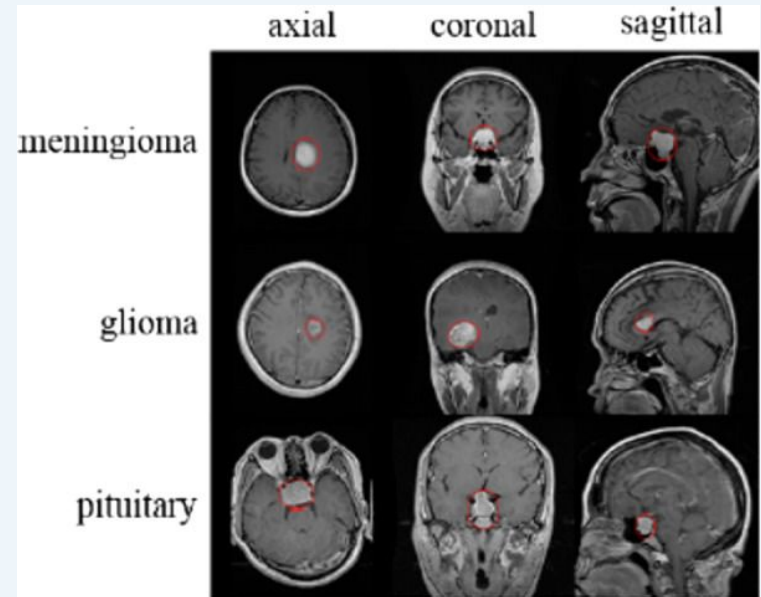
Previous Solutions

Manual MRI Tumor Typing and Grading:

- MRI Segmentation

Cons:

- Time-Consuming
- Subject to human error.



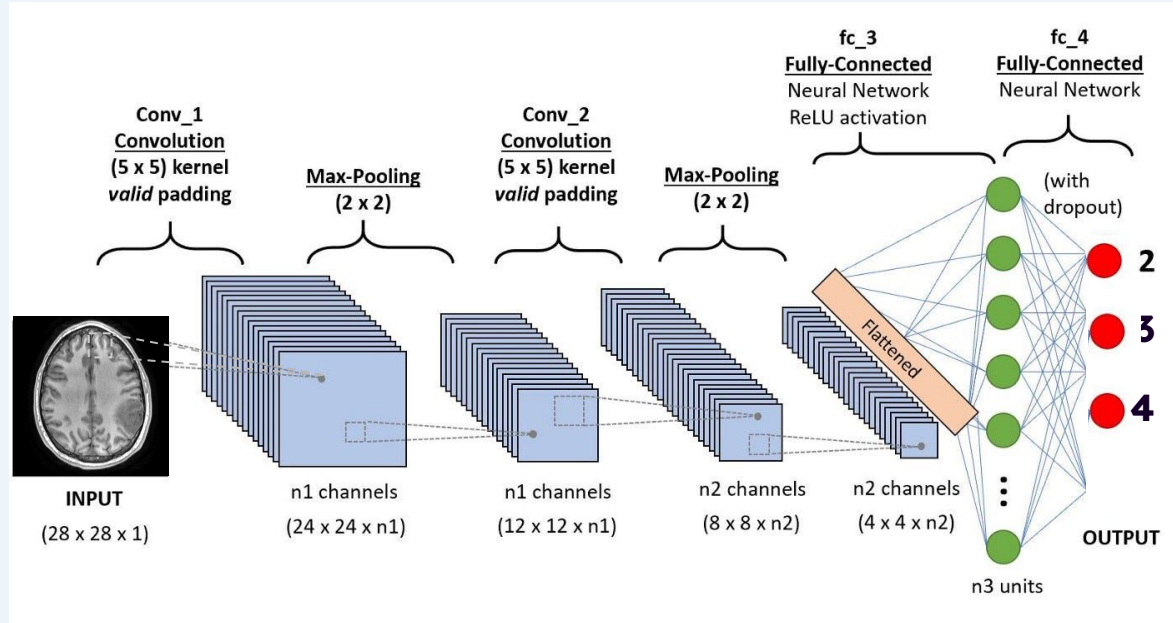
MRI Segmentation

Other Solutions

Existing 2D CNN Models:

- High Accuracy
- Skips Spatial Information

Grading Example



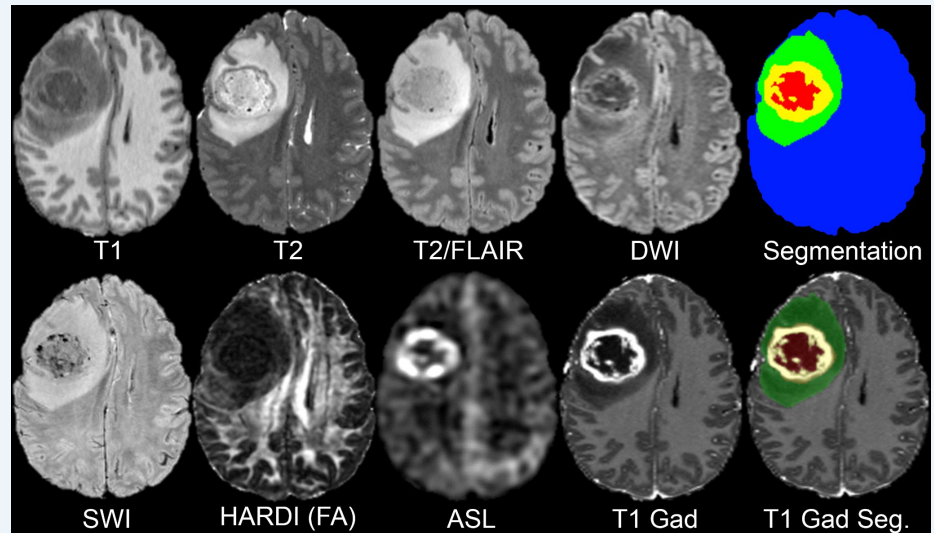
Our Solution

Input: 3D MRI Scans (T2 Flair)

Output: Classification of Glioma Type **and** Grade

The Final Tool:

- locally hosted website
- application.



Types of MRI Scans

Why Is Ours Better?

Possible Higher Accuracy with 3D CNNs:

- Captures Spatial Information

Streamlined Workflow:

- User-friendly platform
- Types AND Grades gliomas

New Classification: In 2021, World Health Organization (WHO) updated their tumor classification categorization [7]

- Many models become outdated

Novelty

Integrated Glioma Typing and Grading: Our project is the first to combine typing, and grading of gliomas into one unified model using 3D data.

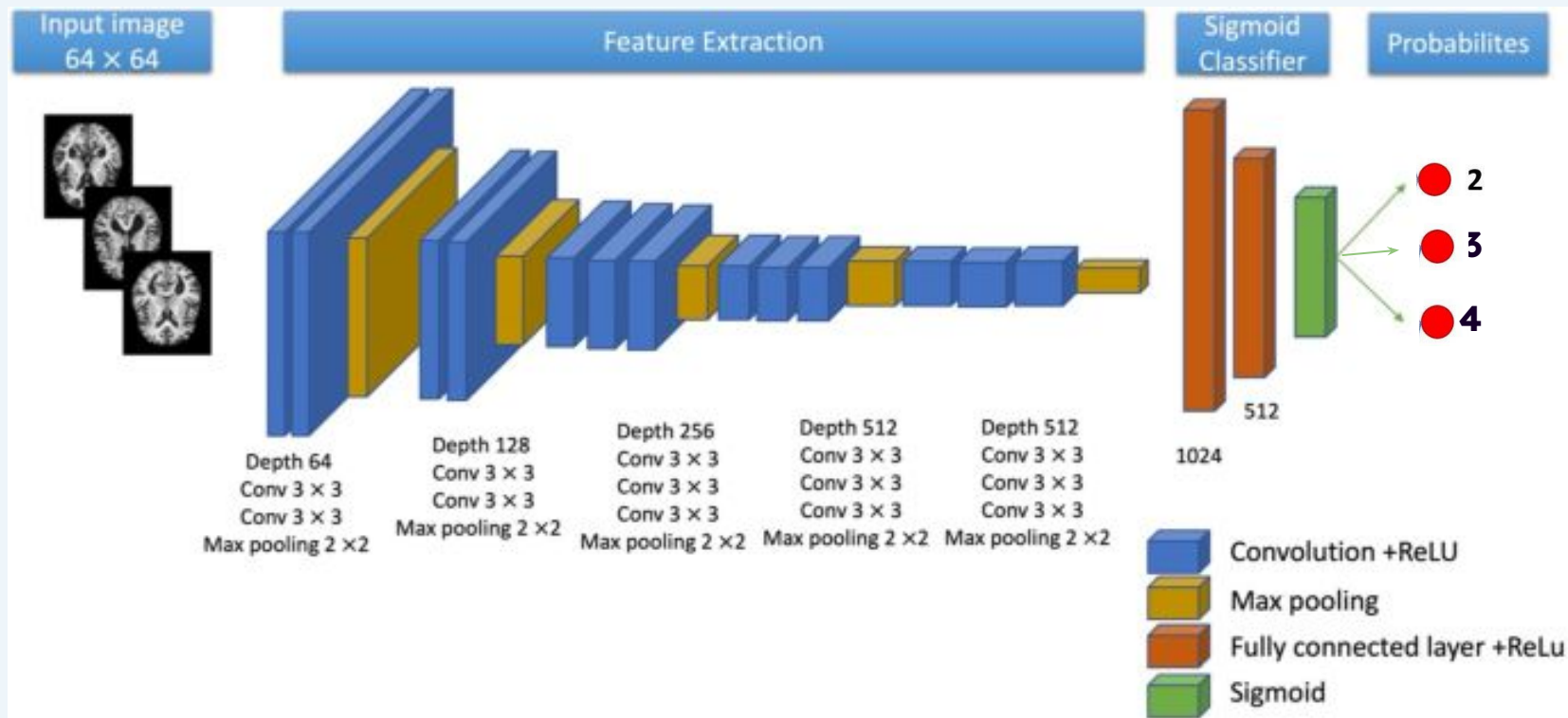
Updated Classification: Our tool will be up to the current WHO Glioma Standard

“One major change between the 2016 and 2021 WHO Classifications is that ... *IDH*-mutant astrocytomas are no longer referred to as glioblastomas” [8]

Project Steps

1. 2D CNN
 - a. Review previous solutions
2. 3D CNN
 - a. Develop new approach

Methods: 2D CNN Architecture (VGG-16)



Methods: 2D CNN

- Methods used for 2D Preprocessing
 - Resizing
 - Skull-Stripping
- Dataset from Kaggle

```
app.py 2 x result.html
app.py > ...
32 def save_image(image, file_path):
33     sitk.WriteImage(sitk.Cast(image, sitk.sitkUInt8), file_path)
34
35 def skull_strip(image):
36     img_array = sitk.GetArrayFromImage(image)
37     mean_intensity = np.mean(img_array)
38     std_intensity = np.std(img_array)
39     lower_bound = mean_intensity - 2 * std_intensity
40     upper_bound = mean_intensity + 2 * std_intensity
41     binary_mask = (img_array > lower_bound) & (img_array < upper_bound)
42     stripped_image_array = np.where(binary_mask, img_array, 0)
43     stripped_image = sitk.GetImageFromArray(stripped_image_array)
44     return stripped_image
45
46 def preprocess_image_for_second_model(image_path):
47     img = read_jpeg_image(image_path)
48     sitk_image = sitk.GetImageFromArray(img)
49     stripped_image = skull_strip(sitk_image)
50     skull_stripped_img_array = sitk.GetArrayFromImage(stripped_image)
51     img_resized = cv2.resize(skull_stripped_img_array, (224, 224), interpolation=cv2.INTER_LANCZOS4)
52     img_resized_3ch = cv2.merge([img_resized] * 3) # Convert to 3 channels
53
54     processed_image_path = os.path.join(app.config['PROCESSED_FOLDER'], 'preprocessed_second_model.jpg')
55     cv2.imwrite(processed_image_path, img_resized_3ch)
56
57     img_array = np.expand_dims(img_resized_3ch, axis=0) / 255.0
58     return img_array, processed_image_path
59
60 def preprocess_image_for_third_model(image_path):
61     img = Image.open(image_path).convert('RGB')
62     img = img.resize((369, 312), Image.LANCZOS) # Resize to the same dimensions used during training
63     processed_image_path = os.path.join(app.config['PROCESSED_FOLDER'], 'preprocessed_third_model.jpg')
64     img.save(processed_image_path)
65     img_array = np.array(img) / 255.0
66     img_array = np.expand_dims(img_array, axis=0)
67     return img_array, processed_image_path
```

Results: 2D

2D Early Development tool

- Typing Accuracy is 93%
 - 0.89 Precision
- Grading Accuracy is 85%
 - 0.82 Precision
- Slicing is hard for Pathologist
- Lacks Spatial Awareness

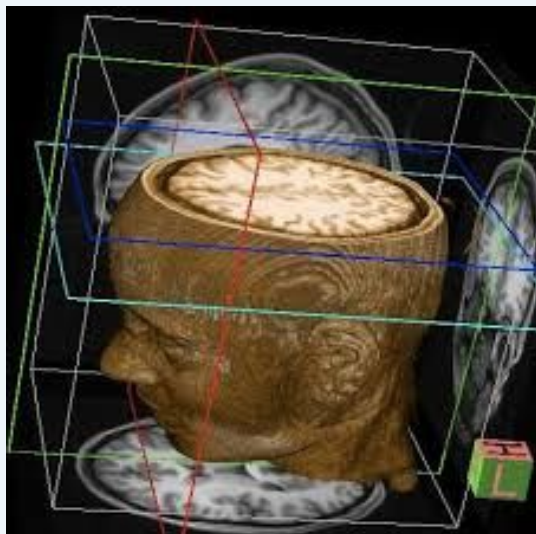
2D CNN Demo Tool



Methods: 3D Convolutional Neural Network

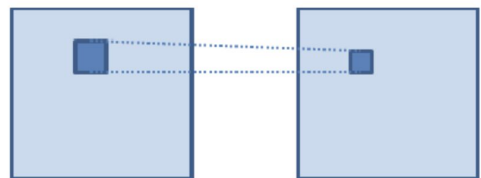
Input: 3D MRI Scan

Output: Classification

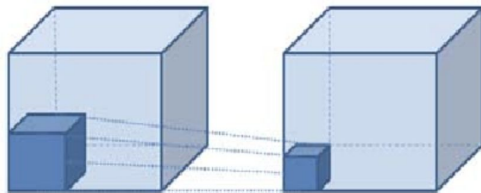


3D CNN

- Uses 3D Kernel instead of 2D



(a) 2D convolution



(b) 3D convolution

Comparison of (a) 2D convolution and (b)

Data Set Details

UC San Francisco (Training) [2]:

- 495 Patients
- WHO 2021 Classification
- Contains T1, T1 Bias, T2, T2 Bias, T2 Flair Scans etc.
- 156 GB
- Skull Stripped and Normalized (Preprocessed)
- <https://www.cancerimagingarchive.net/collection/ucsf-pdgm/>

Erasmus Glioma Database (Testing) [3]:

- 774 Patients
- WHO 2016 Classification
- pre-contrast T1-weighted, post-contrast T1-weighted, T2-weighted, and T2-weighted FLAIR scan
- 68 GB
- Raw (No Preprocessing)
- <https://www.healthinformationportal.eu/health-information-sources/erasmus-glioma-database>

Preprocessing

To **normalize** the data:

- Skull Stripping
 - Removes the high intensity skull values from the MRI
- Bias Correction
 - Corrects intensity variations from bias field within MRI
- Erasmus Glioma Data
 - Needs to be Skull Stripped and Normalized

Additional Preprocessing

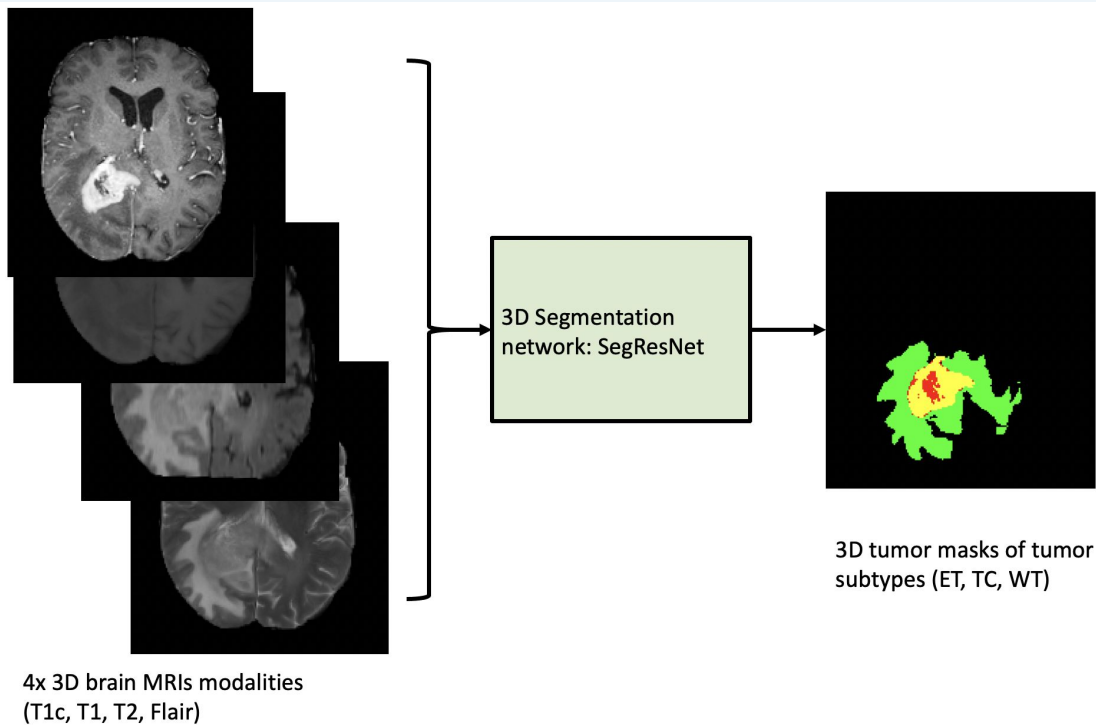
To increase the accuracy:

- Segmentation
 - Identifies the Tumor into 3 regions
 - the "enhancing tumor" (ET)
 - the "tumor core" (TC)
 - the "whole tumor" (WT)

Additional Preprocessing

Needs 4 MRI Types to **create** the segmentation:

- T1c
- T1
- T2
- Flair



Methods (Cont.)

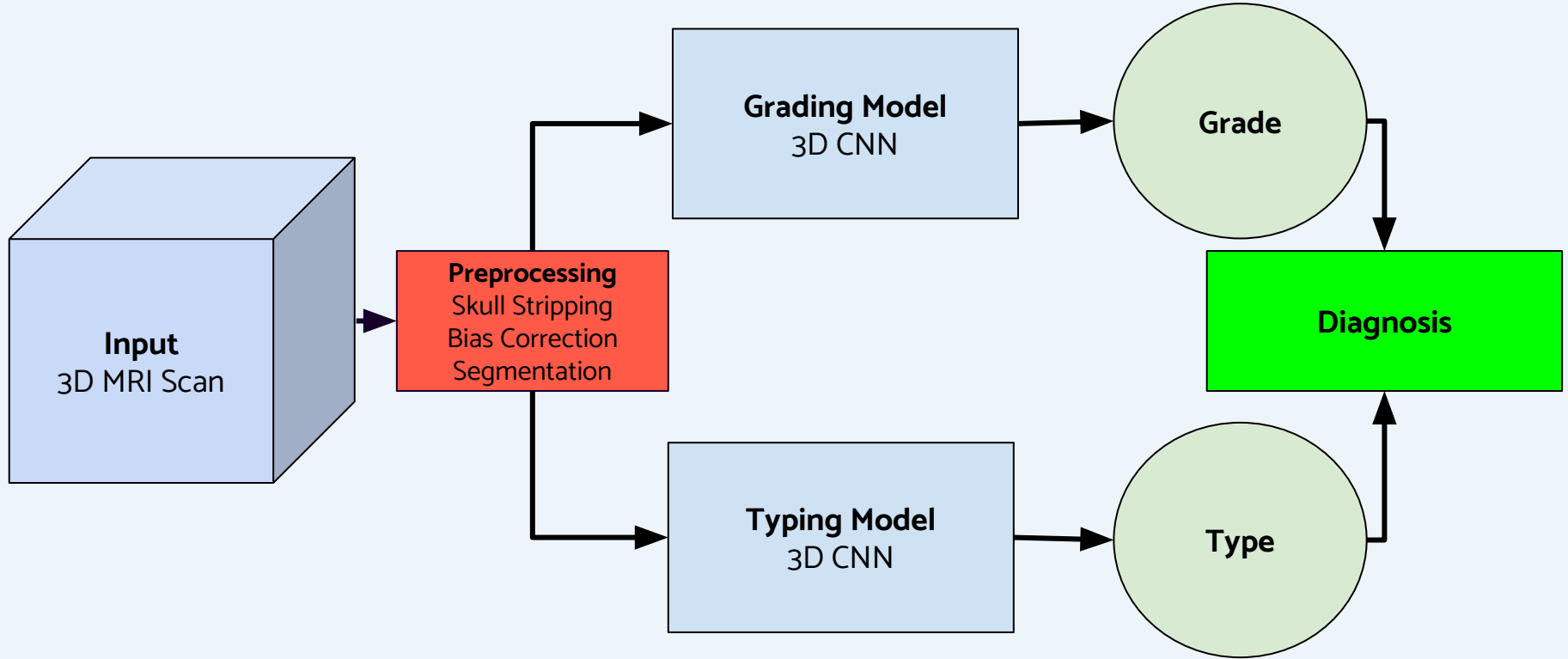
The First 3D CNN Model will classify MRI Scans into 4 classes (Type):

- Astrocytoma (IDH-Mutant)
- Astrocytoma (IDH-Wildtype)
- Glioblastoma
- Oligodendroglioma

The Second 3D CNN Model will classify the MRI Scans into 3 classes (Grade):

- 2, 3, 4

Methods: System Architecture



Methods: 3D CNN Architecture (VGG-16)

Input: (B,1,64,64,64)(B, 1, 64, 64, 64)(B,1,64,64,64)

Conv3D (1 \rightarrow 32) + BatchNorm3D + ReLU

MaxPool3D (halves each dimension \rightarrow (B,32,32,32,32)(B, 32, 32, 32, 32)(B,32,32,32,32))

Conv3D (32 \rightarrow 64) + BatchNorm3D + ReLU

MaxPool3D (\rightarrow (B,64,16,16,16)(B, 64, 16, 16, 16)(B,64,16,16,16))

Conv3D (64 \rightarrow 128) + BatchNorm3D + ReLU

MaxPool3D (\rightarrow (B,128,8,8,8)(B, 128, 8, 8, 8)(B,128,8,8,8))

Conv3D (128 \rightarrow 256) + BatchNorm3D + ReLU

MaxPool3D (\rightarrow (B,256,4,4,4)(B, 256, 4, 4, 4)(B,256,4,4,4))

Flatten \rightarrow (B,256 \times 4 \times 4 \times 4=16,384)(B, 256 \times 4 \times 4 \times 4 = 16,384)(B,256 \times 4 \times 4 \times 4=16,384)

Fully Connected (16,384 \rightarrow 512) + ReLU + Dropout

Fully Connected (512 \rightarrow num_classes)

Methods: Training and Testing

Trained on:

- University of California San Francisco Dataset [2]
 - Already Skull Stripped and Normalized

Tested on:

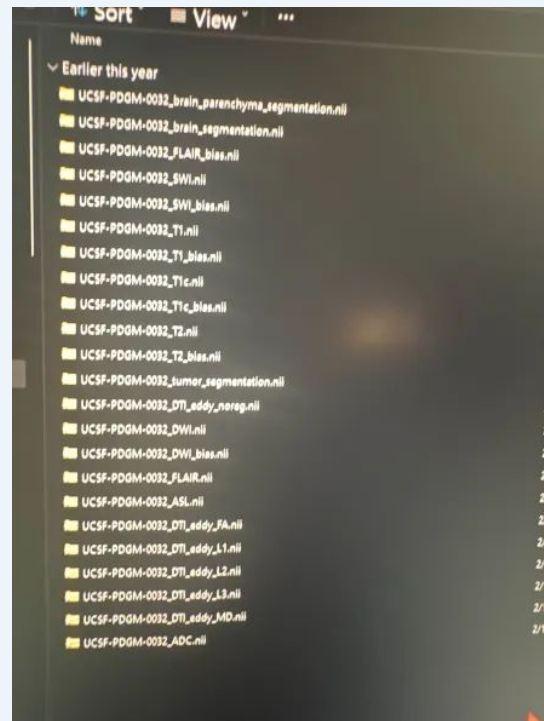
- Erasmus Glioma datasets Dataset [3]
 - Raw (Not Preprocessed)

Training Specifics

- Google Colab

Data Download

- Each contains a variety of scan types
- Segmentation takes the most space
 - Recommended to try
 - Need Funding for Space
- Significant issues downloading



Meta Data Preprocessing

- Data Downloaded
- Data Separated
- Removal of Misc. Class
- Normalizes Instances
- Removes Alt Labels

```
# Mount Google Drive
from google.colab import drive
drive.mount('/content/drive')

# Define paths
T2BiasDataPath = '/content/drive/MyDrive/UCSF_data/T2biasCollected'
csv_path = '/content/drive/MyDrive/UCSF_data/UCSF-PDGM-metadata_v2.csv'

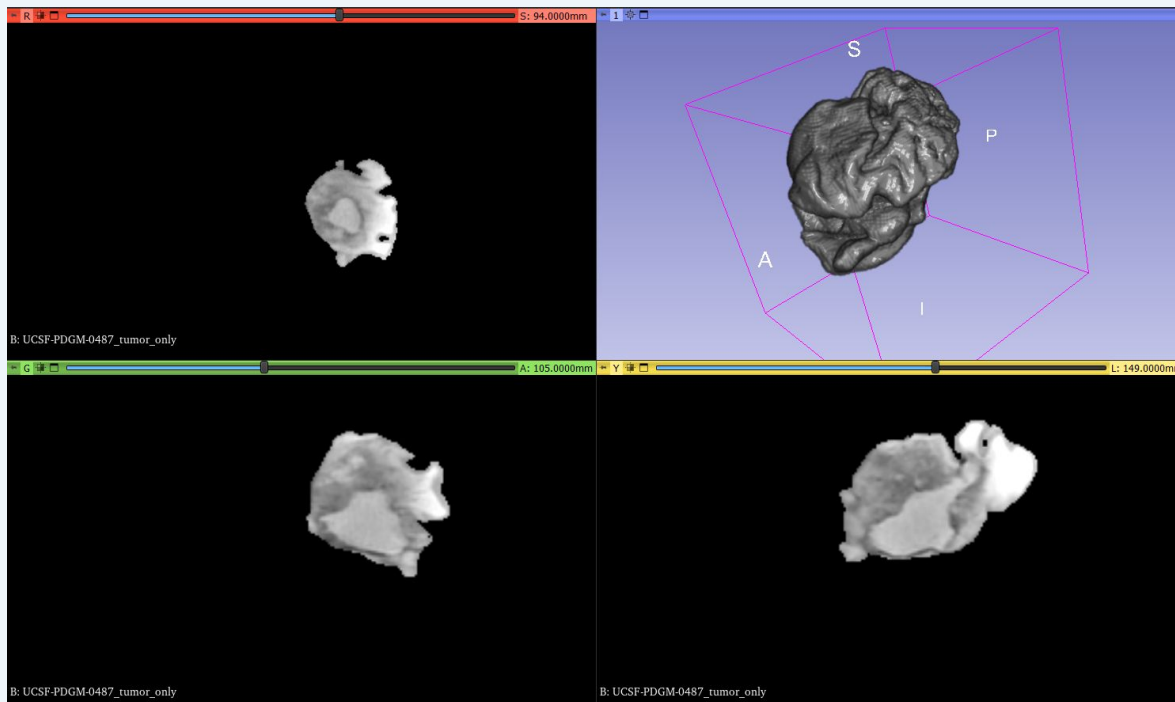
# Load metadata
metadata = pd.read_csv(csv_path)
metadata['ID'] = metadata['ID'].str.replace("UCSF-PDGM-", "").astype(int)
ids = metadata['ID']
labels = metadata['Final pathologic diagnosis (WHO 2021)']

# Define label mapping
label_mapping = {
    'Glioblastoma, IDH-wildtype': 0,
    'Astrocytoma, IDH-wildtype': 1,
    'Oligodendroglioma, IDH-mutant, 1p/19q-codeleted': 2,
    'Astrocytoma, IDH-mutant': 3
}

# Clean and filter metadata
filtered_metadata = metadata[metadata['ID'].isin(ids)]
filtered_metadata['label_idx'] = filtered_metadata['Final pathologic diagnosis (WHO 2021)'].map(label_mapping)
```


Results

- Segmentation Mask
- T2 Flair x Segmentation
- Geodesic CNN
- Increases Complexity



Small Range of Values



Large Range of Values

Results

- Early Results presented at Science Fair
- Judges Impressed
- Inspired by Dr. Yilmaz



Results

3D CNN Models

- Typing Accuracy is 84.57%
- Grading Accuracy is 83.84%

3D CNN Website



Limitations + Future Work

Dataset Issues: Datasets have very different preprocessing done on them. This is an issue as it make the data less normalized and less accurate.

3D CNN :

- Needs Lengthy Training Time
 - Lower Accuracy

Conclusion

3D Machine Learning Models on MRI Scans to Type and Grade Gliomas in Human Brains

Future Work:

Send Tool to Medical Institutions

Peer Review our Work

References

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- [2] Calabrese, E., Villanueva-Meyer, J., Rudie, J., Rauschecker, A., Baid, U., Bakas, S., Cha, S., Mongan, J., & Hess, C. (2022). The University of California San Francisco Preoperative Diffuse Glioma MRI (UCSF-PDGM) (Version 4) [Dataset]. The Cancer Imaging Archive.
- [3] Sebastian R. van der Voort, Fatih Incekara, Maarten M.J. Wijnenga, Georgios Kapsas, Renske Gahrman, Joost W. Schouten, Hendrikus J. Dubbink, Arnaud J.P.E. Vincent, Martin J. van den Bent, Pim J. French, Stefan Klein, Marion Smits,
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- [6] Jesús Vaquero, Roberto Martínez, Miguel Manrique, Stereotactic biopsy for brain tumors: is it always necessary?, *Surgical Neurology*, Volume 53, Issue 5, 2000, Pages 432-438, ISSN 0090-3019,
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Q&A

Any Questions!

THANKS!