BRAIN TUMOR RADIOGENOMIC CLASSIFICATION - AN ADAPTED SWIN TRANSFORMER APPROACH

By

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Computer Science UG Major Project | 2024

Jawaharlal Nehru University

OVERVIEW

- Introduction
- Acknowledgement
- Objective
- Tools and Technologies
- Methodology
- Swin-T Architecture
- Results
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- Conclusion
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INTRODUCTION

- Glioblastoma is a common and deadly type of brain cancer in adults.
- This aggressive cancer has a poor prognosis, making treatment very challenging.
- To understand its genetics, doctors need to perform surgery to get a tissue sample.
- Analyzing the genetic characterization of the tumor through these invasive surgical methods take several weeks.
- Development of an accurate method to predict the genetics of cancer through radiogenomics, refines the type of therapy required.

ACKNOWLEDGEMENT

I would like to express my sincere gratitude to everyone who supported me this project:

- Dr. Anupama Namburu, for her invaluable guidance, insightful feedback, and encouragement throughout this study.
- Sai Sivakesh and Pravith Potluri, for their constructive discussions and suggestions.
- RSNA-MICCAI organizations, for their collaborative effort in formulating the problem statement, organizing the challenge, and providing the BraTS 2021 dataset.

OBJECTIVE

- Genetic sequence O6-Methylguanine-DNA-Methyltransferase (MGMT) promoter methylation acts favourably for prognosis and responsiveness to chemotherapy.
- Develop a predictive model, using the techniques from Computer Vision, Machine Learning, Deep Learning and Radiogenomics.
- By training and testing this model with MRI (Magnetic Resonance Imaging) scans, we estimate the probability of MGMT promoter methylation.
- Improve treatment decision making and enhance patient outcomes.

TOOLS AND TECHNOLOGIES

TOOLS

- Python
- Pandas
- Numpy
- OpenCV
- Pydicom
- Pytorch
- Scikit-learn
- Seaborn

TECHNOLOGIES

- Radiogenomics
- Computer Vision
- Machine Learning
- Deep Learning
- Swin Transformer

METHODOLOGY

PHASE 1

- Visualization
- Analysis
- Preprocessing
- Augmentation

PHASE 2

- Data Loading
- Dataset Retrieval
- Modelling
- Training

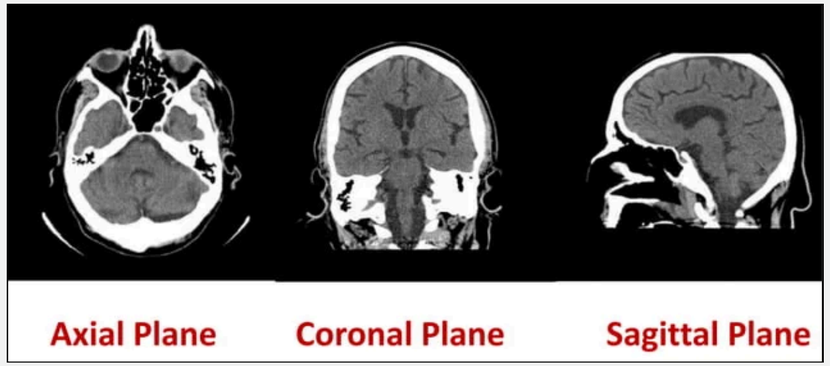
PHASE 3

- Optimization
- Prediction
- Evalution
- Submission

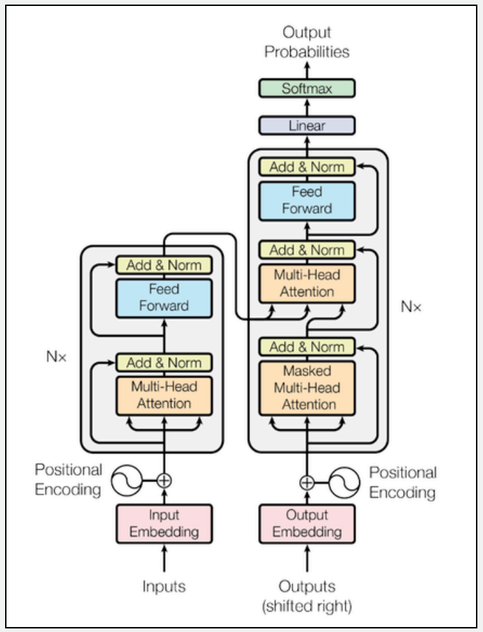
METHODOLOGY

```
Training/Validation/Testing
|
└── 00000
|   |
|   └── FLAIR
|   |   | Image-1.dcm
|   |   | Image-2.dcm
|   |   | ...
|   |
|   └── T1w
|   |   | Image-1.dcm
|   |   | Image-2.dcm
|   |   | ...
|   |
|   └── T1wCE
|   |   | Image-1.dcm
|   |   | Image-2.dcm
|   |   | ...
|   |
|   └── T2w
|   |   | Image-1.dcm
|   |   | Image-2.dcm
|   |   | .....
|
└── 00001
|   | ...
|
| ...
```

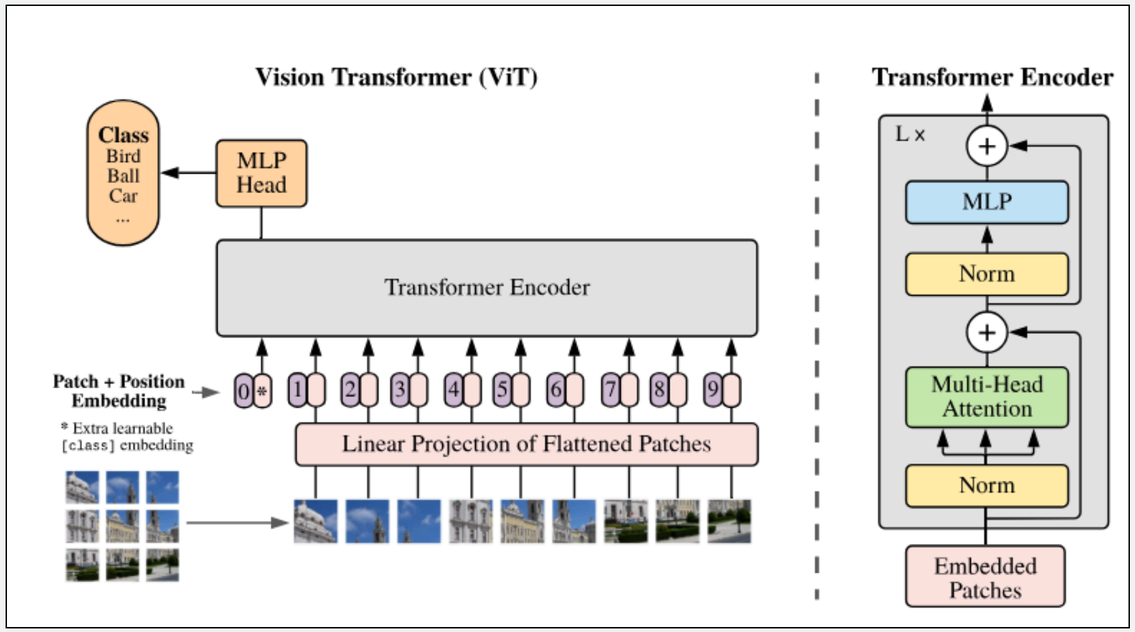
```
BraTS21ID,MGMT_value
00001,0.5
00013,0.5
00015,0.5
etc.
```



SWIN-T ARCHITECTURE

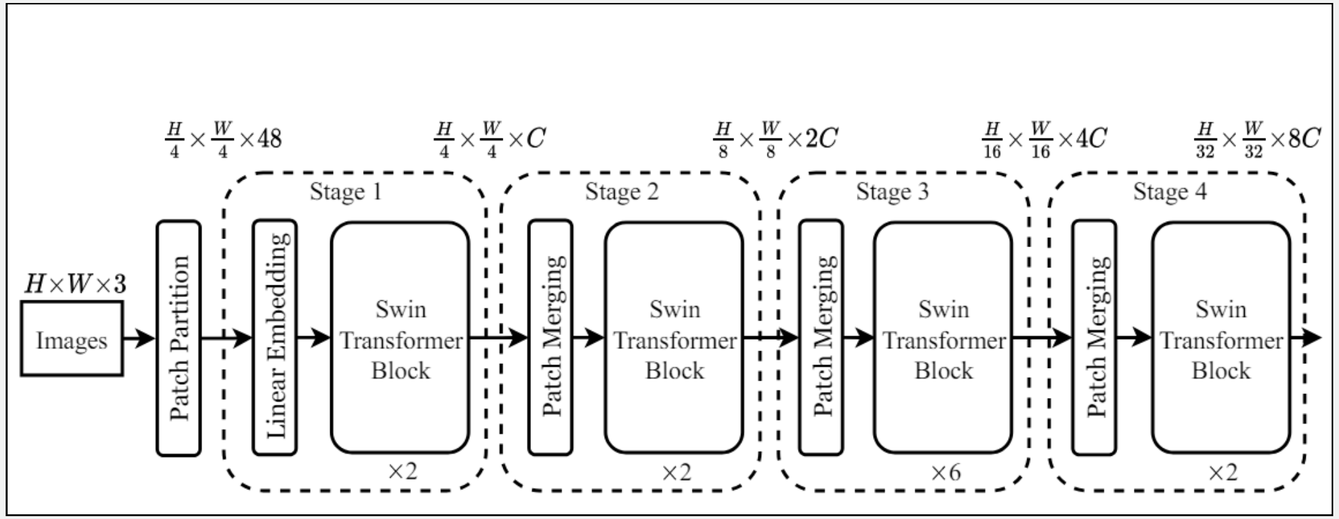


original transformer

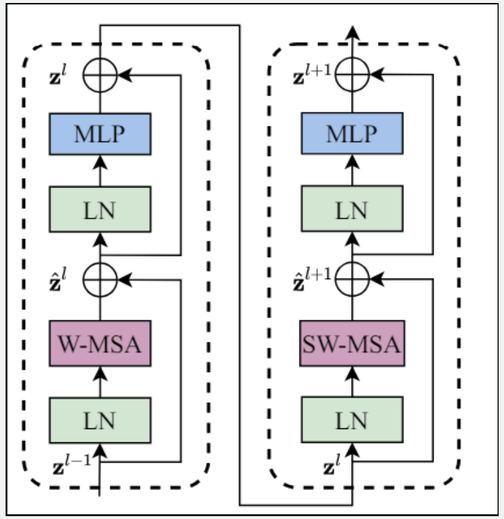


vision transformer

SWIN-T ARCHITECTURE



Architecture of Swin-T



Transformer Block

SWIN-T ARCHITECTURE

IMPLEMENTATION

- Convert the loaded image to sequence of patches
- Patch Embeddings
- Positional Encoding
- Transformer Encoder
- Token Classification
- Training and Fine-Tuning
- Evaluation

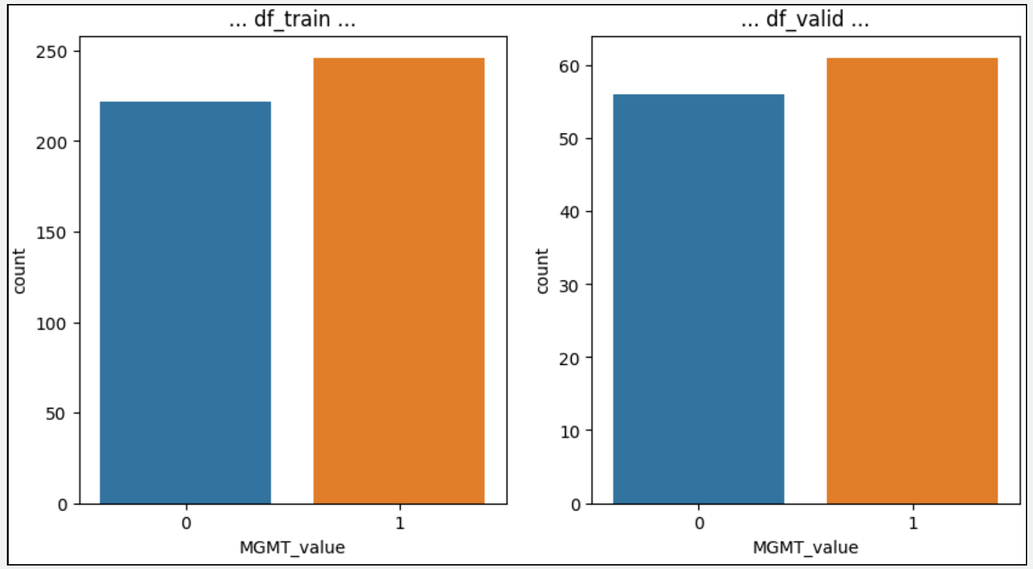
RESULTS

	BraTS21ID	MGMT_value
0	0	1
1	2	1
2	3	0
3	5	1
4	6	1
...	...	...
580	1005	1
581	1007	1
582	1008	1
583	1009	0
584	1010	0

585 rows × 2 columns

df

after splitting df in 80:20 ratio



df_train

df_valid

RESULTS

```
df_train['BraTS21ID_full'][481]
```

```
'00481'
```

```
df_train['FLAIR'][481]
```

```
'../input/rsna-miccai-brain-tumor-radiogenomic-classification/train/00481/FLAIR/'
```

dataframe manipulation for easy access

of the images from each BraTS21_ID folder

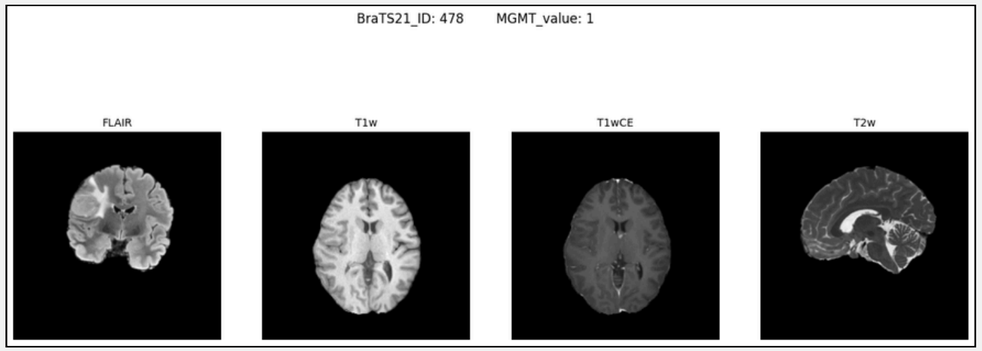
```
df_valid.head()
```

BraTS21ID	MGMT_value	BraTS21ID_full	FLAIR	T1w	T1wCE	T2w
563	0	00563	../input/rsna-miccai-brain-tumor-radiogenomic-...	../input/rsna-miccai-brain-tumor-radiogenomic-...	../input/rsna-miccai-brain-tumor-radiogenomic-...	../input/rsna-miccai-brain-tumor-radiogenomic-...
195	0	00195	../input/rsna-miccai-brain-tumor-radiogenomic-...	../input/rsna-miccai-brain-tumor-radiogenomic-...	../input/rsna-miccai-brain-tumor-radiogenomic-...	../input/rsna-miccai-brain-tumor-radiogenomic-...
28	1	00028	../input/rsna-miccai-brain-tumor-radiogenomic-...	../input/rsna-miccai-brain-tumor-radiogenomic-...	../input/rsna-miccai-brain-tumor-radiogenomic-...	../input/rsna-miccai-brain-tumor-radiogenomic-...
608	1	00608	../input/rsna-miccai-brain-tumor-radiogenomic-...	../input/rsna-miccai-brain-tumor-radiogenomic-...	../input/rsna-miccai-brain-tumor-radiogenomic-...	../input/rsna-miccai-brain-tumor-radiogenomic-...
21	0	00021	../input/rsna-miccai-brain-tumor-radiogenomic-...	../input/rsna-miccai-brain-tumor-radiogenomic-...	../input/rsna-miccai-brain-tumor-radiogenomic-...	../input/rsna-miccai-brain-tumor-radiogenomic-...

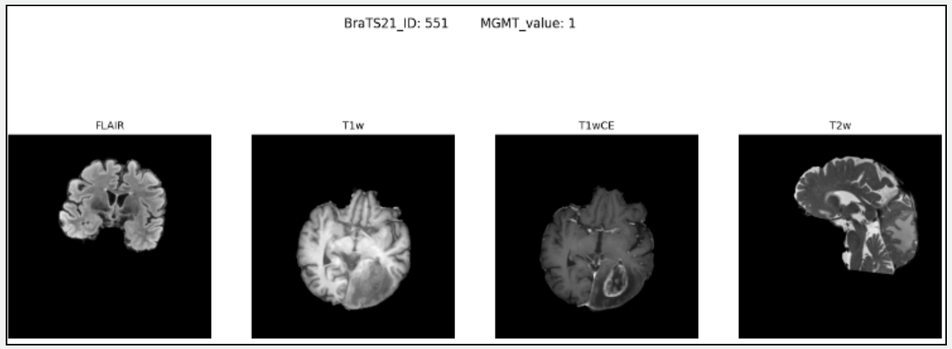
df_valid

RESULTS

Visualisation of different MRI types (FLAIR, T1w, T1wCE, T2w)

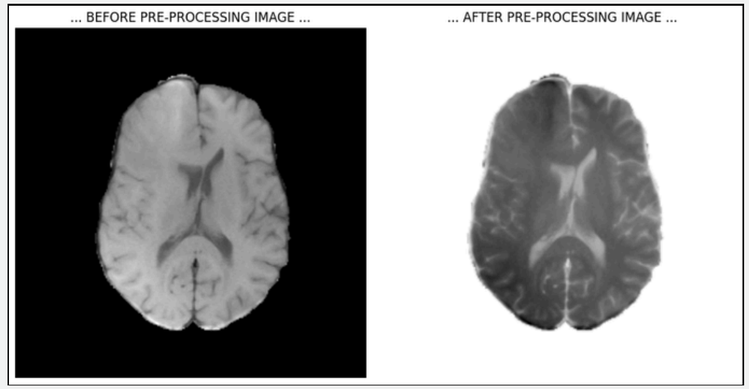


BraTS21_ID (478)



BraTS21_ID (551)

RESULTS




```
a = load_dicom_images_3d("00481")
print(a.shape)
print(np.min(a), np.max(a), np.mean(a), np.median(a))
```

```
(1, 256, 256, 64)
0.0 1.0 0.05419003281395742 0.00012306291639827978
```

apply voit_lut

RESULTS

Parametric values

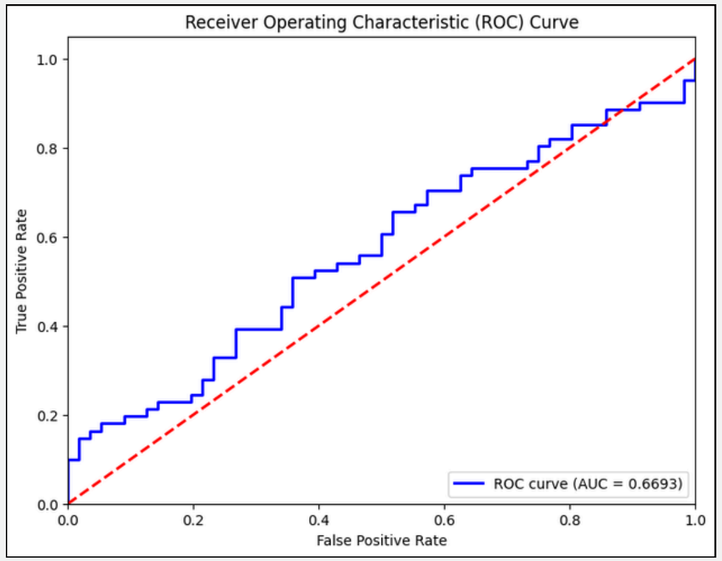
BraTS ipynb version	*Optimizer*	*Learning rate*	*Epochs*	*Patience*	*Batch size*	*Depth*	*Patch embedding*
(VIT Model) - version 2	*Adam*	*0.001*	*10*	*10*	*4*	*2*	*Linear projection*
(Swin VIT Model) - version 1	*Adam*	*0.001*	*3*	*3*	*1*	*12*	*Linear projection*
(Swin VIT Model) - version 4	*Adam*	*0.001*	*5*	*5*	*2*	*12*	*Conv2D projection*
(Swin VIT Model) - version 5	*Adam*	*0.0005*	*10*	*10*	*4*	*16*	*Conv2D projection*
(Swin VIT Model) - version 21	*Adam*	*0.0003*	*15*	*10*	*4*	*16*	*Conv2D projection*
(Swin VIT Model) - version 23	*Adam*	*0.0002*	*25*	*10*	*4*	*16*	*Conv2D projection*

Validation ensemble AUC and accuracy after prediction

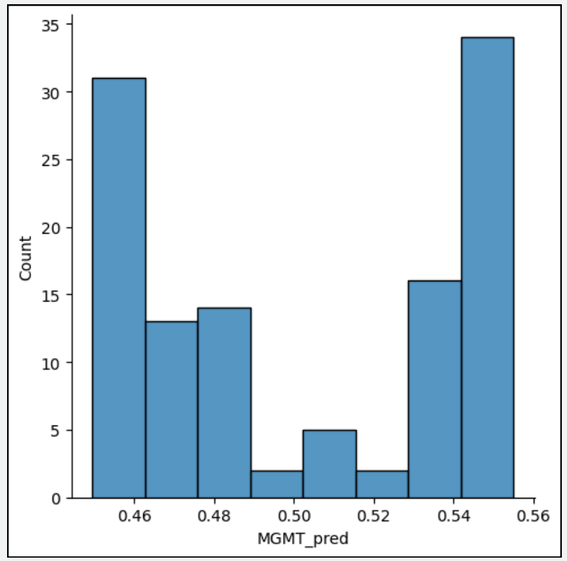
```
df_valid["MGMT_pred"] = 0
for m, mtype in zip(modelfiles,  mri_types):
    pred = predict(m, df_valid, mtype, "train")
    df_valid["MGMT_pred"] += pred["MGMT_value"]
df_valid["MGMT_pred"] /= len(modelfiles)

auc = roc_auc_score(df_valid["MGMT_value"], df_valid["MGMT_pred"])
print(f"Validation Ensemble AUC: {auc:.4f}")

predicted_labels = (df_valid["MGMT_pred"] >= 0.5).astype(int)
actual_labels = df_valid["MGMT_value"]
accuracy = accuracy_score(actual_labels, predicted_labels)
print(f"Validation Ensemble Accuracy: {accuracy:.4f}")
```

```
Predict: FLAIR-best.pth FLAIR (117, 8)
Predict: T1w-best.pth T1w (117, 8)
Predict: T1wCE-best.pth T1wCE (117, 8)
Predict: T2w-best.pth T2w (117, 8)
Validation Ensemble AUC: 0.6693
Validation Ensemble Accuracy: 0.6714
```

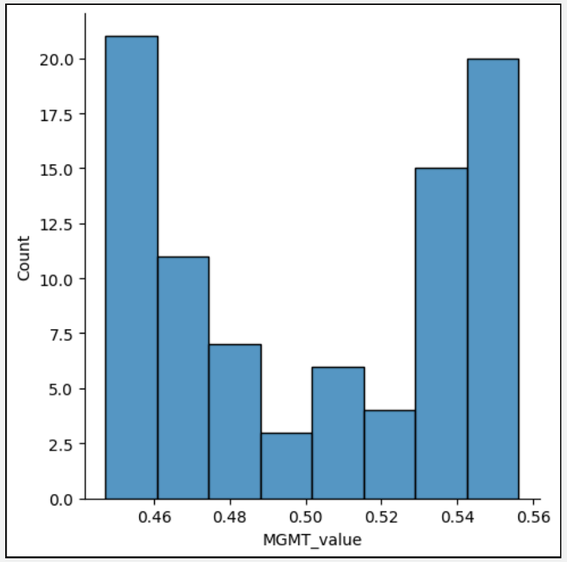
RESULTS



ROC curve obtained on df_valid



df_valid[MGMT_pred]



submission[MGMT_value]

RESULTS

Submission and Description	Private Score	Public Score
BraTS (VIT Model) - Version 2 Succeeded (after deadline) · 1mo ago · BraTS (VIT Model) | Versio...	0.44390	0.43208
BraTS (Swin VIT Model) - Version 1 Succeeded (after deadline) · 1mo ago · Notebook BraTS (Swin VIT...	0.58305	0.56421
BraTS (Swin VIT Model) - Version 4 Succeeded (after deadline) · 1mo ago · Notebook BraTS (Swin VIT...	0.59593	0.58694

Initial submissions and poor performance

Submission and Description	Private Score	Public Score
BraTS (Swin VIT Model) - Version 5 Succeeded (after deadline) · 1mo ago · Notebook BraTS (Swin VIT...	0.61586	0.62896
BraTS (Swin VIT Model) - Version 21 Succeeded (after deadline) · 13d ago · Notebook BraTS (Swin VIT ...	0.61503	0.61945
BraTS (Swin VIT Model) - Version 23 Succeeded (after deadline) · 13d ago · Notebook BraTS (Swin VIT ...	0.61125	0.62262

Best submissions sorted based on private scores

RESULTS

#	△	Team	Members		Score
1	▲ 1039	[Tunisia.ai] I love this competition			0.62174
2	▲ 595	Minh Phan			0.61881
3	▲ 676	Cedric Soares			0.61732
4	▲ 469	Leaky Folds			0.61562

Surpassed the fourth best submission by “Leaky Folds” with a private AUC score of 0.61586

NOVELTY

- Introduction of the latest computer vision techniques, such as Vision Transformers and their variants, in the field of brain tumor radiogenomics.
- Development of a transformer model that incorporates patch embedding and positional embedding layers from the Vision Transformer.
- Incorporation of Shifted Windows and a hierarchical structure from the Swin Transformer, resulting in a hybrid model that combines elements of both the Vision Transformer and Swin Transformer.

CONCLUSION

- Submission was evaluated based on the area under the ROC curve between the predicted probability and the observed target.
- Obtained an AUC score of 0.61586
- Predict genetic subtypes of glioblastoma from MRI scans and reduce invasive procedures to enhance patient outcomes.
- Represents a significant advancement in precision medicine for neuro-oncology

REFERENCES

- Radiogenomic classification for MGMT promoter methylation status
- Structural and Advanced Imaging in predicting MGMT promoter methylation
- RSNA - MICCAI Brain Tumor Radiogenomic Classification Challenge
- Vision Transformer Model
- EfficientNet3D Brain Tumor Radiogenomic Classification

THANK YOU

Presentation by M. Satya Sai Teja