RSNA-MICCAI BRAIN TUMOR RADIO GENOMIC MGMT CLASSIFICATION

(METHYLGUANINE METHYLTRANSFERASE)

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- About Cancer and Gene
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ABSTRACT

- Aim to study the effect of different preprocessing Brain Tumor MRI images
- MRI scan images are quite different from our traditional RGB images
- first preprocess the images data, then fit it to several baseline models to investigate the utility of AI

INTRODUCTION

- ☐ The brain is the most complex part of the human body.
- brain tumor is an uncontrolled development of brain cells in brain cancer
- Brain Tumors can be malignant or benign.

Benign Tumor	Malignant Tumor
Slow rate of growth	Rapid rate of growth
Non invasive (Capsule covered)	Invasive (No capsule) Highly spreadable
Metastasis – Absent	Metastasis – Present (Spread in organs)
Hemorrhage and Necrosis – Absent	Hemorrhage and Necrosis - Present

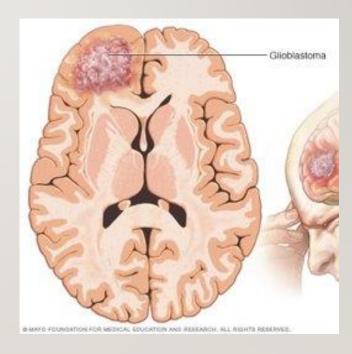
WHAT IS GLIOBLASTOMA?

☐Glioblastoma is an aggressive type of cancer that can occur in the brain.

(Grade IV tumor GBM)

☐ Frontal Lobe is most common but can occur Brainstem, Cerebellum

- **☐**Treatments:
 - **□** Surgery
 - Radiation
 - Chemotherapy



MGMT PROMOTER METHYLATION?

- MGMT Methylguanine Methyltransferase it is an enzyme which removes the molecule to synthesize chemo drug, helps in DNA repair for cancer cell
- Methylated MGMT associated with improved outcome in glioblastoma
- a favorable prognostic factor and a strong predictor of responsiveness to chemotherapy.
- Help in therapy decision making

MOTIVATION

- Currently, genetic analysis of cancer requires surgery to extract a tissue sample.
- Then it takes **several weeks** to determine the genetic characteristics of the tumor.
- An automatic model to detect the presence of MGMT(value) promoter methylation might help faster treatment and avoid surgery for test



Images are in DICOM format.

DATASET



Three cohorts of multi-parametric MRI (mpMRI) scans:

- 1. Training Data
- 2. Validation Data
- 3. Test Data

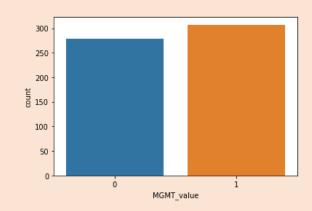
- ▼ □ 00000
 - ▶ □ FLAIR
 - ▶ 🗖 T1w
 - ▶ □ T1wCE
 - ▶ 🗖 T2w
- ▶ □ 00002
- ▶ □ 00003

Four subfolders within cohorts:

- 1. Fluid Attenuated Inversion Recovery (FLAIR)
- 2. T1-weighted pre-contrast (T1w)
- 3. T1-weighted post-contrast (T1WCE)
- 4. T2-weighted (T2)

PREDICTION OF GENETIC CHARACTERISTIC OF GLIOBLASTOMA

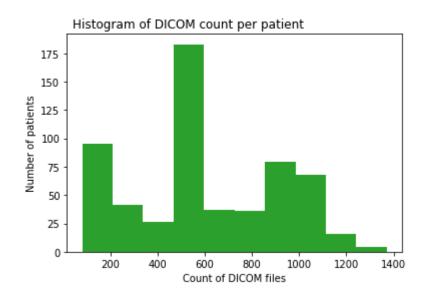
- □The MGMT promoter methylation status data is defined as a binary label (0: unmethylated, 1: methylated)
- □307 Positive Cases (Methylated)
- □278 Negative Cases (Unmethylated)
- □585 Total Patients

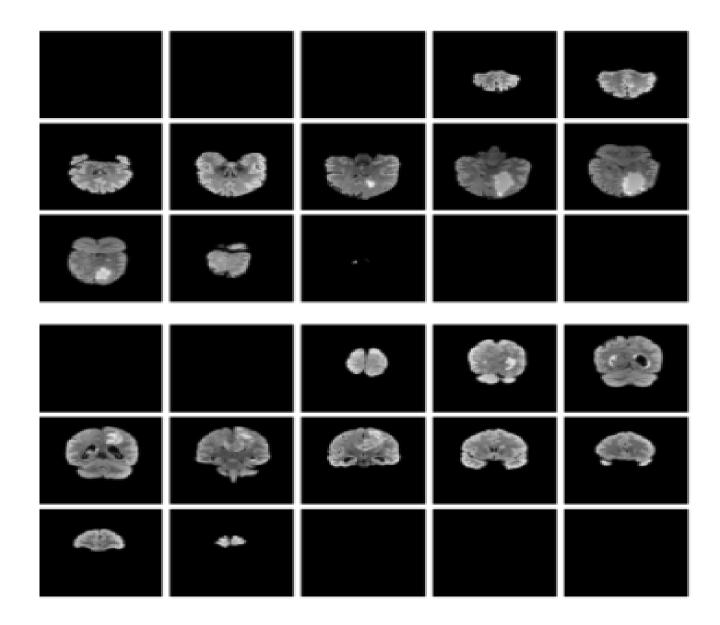


	BraTS21ID	MGMT_value
2	3	0
6	9	0
10	17	0
11	18	0
12	19	0
569	837	0
571	839	0
579	1004	0
583	1009	0
584	1010	0
278 r	ows × 2 col	umns

	BraTS21ID	MGMT_value	
0	0	1	
1	2	1	
3	5	1	
4	6	1	
5	8	1	
577	1002	1	
578	1003	1	
580	1005	1	
581	1007	1	
582	1008	1	
307 rows × 2 columns			

Each patient has several scans for each MRI Type (4 types).





EXPLORATORY DATA ANALYSIS

87 Patients have Similar count of images in subfolder

Total number of patients: 585

Total file count: 348641

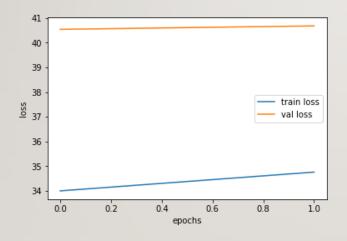
	BraTS21ID	MGMT_value	imfolder	path	FLAIR_count	T1w_count	T1wCE_count	T2w_count	allsame
0	0	1	00000	/input/rsna-miccai- brain-tumor- radiogenomic	400	33	129	408	False
1	2	1	00002	/input/rsna-miccai- brain-tumor- radiogenomic	129	31	129	384	False
2	3	0	00003	/input/rsna-miccai- brain-tumor- radiogenomic	129	33	129	408	False
3	5	1	00005	/input/rsna-miccai- brain-tumor- radiogenomic	400	28	129	424	False
4	6	1	00006	/input/rsna-miccai- brain-tumor- radiogenomic	129	32	129	408	False
580	1005	1	01005	/input/rsna-miccai- brain-tumor- radiogenomic	23	23	23	23	True
581	1007	1	01007	/input/rsna-miccai- brain-tumor- radiogenomic	124	124	124	124	True

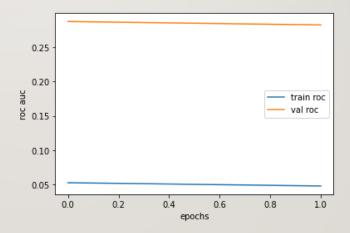
BASELINE MODEL

- A simple solution
 - For each patient, we consider 4 sequences (FLAIR, TIw, TIGd, T2), and for each of those sequences take a slice randomly.
 - Use CNN to perform Classification
- Convolutional Neural Network
 - ResNet50
 - EfficientNet

RESULTS WITH CNN

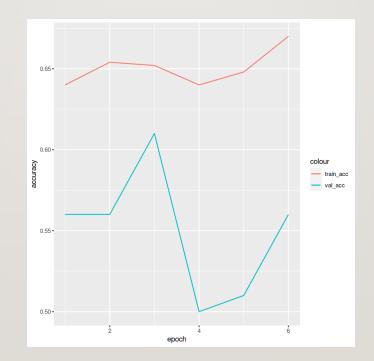
Very poor results – Obvious with very few images

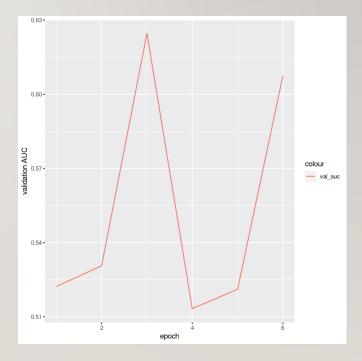




RESULTS WITH CNN – WITH MORE IMAGES

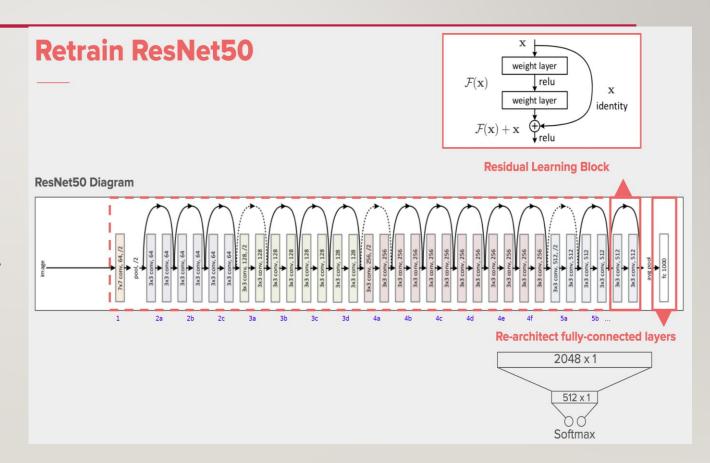
- Still poor results
- Validation Accuracy ~55%
- Training Accuracy ~ 65%
- Validation AUC ~ 0.55



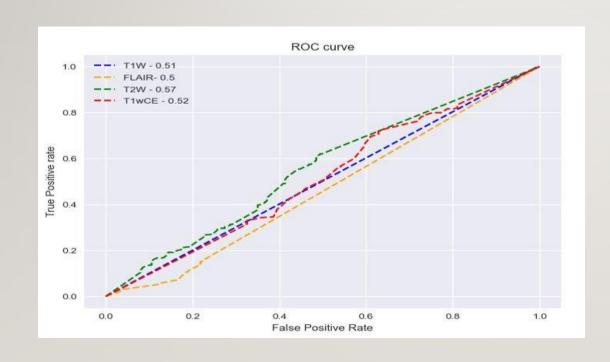


RESNET50

- Deep Learning model for image classification of the Convolutional Neural Network.
- 50 layers deep
- Deep neural networks are susceptible to vanishing gradients
- Resnet used skip connection to propagate information over layers



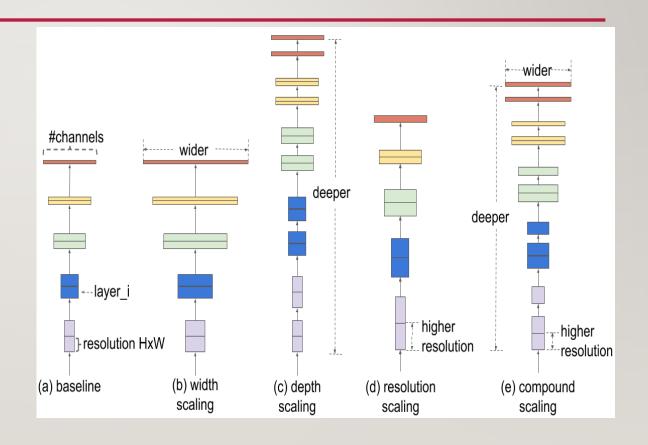
EXPERIMENTAL ANALYSIS [RESNET50]





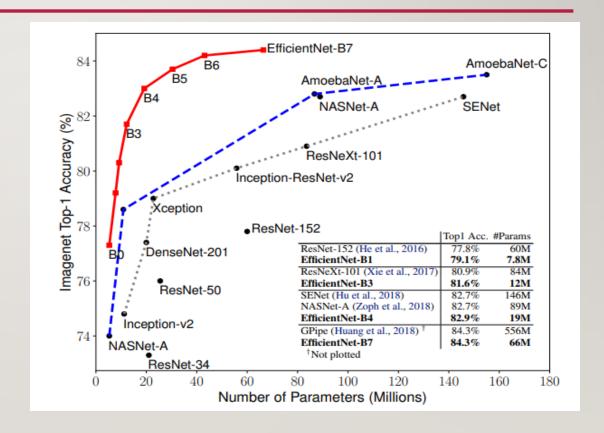
EFFICIENTNET

- EfficientNet, as the name suggests are very efficient computationally.
- Achieved state of art result on ImageNet dataset which is 84.4% top-I accuracy.
- Model scaling is about scaling the network depth (more layers), width (more channels per layer), resolution (input image)

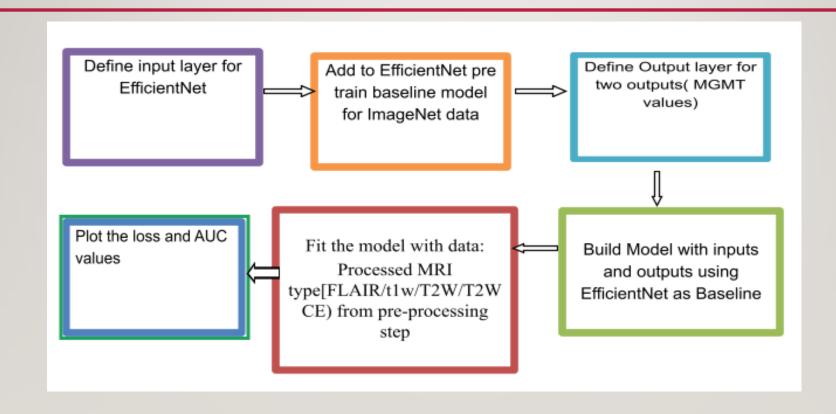


WHY EFFICIENTNET?

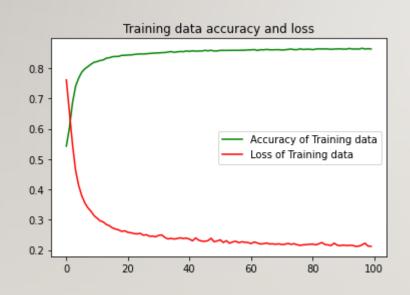
- EfficientNets has large activations which cause a larger memory footprint because
- Use similar FLOPs as ResNet to give better Accuracy
- FLOPs, simply means the total number of floating point operations required for a single forward pass.
 The higher the FLOPs, the slower the model and hence low throughput.

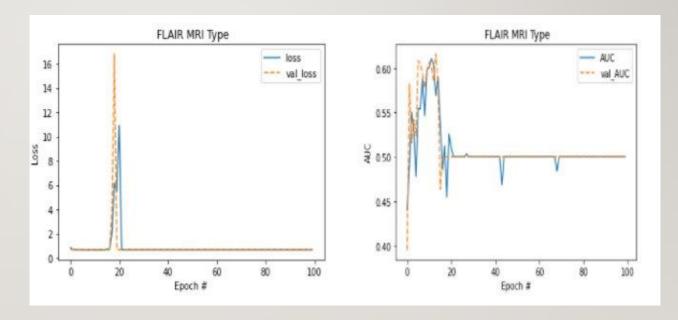


WORKFLOW OF DEEP LEARNING MODEL ARCHITECTURE

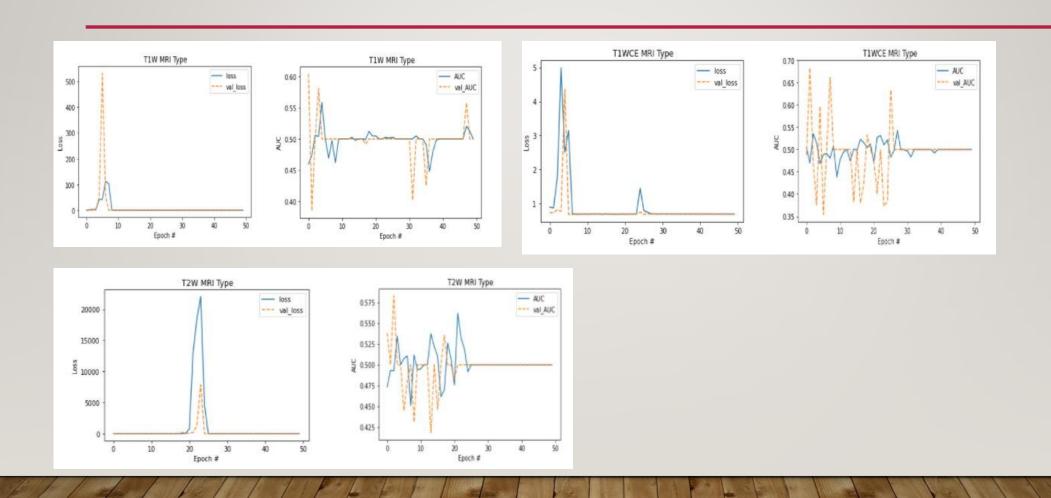


EXPERIMENTAL ANALYSIS [EFFICIENTNET]





EXPERIMENTAL ANALYSIS[EFFICIENTNET]



TEST RESULTS

MRI Type	Test Accuracy	Test AUC
FLAIR	0.7551	0.458
TIw	0.822	0.29
TIGd	0.59	0.91
T2W	0.9125	0.7842

CONCLUSION AND FUTURE WORK

Conclusion

- MRI images are very different from non-medical images
- Pre-trained models for ImageNet may not be as good as baseline
- Unique pre processing may require

Future Work

- Additional, higher quality pre-processed data
- Apply sequence model like LSTM along with CNN
- Use VGG 16 /19 DenseNet or other Pretrained Models

REFERENCES

- The RSNA-ASNR-MICCAI BraTS 2021 Benchmark on Brain Tumor Segmentation and Radiogenomic Classification (arxiv.org/pdf/2107.02314.pdf)
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THANKYOU