Multi-Class Brain Tumor Recognition through MSENet

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AGENDA

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INTRODUCTION

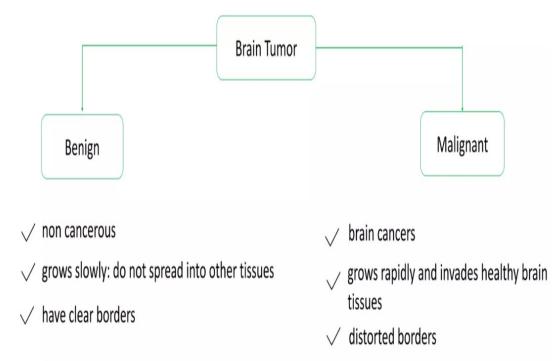
Brain Tumors are masses of unwanted cells that have grown in the brain area and impact the central nervous system.

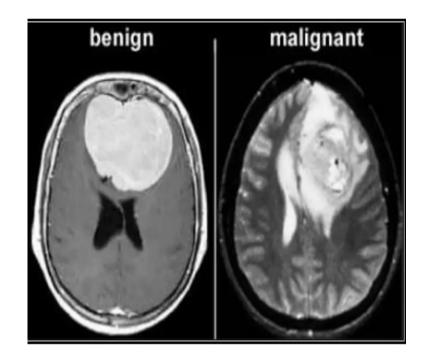
These tumors are classified as benign or malignant depending on their effect.

Benign Tumors are safe and do not spread outside of the growing site.

Malignant Tumors are particularly dangerous since they can quickly apply to surround areas, if left untreated, can lead to death. These malignant tumors are further classified as Meningioma, Glioma, and Pituitary tumors.

INTRODUCTION





MOTIVATION

- Brain tumor classification is one of the most challenging problems in Neuroimaging.
- Manual diagnosis of various tumor variants includes screening Magnetic Resonance (MR) imaging scans of the brain for the presence of a tumor and evaluating the tumor's severity level.
- Any mistake made by radiologists during tumor diagnosis to identify tumor presence or detect tumor severity level costs human life.
- Artificial intelligence and deep learning innovations have made it possible to complete various medical image-processing tasks, such as diagnosing brain cancers.

OBJECTIVE

- To build a simple architecture based on deep learning that results in solid generalization without needing much pre-processing.
- Convolution feature descriptors from different deep pre-trained models are employed to represent tumor images effectively and are input into the proposed MSENet.
- The proposed Multi-modal Squeeze and Excitation model (MSENet) receives various representations of a given tumor image, learns from beginning to end, and accurately predicts tumor severity.



- The MSENet's squeeze and excitation blocks allow the model to prioritize tumor regions while ignoring the rest of the image, acting as an attention mechanism in the model.
- The proposed model has been evaluated on a benchmark brain tumor dataset from the Figshare repository.

Proposed MSENet Model

Multi-modal Squeeze-and-Excitation network (MSENet)

- Proposed MSENet receives vectorized representations (Feature Maps) of Brain tumor images derived from two different deep pre-trained models.
- **MSENet** manages and learns from those two independent brain tumor image representations and produces more generalized predictions.
- Squeeze and excitation (SE) blocks are added to enable the model to pay particular attention to the features that define tumor regions.

Multi-modal Feature Preparation

The process of multi-modal feature preparation involves several steps,

- 1. Data collection and preprocessing
- 2. Feature extraction
- 3. Feature normalization
- 4. Feature fusion
- 5. Feature selection

Multi-modal feature preparation is an important step in ML & DL applications that involve heterogeneous data sources, as it allows for a more comprehensive and representative feature representation of the data, which can lead to improved accuracy and performance of the machine learning algorithm.

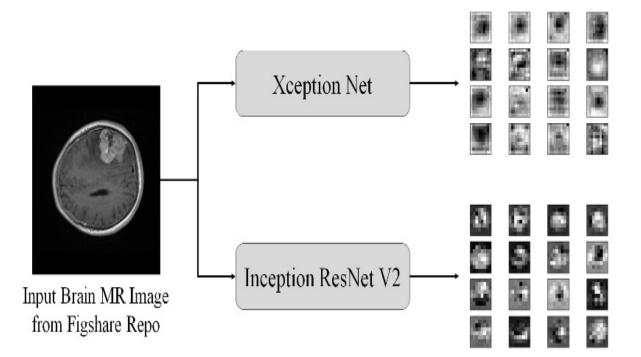
Feature Extraction:

Proposed model MSENet uses two different pre-trained deep CNNs, **XceptionNet** and **InceptionResNetV2 (IRV2)** to extract features.

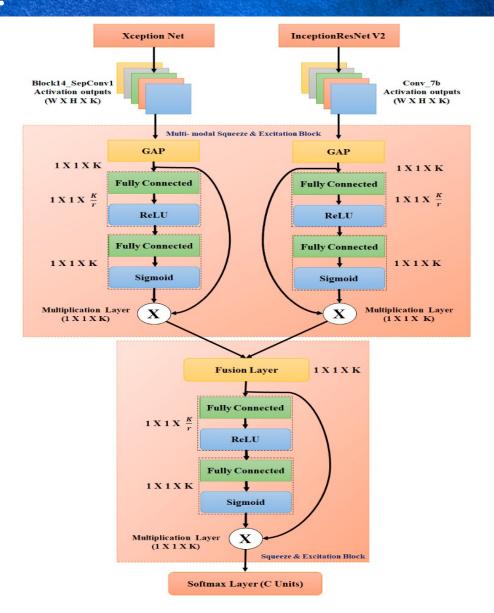
Why Pre-trained Models?

- Our dataset is very small which may not produce generalized results.
- The pre-trained models are learned using the ImageNet dataset (1.4M images), the weights of these pre-trained models are used to extract feature maps, which is also known as Transfer Learning.

- Feature sets from two separate deep CNNs can be used as input to the proposed MSENet.
- Each local descriptor is of dimension (W × H × K).
- The proposed model obtains one such representation from the Xception network and another from the IRV2 network and offers multi-modal feature representations of tumor images as input to the model MSENet.







Squeeze and Excitation Blocks for Attention

Squeeze and Excitation (SE) blocks are a type of attention mechanism commonly used in convolutional neural networks (CNNs) for image classification tasks.

The main objective of SE Blocks is to capture the channel-wise dependencies in the feature maps of the CNNs by adaptively weighting the importance of each channel.

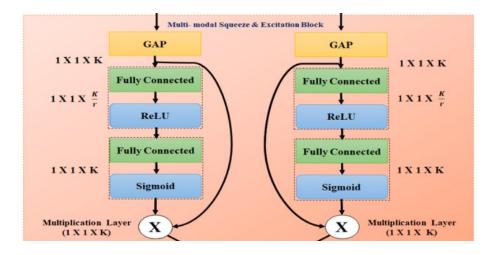
The SE block consists of two primary operations: **squeezing** and **exciting**.

Squeezing block, feature maps by from pre-trained models ExceptionNet & IRv2Net are taken as input and global average pooling is applied.

This reduces the spatial dimensions of the feature maps to 1x1 while preserving the channel dimension.

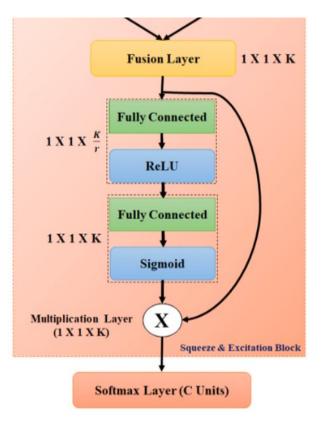
Exciting block, the resulting 1x1 feature map is fed through a set of fully connected layers that learn channel-wise dependencies and produce a set of scaling coefficients.

These coefficients are then used to rescale the original feature maps, emphasizing the important channels while suppressing the unimportant ones.



Fusion Layer

- The two weighted feature descriptors generated simultaneously from SE blocks are aggregated using a fusion layer to get a single consolidated representation.
- This merged representation is now passed through another SE block to ensure that the network learns to selectively emphasize informative features while suppressing less useful features.
- The final softmax layer of the model serves as a classification layer and produces the type of the tumor present in the input MR images as output.



Why SE Blocks? Why Not CNN's?

- A standard neural network model treats each input descriptor with equal priority, which may not be appropriate for such tasks as medical image processing.
- Providing a strong orientation to features representing tumor regions will contribute a great deal to the final classification of tumor type.
- Squeeze and Excitation (SE) block will resolve this issue, which gives different degrees of focus to different local descriptors of the tumor images.
- Each SE block is a combination of a squeeze and an excitation operation.

Input: Let D be the dataset of Contrast Enhanced-MRI brain images from Figshare repository, where $D = \{(Xi, yi)\}$ 3062 and yi is the severity level i=1 of brain tumor associated with Xi.

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Output: yi \in {0, 1, 2} representing Meningioma, Glioma, and Pituitary brain tumors.

Algorithm

Step 1: Pre-Processing: Each image Xi in dataset D is pre-processed such that they are compatible (re-sized) with deep pre-trained models, i.e., for Xception and Inception-ResNet v2.

Step 2: Feature Extraction: Each pre-processed image is passed through pre-trained Xception and IRV2 models to get two sets of 2-D feature representations as follows:

F1 \leftarrow Features from the first depth-wise separable convolution layer of block-14 of the Xception network.

F2 \leftarrow Features from the first convolution layer of the seventh block of IRV2.

Where $F1 \in R\{16 \times 16 \times 1536\}$ and $F2 \in R\{14 \times 14 \times 1536\}$. Now, each $xi \in D$ has two high-dimensional representations F1 and F2.

Step 3: Dataset Partition: Preparing the dataset, D, for Split the dataset D into train and test partitions, 80 and 20 % respectively.

Step 4: Model training and evaluation: Supply the training data's high dimensional feature representations F1 and F2 to the proposed MSENet and train the model. Get tumor severity predictions for all the samples, xi in Di.

Compute all the required performance measures by comparing the model predictions with ground truth labels.

Step 5: Evaluating Model Performance:

Repeat Step - 3 for $I \in \{1, 2, 3, 4, 5\}$ and obtain the model predictions for the split Di.

Why only MSENet?

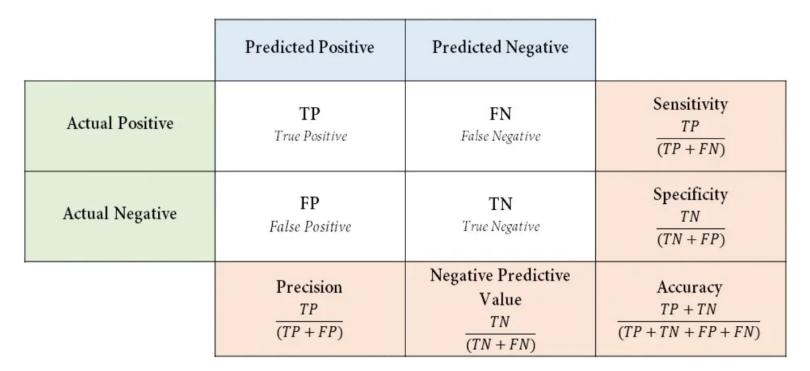
- No need of pre-processing steps. Resize input image 512 X 512 X 3.
- Segmentation and Augmentation Techniques are not at all used.
- Use of Transfer Learning mechanism made model to generalized predictions.
- Used Attention Mechanism which made the model focus on the tumor regions rather than giving equal importance to whole image.

Dataset Summary

- Brain Tumor Dataset was collected from the figshare repository.
- This dataset includes 3064 images of 233 patients.
- Each image in the dataset represents one of the brain tumor (Meningioma, Glioma, and pituitary) types.

Tumor Type	# Patients	MRI view	# Images	Total
		Axial	209	
Meningioma	82	Coronal	268	708
		Sagittal	231	
		Axial	494	
Glioma	89	Coronal	437	1426
		Sagittal	495	
		Axial	291	
Pituitary	62	Coronal	319	766
-		Sagittal	320	
Total	233	-	3064	3064

Evaluation Metrics



Confusion Matrix Metrics

ClassWise Model Performance

	precision	recall	f1-score	support
Meningima Glioma Pituitary	0.9143 0.9577 0.9684	0.9014 0.9510 0.9892	0.9078 0.9544 0.9787	71 143 93
accuracy macro avg weighted avg	0.9468 0.9509	0.9472 0.9511	0.9511 0.9470 0.9510	307 307 307

Model Comparision

SNo	Approach	Accuracy
1	Intensity Histograms $+$ SVM	87.54
2	GLCM + SVM	89.72
3	CNN + Fully connected NN	91.43
4	BoW + SVM	91.28
5	Statistical Features + BPNN	91.90
6	Capsule Network	90.89
7	CNN + Augmentation	94.39
8	Fine tuning VGG16	94.65
9	Two-Channel DNN	94.23
10	Fine tuning VGG19 (B1-B6)	94.82

MSENet Model Performance

Accuracy: 95.11 Macro Precision: 94.68 Macro Recall: 94.72 Macro F1-Score: 94.7 Quadratic Kappa Score: 93.55

DEMONSTRATION



Appliaction UI & Technology

- Built a web application using HTML/CSS, JavaScript for frontend.
- Python Flask framework for Backend.
- Sqlite for DB which is easily integrated with Flask Framework.
- MSENet was integrated with this Web Application and make generalized predictions.
- Demo Link: <u>http://127.0.0.1:5000/</u> (Application Running Locally on Port 5000)

Conclusion

- Main Objective is to build a robust model with no pre-processing steps and without using segmentation and augmentation techniques.
- The proposed MSENet model performance was built and evaluated using the Brain Tumor dataset from Figshare Repository.
- MSENet model outperforms all the existing models by achieving an accuracy of 95.11%.
- Due to less computational power this model is built and evaluated using small scale unbalanced dataset.
- To achieve precise results we need to use a larger dataset and also use some other Granular computing methods for pre-processing those unbalanced data.

Questions & Suggestions?



THANK YOU

