Brain Tumor Detection using Magnetic Resonance Imaging and Machine Learning

CMPE 351 | Machine Learning Design Project Final Presentation

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01 Introduction



Background

Overview

Early diagnosis of brain tumors is important for patient prognosis

Magnetic resonance imaging (MRI) is used for **glioma** diagnosis

Currently-adopted practices

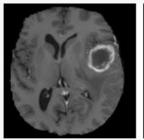
Manual segmentation of brain tumors by radiologists

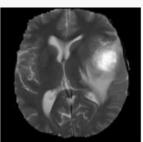
LIMITATIONS

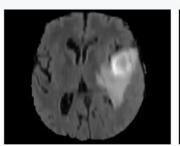
Time-consuming and resource-heavy

Inter- and intra-rater variability → fragile replicability

Complicated data











Background

Automatic segmentation

Convolutional neural networks (CNN) used for automatic segmentation

Focus on network architecture, e.g. 4D vs. 2D architectures

Current progress

Mature task propelled by BraTS competition

Research now focuses on reducing computational complexity and combining CNNs with other classification techniques

REMAINING CHALLENGES

Reducing computational complexity for usage in clinical settings

Increasing accuracy of segmentation due to irregularity of tumor shapes, sizes, and boundaries



Research Questions

RQ 1: How can transfer learning be effectively utilized?

RQ 2: Can pre-processing be reduced and what are the implications?

RQ 3: Can model accuracy be sustained with lower computational complexity?



02 Dataset



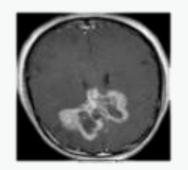
Dataset

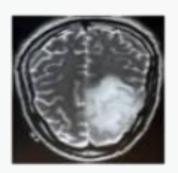
Overview

Open-source dataset from Kaggle provided by Navoneel Chakrabarty and his research in Brain MRI Images for Brain Tumor Detection

Contains 253 T1-weighted images; 98 healthy scans and 155 scans contain lesions

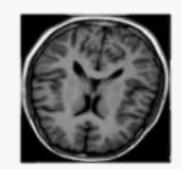
Since the dataset is small, data augmentation is used to create more images and solve the imbalance between tumorous and non-tumorous images





CONTAINS TUMOR

155 images





DOES NOT CONTAIN TUMOR

98 images



Summary Statistics

98 healthy scans and 155 tumorous scans

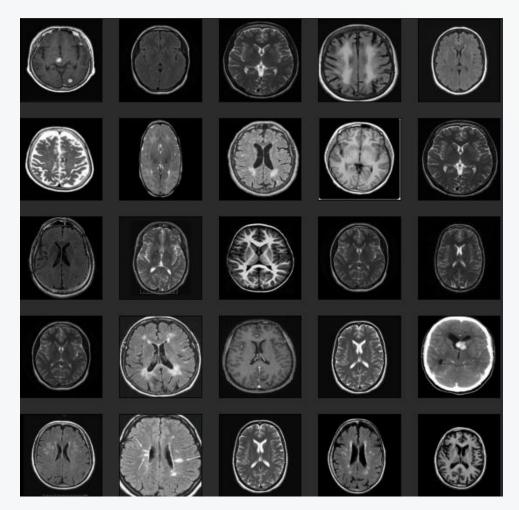
All the files are .jpg images

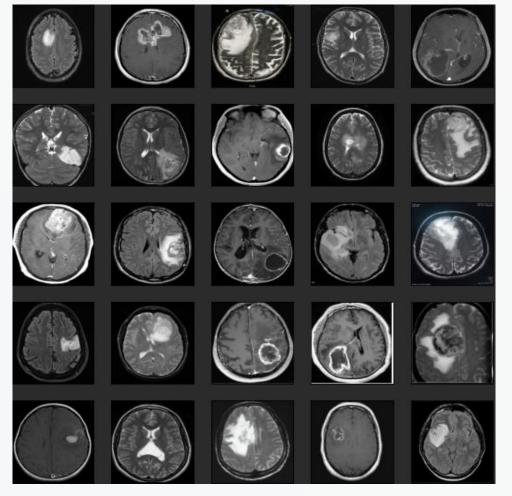
All images have 3 channels

	MIN HEIGHT	MEAN HEIGHT	MAX HEIGHT	MIN WIDTH	MEAN WIDTH	MAX WIDTH	MEAN CHANNELS	
Healthy	168	342.23	1080	150	343.16	1920	3.0	
Tumorous	173	413.70	1427	178	361.24	1275	3.0	



Data Exploration







Tumorous Set

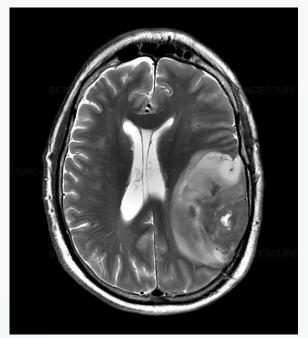
03 Methodology



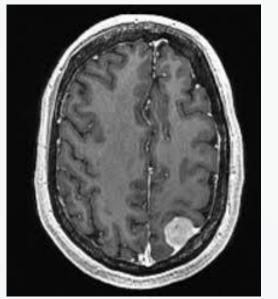
Data Preprocessing

Size Differences and Wasted Space

- Images in the dataset do not have the same dimensions
- CNNs input layer in Keras required images to be of the same size (height, width, channels)
- A significant portion of each image contains insignificant data
- The CNN only needs information about the brain itself, not the black border



y162.jpg



y56.jpg

IMAGE

Dimensions	1059x1200
Width	1059 pixels
Height	1200 pixels

IMAGE

Dimensions	211x239
Width	211 pixels
Height	239 pixels



Data Preprocessing

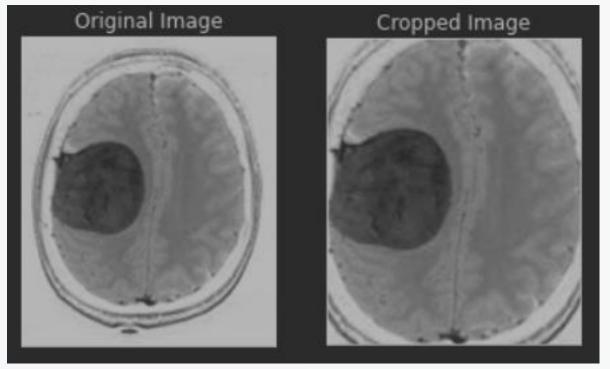
Size Differences and Wasted Space

Average Image Dimensions

	Height	Width	Channels
Healthy	342.23	343.16	3.0
Tumorous	412.70	361.24	3.0

- Brain contour: four most extreme points in each corner
- Cropped based on brain contour

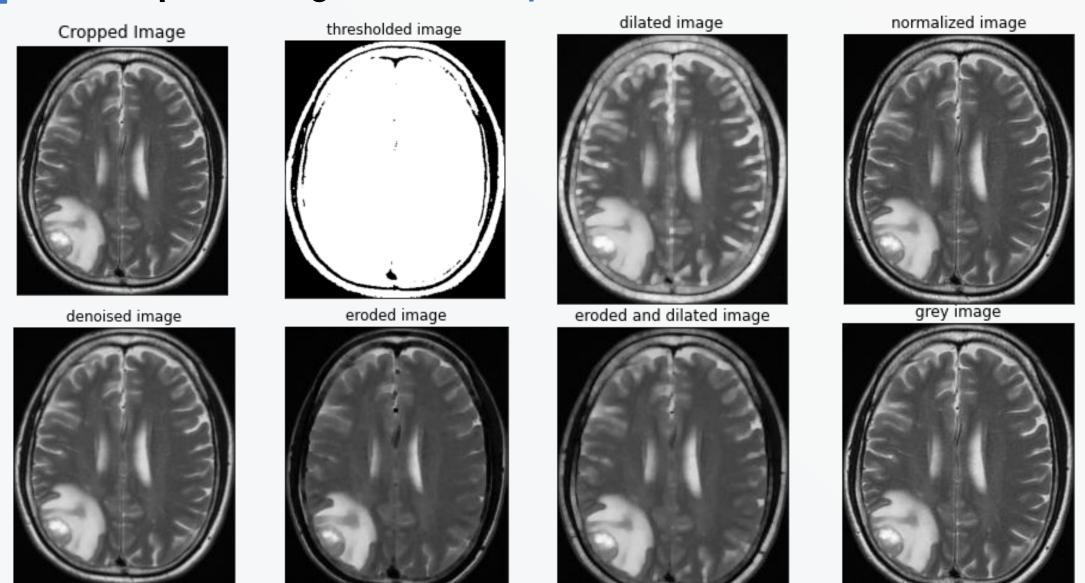
Image Cropping



Y1.jpg before and after applying the cropping technique



Data Preprocessing: Other techniques

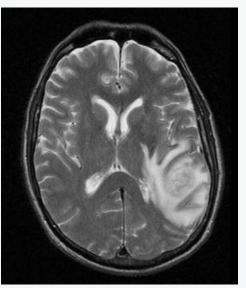




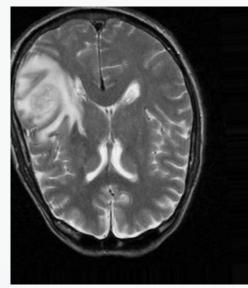
Feature Engineering

Data Augmentation

- 61% of images are tumorous and 39% of images are healthy
- Create 9 new images for each healthy scan
- Create 6 new images for each tumorous scan
- rotation_range: range for random rotations (in degrees)
- width_shift_range: shift, fraction of total width
- height_shift_range: shift, fraction of total height
- **shear_range**: shear angle in counter-clockwise direction in degrees
- **brightness_range**: range for randomly choosing a brightness shift
- horizonal_flip: randomly flips an image horizontally
- vertical_flip: randomly flips an image vertically
- **fill_mode**: how to fill points outside the input, but within the image boundary



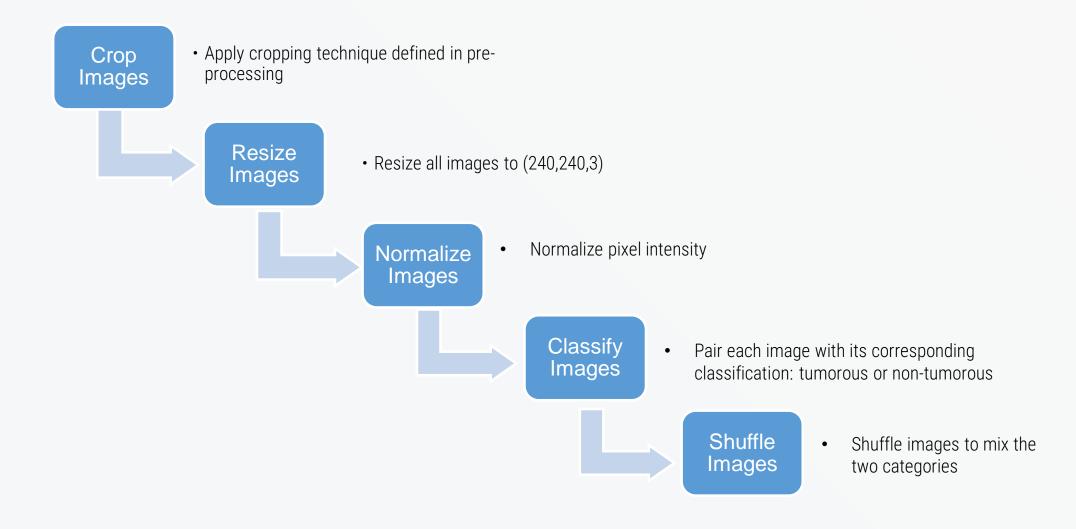




Y71 Augmented

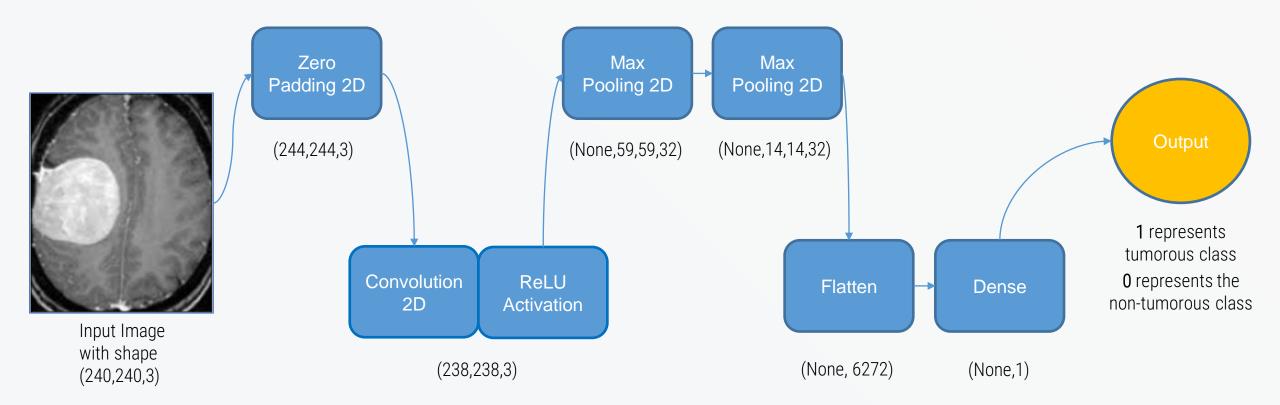


Data Loading and Splitting





Neural Network Architecture





Question 1 Self-taught Case 1 How can transfer learning be effectively utilized? Learning No labeled data in source domain **Inductive Transfer** Learning Labeled data are available in a Labeled data are available in a target source domain domain Source and target Case 2 Multi-task tasks are learnt simultaneously learning Transfer Learning Labeled data are available only in a source domain Assumption: Transductive No labeled data in both Domain different domains Transfer source and target domain Adaptation but single task Learning Assumption: single Unsupervised Sample selection domain and single

Transfer Learning

task

bias/covariance

shift

With image dimensions (340, 340, 3)

Question 2

3. Normalization

4. Denoise

Can preprocessing be reduced and what are the implications?

	oproceeding be read	ioca and imat are the improductions.
	Pre-processing step(s):	Justification:
	1. No pre-processing	Use as a baseline for comparison
	 Cropping Dilation 	Reduce memory required for preprocessing
	 Crop Dilation Normalization 	Normalize pixel values for memory considerations
	 Crop Dilation Denoise 	Eliminate artifacts and noise from images to improve true tumour detection
	 Crop Dilation Denoise Normalization 	 Normalize pixel values after denoising to avoid losing information about artifacts and noise
	1. Crop 2. Dilation	 Normalize pixel values before denoising for memory considerations

With cropping and normalization

Image Dimensions
(140, 140, 3)
(240, 240, 3)
(340, 340, 3)
(440, 440, 3)



Question 3

Can model accuracy be sustained with lower computational complexity?

1 Convolutional Layer and Batch Size of 32

Epochs	Acc	Loss	Time	
5				
10				
15				
20				

1 Convolutional Layer and 10 Epochs

Batch Size	Acc	Loss	Time	
32				
64				

4 Epochs and Batch Size of 32

Convolutional Layers	Acc	Loss	Time
1			
2			



04 Results



RQ2 Results

4. Denoise

	Pre-processing step(s):	Justification:	Acc	Loss	Time
	1. No pre-processing	Use as a baseline for comparison	Model: 0.8672 Validation: 0.7629	Model: 0.3042 Validation: 0.6508	0:12:59.9
	 Cropping Dilation 	 Reduce memory required for preprocessing 	Model: 0.9072 Validation: 0.8362	Model: 0.2064 Validation: 0.5987	0:12:37.5
With image	 Crop Dilation Normalization 	 Normalize pixel values for memory considerations 	Model: 0.9547 Validation: 0.8621	Model: 0.1442 Validation: 0.3361	0:14:38.5
dimensions (340, 340, 3)	 Crop Dilation Denoise 	 Eliminate artifacts and noise from images to improve true tumour detection 	Model: 0.9002 Validation: 0.7974	Model: 0.2312 Validation: 0.6396	0:13:53.3
	 Crop Dilation Denoise Normalization 	 Normalize pixel values after denoising to avoid losing information about artifacts and noise 	Model: 0.9271 Validation: 0.8793	Model: 0.2053 Validation: 0.3175	0:13:39.2
	 Crop Dilation Normalization 	 Normalize pixel values before denoising for memory considerations 	Model: 0.9406 Validation: 0.8750	Model: 0.1549 Validation: 0.2906	0:14:08.3



RQ2 Results (Continued)

With Cropping and Normalization

Image Dimensions	Acc	Loss	Time
(140, 140, 3)	Model: 0.8656 Validation: 0.8017	Model: 0.3236 Validation: 0.4038	<mark>0:02:26.4</mark>
(240, 240, 3)	Model: 0.9212 Validation: 0.8707	Model: 0.2146 Validation: 0.2828	0:12:17.6
(340, 340, 3)	Model: 0.9498 Validation: 0.8836	Model: 0.1475 Validation: 0.3196	0:13:21.4
(440, 440, 3)	Model: 0.9504 Validation: 0.8750	Model: 0.1461 Validation: 0.3433	0:42:5.4



RQ3 Results

1 Convolutional Layer and Batch Size of 32

Epochs	Acc	Loss	Time
5	Model: 0.8721 Validation: 0.8362	Model: 0.3050 Validation: 0.3867	0:7:26.9
10	Model: 0.9498 Validation: 0.8836	Model: 0.1475 Validation: 0.3196	0:13:21.4
15	Model: 0.9892 Validation: 0.8276	Model: 0.0695 Validation: 0.5006	0:20:15.9
20	Model: 0.9978 Validation: 0.8879	Model: 0.0224 Validation: 0.3900	0:27:49.5

1 Convolutional Layer and 10 Epochs

Batch Size	Acc	Loss	Time
32	Model: 0.9342 Validation: 0.8578	Model: 0.1765 Validation: 0.3844	0:13:50.6
64 4 Epochs and I	Model: 0.9153 Validation: 0.8362 Batch Size of 32	Model: 0.2293 Validation: 0.3803	0:19:50.6
Convolutional Layers	Acc	Loss	Time
1	Model: 0.8322 Validation: 0.8190	Model: 0.3889 Validation: 0.4016	0:5:32.1
2	Model: 0.8554 Validation: 0.6681	Model: 0.3353 Validation: 0.8161	0:39:38.8



05 Discussion



Discussion

Machine Power

Compute Resources Available

Novelty

Boosting accuracy while applying transfer learning techniques

Availability of Data

Large-scale, industry- data is not open-source

What worked? What Didn't?

Hyper-parameter tuning



Thank you for listening!

Please feel free to reach out with any additional questions: Madison Boem – 16mab11@queensu.ca Caroline Kim – kim.caroline@queensu.ca Eric Venditti – eric.venditti@queensu.ca Jade Watson – 16jw73@queensu.ca

