Breast Cancer Classification Using Neural Networks

Rohan Raman

Vellore Institute of Technology

Abstract- Breast cancer (BC) is the most common type of cancer in adult women. The need for a system for early detection of BC is evident and consequently there is a demand for it in the healthcare industry. This manuscript attempts to solve this problem by proposing a solution based on convolution neural networks. The model is trained on histopathological images as opposed to the normally used mammography images for better accuracy from the BreakHis dataset. Various pre-existing architectures were tried, ultimately a trimmed down version of the VGG-16 architecture gave the best results. The proposed model was evaluated using various metrics and gave better results than most of the pre-existing models.

Keywords- Convolution Neural Networks, Neural Networks, Breast Cancer, Deep learning, Histopathology

I. INTRODUCTION

The National Cancer Institute defines histopathology as "the study of diseased cells and tissues using a microscope". The target tissue is obtained from the body and then stained with a suitable colouring agent to make the features visible easily. This stained tissue is then placed on a slide and observed under a microscope for further study. A histopathology report is also called a biopsy report.

This manuscript attempts to classify the images into 5 categories based on the features from the histopathological images. Benign being non-cancerous while malignant, that is cancerous being further classified as ductal carcinoma, lobular carcinoma, mucinous carcinoma and papillary carcinoma.



A neural network is based on how the human brain works.Artificial neuron is conceived as an analogy of biological neuron, where it takes a number of signals as input, and fires an output if the combined input signal strength exceeds a certain threshold. When a number of artificial neurons are connected together, it is called an artificial neural network. The ability of an artificial neuron is limited if it simply performs a weighted sum of all inputs, so we pass the weighted sum of inputs o a non-linear function called the activation function. The hidden layer in neural networks generally refers to the biases to be added to the weighted sum along with the activation function to which it is passed. The hidden layer is expected to extrapolate or highlight the salient features from the input layer and give the result as an output layer. Neural networks given enough data can find patterns in almost anything and is thus used with unstructured data like video, text, images, speech etc. A basic neural network is shown in the diagram below.

Deep learning is a set of techniques that utilize the concept of a neural network. Here I have used convolution neural networks to extract the features from the histopathological images and train the model on these features.



II. EXISTING CNN ARCHITECTURES

There are mainly 4 model architectures that are considered for image classification:

Alexnet:

- 5 Convolution Layers
- 3 Fully Connected Layers
- Activation function: Rectified Linear Unit (ReLU)

The block diagram is given below:



Alexnet has about 62 million parameters, as elaborated in the following table:

	AlexNet Network - Structural Details												
Input			Output		out	Layer	Stride	Pad	Kernel size		in	out	# of Param
227	227	- 3 -	55 55 96		96	conv1	4	0	11	11	3	96	34944
55	55	96	27	27	96	maxpool1	2	0	3	3	96	96	0
27	27	96	27	27	256	conv2	1	2	5	5	96	256	614656
27	27	256	13	13	256	maxpool2	2	0	3	- 3 -	256	256	0
13	13	256	13	13	384	conv3	1	1	3	- 3	256	384	885120
13	13	384	13	13	384	conv4	1	1	3	3	384	384	1327488
13	13	384	13	13	256	conv5	1	1	3	- 3	384	256	884992
13	13	256	6	6	256	maxpool5	2	0	3	3	256	256	0
	fc6 1 1 9216 4096								37752832				
	fc7 1 1 4096 4096									16781312			
	fc8 1 1 4096 1000										4097000		
						Total							62,378,344

VGG16:

- 13 Convolution Layers
- 3 Fully Connected Layers
- Activation function: Rectified Linear Unit (ReLU)

The block diagram is given below:



VGG16 has about 138 million trainable parameters, as elaborated in the following table:

	VGG16 - Structural Details												
#	In	put li	nage		outpi	ıt	Layer	Stride	Ke	rnel	in	out	Param
1	224	224	3	224	224	64	conv3-64	1	3	3	3	64	1792
2	224	224	64	224	224	64	conv3064	1	3	3	64	64	36928
	224	224	64	112	112	64	maxpool	2	2	2	64	64	0
3	112	112	64	112	112	128	conv3-128	1	3	3	64	128	73856
4	112	112	128	112	112	128	conv3-128	1	3	3	128	128	147584
	112	112	128	56	56	128	maxpool	2	2	2	128	128	65664
5	56	56	128	56	56	256	conv3-256	1	3	3	128	256	295168
6	56	56	256	56	56	256	conv3-256	1	3	3	256	256	590080
7	56	56	256	56	56	256	conv3-256	1	3	3	256	256	590080
	56	56	256	28	28	256	maxpool	2	2	2	256	256	0
8	28	28	256	28	28	512	conv3-512	1	3	3	256	512	1180160
9	28	28	512	28	28	512	conv3-512	1	3	3	512	512	2359808
10	28	28	512	28	28	512	conv3-512	1	3	3	512	512	2359808
	28	28	512	14	14	512	maxpool	2	2	2	512	512	0
11	14	14	512	14	14	512	conv3-512	1	3	3	512	512	2359808
12	14	14	512	14	14	512	conv3-512	1	3	3	512	512	2359808
13	14	14	512	14	14	512	conv3-512	1	- 3	3	512	512	2359808
	14	14	512	7	7	512	maxpool	2	2	2	512	512	0
14	1	1	25088	1	1	4096	fc		1	1	25088	4096	102764544
15	1	1	4096	1	1	4096	fc		1	1	4096	4096	16781312
16	1	1	4096	1	1	1000	fc		1	1	4096	1000	4097000
							Total						138,423,208

ResNet18:

- 17 Convolution Layers
- 1 Fully Connected Layers
- Activation function: Rectified Linear Unit (ReLU)

In order to tackle the vanishing gradient problem ResNet introduced two types of shortcut connections, the identity shortcut and the projection shortcut.

ResNet18, eighteen being the number of layers in the network has about 11 million trainable parameters.

	ResNet18 - Structural Details													
#	In	put L	mage		outpu	ıt	Layer	Stride	Pad	Ker	rnel	in	out	Param
1	227	227	3	112	112	64	conv1	2	1	7	7	3	64	9472
	112	112	64	56	56	64	maxpool	2	0.5	3	3	64	64	0
2	56	56	64	56	56	64	conv2-1	1	1	3	3	64	64	36928
3	56	56	64	56	56	64	conv2-2	1	1	3	3	64	64	36928
4	56	56	64	56	56	64	conv2-3	1	1	3	3	64	64	36928
5	56	56	64	56	56	64	conv2-4	1	1	3	3	64	64	36928
6	56	56	64	28	28	128	conv3-1	2	0.5	3	3	64	128	73856
7	28	28	128	28	28	128	conv3-2	1	1	3	3	128	128	147584
8	28	28	128	28	28	128	conv3-3	1	1	3	3	128	128	147584
9	28	28	128	28	28	128	conv3-4	1	1	3	3	128	128	147584
10	28	28	128	14	14	256	conv4-1	2	0.5	3	3	128	256	295168
11	14	14	256	14	14	256	conv4-2	1	1	3	3	256	256	590080
12	14	14	256	14	14	256	conv4-3	1	1	3	3	256	256	590080
13	14	14	256	14	14	256	conv4-4	1	1	3	3	256	256	590080
14	14	14	256	7	7	512	conv5-1	2	0.5	3	3	256	512	1180160
15	7	7	512	7	7	512	conv5-2	1	1	3	3	512	512	2359808
16	7	7	512	7	7	512	conv5-3	1	1	3	3	512	512	2359808
17	7	7	512	7	7	512	conv5-4	1	1	3	3	512	512	2359808
	7	7	512	1	1	512	avg pool	7	0	7	7	512	512	0
18	1	1	512	1	1	1000	fc					512	1000	513000
							Total							11,511,784

ResNet has a number of variations, ResNet50 and ResNet101 being the most commonly used.

Inception:

Each inception network consists of a several modules. Every inception module essentially comprises of four operations in parallel

- 1x1 conv layer
- 3x3 conv layer
- 5x5 conv layer
- max pooling



The respective outputs from the four parallel operations are concatenated in a depth wise fashion in the filter concatenation block. The structural details of GoogleNet, a type of inception net, are given below:



Initially I was looking at Resnet, VGG and inception but I realised that with our dataset defeats the purpose of using inception net as a consistent portion of every image consists of the tumor. Resnet wasn't used because the skip connection was only considerably useful in very deep neural networks, whereas if we go that deep with the proposed model, the model will most likely overfit. So,I decided to use VGG and applied necessary changes by removing certain layers to improve the accuracy as it was more suited to our use case.

III. METHODOLOGY

Data Preparation:

The model was trained on the histopathological images from the BreakHis dataset. The dataset consists of over 8000 images categorised as malignant and benign. It was further split up into the various types of malignant and benign tumors. The subcategories contained images in various magnifications.

First, the images of all the magnifications were grouped and placed together under the name of the subcategory. For the benign images, the subcategorization was removed and all the images were labelled as benign. This give us our 5 classes for classification, as ductal carcinoma, lobular carcinoma, mucinous carcinoma papillary carcinoma and benign.

Image Augmentation:

Deep learning models require a considerable amount of training data to produce desirable results. Image augmentation is a way of supplementing the original dataset with processed images in the form of random rotations, shits etc thereby boosting the performance of the model.

For image augmentation I used the ImageDataGenerator function in the keras library. The code for augmentation is hosted athttps://github.com/romanronin/breast-cancerhistopathology-classification under the name 'augmentation.py'.

Model:

About the model:

- 1. Removed dropout layers so that the number of parameters is not reduced, to get a better accuracy.
- 2. Increased the filters for the convolution layers (32-64-128) respectively.
- 3. Reduced the pool size for better and finer patterns.
- 4. First dense fully connected layer has 1024 dimensions.
- 5. The second dense fully connected layer has 5 dimensions for classification into five classes.
- 6. Batch size is 55.
- 7. The learning rate is set to $1 e^{3}$.

The detailed architecture:



The model summary is given below:

Layer (type)	Output	Shape	Param #
conv2d_6 (Conv2D)	(None,	96, 96, 32)	896
activation_8 (Activation)	(None,	96, 96, 32)	0
batch_normalization_6 (Batch	(None,	96, 96, 32)	128
max_pooling2d_4 (MaxPooling2	(None,	32, 32, 32)	0
conv2d_7 (Conv2D)	(None,	32, 32, 64)	18496
activation_9 (Activation)	(None,	32, 32, 64)	0
batch_normalization_7 (Batch	(None,	32, 32, 64)	256
conv2d_8 (Conv2D)	(None,	32, 32, 64)	36928
activation_10 (Activation)	(None,	32, 32, 64)	0
batch_normalization_8 (Batch	(None,	32, 32, 64)	256
<pre>max_pooling2d_5 (MaxPooling2</pre>	(None,	16, 16, 64)	0
conv2d_9 (Conv2D)	(None,	16, 16, 128)	73856
activation_11 (Activation)	(None,	16, 16, 128)	0
<pre>batch_normalization_9 (Batch</pre>	(None,	16, 16, 128)	512
conv2d_10 (Conv2D)	(None,	16, 16, 128)	147584
activation_12 (Activation)	(None,	16, 16, 128)	0
<pre>batch_normalization_10 (Batc</pre>	(None,	16, 16, 128)	512
<pre>max_pooling2d_6 (MaxPooling2</pre>	(None,	8, 8, 128)	0
flatten_2 (Flatten)	(None,	8192)	0
dense_3 (Dense)	(None,	1024)	8389632
activation_13 (Activation)	(None,	1024)	0
dense_4 (Dense)	(None,	5)	5125
activation_14 (Activation)	(None,	5)	0
Total params: 8,674,181			

Trainable params: 8,673,349

Non-trainable params: 832

IV. RESULTS

The overall accuracy of the proposed system is 90.45 %. Other evaluation metrics were also used like the confusion matrix, precision, recall and f1 score. The metrics are summarized below.

[[829	3	8	20	4]		
[33]	354	12	4	15	1		
Î 3	15	231	1	6	i		
r 17	4	29	268	3	i		
[20	2	1	5	260	i 1		
testin	т а(- Cure		0 0	0/517	021008	1360
restri	6 a.	cuit	acy-	0.5	04511	991990	1202
		preci	sion	recall	f1-score	support	
	Benigr	1 0	0.96	0.92	0.94	902	
Ductal_Ca	rcinoma		0.85	0.94	0.89	378	
Lobular_Ca	rcinoma		0.90	0.82	0.86	281	
Mucinous Ca	rcinoma		0.83	0.90	0.87	298	
Papillary1_Ca	rcinoma	•	0.90	0.90	0.90	288	
a	ccuracy				0.90	2147	
ma	cro ave		0.89	0.90	0.89	2147	
weigh	ted ave		0.91	0.90	0.90	2147	

Confusion matrix:

It is a N * N matrix used for evaluation of classification problems. Where N is the number of classes, hence the 5 * 5 matrix. It gives a holistic view of our model and the errors in it. The rows represent the predicted values and the columns represent the actual values. Ideally, the main diagonal should have values much larger as compared to the rest of the matrix as is the case in our matrix.

Precision:

Precision by definition the true positives divided by the total predicted positives. It gives us an idea out of the predicted positives how many are actually positive. The higher the better.

Recall:

Recall by definition is the true positives divided by the total actual positives. It gives us an idea out the actual positives how many were correctly identified as positive. The higher the better.

F1 score:

F1 score is the harmonic mean between precision and recall. It takes into account both the false positives and false negatives. It is commonly used as a metric for model selection besides accuracy. The higher the better.

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