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Comparative Analysis of Multiple Categorizations of Oncology Images for Cancer Cell Identification Using Parallel Transfer Learning Algorithms

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Abstract

Cancer is a destructive, lethal, hazardous, and erratic disease. Predicting the condition, diagnosing it quickly and properly, and accurately predicting the prognosis are all necessary to lower the chance of mortality in this disease. As a disease, cancer has been found to have several distinct forms. As early cancer research has shown, it is essential to the medical treatment of patients to test for and follow a specific course of therapy for a certain cancer type at the earliest possible stage. Researchers from many different backgrounds have looked at how ML and Deep Learning techniques might be used in the fields of biology and bioinformatics to better categorize cancer patients into high- and low-risk groups. Algorithms from the fields of artificial intelligence (AI), machine learning (ML), and deep learning (DL) are already being put to good use in the healthcare system. A) is a simulation of human intellect that makes predictions using data, rules, and knowledge that has been put into it. In the realms of machine learning and artificial intelligence, deep learning (DL) has found widespread use in fields as diverse as healthcare and the development of new medicines. The prognosis for cancer is an assessment of the patient's likelihood of surviving the disease. Patients with cancer would benefit immensely from a prompt and precise diagnosis and prognosis. As a result of the widespread availability of powerful computers, DL has become the go-to method of data analysis. We investigate how AI aids in cancer diagnosis and prognosis, focusing on its remarkable accuracy, which is even greater than that of conventional statistical applications in oncology. AlexNet, GoogleNet, and, DenseNet, convolutional neural networks (CNNs are just some of the methods used in the advancement of forecasting models for predicting a cure for cancer. We show how these techniques contribute to the field's progress as well. The experiments are carried out on three different datasets, Cancer Genome Atlas Lung Adenocarcinoma (TCGA-LUAD), Digital Database for Screening Mammography's Curated Breast Imaging Subset (CBIS-DDSM), and Brain MRIs.

Keywords: Oncology Images, Cancer cell identification, Transfer Learning, Artificial Intelligence, Convolutional Neural Networks, Categorization schemes, Data analysis.

1. Introduction

In the United States, it is expected that there will be 1.7 million new cases of cancer in 2019, with 0.6 million deaths as a direct result of the disease [11]. Modern laparoscopic surgery, robotic surgery, tumor adjuvant treatment, and other

emerging technologies are more important for enhancing survival time and decreasing the risk of local recurrence as cancer rates and deaths continue to climb dramatically [12]. Numerous approaches exist for dealing with cancer now [13-15]. A lot of progress has been made in the efficacy of cancer treatment during the 2010s [11-15]. But due to diagnostic ambiguities, even with the plethora of new procedures, scientifically adequate therapeutic results for each afflicted individual are elusive. An accurate prognosis would allow for the implementation of treatment plans tailored to the individual patient. In fact, if doctors could better forecast how their patients would respond to various therapies, they might better plan for their patient's care and ultimately alleviate the physical and psychological suffering that often accompanies diseases like this. Erroneous prognostic predictions continue to be a bottleneck for clinicians despite the fact that fundamental clinical findings can be blended with the application of the conventional Staging system approach (based on the size of the tumor (T), the dispersion of cancer into adjacent lymph nodes (N), and the expanded of cancer to other parts of the body (M, for metastasis) in empirical tests [16]. Clinical researchers still face a significant barrier in attempting to improve prognosis accuracy using cutting-edge AI technologies.

Current developments in elevated computing and ground-breaking deep-learning algorithms [8] are being used to integrate the massive amounts of data obtained from multi-omics investigations into the precision oncology landscape, which is being reshaped by AI. In particular, AI is finding more and more uses, with recent examples including novel methods for diagnostic imaging, screening, treatment, and classification; characterization of cancer genomics; evaluation of tumor cells; evaluation of biomarkers for prognostic and forecasting purposes; and evaluation of methods for follow-up and drug development [9-10].

DL algorithms show potential for enhancing the accuracy of cancer diagnostic picture interpretation. Diagnostic imaging techniques including MRI, CT, and x-ray images have been used to verify DL-generated models, showing classification accuracy that often exceeds that of skilled doctors. [1-3] Nonetheless, DL models' universal applicability and robustness are crucial to their success. It has been demonstrated that DL algorithms' output varies depending on subtle shifts in the input data. Observing such variation in reaction to very slight modifications may indicate an unstable algorithm, which may in turn cause misclassification and transferability issues. However, DL models' vulnerability to adversarial assaults is a serious drawback. Adversarial pictures are photos that have had subtle changes made to them at the pixel level in order to trick deep learning algorithms. [4] Adversarial pictures' pixel-level variations, which are frequently undetectable to humans but can have significant effects on the model's prediction accuracy. [5] Concerns regarding the generalization of Learning algorithms and the reliability of their useful purposes in medicine are raised by their poor performance against adversarial pictures. As deep learning (DL) methods for diagnostic picture analysis grow more commonplace in healthcare settings, adversarial images pose a future security risk. [6-7] Instability in DL models that try to approximate the classification precision of radiologists is further supported by their sensitivity to adversarial assaults.

In this article, we propose a categorization method that is both accurate and automated, and it was developed for the three different forms of malignant tumors. The implementation uses a deep transfer learned CNN model for feature extraction from images. The retrieved characteristics are then categorized with the assistance of tried and tested classifiers. After then, an exhaustive analysis of the system that has been proposed is carried out. When assessed using the open dataset, the suggested system had the best classification performance of all the comparable efforts. This was the case when compared to other systems. In addition, it has been discovered that the suggested algorithm may provide satisfactory outcomes with a much-reduced amount of training examples.

The remaining portion of this article will be structured in the following manner. The following is presented after Section 2's introduction to the concepts of transfer learning and benchmark models and Section 3's description of the detailed architecture of the proposed classification algorithm. Section 4 describes the experiments conducted and the dataset used in this study. The findings of the evaluation are presented in section 5, along with a commentary of the outcomes. This study comes to a close with the discussion included in Section 6.

2. Related Works

Artificial intelligence's usage of deep learning (DL), which uses complicated computer models to represent abstractions gleaned from data, has skyrocketed in recent years, finding widespread use in fields as diverse as speech processing and visual processing. These techniques are effective because they use a backpropagation algorithm to find subtle patterns in

massive, frequently complicated datasets. Conventional approaches, including machine learning-based methods, have difficulties handling natural data in its raw form without preprocessing [17], but DL overcomes these difficulties. In the realm of deep learning (DL), Convolutional Neural Networks (CNNs) have the ability to learn invariant features. A convolutional neural network (CNN) is a collection of layers, including a filter bank, feature pooling layer, batch normalization layer, dropout layer, and dense layer, that collaborate to generate patterns for various object identification tasks, such as detection, segmentation, and classification. With CNNs, training involves redistributing inputs over several layers of the hierarchy. Pre-processed inputs, including those produced by whitening, etc., are extremely desirable to gain higher performances across jobs [18]. Other CNN versions, like the DenseNet architecture, have shorter connections that can help with feature circulation and allow for a lower number of hyperparameters to be used in the design of more effective designs [19]. Focused and non-focused EEG signals have been studied and recognized using feature selection and neural network techniques in the adjustable Q-factor wavelet transform domain [20]. In a recent paper [21], researchers explored the use of low-density parity-check (LDPC) codes in IoT networks by employing a unique approach to retrieve the first two minima of the check-node update operation of the min-sum-LDPC decoder.

Artificial intelligence (AI), machine learning (ML), and deep learning (DL) strengthen the practice of predicting the likelihood of developing cancer. All of these algorithms employ information gathered from a patient's medical record, including their medical history, tests, scans, and other diagnostic procedures [31]. There is a wide range of obstacles in the path. In the field of medicine, for instance, the use of AI has traditionally been limited to a select few groups, with minorities and new types of patients often being excluded [31]. Correctly diagnosing various malignancies and distinguishing tumors from benign growth or any other condition can be challenging and need a great deal of accuracy and years of expertise. Knowing the prognosis is important since it forms the foundation of the treatment strategy. Scientists are working on image-based risk models, but they need to be confirmed by widespread scientific demonstration in several hospitals and computational progress [31]. The likelihood of a negative consequence occurring in the future can be assigned to a person using a factor model [32].

In addition, future resilient networks, including several 6G scenario examples, have been reviewed and addressed in [22]. ResNets, Xception, and Google Net are some more prominent CNN designs of recent years. Degradation in performance across jobs as the network gets deeper, the requirement for multiscale processing, and the hunt for better designs with fewer parameters [23–26] all point to the necessity of such networks. Storage capacity for long periods of time is another important concern in DL. Long-term, short-term memory is one potential approach (LSTM). The LSTM architecture achieves its results by the enforcement of a non-global error flow in space and time via the states of specialized units [27].

In DL, the concept of transfer learning is also important to discuss. Features from deep CNNs are mined for transfer learning, which then applies to fresh problems. This is necessary because there may not be enough labeled data or other data to train or adapt a DL architecture to new tasks, especially when generic tasks differ significantly from the original tasks. Simple strategies may be used reliably through transfer learning to modify characteristics so that they convey adequate generalization [28–30]. Optimizing DL model architecture design parameters is a challenge worth tackling. The use of reinforcement learning strategies can be helpful in this endeavor. The NASNet architecture is illustrative; it employs many distinct network topologies to discover recurrent motifs that may be chained together to process inputs with variable spatial dimensions and depth[33][34].

3. Materials and Methods

Using enriched cancer datasets, we investigate and assess several of the most well-known CNN designs, including AlexNet, GoogLeNet, and Densenet. Transfer learning strategies are implemented with these pre-trained CNN architectures in order to get the visually discriminative and rich features. At this point, the visual patterns are given a classification using a log-based softmax layer. The following subsections will go through the most important aspects of the proposed framework. After that, we go on to a discussion of the measurement matrices in order to evaluate the performance of our suggested systems.

3.1 CNN Model

Computational models known as convolutional neural networks (CNNs) are constructed of numerous processing layers to recover features from raw data using multilayer interpretations and progressive abstraction [19]. Convolutional layers, full-connection layers, pooling layers, and input and output layers, make up the overall structure of CNN models, as depicted on the right side of Figure 1. CNN uses 4 convolutional layers, 2 full-connection layers,2 pooling layers, and 6 softmax, tanh, and ReLu layers, as shown in Figure 2. Several methods can be incorporated, including nonlinear filtering, data augmentation, local response normalization, hyper-parameter optimization, and multiscale representation, to improve object classification even further. Nowadays, VGG, LeNet, Resnet101, U - net, Imagenet, YOLO, R-CNN, and Long short-term memory, GoogleNet are among the most popular deep learning models.

The Convolution Neural Network, often known as CNN, is a type of neural network that is typically used to analyze, identify, or categorize pictures since it helps to simplify the images for more effective analysis. The fact that this network requires fewer human efforts and less pre-processing makes it an attractive option. Backpropagation is a component of the learning process that contributes to the development of a more accurate network. It is conceptually somewhat similar to the MLP in that it has an input layer of neurons, many hidden layers, and an output layer. Moreover, it also has numerous hidden layers. Every neuron in one layer is coupled to each and every neuron in the layer that follows it. The image that has to be categorized or analyzed is taken through a number of different layers. After executing convolution on the picture, the convolution layer is then utilized to apply a filter to it in order to accentuate the features. After that, pooling layer-down samples of the sample of features extracted will (lower the sample size of) the sample.

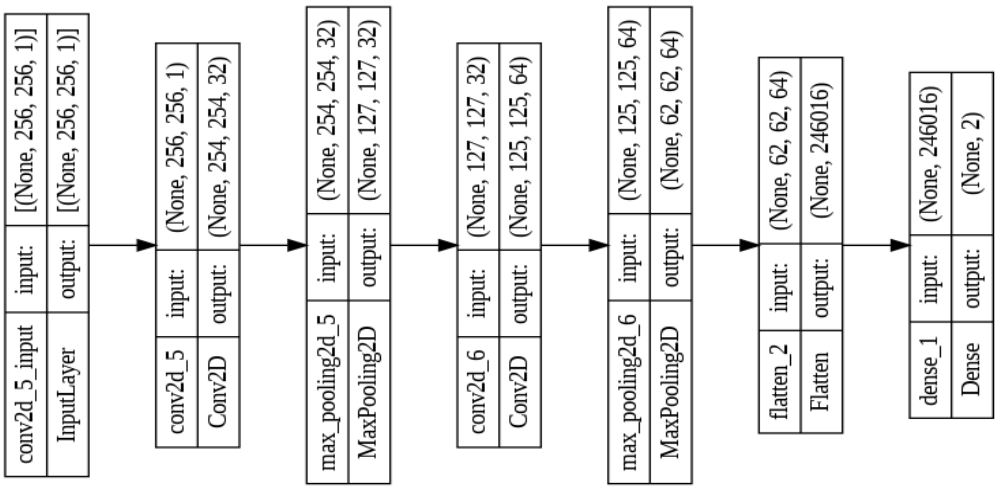


Figure 1. The Model structure of CNN -1

As a result, the procedure will go more quickly when the parameters are decreased. The largest amount that may be achieved by pooling is referred to as "Max pooling," whereas the average quantity gained through pooling is referred to as "Average pooling." Rectified Linear Unit is the name of the activation function that is employed in CNN to guarantee that the network is not linear. The output is forecasted into classes once it has been processed via a layer that has all of its connections established. As a result of its ability to resolve the issue of signal transition and effectively extract features, this network frame is finding growing use in image processing. Because of its capability of image retrieval that can be utilized to improve and readily observe malignancy in breast lesions, the CNN architecture has been applied in the detection and classification of breast cancer. This is due to its capacity to detect breast cancer earlier. So, contributes to the process of early breast cancer identification, which enables the disease to be treated at an earlier, less advanced stage, before it has a chance to spread further.

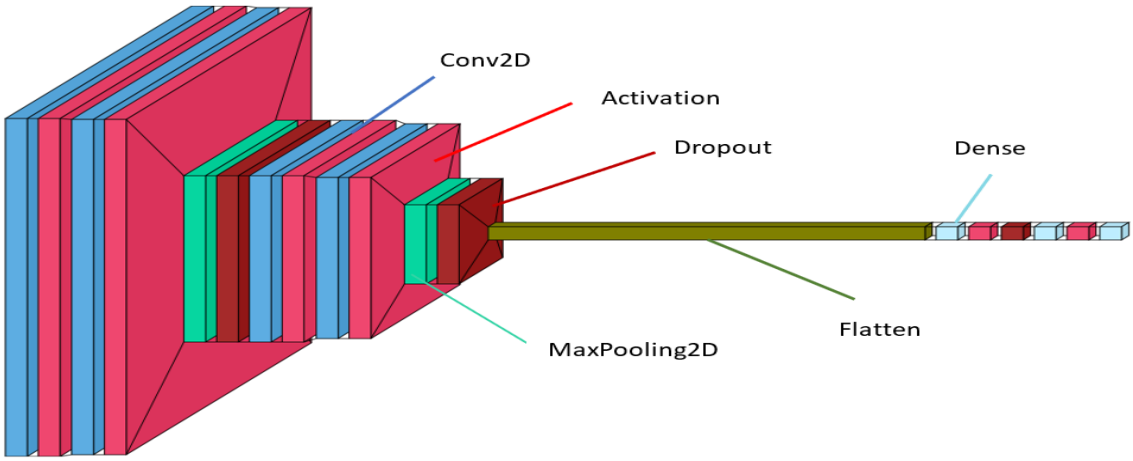


Figure 2. The Model architecture of CNN -2

The following mathematical description provides an overview of the process of employing a trained CNN-based model for lesion malignancy prediction. The output of a convolutional neural network (CNN) model, given a suspicious area (S_x), may be written as where H is the number of hidden layers and a_j is the activation function in the jth layer.

$$O = f(S_x) = f_H(f_{H-1}(\ldots\ldots f(S_x))) \quad (1)$$

While evaluating the performance of the network, we utilized a method known as k-fold cross-validation. Both of the methods that were used, which were both different from one another, comprised of a 10-fold cross-validation. The first method, known as record-wise cross-validation, consisted of arbitrarily dividing the data into ten groups that were roughly equivalent to one another. This was done to ensure that each type of tumor was represented in the same proportion across all of the groups. The second method included randomly dividing the data into ten sets, each of which had nearly the same amount of information, but the information pertaining to a certain issue could only be discovered in one of the sets. This method, known as subject-wise cross-validation, ensures that each data set has information from at least two individuals, irrespective of the kind of tumour being studied. The second strategy was put into action in order to evaluate the generalisation potential of the network in the context of medical diagnostics. The capacity to anticipate the diagnosis based on the data collected from participants for whom there are no observations during the training phase is what is meant by the term "generalisation capability" in clinical practise. As a result, the observations made by individuals who were part of the training set cannot be included in the test set. In the event that this is not the case, complex predictors have the potential to pick up on a confounding link between identification and diagnostic status, which would result in an unreasonably high prediction accuracy.

3.2 Transfer Learning

As shown in Fig. 2, AlexNet and GoogleNet is used to investigate transfer learning strategies. In the case of a fine-tune approach to the pretrained AlexNet, we have tested several settings to provide the best possible results in terms of network performance and accuracy. Following the guidelines in Table 1, we have trained the network using the sgdm, adam, and rms prop basic solvers with varying batch sizes and verification frequencies.

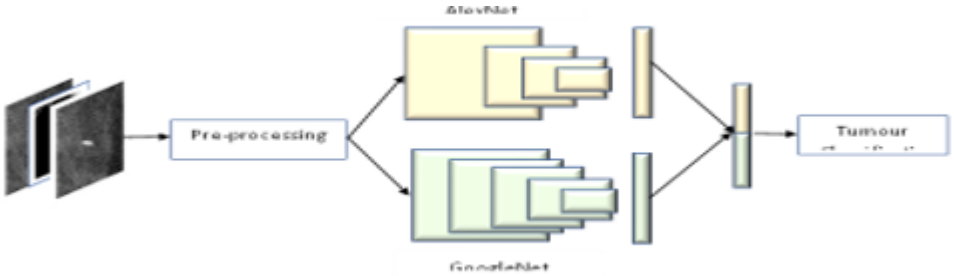


Fig.2. Parallel Transfer Learning Model for deep feature extraction

Using SGDM, adam SGDM with a batch size of 20, validating frequency of 200, and the best network, you can get an accuracy of 97.39 percent. Both convolutional and fully connected layers are explored for feature extraction in the event of a frozen approach to the pre-trained AlexNet. We have taken the generic representation of the pictures in the source dataset and retrieved features from the convolutional layers. In order to get a more complete and accurate representation of the pictures in the source dataset, we additionally collected features from fully connected layers. According to the reports, AlexNet's Conv5 produces the most accurate findings at 99.8 percent.

Table 1. Hyperparameter tuning

Hyper-Parameter	CNN	Alexnet	GoogleNet
Optimizer	Adam	Adam, rms prop	nAdam
Batch size	64	20	128
Validation Frequency	300	200	300
Epochs	200	100	100
Learning Rate	0.0001	0.00001	0.0001
Activation	ReLu, softmax	ReLu, Softmax	Tanh, Softmax

Figure 2 depicts the architecture of GoogleNet, a convolutional neural network. This network's model was supposedly created to take into consideration high image features utilizing a million photos of commonplace objects included in the massive dataset known as ImageNet. It can recognize patterns in around a thousand photos. It makes use of only a twelfth as many parameters as Alexnet. This model takes in pictures as input and output labels of one of its learned classes together with the level of confidence, just like other neural networks used in computer vision applications. GoogleNet has 22 layers, with 9 of them being inception units. A modified Inception module that employs learnable filters ranging in size from $(1x1)$ to $(5x5)$ to conduct convolution in parallel, therefore facilitating the collection of features at varying degrees of detail [35].

4. Experimental setup

4.1 Dataset

The Cancer Genome Atlas Lung Adenocarcinoma (TCGA-LUAD) [33] data gathering is part of a wider initiative to develop a research community focused on linking cancer phenotypes to genomes by offering health pictures matched to participants from the Atlas. The Genomic Data Commons (GDC) Data Portal holds clinical, genomic, and pathological data, while The Cancer Imaging Archive holds radiological data. Researchers may search the TCGA/TCIA datasets for tissue genotyping, radiological phenotype, and clinical outcomes using matched patient IDs. To meet accrual objectives of 500 specimens per cancer type, TCGA gathered tissues from various sites worldwide. This makes image data sets quite varied in scanner modalities, vendors, and acquisition techniques. Most of the photos were taken during ordinary

treatment, not clinical trials. The information is a small sample of cancer imaging data as shown in figure 2. These are the middle section of all CT scans with properly tagged age, modality, and contrast. The final tally is 475 series representing 69 unique patients.

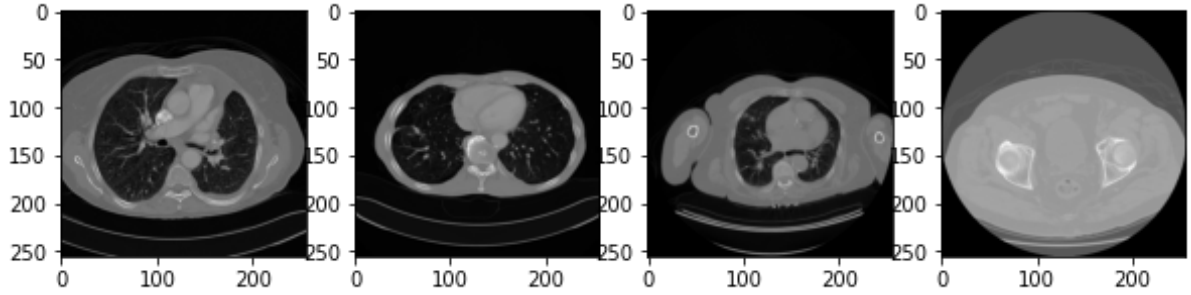


Fig.2. Sample CT images from the TCGA/TCIA dataset.

From the Digital Database for Screening Mammography's Curated Breast Imaging Subset (CBIS-DDSM), a total of 1,696 lesions were imaged. So far, [34] the CBIS DDSM has accumulated 1,566 mammograms from four different locations in the United States. Clinical information was utilized to generate areas of interest that were then used to obtain mammographic lesions for DL model training. Verified pathologic reports were used to establish the existence of malignancy.

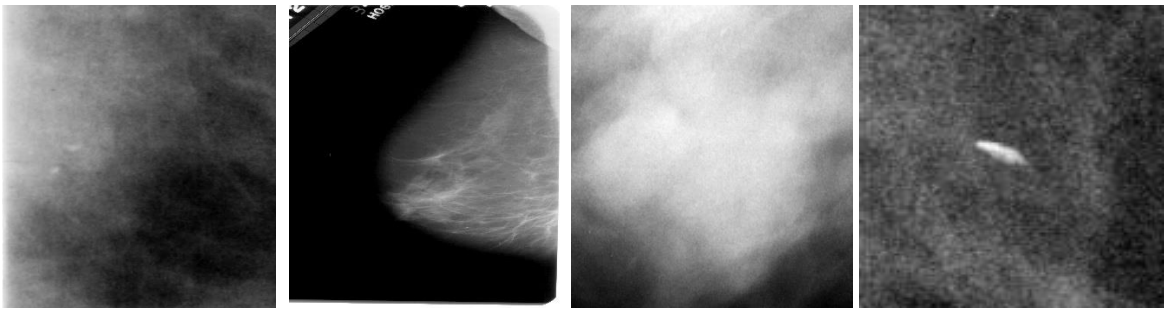


Fig.3. Mammography images from CBIS-DDSM

Brain MRIs were collected from 831 individuals who were enrolled in a brain metastases registry at a single institution. [35] Almost 4,000 MRI-detected brain lesions were evaluated for malignancy. Radiologists, neurosurgeons, and radiation oncologists all worked together to pinpoint the areas of interest. Pathological evidence or a general medical opinion established the diagnosis of cancer.

4.2 Data augmentation

When there isn't enough data for training, data augmentation can help. By operations like lightening, scaling, and flipping the original data, new pictures may be created while maintaining the same label; this is known as data augmentation. When given more data, deep learning models tend to perform better. To improve the model's training, we supplement photos in real-time, increasing the total amount of images. By improving the training dataset, which is the source of the problem, rather than depending on modifications to the model's structure, data augmentation is viewed as a sort of regularisation applied on the dataset level. This helps to prevent overfitting and improve generalization performance. Oversampling the underrepresented group in the training set is one way that data augmentation can address the issue of class imbalance and produce more representative results.

To improve contrast and eliminate noise in MRI scans, CT and Mammography are the major goal of medical image analysis. The various techniques of acquisition used for MRI, CT, and mammography might produce artifacts and incorrect intensity of exercise. Because of this, a variety of machine learning and image processing methods were used to improve the contrast of MRI scans. The high-resolution contrast pictures were created with the help of the contrast

stretching algorithm of pre-processing. Low-contrast pictures can benefit from contrast stretching since it expands the range of grayscale values seen in such images. Using this relationship, we can improve the contrast of scans.

$$f(a,b) = \frac{f(a,b) - f_{mn}}{f_{mx} - f_{mn}} \times 2 \quad (2)$$

4.3 Performance Evaluation

In order to evaluate the efficacy of our network in relation to that of other cutting-edge methodologies, we also conducted tests on our network in the absence of k-fold cross-validation (one test). In each of the aforementioned strategies, the testing phase utilised two data subsets, the validation phase utilised two data subsets, and the training phase utilised six data subsets. Each approach was applied to both the original and the modified datasets to see how they performed.

For training, an Adam optimizer was used with a mini-batch size of 16, and data was shuffled between iterations. While training a network, the early-stop situation suggests when the operation should be terminated. To be more exact, it was designed to complete the training process after one epoch, which is the point where the loss begins to rise. Both the regularisation factor and the starting learning rate were set to 0.004 at this point in the process. An initializer called a Glorot initializer, which is also known as a Xavier initializer, was utilised to provide the convolutional layers their initial weights. When the loss on the validation set reached a level that was more than or equal to the preceding lowest loss for 11 times, the training procedure came to an end.

5. Result and Discussion

One of the most used metrics for evaluating classification models is accuracy. It's a representation of the proportion of accurate forecasts to total predictions. Obtaining high accuracy that is skewed towards the class with the largest instance count is possible for an unbalanced dataset. To maximise accuracy, the classifier may potentially classify every test case as belonging to the big class, with the result that the classifier's performance would be proportional to the proportion of the more common labels in the test set. Because of this, precision is not always the best indicator of performance. The following Equation, where l denotes the number of classes, shows that the balanced accuracy, which may be defined as the average accuracy attained on either class, is a superior generalizability metric. We obtained 98%,97% and 100% accuracy for lung cancer, Breast cancer and Brain tumour.

In order to determine whether or not the proposed tumour and detection system is successful, evaluation metrics are determined based on the four major results that are utilized to test the classification algorithm: true positives (tr_p), false positives (fa_p), true negatives (tr_n), and false negatives (fa_n). The following metrics are used to determine the system's effectiveness.

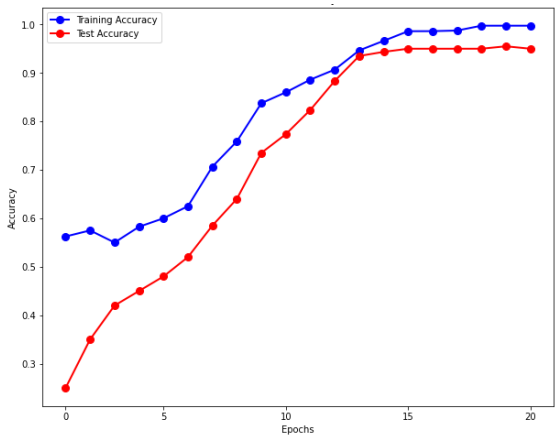
Correctly differentiating between different forms of brain tumours depends on how accurate the diagnosis is. We may measure a test's precision by computing the ratio of true positives to false negatives across all instances using the following relations:

$$Accuracy(Ac) = \frac{tr_p + fa_n}{tr_p + fa_n + fa_p + tr_n} \quad (2)$$

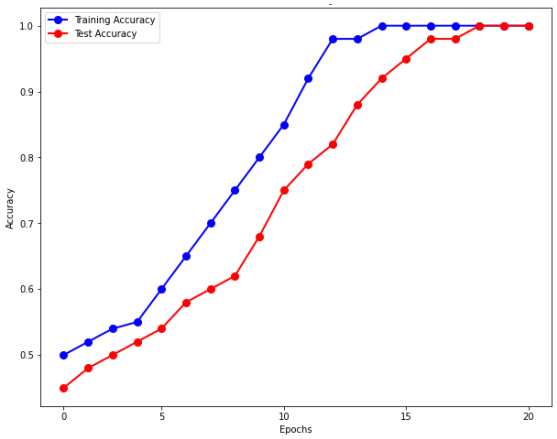
The percentage of correct diagnoses is used to determine the system's level of sensitivity for detecting brain cancers.

$$Sensitivity(Se) = \frac{tr_p}{tr_p + fa_n} \quad (3)$$

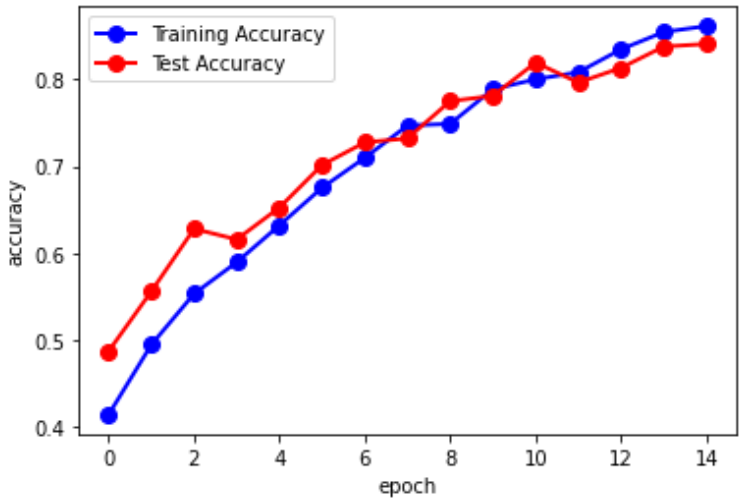
The figure 3 depicts the accuracy of the transfer learning model on the three dataset.



(a) Lung Cancer



(b) Breast Cancer



(c) Brain Cancer

Fig.3. Accuracy of the Parallel Transfer Learning Model

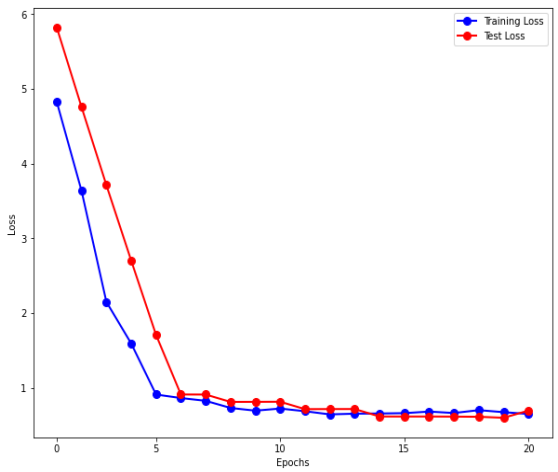
The figure 4 shows the loss value obtained from the transfer learning model. Compared to the baseline model, the minimum loss value is obtained.

The model's specificity, or its ability to correctly identify the true brain tumour kind, is measured as

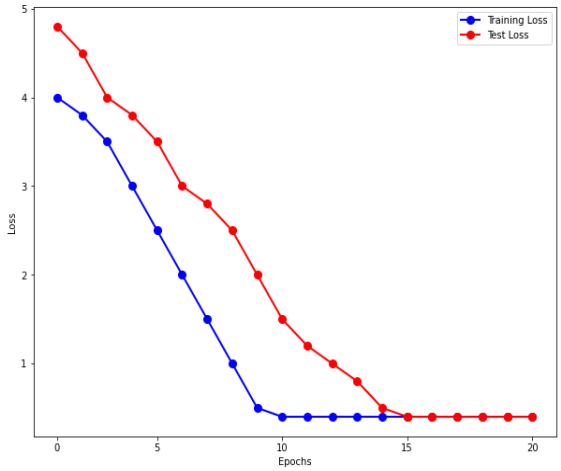
$$Specificity(Sp) = \frac{tr_n}{tr_n + fa_p} \quad (4)$$

The genuine positive measure is precision, which may be calculated with the following relation:

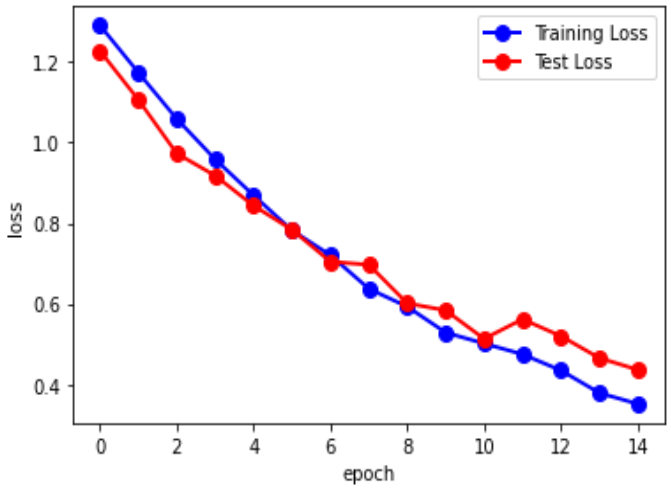
$$Precision(Pr) = \frac{tr_p}{tr_p + fa_p} \quad (5)$$



(a) Lung Cancer



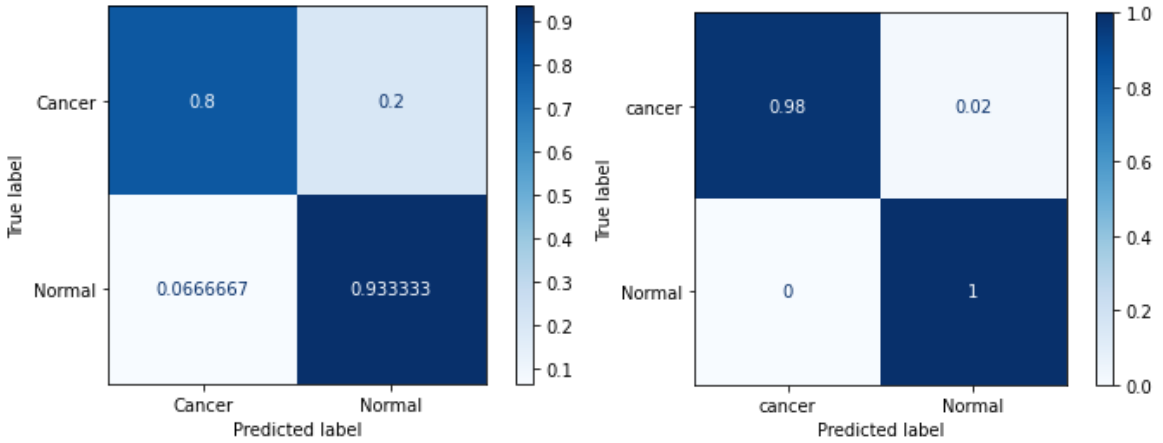
(b) Breast Cancer



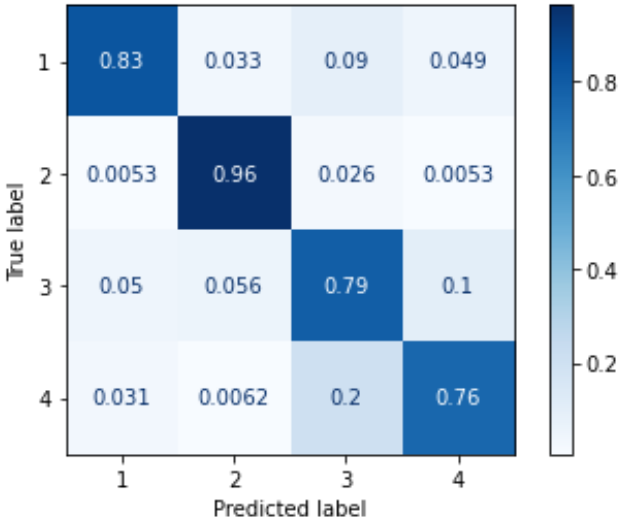
(c) Brain Cancer

Fig.4. Loss of the Parallel Transfer Learning Model

The accuracy plot shows that after around 100 iterations, the algorithm begins to stabilise within half a standard deviation of the final result. It's also been noted that the algorithm's training process is prone to volatility. Non-uniform imaging circumstances are to blame for these variations in the results. Also, the data augmentation added an extra layer of difficulty to this task. Yet, when a deep learning model is applied to real-world issues with imperfect data, it is presumed that these conditions are the norm. In addition, the findings demonstrate that the trained model attained a sensitivity of 99.08% and a specificity of 99.7%. Because the major goal of classification models is to increase the sensitivity, which manifests the success or hit rate, while maintaining the specificity, which represents the real negative rate , it is imperative that these models be able to achieve this goal. The values obtained by these metrics reflect the legitimacy of the proposed structure (ROI retrieval preceded by deep learning) in classifying data of similar modalities, and this is especially true when compared to the same algorithm that was applied without any pre-processing that was also implemented by the writers, which scores somewhere around 100% accurateness. These measures were presented here. Figure 5 provides a presentation of the confusion matrix for the results that have been described.



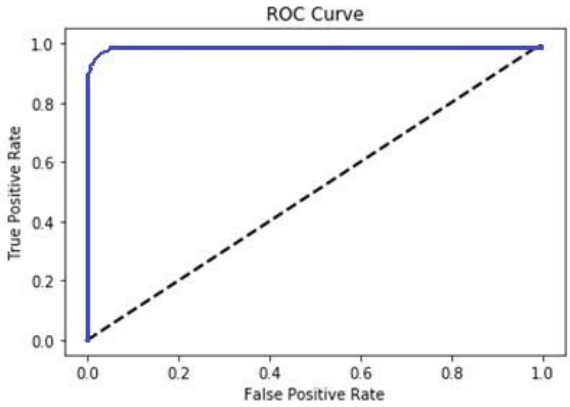
(a) Lung Cancer **(b) Breast Cancer**



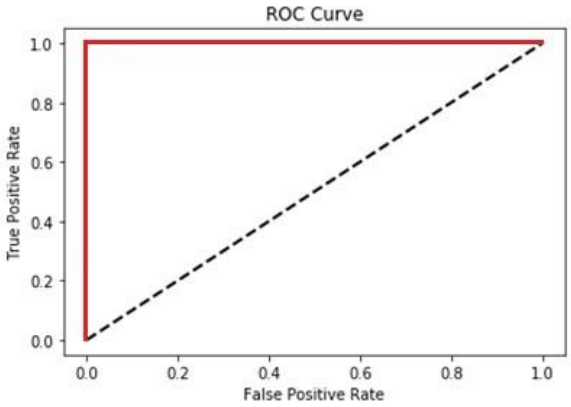
(c) Brain Cancer

Figure 5. confusion matrix for all three datasets

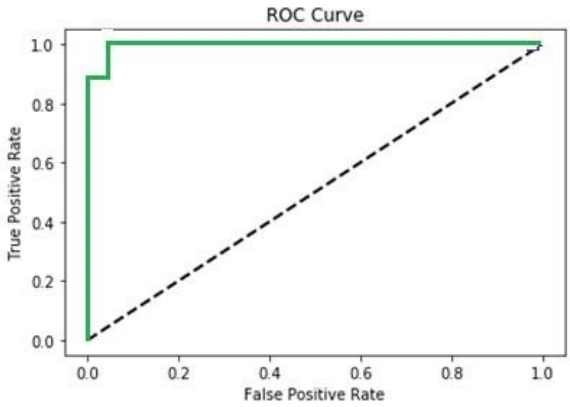
We show that ROC curves in their conventional form, which do not include threshold values, have an unpredictable shape even when accounting for the same area under the curve (AUC). This makes it difficult to compare the performance of different models depending on the threshold. By comparing ROC curves with categorization plots, which provide sensitivity and specificity based on risk thresholds, we find that ROC curves provide a more accurate picture. The figure 6 shows the ROC curves of the cancer predictions aimed in this paper.



(a) Lung Cancer



(b) Breast Cancer



(c) Brain Cancer

Figure 5. ROC of all three datasets

The results of the classification accuracy tests conducted on the fine-tuned transfer learning approach and the CNN model are presented in Table 2. When compared to other models, it is clear that the GoogleNet + AlexNet model that was fine-tuned to reach optimal performance got superior results. The vast majority of the accuracy scores that were achieved are at or above 90%. In the breast cancer dataset, we achieved the maximum accuracy score possible, which was 100%. In addition to that, a score of one hundred percent accuracy was achieved in the lung cancer dataset. DenseNet and GoogleNet produced the most appropriate results, with accuracy rates of 99% and 98%, respectively.

Table 2. Performance Evaluation of the model we used in this study

Model	Lung Cancer				Breast Cancer				Brain Cancer			
	Accuracy	Precision	Recall	F1-Score	Accuracy	Precision	Recall	F1-Score	Accuracy	Precision	Recall	F1-Score
CNN	98%	97%	98%	97%	98%	99%	99%	97%	96%	97%	97%	98%

AlexNet	**99%**	**98%**	**98%**	**99%**	**99%**	**98%**	**98%**	**97%**	**97%**	**96%**	**98%**	**99%**
GoogleNet	**96%**	**97%**	**96%**	**96%**	**96%**	**97%**	**97%**	**96%**	**96%**	**97%**	**96%**	**97%**
DenseNet	**98%**	**98%**	**97%**	**97%**	**97%**	**96%**	**95%**	**95%**	**95%**	**96%**	**96%**	**95%**
GoogleNet + AlexNet	**100%**	**100%**	**99%**	**99%**	**100%**	**100%**	**100%**	**100%**	**98%**	**99%**	**98%**	**98%**

According to the findings, the accuracy rates of the Alexnet and GoogleNet designs were found to be 99% and 97%, respectively. The results demonstrated that the Alexnet architecture was superior than the GoogleNet architecture. In addition, the amount of time needed to train the AlexNet is far less than that required for the GoogleNet. Consequently, in comparison to GoogleNet, the brain tumour type categorization according to AlexNet is regarded as being of higher quality.

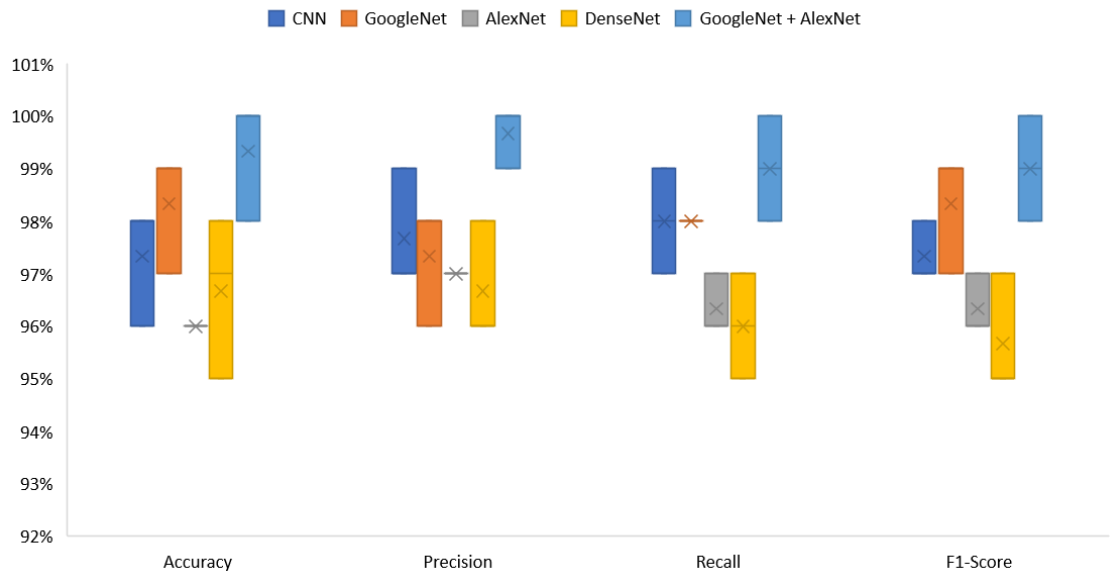


Figure 6. Comparative analysis of the model's performance that is proposed in this article

It can be seen from figure 6 that the combination of GoogleNet and AlexNet results in the best similar accuracy to the other baseline models. This is because in our design, we add the functionality of transfer learning to the last three levels as replacement layers. This causes this result. Transfer learning may enhance the training process in one arena by passing data from related domains. In order to do this, a fully interconnected (FC) picture is used as an input, and a softmax analysis is carried out using both of the nodes in the layer. This is why doing this is requisite because transfer learning can achieve better the learning inside one realm. As we analysed and compared the outcomes of each design by applying the fine-tuned approach, as shown in Figure 6, we were able to see that all structures of convolutional neural networks outperformed with just a small difference between them. Yet, out of the three CNN architectures, GoogleNet and AlexNet achieves the maximum accuracy by generalising the medical pictures.

6.Conclusion

In a nutshell, the work that was presented is a ground-breaking study in the field of brain tumour classification that makes use of transfer learning and deep CNN architectures. We used transfer learning algorithms on natural photos from the dataset, and we identified tumours from the dataset to determine the type of brain tumour each patient had. In order to determine the nature of the tumour, we used three sophisticated deep CNN architectures (AlexNet, GoogLeNet, and DenseNet) to analyse medical images. Two studies of transfer learning, known as fine-tune and freeze, are being carried out to extract the visually distinguishable characteristics and patterns present in MRI slices in order to evaluate and investigate the performance of deep neural networks. By utilising the fine-tune GoogleNet network, we were able to achieve the maximum accuracy of 100% across all of our trials.

In spite of the fact that this work analysed three architectures of deep CNN and transfer learning techniques for brain tumour, breast cancer and lung cancer in the medical imaging arena, there is still a great deal that has to be researched. In the near future, we will investigate various vital and strong deep neural network topologies for the categorization of brain tumours that need less time complexity.

Compliance with Ethical Standards

Conflict of interest : The authors declare that they have no conflict of interest.

Human and Animal Rights: This article does not contain any studies with human or animal subjects performed by any of the authors.

Informed Consent: Informed consent does not apply as this was a retrospective review with no identifying patient information.

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Availability of data and material: Data sharing is not applicable to this article as no new data were created or analyzed in this study.

Code availability: Not applicable

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