Abnormality Detection in Breast Images Using Deep Convolution Neural Network

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Abstract: Breast cancer is a fast-rising disease that is occurring at a distressing degree midst the females. However, prediction of breast cancer at its initial phase may be curable and can reduce the hazard of life threats. The histopathological analysis is effective to localize and detect the malignant tumor because of its capability to analyze at cellular level. However, manual inspection followed by analysis is time-taking, labor intensive and mostly have strong subjective biasness in making the accurate decision. Therefore, a computer assisted conclusion system for estimation of the breast tumor stands out to be current field of learning. In this paper, a framework is design based on the applications of Convolutional Neural Network for accurate prediction and classification of normal and abnormal histopathological images. The framework consists of MOBILENETV2 architecture with two output neurons to represent the normal histopathological images and another representing the abnormal histopathological images. The analysis of the framework has been carried out in publicly available BREAKHIs Benchmark Dataset. From the experimental results it is observed that framework achieved accuracy, specificity, and sensitivity of 83%, 80%, and 85% respectively for classification of the logical images.

Keywords: Breast cancer identification, Convolutional Neural Network, Histopathological images, MOBILENETV2

Introduction:

The medical diagnosis of any illness is one of the highlights of the most important research today. Cancer has become a major global attention and threat to the population around the globe. Cellulites are an ailment that grows inside the physique as well as on the body due to development of anomalous cell. Cells that work together as a unit make form the tissues that make up an organ. Under normal circumstances, the process of cell multiplication, which occurs in all cells, allows for the replacement of damaged cells with healthy ones. The authors in [1] states that tissues or cell mass form because these cells proliferate uncontrollably and grow out of control, resulting in tumors or cancers, which are considered to be the masses or masses of cells that exceed their natural environment. There are various types of frequently stirring cancers in today's world, namely colon cancer, throat cancer, mouth cancer, gastrointestinal cancer and liver cancer. These days breast cancer is also frequently happening midst the womenfolk. The 2020 statistics of occurrence of various types of cancer is depicted in Fig. 1

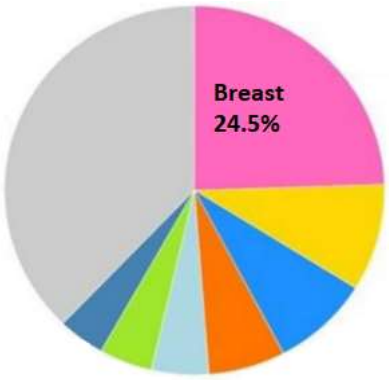

Figure 1: Statistics of Breast Cancer in India

In earlier days, manual processing of the medical images was usually done. Beside this, there are several issues that can create negative influence on the histopathological image classification as epitomized as: The first is the lack of many pathologists at one location. Second, manual analysis of medical image is an extremely time-consuming and demanding process. Thirdly, the detection of breast cancer depends greatly on the pathologists' professional experience and subject-matter expertise. Therefore, computer assisted detection of breast cancer utilizing deep learning-based approaches is crucial to avoid misdiagnosis in the early stages. The computerized exposures of the ailment will innate individuals of the isolated parts for precise finding of the breast melanoma followed by suitable treatment monitoring. The objectives of the work:

i. Survey on existing benchmark datasets for breast cancer detection and various deep learning-based methods adopted by the research community for automated breast cancer detection.

ii. Collection of available benchmark histopathological image dataset (BREAKHIs Bench-mark Dataset) for breast cancer detection.

iii. Designing of a CNN based framework based on fine-tuned MOBILENETV2 architecture for classification of benign and malignant histopathological cell images.

iv. Performance Evaluation of the proposed framework for breast cancer detection (i.e., classification) towards disease diagnosis.

The paper is organized into five segments. The literature survey elaborately describes the existing literature for breast cancer detection methods. The framework for breast cancer prediction in terms of breast abnormality (i.e., classification) using deep learning method is discussed. Segment 4 presents the results and discussion of the framework for breast cancer prediction using deep CNN method. Finally, segment 5 completes the paper and offers some future directions of the proposed study.

Related Work:

In this section, the literature review on the existing datasets and computer-aided methods for breast cancer detection is described. The study conducted in [2] mentions that breast melanoma is one of the most dominant malignancies in women and is a universal public health matter. As shown by the numbers in Figure 1, breast cancer surpassed all other cancer types in terms of global diagnoses in 2020. In the year2020, the International Agency for Research on Cancer (IARC)forecasts that approximately more than 2.25 million new examples of breast tumor and about 685,000 numbers of deaths caused due to breast cancer annually. The utmost recurrent reason of cancer-related death in female population was mostly due to breast melanoma. An important aspect of the global breast cancer mortality crisis is inequality. In high-income countries, where the prognosis for people with breast cancer is frequently rather favorable, there are disparities in survival rates between various socioeconomic levels. Due to difficulties in identification and treatment, women have a substantially lower chance of surviving the illness in developing nations. Approximately half a million women in developing nations passed away from breast cancer in 2020; these nations accounted for about 75 percent of all breast cancer fatalities worldwide. The study in [3] projects that real-world scenarios now allow for the detection of breast cancer using imaging techniques like magnetic-resonance-tomography, analytical mammograms, ultrasonography and histopathological imageries. But among these, a biopsy is still the only way to make a certain finding. The paper in [4] highlights that the most popular biopsy methods are Surgical Open Biopsy (SOB), void- aided, central needle culture, and fine indicator objective. Pathologistsmust examine the tissue biopsy under a microscope after enhancing the sample, which is often taken from biopsy samples or specimens collected. This procedure can be quite time taken and may be impacted by the medical and clinical experience. It is crucial to adopt computer aided decision system, which can reduce the stress on pathologists, because it saves time and reduces the possibility of human mistake. Imaging techniques like analytical mammograms, echography, magnetic reverberation imagery, and histopathological imageries. But among these, a surgery is still the lone method to make a certain analysis. The most popular biopsy methods are surgical open biopsy (SOB), central indicator culture, and fine needle aspiration. Pathologists must examine the tissue biopsy under a microscope after enhancing the sample, which is often taken from biopsy samples or specimens collected. This procedure can be quite time taken and may be impacted by the medical and clinical experience. It is crucial to adopt computer aided decision system, which can reduce the stress on pathologists, because it saves time and reduces the possibility of human mistake. In the paper [5], it is found that among several imaging modalities; histopathological images are one of the significant considered to be the second most gold standard method for diagnosis towards breast cancer. Even though breast cancer diagnosis using mammography is considered to be gold-standard method but it has more-false positive rate. During the histopathological examination, a biopsy sample is examined under a microscope by a pathologist/ expert to assess the growth of cancer in the organs. In the proposed papers,the aim is to detect the breast cancer (i.e., breast abnormality detection) thereby utilizing the convolutional Neural Network (CNN) architecture from histopathological images. Proceeding to the diagnostician's examination of the cell illustration, a histological tissue slide is formed. The physician determines the illness based on the cell distribution inthe histopathological pictures. Typical histological specimens have a large number of cells and surfaces that are roughly and asymmetrically gathered and distributed by a diverse set of various tissue kinds. Some of the sample images of the normal and abnormal histopathological images are shown in Figure 2. It also improves the effectiveness of histopathological process thereby providing a trustworthy alternative decision opinion for reliable analysis, which boosts their diagnosis.

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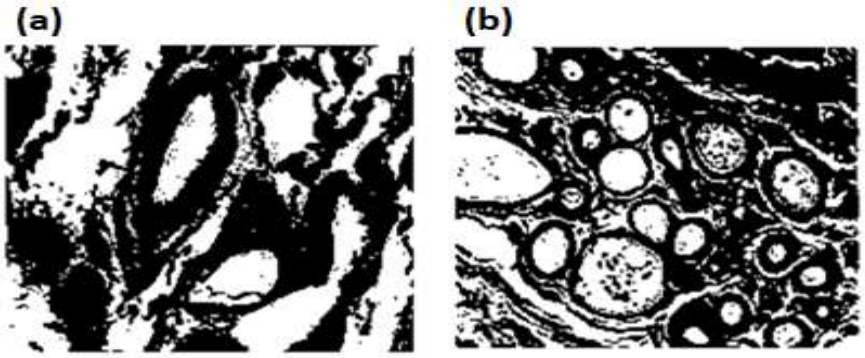


Figure 2: Histopathological Image sample (a) Normal Image, (b) Abnormal Images

Methodology:
This segment focuses on the framework for breast tumor classification for normal besides abnormal categories from the histopathological imageries using deep learning method is elaborately described. The overall flow representation of the framework for breast cancer (i.e., breast abnormality) detection is shown below. The Figure 3 depicts the framework of breast tumor detection using histopathological pictures by using CNN methods.

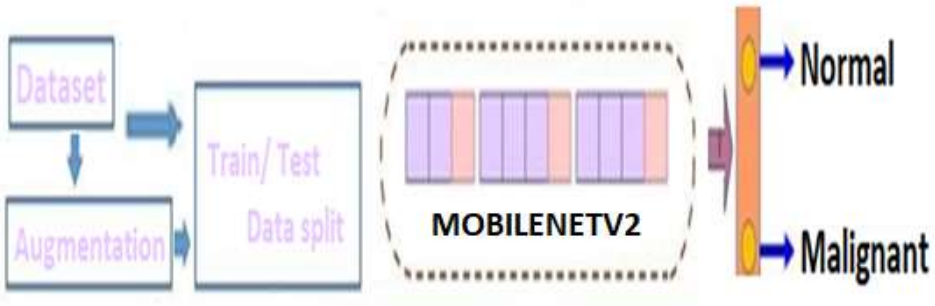


Figure 3: Framework for breast abnormality detection from Histopathological Images

Total number of Histopathological images was approximately 8000, that was considered for the study.

3.1 BREAKHIs Benchmark Dataset

BreakHis is an online available benchmark datasets for the medical research community toward breast cancer detection thereby utilizing the histopathological images [12]. The dataset comprises of around 8000 samples of histopathological pictures of chest tumor at cellular level method attained from affected ones via varied set of scaling factors in terms of magnification. The dataset encompasses 2,480 benevolent (i.e., normal histopathological images) and 5,429 malignant samples (i.e., abnormal histopathological images) with a standard resolution of 700X460 pixels at three channel RGB with 8-bitdepth in each of the considered channels. All the images are preserved in .PNG format. Some of the model images of the BREAKHIs standard dataset is exhibited as follows.

3.2 Data Augmentation

A huge volume and variety of dataset is necessary for the deep learning-based techniques to function well. However, by enhancing the data we currently have, we can make the model perform better. Deep learning frameworks often come with built-in data augmentation tools; however, they sometimes aren't very effective or don't have all the necessary features. To increase the volume and variety of the dataset we have applied certain geometric augmentation techniques on the BREAKHIs Benchmark Dataset [12].By diagramming each pixel in the original picture onto a new place in the new image, geometric augmentation creates additional data samples. The detailed description of the augmentation techniques adopted on our proposed dataset is provided below:

Augmentation in terms of Shift: Shift augmentation is the process of moving all of the pixels in a picture from one place to another. Shift augmentation comes in two forms: vertical shift augmentation and horizontal shift augmentation. The term" horizontal shift augmentation" refers to the horizontal shift of all pixels inside a picture. Vertical shift augmentation, on the other hand, refers to the vertical shift of all pixels in a picture.

Augmentation in terms of Flip: An image is alternated in a parallel or perpendicular alliance. Flicking happens on a

perpendicular axis in a parallel flip and a horizontal axis in an upright flip.

Augmentation in terms of Rotation: In rotation-based augmentation, the considered images are rotated at random in a clockwise manner from 0 to 360 degrees.

Augmentation in terms of Brightness: Improvement of random brightness depending on the specified brightness range, the picture brightness can be change to brilliant or dark. The picture becomes darker when the brightness range is less than 1.0 percent.

Augmentation in terms of zooming: Zoom augmentation adds extra pixels to the picture when zooming it at random. The augmented results of the histopathological images from BREAKHIs are shown in Figure 4.

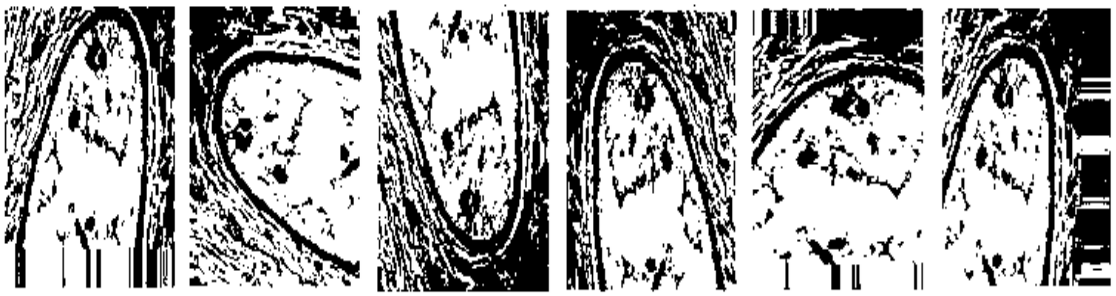


Figure 4: Augmented Histopathological Images of BREAKHIs Dataset

3.2.1 Training, Validating and Testing the Dataset

After effective augmentation of the BREAKHIs Benchmark Dataset using geometric trans-formation-based augmentation techniques, data preparation for effective training, validation and testing was done. In this work, to train the CNN model, augmented images with their corresponding images along with the corresponding class labels were used. At the beginning of the training process, augmented images were randomly shuffled before feeding into the CNN. The augmented images were split into 80:20 ratio that shows the two sets depicting training and testing correspondingly. For enduring the process of training, the training set is further slatted into 8:2 ratios.

3.2.2 Architectural Description for Breast Cancer Identification

In this study, MOBILENETV2 architecture, proposed by K. Simonyan etal. [25] from the University of Oxford was used. This MOBILENETV2 is a convolution Neural Network style, which was employed against ILSVR (Imagenet) race in 2014. This architecture is viewed as the outer executed visualization classical styles formed till date. VGG16 is mostly preferred method since it has 3x3 sized strainers in the convolution layers for pace 1 and 2x2 sized filters with a skipping step in terms of step2. In the full proposal, intricacy and max pool coats are organized in the identical style. Two fully linked layers are existing at the very end, sequenced by a soft max for prediction of the output. In this study, the last layers made up of two neurons were replaced with a MOBILENETV2 architecture that was pre-trained on the ImageNet challenge database [26]. The CNN films comprise of participation and yield layers along with a sequence of concealed layers. CNN hidden layer chiefly contains the following Convolution Layer, Initiation Layer, Assembling Layer and Completely Linked Layer. Detailed description of modified MOBILENETV2 style is provided below:

3.2.2.1 Convolution Layer

The Image features are extracted from the dataset by utilizing convolution films. It pertains pixels information of images in the dataset by understanding the features. In this layer, a filter slides over the input data and computes the output volume by computing dot product between all filter pixels and image pixels. The output of this layer is known as Feature Map (FM) or Convolved Feature [27].

Mathematical representation of the convolution coat is depicted in Equation3.1

$$C[m,\ n] = (f * h)[m,\ n] = \sum_{j}\sum_{k} h[j,\ k]\, f[m-j,\ n-k] \quad \ldots\ldots\ldots\ldots\ldots\ldots 1$$

The process to form a feature map involves smearing a kernel or filters to the input feature map and then calculating the element-based product among each entry of the kernel that is being measured and the input feature map under consideration at each location that is being considered in order to get the output value at the equivalent location of the output feature plot of the convolution mean.

The involvement image in this case is f, and the filter is h. The row wise entries and column wise entries of the result matrix's indexes are denoted by the numbers m and n, respectively. In addition, j and k, respectively, are used to indicate the filters' row and column indices.

Activation Function Layer:

This layer accomplishes element-wise initiation function of the measured feature plot, and extent of feature map remains sun bothered. The ReLU initiation function is utilized those exchanges negative values in the output of the convolutional layer by zero, and the positive value remain sun changed. The output of Activation function is called Rectified Feature Map (RFM). The mathematical representation of ReLU activation function (f(x)), as shown in Equation (3.2) [28]. Here, p is the selected pixel value.

$$f(p) = 0 \text{ if } f < 0 \\ = 1 \text{ if } f > 0 \quad \ldots\ldots\ldots\ldots\ldots\ldots\ldots\ldots 2$$

Pooling Layer:

The important motivation of utilizing pooling layer is to decrease the overall dimension of the rectified feature map, which makes the computation fast, reduces memory, and prevents from over-fitting. Pooling makes these presentations smaller and more manageable by reduces the dimensionally of each rectified feature map, and it also preserve each activation map independently. Here, we use Max pooling, which is defined by spatial neighborhood. Max pooling takes the biggest value from the convoluted feature matrix. A feature map, sometimes referred to as an output value, is produced by applying a kernel or sometimes termed as filters over the input feature map and then computing the access wise produce amid individually of the careful component of the kernel and the feature map at separately surveyed positions before hand.

Fully-Connected Layer:

It is common for the final convolution or pooling layer to flatten, or convert, its output feature maps into one-dimensional (1D) arrays of feature values (in the form of vectors), and then connect them to several impenetrable films, also named as completely linked films, where every considered contribution and equivalent yield is related by trainable mass. The characteristics produced by the density films and the considered down cast specimen sheets are then mapped to the system concluding yields, such as the generated probabilities for each considered group in cataloguing responsibilities, by a picking a fully connected layer. Finally, the completely linked film, the sequential number of output nodes often corresponds to the number of classes. Each layer that is fully coupled to a nonlinear function, such as RELU is followed.

The fully connected CNN is the player and utilizes a soft-max function in the output layer to classify images based on the neuron's greatest probability value. This layer is regular neural network layer, which takes input from the earlier layer, and works out the class scores of every neuron. The final fully connected output layer collects a dissimilar initiation role from the rest. Every job wants a diverse stimulation role, which must be selected consequently. The last fully connected layer's output real values are normalized by the proposed methodology's usage of a softmax activation function to target class probabilities, where each value ranges from 0 to 1 and they all add up to 1. And the class is assigned based on the highest probabilities core of the neurons in the last layer (i.e., the neuron having highest probability score is its class). Thus, in our work, the last layer gives an output using the soft-max function on a one-dimensional array of size is similar to the number of classes. The main motivation of a fully connected layer is to utilize the features for test image classification based on the train image data. In this work, the last film of the pre-qualified MOBILENETV2 process is substituted by two neurons(i.e., 0representing benign class and1 representing malignant class).

Experimental Result and Analysis:

In this chapter, the qualitative and quantitative evaluation of the CNN based frame work for classification of normal and abnormal histopathological images of breast cancer has been described.

4.1 Training the Framework for Histopathological Image Classification

The process of training a network involves locating weights in fully connected layers and kernels in convolutional layers that minimize discrepancies between the considered output predictions and supplied class labels (i.e., considered ground truths) on a training dataset.

The gradient descent optimization algorithm, loss function, and back propagation technique a real often used while training neural networks. A neural network loss function assesses the prediction performance of the model with particular considered kernels and weights on the considered training dataset. Then, various learnable or trained parameters like kernels and

weights are modified using an optimization approach like back propagation or gradient descent in line with the loss value. As illustrated in the following equation 4.1, binary cross entropy loss is determined in this work to update the weights throughout the network. A is considered as tag, and p(A) represents estimated possibility of copy for each of the M points that are engaged

$$BCL\ (q) = -\frac{1}{M}\sum_{i=1}^{M} A.\log_i(p\ (A)) + (1 - A).\log_i(1 - p\ (A)) \quad \ldots\ldots\ldots\ldots\ldots\ldots\ldots\ldots 3$$

The accuracy and loss diagram of the model for train and test is shown in Figure 5.

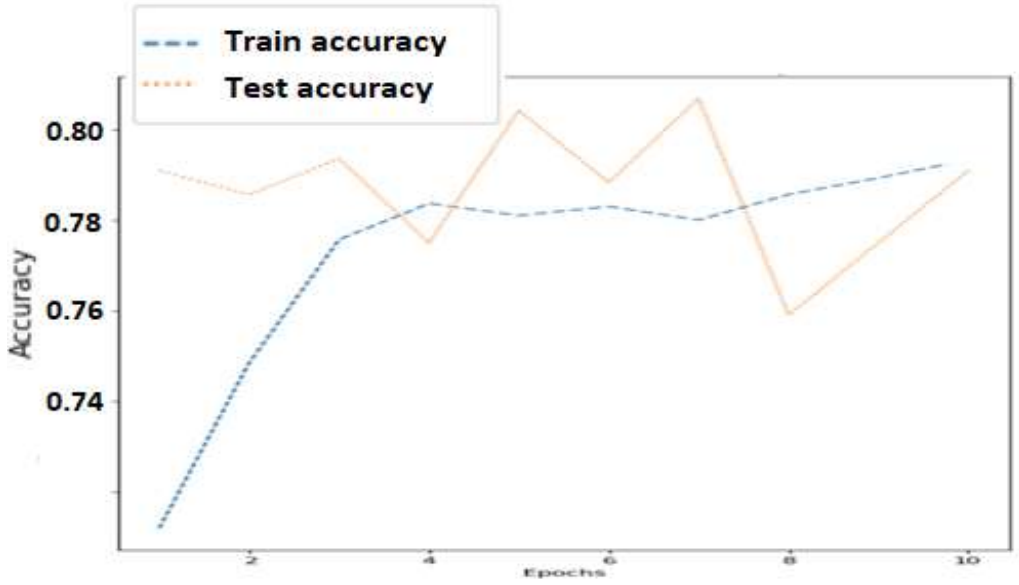
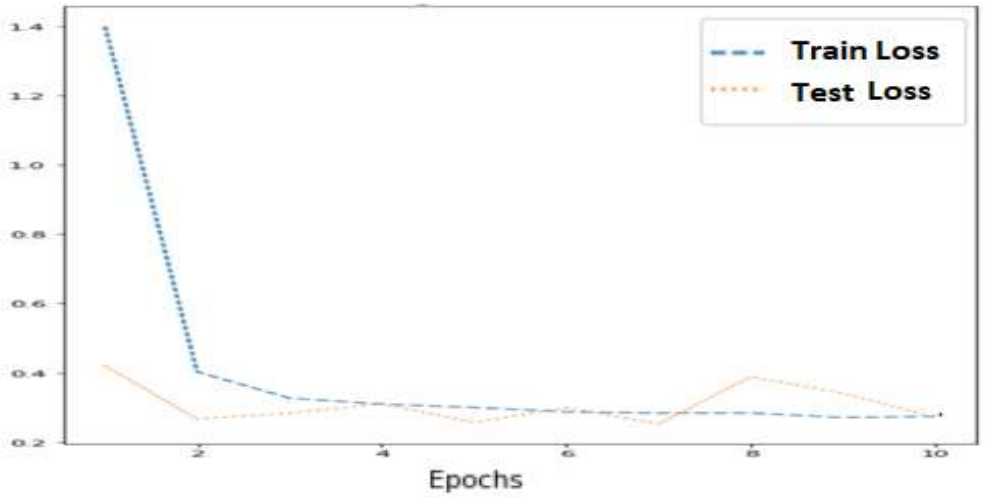


Fig. 5 (a) Accuracy of the model



(a) Loss of the model

Fig. 5 (b) Model diagram in terms of loss

Parameter Settings:

For effective and optimized training, two parameters i.e., learning rate and weighting decay are adjusted empirically to 0.001 and 0.0002 respectively, loss function is Binary Cross Entropy Loss, Optimizers is SGD (stochastic gradient descent) [29]),

and total epochs are considered to be 100 with batch size of 50 histopathological images. The train, accurateness and loss graph of the proposed framework for histopathological images are shown in diagram 6and 7. It is detected from the graph, after 100 epochs the models fixes to the maximum accuracy and sustains further. Therefore, we have used the model after 100 epochs for testing purpose.

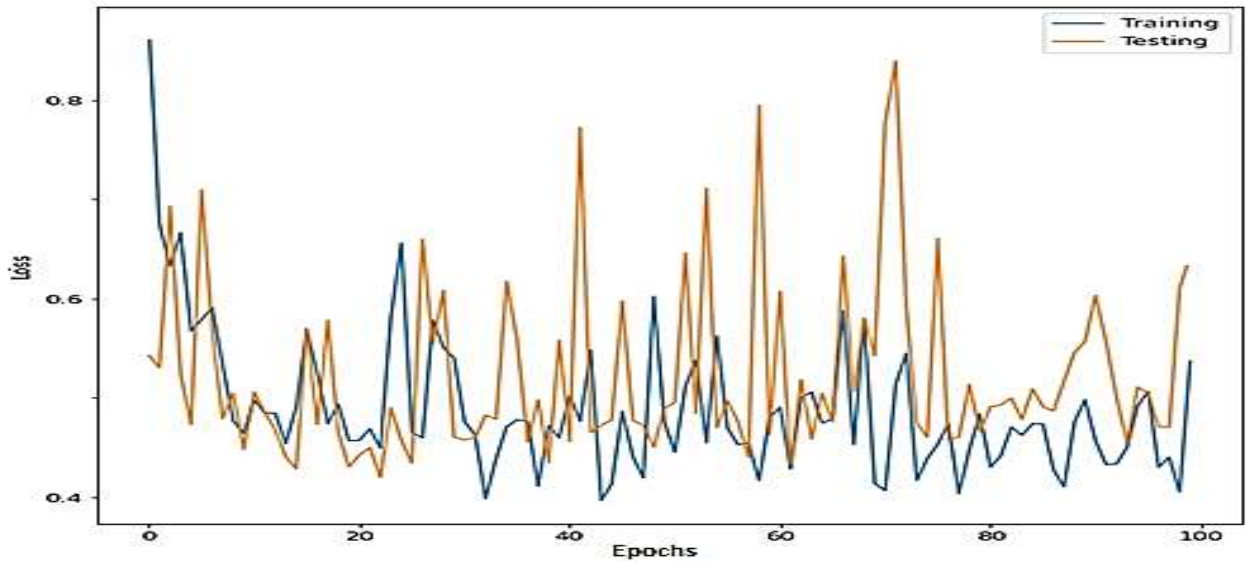


Figure 6: Train and Test Loss Graph of Normal and Abnormal Histopathological Images

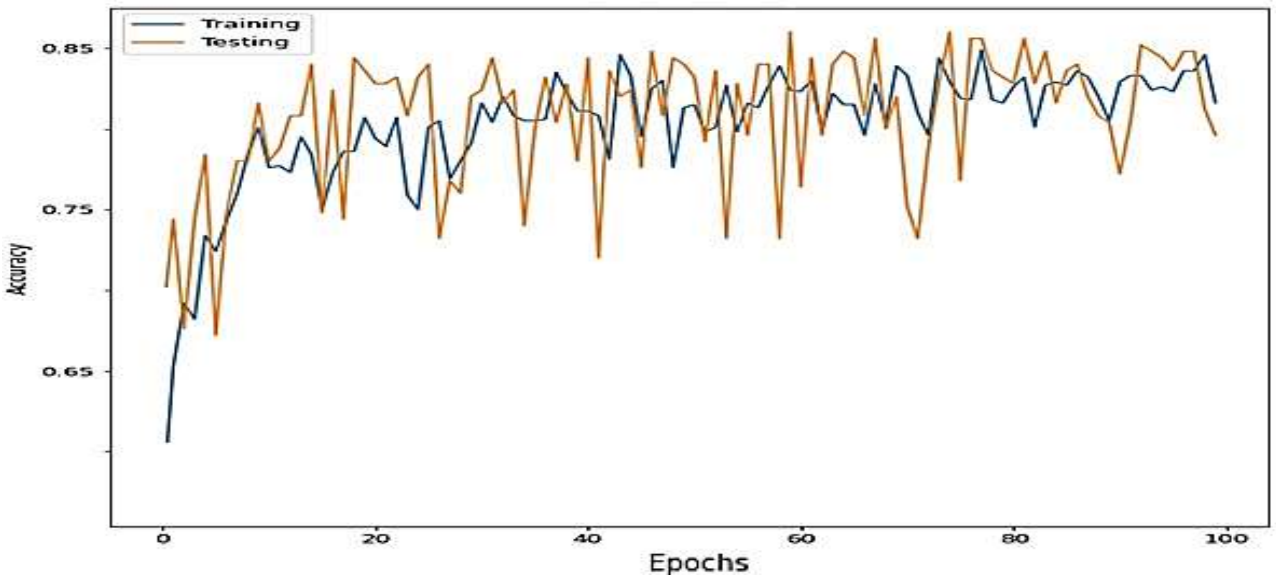


Figure7: Train and Test Accurateness Graph for Normaland Abnormal Histopathological Images

Performance Evaluation Measures:

For effective comparison, the testing performance of the classification method is computed and quantitatively measured in terms of accuracy, specificity and vulnerability defined by the following equations [30]:

$$\text{Accuracy} = \frac{TP + TN}{TP + TN + FP + FN} \quad \ldots\ldots\ldots\ldots\ldots\ldots\ldots\ldots\ldots\ldots 4$$

$$\text{Sensitivity} = \frac{TP}{TP + FN} \quad \ldots\ldots\ldots\ldots\ldots\ldots\ldots\ldots\ldots\ldots\ldots\ldots\ldots\ldots 5$$

$$\text{Specificity} = \frac{TN}{FP + TN} \quad \ldots\ldots\ldots\ldots\ldots\ldots\ldots\ldots\ldots\ldots\ldots\ldots\ldots\ldots 6$$

Here in equation 4, 5, and 6, TP (True Positives) and FP (False Positives) denote the numbers of correctly detected and incorrectly detected pixels, and TN (True Negatives) and FN(False Negatives) denote the numbers of accurately and in accurately missed pixels.

Experimental Results and Discussions:

The visual detection results of the framework for classification of normal and abnormal histopathological images are displayed in Figure4.2.Also, quantitative measures of the framework for actual cataloguing of histopathological imageries on the testing set of BREAKHI Standard Database is shown in Table 4.1.

The images shown in Fig. 8 and Fig. 9 through the framework achieves better performance for histopathological image classification with an average accuracy, specificity, and sensitivity of 83%, 80%, and 85%respectively.

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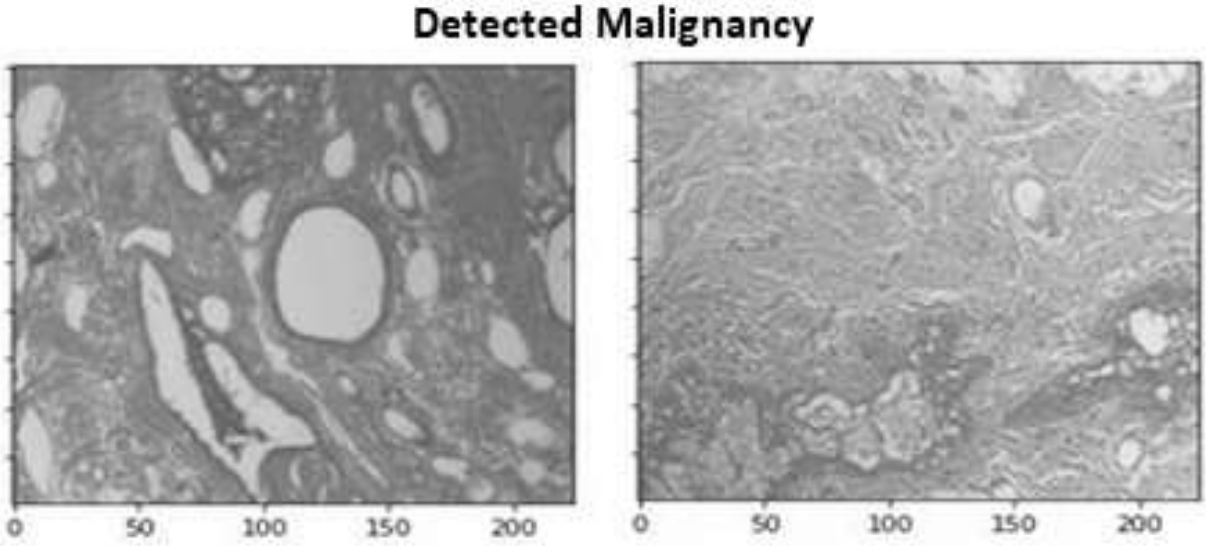

Figure 8: Experimental Results of Malignant Images

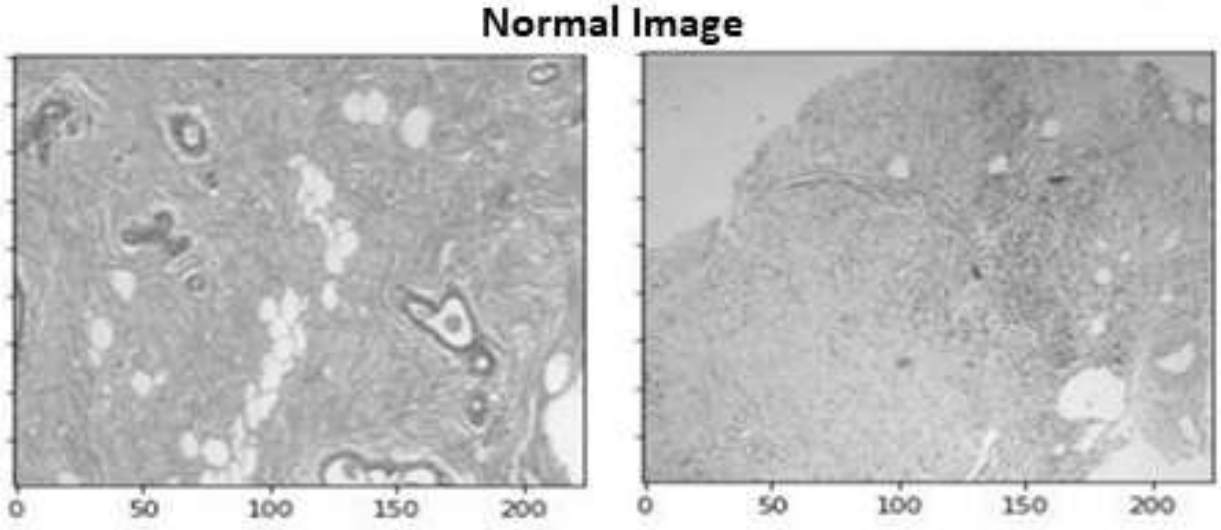

Figure9: **Experimental Results of Normal Images in the Framework**

Table 4.1: Quantitative Results for Histopathological Image Classification using our Framework

Performance Evaluation Measure	Performance
Accuracy	83%
Specificity	80%
Sensitivity	85%

Conclusion and Future Work:

The recurrent factors of deaths are due to cancer, which develops when body cells grow abnormally so as observed in the patients of breast cancer. It is increasingly becoming a serious issue for people everywhere and posing a threat to their safety and welfare. Among this, foremost reasons of death for females worldwide are Breast Melanoma, and particularly common in the United States. A number of imaging techniques, i.e., mammography, computed tomography, MRI, echography, and surgeries can be used for classifying breast cancer. Among various medical imaging modalities, a histopathology analysis (i.e., biopsy) is mostly done, which provides the analysis of breast cancer for accurate detection and diagnosis. The foremost inspiration of the study was a proposal to plan a CNN based outline for breast cancer recognition. For this, we have designed a fine-tuned MOBILENETV2 architecture for two stage classification i.e., normal and abnormal histopathological images. The experiments have been carried out in BREAKHIs Benchmark Dataset. It has been observed that the model achieved prediction performance of accuracy, specificity, and sensitivity of 84.83%, 81.48%, and 87.92% respectively. In future, I will enhance the framework by including extra modules so as to increase the performance for histopathological image classification. In addition, in future the proposed framework for multi-class classification of histopathological images will be used.

References:

1. Xiang Yu et al. “A systematic survey of deep learning in breast cancer”. In: International JournalofIntelligentSystems37.1(2022), pp.152–216
2. M. Masud, A. E. Eldin Rashed, and M. S. Hossain, “Convolutional neural network-based models for diagnosis of breast cancer,” *Neural Computing and Applications*, vol. 5, 2020.
3. G. Muhammad, M. S. Hossain, and N. Kumar, “EEG-based pathology detection for home health monitoring,” *IEEE Journal on Selected Areas in Communications*, vol. 39, no. 2, pp. 603–610, 2021.
4. M. Chen, J. Yang, L. Hu, M. S. Hossain, and G. Muhammad, “Urban healthcare big data system based on crowdsourced and cloud-based air quality indicators,” *IEEE Communications Magazine*, vol. 56, no. 11, pp. 14–20, 2018.
5. M. S. Hossain, “Cloud-supported cyber-physical localization framework for patients monitoring,” *IEEE Systems Journal*, vol. 11, no. 1, pp. 118–127, 2017.
6. S. A. Alanazi, M. M. Kamruzzaman, M. Alruwaili, N. Alshammari, S. A. Alqahtani, and A. Karime, “Measuring and preventing COVID-19 using the SIR model and machine learning in smart health care,” *Journal of Healthcare Engineering*, vol. 2020, Article ID 8857346, 12 pages, 2020.
7. Y. Zhang, X. Ma, J. Zhang, M. S. Hossain, G. Muhammad, and S. U. Amin, “Edge intelligence in the cognitive internet of things: improving sensitivity and interactivity,” *IEEE Network*, vol. 33, no. 3, pp. 58–64, 2019.
8. M. M. Kamruzzaman, “Architecture of smart health care system using artificial intelligence,” in *Proceedings of the 2020 IEEE International Conference on Multimedia & Expo Workshops (ICMEW)*, pp. 1–6, London, UK, July 2020.
9. W. Min, B.-K. Bao, C. Xu, and M. S. Hossain, “Cross-platform multi-modal topic modeling for personalized inter-platform recommendation,” *IEEE Transactions on Multimedia*, vol. 17, no. 10, pp. 1787–1801, 2015.
10. M. M. Kamruzzaman, “Arabic sign language recognition and generating Arabic speech using convolutional neural network,” *Wireless Communications and Mobile Computing*, vol. 2020, Article ID 3685614, 9 pages, 2020.
11. M. S. Hossain, S. U. Amin, M. Alsulaiman, and G. Muhammad, “Applying deep learning for epilepsy seizure detection and brain mapping visualization,” *ACM Transactions on Multimedia Computing, Communications, and Applications*, vol. 15, no. 1, pp. 1–

17, 2019.
12. J. L. Wang, A. K. Ibrahim, H. Zhuang, A. Muhamed Ali, A. Y. Li, and A. Wu, "A study on automatic detection of IDC breast cancer with convolutional neural networks," in *Proceedings of the 2018 International Conference on Computational Science and Computational Intelligence (CSCI)*, pp. 703–708, Las Vegas, NV, USA, December 2018.
13. M. S. Hossain and G. Muhammad, "Emotion-aware connected healthcare big data towards 5G," *IEEE Internet of Things Journal*, vol. 5, no. 4, pp. 2399–2406, 2018.
14. Cruz-Roa, A. Basavanhally, F. González et al., "Automatic detection of invasive ductal carcinoma in whole slide images with convolutional neural networks," *Medical Imaging 2014: Digital Pathology*, vol. 9041, no. 216, p. 904103, 2014
15. S. U. Amin, M. Alsulaiman, G. Muhammad, M. A. Bencherif, and M. S. Hossain, "Multilevel weighted feature fusion using convolutional neural networks for EEG motor imagery classification," *IEEE Access*, vol. 7, pp. 18940–18950, 2019.
16. N. Wahab and A. Khan, "Multifaceted fused-CNN based scoring of breast cancer whole-slide histopathology images," *Applied Soft Computing*, vol. 97, p. 106808, 2020.
17. M. Gravina, S. Marrone, M. Sansone, and C. Sansone, "DAE-CNN: exploiting and disentangling contrast agent effects for breast lesions classification in DCE-MRI," *Pattern Recognition Letters*, vol. 145, pp. 67–73, 2021.
18. L. Tsochatzidis, P. Koutla, L. Costaridou, and I. Pratikakis, "Integrating segmentation information into CNN for breast cancer diagnosis of mammographic masses," *Computer Methods and Programs in Biomedicine*, vol. 200, p. 105913, 2021.
19. M. Malathi, P. Sinthia, F. Farzana, and G. Aloy Anuja Mary, "Breast cancer detection using active contour and classification by deep belief network," *Materials Today: Proceedings*, 2021.
20. M. Desai and M. Shah, "An anatomization on breast cancer detection and diagnosis employing multi-layer perceptron neural network (MLP) and Convolutional neural network (CNN)," *Clinical eHealth*, vol. 4, pp. 1–11, 2021.
21. D. Abdelhafiz, J. Bi, R. Ammar, C. Yang, and S. Nabavi, "Convolutional neural network for automated mass segmentation in mammography," *BMC Bioinformatics*, vol. 21, no. 1, pp. 1–19, 2020.
22. H. Rezaeilouyeh, A. Mollahosseini, and M. H. Mahoor, "Microscopic medical image classification framework via deep learning and shearlet transform," *Journal of Medical Imaging*, vol. 3, no. 4, Article ID 044501, 2016.
23. G. Murtaza, L. Shuib, A. W. Abdul Wahab et al., "Deep learning-based breast cancer classification through medical imaging modalities: state of the art and research challenges," *Artificial Intelligence Review*, vol. 53, no. 3, pp. 1655–1720, 2020.
24. M. F. Alhamid, M. Rawashdeh, H. Al Osman, M. S. Hossain, and A. El Saddik, "Towards context-sensitive collaborative media recommender system," *Multimedia Tools and Applications*, vol. 74, no. 24, pp. 11399–11428, 2015.
25. S. Qian, T. Zhang, C. Xu, and M. S. Hossain, "Social event classification via boosted multimodal supervised latent dirichlet allocation," *ACM Transactions on Multimedia Computing, Communications, and Applications*, vol. 11, no. 2, pp. 1–22, 2015.
26. D. Singh, S. Singh, M. Sonawane, R. Batham, and P. A. Satpute, "Breast cancer detection using convolution neural network," *International Research Journal of Engineering and Technology*, vol. 5, no. 6, pp. 316–318, 2017.
27. M. M. Jadoon, Q. Zhang, I. U. Haq, S. Butt, and A. Jadoon, "Three-class mammogram classification based on descriptive CNN features," *BioMed Research International*, vol. 2017, Article ID 3640901, 11 pages, 2017.
28. T. Kooi, A. Gubern-Merida, J.-J. Mordang et al., "A comparison between a deep convolutional neural network and radiologists for classifying regions of interest in mammography," in *International Workshop on Breast Imaging*, pp. 51–56, Springer, 2016.
29. P. Simard, B. Victorri, Y. LeCun, and J. Denker, "Tangent prop-a formalism for specifying selected invariances in an adaptive network," *In Advances in Neural Information Pro-cessing Systems*, pp. 895–903, 1992.
30. S. Noguchi, M. Nishio, M. Yakami, K. Nakagomi, and K. Togashi, "Bone segmentation on whole-body CT using convolutional neural network with novel data augmentation techniques," *Computers in Biology and Medicine*, vol. 121, article 103767, 2020.