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FA -WSI -CNN Model for Predicting Breast Cancer using Deep Learning

Dr.P.Rama[1]
[1] Assistant Professor Department of Computing Technologies, College of Engineering and Technology, Faculty of Engineering and Technology, SRM Institute of Science and Technology, SRM Nagar, Kattankulathur, 603203, Tamilnadu, India.
e-mail: ramaponnuvarman@gmail.com

Dr.V. Angayarkanni[2]
[2] Assistant Professor Department of Computing Technologies, College of Engineering and Technology, Faculty of Engineering and Technology, SRM Institute of Science and Technology, SRM Nagar, Kattankulathur, 603203, Tamilnadu, India.
e-mail: angayarv@srmist.edu.in

Dr. J. Premalatha[3]
[3] Assistant Professor , Dhanalakshmi Srinivasan Arts and Science College ECR, Mamallapuram, Chennai .
E-mai: premalathasaro@gmail.com

Mrs. Geetha Rani K[4]
[4] Assistant Professor,Department of Computer Science and Engineering, Jain (Deemed-to-be University),Bangalore.
E-Mail: ramagetu2015@gmail.com

Abstract—Deep Learning is used for predicting a large volume of data sets in the medical field particularly for breast cancer prediction and diagnosis. The most effective and broadly applied model for detecting breast cancer is the Conventional Neural Network (CNN) among the various deep learning algorithms available. The existing CNN models are lacking in the analysis of a fully labeled Whole Set Image (WSI) data set. The proposed Fully Automate WSI with the CNN model will analyze the whole slide images and patch the input image for improving the accuracy. Then CNN model will get input from patched images and creates classified data for predicting breast cancer. The scikit-learn deep learning framework with Python is used to analyze the result and build a generalized tissue classifier, the WSI data set should include tissues generated under numerous different preparation circumstances. The proposed model experimental results shows promising WSI patch values, accuracy, precision, re-call, and F1 score of the breast cancer tissues which are used for diagnosis purposes. The FA -WSI -CNN model can reduce the training time by evaluating the inference time

Keywords- Conventional Neural Network;Whole Set Image; Breast Cancer; Tissue classifier; Accuracy; Precision.

I. INTRODUCTION

In recent days majority of women are facing the cancer problem, especially breast cancer. The breast cancer death ratio is 3:1 among the world and every year it is increased to 48% from 90s to '20s as shown in Figure 1. CAD(computer-aided design) has just been created to identify breast cancer easier. Rationalistic computer-aided design systems of rules, on the additional hand, frequently rely on manually made features, which degrades overall performance. Deep learning-based techniques for detecting breast cancer have been recently researched over all development of artificial intelligence (AI) and machine learning methods [1].

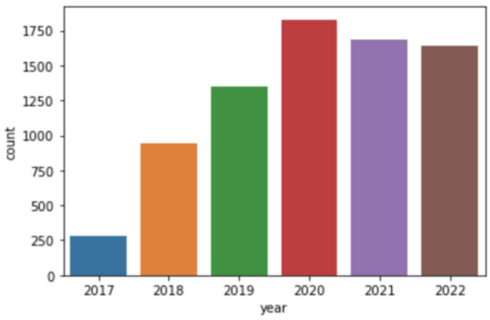

Figure 1. Comparison chart of Brest cancer count

The convolutional region , the pooling region are the important layers that get up the deep CNN architecture, which is employed in image processing. By swapping weights and biases, the convolutional layer calculates the end product of nerve cell adjacent to a local area network at the signal location. The final result of the convolutional layer of the algorithm is sampled and the pooling layer reduces the data volume as used in learning process. The fact that a deep CNN must learn millions of parameters and have access to its growth of medical field and many advanced deep CNNs algorithms are invoked in the medical domain.

In digital mammography, a computerized technique can service as selection assistance and a intermediate public opinion for the primal diagnosis of breast cancer, particularly in compact and extremely heavy conditions. The development of computer vision technologies and algorithms over the past ten years has produced promising results in the early stage of breast cancer detection and in supporting radiologists' diagnosing. Deep learning models are relatively new and are becoming more prevalent, which can make help more valuable since they have demonstrated amazing achievements in numerous domains.

This paper is evaluating breast cancer identification, which can be utilized to identify breast cancer in the early stage. The CNN model is the best model to segregate the images for the classification of positive and negative values. The first section is an introduction to breast cancer and its current methodologies. The second section will be discussed the literature review and it will be continued. The rest of the paper has discussed the proposed works, further, it has continued the result and analysis section. Finally, this paper were highlight the performance of the proposed work with a chart and concluded with major advantages.

template, modified in MS Word 2007 for the PC, provides authors with most of the formatting specifications needed for preparing electronic versions of their papers. All standard paper components have been specified for three reasons: (1) ease of use when formatting individual papers, (2) automatic compliance to electronic requirements that facilitate the concurrent or later production of electronic products, and (3) conformity of style throughout conference proceedings. Margins, column widths, line spacing, and type styles are built-in; examples of the type styles are provided throughout this document and are identified in italic type, within parentheses, following the example. Some components, such as multi-leveled equations, graphics, and tables are not prescribed, although the various table text styles are provided. The formatter will need to create these components, incorporating the applicable criteria that follow.

II. RELATED WORKS

Thus, the author mentioned [1] CNN model were more accurate for predicting the breast cancer, and also accuracy criteria level is more high. This CNN models are more popular and give better performance metrics in research side. But investigating in depth knowledge in side the research area is very complicated. The study of histology pictures is a booming and important scientific area that aids in disease diagnosis. The difficulties of histology image analysis are discussed in this work [2].

With less reliance on strict oversight, WSI analysis can now address problems like patient survival and recurrence prediction, where the true state of affairs is only known at a level beyond patching.[3]. An automated approach for identifying invasive carcinoma of the ducts (IDC), the most prevalent sub-type of breast cancer, is introduced using deep transfer learning. To address the IDC spotting challenges, pre-trained deep learning models ResNet-50 and DenseNet-161 were employed.[4]. The CNN method evaluates the IDC body part areas of WSIs for the self-regulating detection of this cancer.The article describes three distinct CNN field of study and compares them. The proposed method, which leverages CNN Model 3, achieves an accuracy of 87%.The major disadvantage of the current research was that it relied on a secondary database like Kaggle, and subsequent research should rely on primary data to improve the accuracy of the outcomes of the spotting of breast cancer[5,6].

The authors re-commands the best breast cancer prediction and development areas in research and also author can evaluate about deep learning models with comparisons. CNN models with number of layers and somatic cell, along with determination on larger cohorts, have deeper configurations [7,8]. In general identification of breast cancer classified in this article is three ways: classification, detection and segmentation. In this way CNN with diagnosis has give better success rate.Fully Convolutional Networks (FCN) can handle greater image sizes (500 500 pixels) for semantic segmentation. ABecause a CNN would need cardinal or large indefinite quantity of parameters for a WSI, applying CNNs directly to WSI is not viable. By combining our method with an FCN method and using GPUs, it may be possible to analyse and examine large full slide photos more quickly[9,10].

Deep learning along with ultrasonic images giver greater prediction ration to breast cancer analysis. It allow to establish efficient system for BC diagnosing, assisting in timely diagnosis and treatment [11,12].There is an absence for a user surface with pre- or post-processing or handmade functions in the new framework. The greatest accuracy can be achieved by enriching data by using updated segmentation of the U-Net model and the InceptionV3model. When compared to cutting-edge CAD systems, deep convolutional neural networks (DCNN) dependability obtained by combining deep features fusion for both datasets was found the greatest value. [13,14]. The end-to-end UNet scheme for one-stage pre-processing identification, the process of segmentation and categorical of breast cancer. Data augmentation, cross validation, fine-tuning more model parameters, increasing how many training epochs there are, and applying transfer learning are all possible.Other breast tumour traits that the multi-stage framework could not discover will be combined into a more thorough diagnosis to compute the property of disease of the breast growth [15].

Recent advancements in mammography CNNs are demonstrated through an analysis of viewpoints, data, and literature. CNN-based CAD can be used in conjunction with clinicians and offers a multitude of clinical and computational innovation opportunities [17]. Applied mathematics, LBP, categorization, and other dynamical attribute are extracted from the data set for Train Validation and Test data sets using an automatic Diverse Features based Breast Cancer Detection (DFeBCD) scheme using a procedure[18,21]. The MIAS, the DDSM, and the INbreast are three standard data sets that the authors in use to assess the performance of their proposed model. By incorporating extended and narrowed pooling kernels, the vector pooling block (VPB) for the CCN method collect the both global and local characteristics, in contrast to the standard pooling layer that gathers data from a constant square kernel. Future work will concentrate on pooling models that are source-dependent so that they can be used for a range of computer vision issues, building on the creative VP [19–20].

III. FULLY AUTOMATED WSI WITH CNN MODEL

The proposed FA-WSI with CNN model is identifying the breast cancer cells in an early stage and it is initiated by a whole slide image (WSI) as input sample image as mentioned in the Figure 3. Next, the input image has to be patched for accurate evaluation of results and it is very easy to train the data with CNN to predict the breast cancer tissues. Next, the patched image can be trained by using the CNN model. The CNN model classifies the positive tissue and negative tissue and from the classified data final result is evaluated with the prediction of breast cancer cells as shown in Figure 2.

WSI is a wide range of images to get a whole slide of data in a particular image. These WSI data slides demand in situ molar data connected with whole cells. When evaluating the WSI, it is possible to visualize the cancer cell protein; it can expose the mutable multiplex-labelled data.This will help to find out the cancer tissues easily and also the labeled data to reach the various levels of analysis when imposing the deep learning technology. Data availability is more challenging in a normal scanner image when compared with WSI. Enormous data is

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available in the WSI scanner image with bright, high illumination and different type size shown in Figure 4.

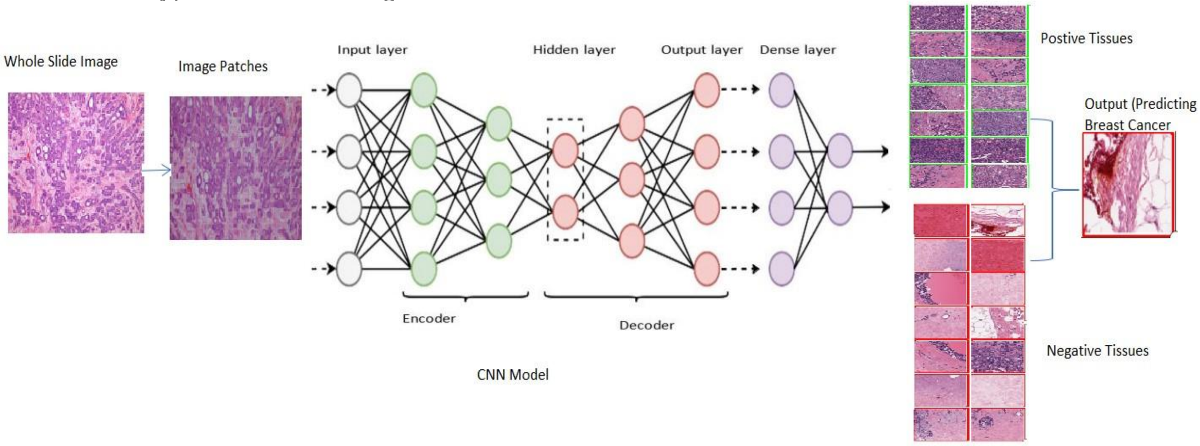

Figure 2.Fully Automated WSI with CNN Model

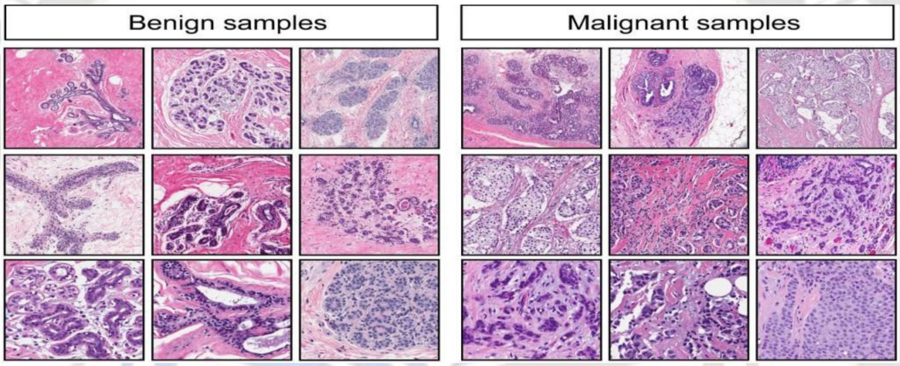

Figure 3. Sample Image taken for analysis

Generally, WSI is not possible to give input in the deep learning training process. Before feeding the input WSI is split into some parts and extract the exact patches from the images. The image patch process has been multiply produce significant results for the identification of cancer tissues.

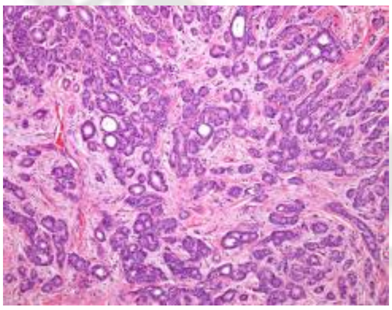

Figure 4. Whole Slide Image

Common image patch region 1000 squares size range is 32x32 pixels in the smaller size and the larger size is 512x512. It is the more complex region or multi-cellular combined objects. The patch size is Wx H = 128x128 and the image sample 512.jpg has dimensions MxN = 512x512. where the letter x is the least number, it is larger than or equal to x. Blue dots indicate patch centres, and red and pink dots indicate patch borders.The total number of produced image patches is displayed in Figure 5.

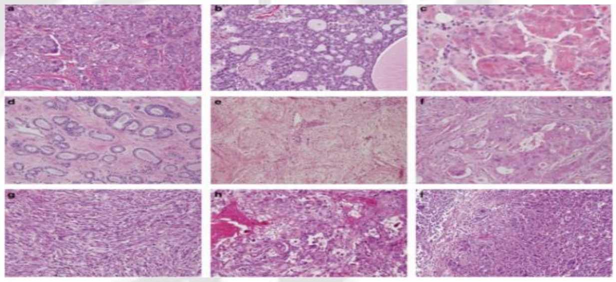

Figure 5.Over all number of created patches

To calculate the overall number of patches created in a WSI by invoking equation 1,

$$K = \left[\frac{M-\ W+1}{Sx}\right]x\left[\frac{N-\ H+1}{Sy}\right] \quad (1)$$

The total number of spots produced is calculated using Eqn(1). K is the total number of spots, W&H is Width and Height H (in pixels), Sx-Sy is the Horizontal and vertical offset of the image MxN is the dimension of the image.

The proposed CNN model has introduced an automatic diagnostic extraction of features and image classification for the prediction of breast cancer as deployed in Figure 6. The image I is captured and convolved using several kinds of kernels to create a property map in the CNN, which belongs to many

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convolutional layers. The image feature maps at position (i, j) at a particular layer l is designated as hl ij, the weight as Wl, and the bias as bl. The feature map's equation 2 is provided as follows:

hlij=ReLU((Wl*I)ij+bl) (2)

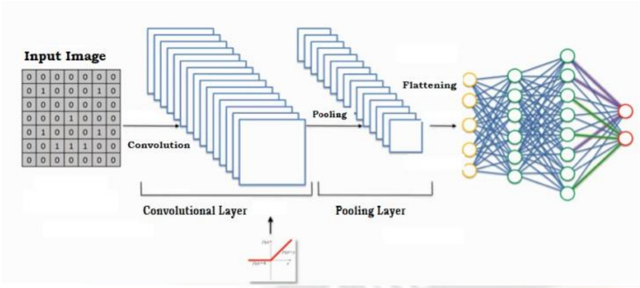

Figure 6. Proposed CNN Model for Analysis

The Rectified Linear Unit (ReLU) is used here. The ReLU function regulates the output; this is one of the parts of algorithm activation.

$$ConvOutputSize = [((Iw - Kw + 2p/s) + 1) * ((Ih - Kh + 2p/s) + 1) * f^2 \quad (3)$$

$$PoolOutSize = [((Iw - Kw/s + 1) * ((Ih - Kh/s + 1) * Nc \quad (4)$$

$$ParamNo = fl * (fl - 1 * Kw * Kh + 1) \quad (5)$$

The equations 3, 4 and 5, compute the property of the result for the convolution layer, Pooling layer is image size, and the quantity of result image parameters for the convolution layer. where Iw, Ih are the input image's width and height, in correspond to the previous layer's product image dimensions; Kw, Kh are the kernel's width and height; p stands for padding; s for stride; and f stands for the performance of kernels (piece & filter out). The depth of the stimulant image, also known as Nc, same layer values.

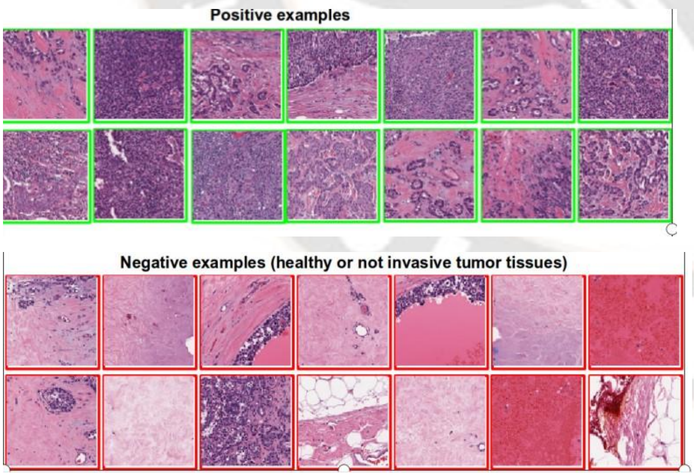

Figure 7. Classified image

The output value of CNN model ranges from 0 to 1, and the output value holds from positive class neurons, these neurons classified patches applied in the mathematical notation. Each patch has the primary coordinates of WSI. Corresponding coordinates will map the probability values over the WSI. CNN model has two types of output between 0 to 1, 0 is a negative value no Cancer tissue found, and 1 is a positive value means cancer tissue found. The final output is to predict breast cancer tissues as Mention in Figure 7 and 8.

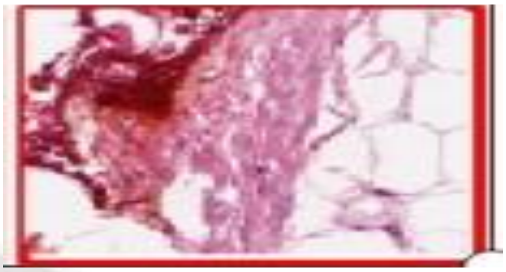
Figure 8. Final Breast Cancer Prediction

The proposed model is fully automated when it predict the cancer tissues. The CNN model without any human guidance it automatically detects the important features of cancer cell. Prediction process having many steps in that majorly consider in the proposed system is image patching, Separating Your Training and Testing Data sets,Transforming the Data Building the CNN ,Running Predictions on the Test Set by segmentation of positive and negative values, Making a Single Prediction,Improving the Model Accuracy.The CNN model performance can be evaluated based on test accuracy comparison,Convergence Rate Comparison and Training, Validation and Testing Results Comparison.

IV. Experimental Results

Thus, the scikit-learn deep learning framework to carry out in Python for output execution, it the most popular and less costly method. The scanned hospital images database was gathered online Shown in Table 1, which was then made public with the ethics committee's blessing and a patient consent form.500 frontal thermogram picture with a resolution of 640 x 480 pixels are taken with a scanner and used in this investigation (with 250 normal and 250 aberrant subjects). These pictures show diverse-sized and shaped breasts. The CNN model should not get WSI directly as an input for training and classification, because in general WSI without a patch have not produce an accurate result. So, Patching is allow the replacement of arbitrarily shaped parts on an image with a skin-deep to other arbitrarily shaped regions plus a synthetic noise component. For example, the sample input image has two output before and after patching values which are used in our experiment, that is before Patching the Normal breast cancer cell value is 0.993264, and Invasive Ductal Carcinoma is 0.006736 after patching the Normal breast cancer cell value is 0.133048, Invasive Ductal Carcinoma: 0.866952.

TABLE I. DATA SET

Magnification	*Benign*	*Malignant*	*Total*
50X	500	1345	1845
100X	623	1453	2076
150X	345	1234	1579
480X	657	1456	2113
Total of Images	2125	5488	7613

Thus, the patched image output is the input of the CNN model. Hence, during the CNN model, multiple layers were involved to train the image for predicting the cancer tissues. In

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this system the CNN architecture having four layers is initiated by 16,32,128 and 512 neurons, it's fully connected with each layer. This model employed a rigid convolutional kernel of size 8*8 and a pool kernel of size 2*2. The CNN model can get two types of classification data, says positive and negative. If the positive values are found in Python coding results, there are no breast cancer tissues affected in the image, otherwise negative found breast cancer tissue is found in the image. Finally, can we evaluate the demonstration of the CNN model by precision, recall, and F1-score.

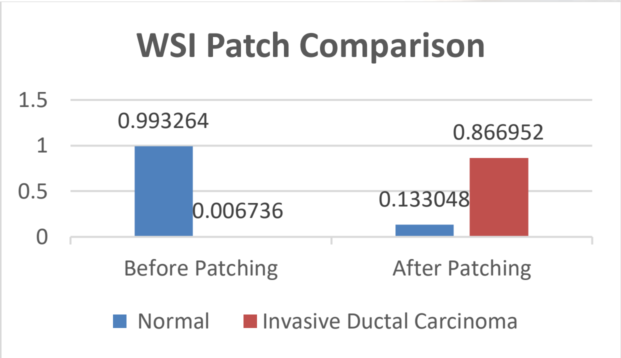

Figure 9. WSI Patch Comparison chart

To calculate the ,

$$\text{Accuracy} = \frac{TP + TN}{TP + FP + TN + FN} \quad (6)$$

$$\text{Precision} = \frac{TP + TN}{TP + FP} \quad (7)$$

$$\text{Re call} = \frac{FN}{FP + TP} \quad (8)$$

$$\text{F1 - Score} = 2 * \frac{(\text{precision} \bullet \text{Re call})}{(\text{precision} + \text{Re call})} \quad (9)$$

$$Training\ time(h) = \frac{1}{3600}\sum_{i=1}^{n=100}(Tt)I \quad (10)$$

$$Inference\ time(s) = \frac{1}{10}\sum_{i=1}^{n=10}\left(\frac{Tf-Tin}{Ns}\right)I \quad (11)$$

Where,
TP – True Positive
FP – False Positive
FN – False Negative
TN – True Negative
Tf – Ending Prediction time Whole slide Image
Ti – Staring Prediction time for Whole slide Image
Tt – Training Time
Ns – Number of Test Sample

$$\text{Accuracy} = \text{number of correct predictions}/\text{total number of predictions} \quad (12)$$

Accuracy can be evaluated by the predicted values. The predicted positive values with total number of predicted values are estimated. Accuracy serves as the most popular performance indicator for models.

Positive data that was correctly predicted is approximated. The diagonal is the value that matters the most powerful evaluation of negative data was negative. It is the sum of all values in the confusion matrix, except the linked class's row and column. The assessment of negative data was positive. It is the sum of all values in the applicable column, excluding TP, for each class. False Negatives (FN) are when positive data is interpreted as negative. It is the sum of all values in the pertinent row, excluding TP, for each class.

From the Equation 10 and 11 the training time calculate in hours and inference time has been calculated in seconds. The FA-WSI-CNN model trained on the data set as low inference time that indicate the results can be predicted in a shortened period and short training period. The output can be expected less than 0.1 s. The maximum prediction speed 0.0404 s, minimum prediction speed is 0.2371 s and FA-WSI-CNN model can be trained in 05h.

Table 2 explains the accuracy, precision, F1-Score, and Recall of the proposed FA-WSI-CNN model and existing model values. In the research results, the FA-WSI-CNN model has given better accuracy, precision, F1-Score, and recall as mentioned in Figure 10. When compared to existing models, the FA-WSI-CNN model produces the greatest prediction values for breast cancer.

TABLE II. COMPARISON OF PROPOSED AND EXISTING SYSTEM MODELS

Methods	***Accuracy***	***Precision***	***Re call***
FA-WSI-CNN	99%	99%	99%
ResNet-18	93%	94%	85%
Shufflenet	90%	92%	75%
AlexNet	92%	93%	89%

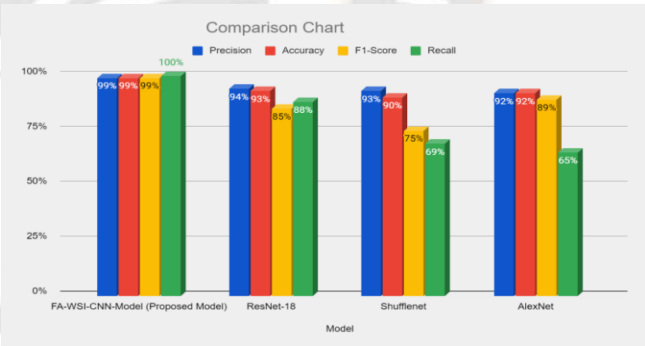

Figure 10. Breast cancer prediction map

V. CONCLUSION

FA-WSI-CNN model has shown the best performance in a multi-dimensional way for predicting breast cancer. Then CNN version gets input from patched snap shots and creates categorised records for predicting breast cancer. The scikit-learn deep learning framework with Python is used to analyze the end result and construct a generalized tissue classifier, the WSI records set should consist of tissues generated below numerous extraordinary training situations. Finally, the CNN model will produce the classified data in the positive and negative values. From the classified data, breast cancer tissues can be predicted. The FA-WSI-CNN model is carried out with various parameters based on performance analysis like; accuracy, precision, F1-Score and Recall the corresponding values 99%, 99%, 99%, and 100% respectively. These values are carrying out the proposed FA-WSI-CNN models when predicting breast cancer and also the proposed model were reduce the training time by evaluating the inference time. Further research can be improved in various types of cancer tissue identification.

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