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IoMT Cloud-Based Intelligent Prediction of Breast Cancer Stages Empowered With Deep Learning

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ABSTRACT Breast cancer is often a fatal disease that has a substantial impact on the female mortality rate. Rapidly spreading breast cancer is due to the abnormal growth of malignant cells in the breast. Early detection of breast cancer can increase treatment opportunities and patient survival rates. Various screening methods with computer-aided detection systems have been developed for the effective diagnosis and treatment of breast cancer. Image data plays an important role in the medical and health industry. Features are extracted from image datasets through deep learning, as deep learning techniques extract features more accurately and rapidly than other existing methods. Deep learning effectively assists existing methods, such as mammogram screening and biopsy, in examining and diagnosing breast cancer. This paper proposes an Internet of Medical Things (IoMT) cloud-based model for the intelligent prediction of breast cancer stages. The proposed model is employed to detect breast cancer and its stages. The experimental results demonstrate 98.86% and 97.81% accuracy for the training and validation phases, respectively. In addition, they demonstrate accuracies of 99.69%, 99.32%, 98.96%, and 99.32% for detecting ductal carcinoma, lobular carcinoma, mucinous carcinoma, and papillary carcinoma. The results of the proposed intelligent prediction of breast cancer stages empowered with the deep learning (IPBCS-DL) model exhibits higher accuracy than existing state-of-the-art methods, indicating its potential to lower the breast cancer mortality rate.

INDEX TERMS Internet of Medical Things, breast cancer prediction, deep learning, convolutional neural network.

I. INTRODUCTION

The human body is composed of microscopic cells. Cellular reproduction is a continuous process where new cells replace old cells. This process is typically uniform; however, overly abundant cell production leads to abnormal growth. This abnormal growth can be a cause of cancer [1]. For decades, cancer has often been a fatal disease, spreading rapidly worldwide [2]. Breast cancer is the second-most common cancer, and it is most often diagnosed in females [3]. Breast cancer is the primary cause of the increasing mortality rate among females aged 20 to 59 years old [4]. Thus, early detection of breast cancer can lower the female mortality rate. There are two main methods of detecting breast cancer: mammography and biopsy. Mammography is the most commonly used method for the early detection of breast cancer. Radiologists administer this test to diagnose breast cancer, decreasing the mortality rate by up to 25%. Mammography is an effective method, but reading mammographic images is quite challenging. According to the US National Cancer Institute, almost

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10-30% of the breast glands depicted in mammographic images cannot be identified by radiologists [5].

The biopsy is another effective and precise breast cancer detection method. It involves taking a tissue sample from an affected part of the breast. This sample is then examined through a microscope by a pathologist, who detects and classifies the tumour. This method has recently played an important role in diagnosing breast and other types of cancers [6]. Biopsies allow pathologists to identify two types of lesions: benign and malignant. Benign cells exhibit abnormalities that are not cancerous. However, a malignant cell's behaviour is abnormal, and its growth is uneven. Due to the similarly irregular behaviour of these two types of cells, it has become challenging for radiologists to manually distinguish between the two [7].

Breast cancer has many causes, including excessive alcohol use, old age, family history, infertility, pregnancy after 30 years of age, consumption of foods with animal fat, living an unhealthy lifestyle, and physical idleness. [8]. The timely detection of breast cancer increases treatment opportunities [9]. Artificial intelligence (AI) techniques play important roles in every domain of life but are particularly prominent in the medical field. Many clinical procedures are automated, and AI presents a second opinion in detecting various diseases [10]. Computer-aided detection (CAD) systems have been used to improve different aspects of life, particularly in the health sector, for the last 20 years. Radiologists are currently utilizing CAD to detect cancer; however, CAD technology requires further improvement to produce accurate results. In 2012, the deep convolutional neural network (CNN) demonstrated remarkable image detection performance and is now approaching human performance. The techniques based on the CNN exceeded all traditional approaches used for CAD solutions, analyzing medical images more effectively and efficiently [11].

Medical experts require histopathological images to analyze breast cancer, which is critical and time-consuming. The existing methods, tools, and software can assist in diagnosis and, as a result, decrease cost and detection efforts. Many studies have been conducted on computational techniques [12]. Zhang *et al.* proposed a model based on the CNNs to classify mammogram and tomosynthesis images. The researchers obtained data composed of 3000 images from the University of Kentucky. Due to the dataset's small size, the researchers used the transfer learning and data expansion method to enhance and train the proposed model. The results were analyzed through a mammogram and a biopsy, as well as verified by a specialist. Transfer learning techniques and data expansion were applied to this model. This method could not conduct image preprocessing and normalization; it also lacked key features and data extraction capabilities [13].

Zuluaga-Gomez *et al.* [14] described that the rapidly increasing mortality rate is due to a lack of early diagnostic techniques. They stated that while many techniques are available for breast cancer detection, mammography is the most efficient. Their proposed model classified mammographic images by region of interest. The IRMA dataset consisted of 355 images, including 233 normal, 72 benign, and 83 malignant images, converted into wavelets. Afterward, the shape and texture features were applied to classify the proposed model; these features were helpful. This model, which was based on the support vector machine (SVM) and the extreme learning machine (ELM), obtained an accuracy of 94.11%. However, it was unable to identify the class inequity issue and did not consider noise removal. In addition, early diagnosis is beneficial only if the exact area of breast cancer is predicted [14]. Gomes proposed an innovative model that uses thermal images for predicting breast cancer. Data preprocessing and expansion techniques were used to decrease bias and overfitting. A DMR-IR database was used after reviewing the previous studies. The researchers found accurate results using database split techniques to overcome prejudice and overfitting during the training phase [15].

The present study found that the early detection of breast cancer is a challenging but essential task. The proposed IPBCS-DL model is used to detect breast cancer and its stages. Image-based datasets of breast cancer patients have been collected for testing and validation purposes. The preprocessing technique applied to the data and the deep learning-based convolutional neural networks is applied to train and validate the model to predict breast cancer and its stages.

II. LITERATURE REVIEW

Computational intelligence approaches, such as fuzzy system neural networks and swarm intelligence, and evolutionary computing approaches, such as genetic algorithms, classifiers, and SVMs, are practical approaches in the field of smart health [16]. According to the study of Ting *et al.* [17], medical experts receive assistance from the proposed CNN Improvement for Breast Cancer Classification (CNNI-BCC) model to detect breast cancer. The proposed approach classifies breast cancer types according to a supervised deep learning neural network. The results exhibit an accuracy of 90.50%, according to 221 real patients' data. This model automatically categorizes and diagnoses breast cancer lesions without requiring any previous knowledge. Proving to be an improvement of previous methods, an evaluation of this model demonstrates that it could analyse the situation of affected patients during the detection process.

Ahmed *et al.* [18] described CAD as dealing with various abnormalities in tissues and diagnosing the disease. The researchers introduced a CAD model based on a deep belief network (DBN) to automatically detect breast cancer and categorize breast regions into normal, benign, and malignant. Two techniques were introduced, considering the areas of interest; the first technique was intended for an anticipated target that is small in size. The second technique was for when the total mass was targeted. A total of 347 images are obtained to train and test the proposed model. The proposed CAD model's accuracies for the two techniques are 92.86% and

90.84%, respectively. The obtained results exhibit improved efficiency when compared to other existing CAD systems.

Luqman Ahmed's [19] machine learning data have demonstrated substantial utility in health care. The explosion of big data is challenging to manage and requires effective management systems. Deep learning expert systems demand a large amount of data upon which various techniques can be applied to obtain valid and accurate results; this is particularly important for medical applications. Medical datasets have many issues, such as inadequate datasets, limited sampling, sampling biases, and large-scale application difficulties. Ahmed's study focused on a large medical image dataset, and various learning techniques, such as transfer learning, were trained through a limited dataset. The study was based on breast cancer classification, cancerous region divisions, and pattern mammogram extraction. For the proposed model, preprocessing, such as noise removal, is applied to mammogram images, and feature extraction filters excessive data elements. Classification and segmentation are applied to the breast ultrasound dataset through CAD. Image classification is performed through the transfer learning technique with a pretrained model, and then all images are categorized as either cancerous or noncancerous. Finally, the R-CNN technique is used to identify the tumour region in affected images.

Sha *et al.* [20] developed a multilevel mitotic-cell identification method consisting of Faster-RCNN, postprocessing, and deep CNNs. Their proposed model was divided into three steps. The first step was the initial diagnosis, the second step was quality enhancement through postprocessing, and the third step was a score-level fusion of the deep CNN. The output combined all three phases, and the Rasnet-50 and DenseNet-201 classifiers were used for feature extraction in all three stages. The ICPR 2012 and ICPR 2014 databases were used to train and test the designed model. For the evolving automation of the proposed technique, this system was used for having a second opinion by pathologists. Croock *et al.* [21] designed an inclusive method for the mammographic detection of breast cancer. The median filter was used to remove noise from images in the preprocessing phase, and a CNN was applied to identify the cancerous region. Related features were extracted through the optimum technique to eliminate unnecessary features, and these features were trained using a support vector machine classifier for both cancerous and noncancerous areas. The grasshopper optimization algorithm (GOA) was used for the optimization of image features and segmentation. Two databases, MIAS and DDMS, were used for result simulation.

Zheng *et al.* [22] designed an early diagnosis system for breast cancer system-based mammography images. They applied the software engineering model to the proposed algorithm to provide consistency, flexibility, and stability. The detection system used deep learning technology to detect soft tissue abnormalities in mammographic images. Their proposed model consisted of a website that was easily accessible to doctors and patients regardless of location. In addition, the model measured the risk factor and informed patients of this risk factor. The evaluation was performed in two steps. First, the accuracy of the designed system was quantified, and then the complete model from the website was tested. The proposed model provided efficient and accurate information for the early detection of breast cancer.

Chaves *et al.*[23] proposed the deep learning-assisted efficient AdaBoost algorithm (DLA-EABA) to detect breast cancer. The AdaBoost algorithm uses classifiers to predict breast cancer, and DLA-EABA improves its performance through the CNN deep learning approach. Deep learning techniques are used for specific features of a dataset, and separate models are created for each dataset. The proposed approach could detect early breast cancer, and thus, decrease the mortality rate. The results demonstrated that DLA-EABA has an accuracy rate that is higher than that of other methods. Agnes *et al.*[24] presented a novel model for early breast cancer diagnosis using infrared images. His proposed technique could more easily detect abnormalities in the breast than mammography. The CNN technique was applied to infrared images to categorize them into two classes: normal and pathology. This model's primary objective was to examine images, and thus, categorize patients automatically.

López-Cabrera *et al.* [25] proposed the classification of mammographic images using the multiscale all-convolutional neural network (MA-CNN) model. MA-CNN performed feature extraction through convolutional neural networks and classified mammography images into three types: normal, benign, and malignant. MA-CNN was found to be accurate and efficient in the detection of breast cancer. Qasim *et al.* [26] enlightened the mammography images to be used for the detection of breast cancer. Various pre-trained convolutional neural network models were applied to classify the images. The transfer learning technique was adopted for the Inception v3 pretrained network. Two CNN methods were implemented, and the three classes were normal, benign, and malignant. The experimental results exhibited an accuracy of 86.05%, and radiologists found it to be a useful tool for early breast cancer detection. Qasim *et al.* [27] presented a breast cancer detection model based on the CNN (BCD-CNN) system to detect breast cancer and categorize the mammographic image as either cancerous or noncancerous. This model's objective was to diagnose and classify breast cancer rapidly. BCD-CNN system operated in three steps. The first step was image data acquisition; the second step was feature extraction using a CNN; the third step was to classify mammographic images through the CNN classifier [28], [29]. The results demonstrated accuracies ranging from 84% to 88%, and the obtained resolution was high compared to other existing models. Similarly, a support vector machine [30] classifier was used to detect various diseases.

This review of related studies reveals that certain irregularities need to be addressed in the image database. These irregularities affect the efficiency of the deep learning models. The present study focuses on detecting the causes of these irregularities and identifying a comprehensive solution.

The main contributions of the proposed study are as ' follows:

a. The primary goal is to increase the detection accuracy and decrease the miss rate in the breast cancer detection process.
b. For better accuracy, breast cancer stages have also been predicted.
c. Finally, we evaluate our proposed deep learning-based model with other existing and state-of-the-art methods, such as using deep belief networks [18], support vector machines [21], and type 1 fuzziness [16]. In addition, the IPBCS-DL model was evaluated on an image-based breast cancer dataset [27].

The rest of this article is organized as follows: in Section III, the proposed breast cancer and its stage detection model are presented. Section IV presents the simulation results and discussion. Section V presents the conclusion of the study. Finally, Section VI contains the limitations and future work.

III. PROPOSED IPBCS-DL MODEL

The rapid expansion of deep learning has transformed the world of image processing. The deep learning approach has been applied to medical image processing for the last few years. It is helpful to analyze and categorize the entity in the domain of medical data. In particular, the early prediction of breast cancer can play a significant role in decreasing the mortality rate.

The rapid spread of breast cancer can be minimized by proper detection. Many artificial intelligence approaches are being utilized for the early detection of breast cancer in its various stages. Deep learning is an intelligent approach that assists radiologists and pathologists in breast cancer detection. The proposed IPBCS-DL model uses a deep learning approach to detect breast cancer and its stages. It obtained data from IoMT devices, as shown in Fig. 1. Data is obtained from different tests, such as a computed tomography scan (CT-Scan), magnetic resonance imaging (MRI), and positron emission tomography (PET). The preprocessing technique activates image resizing, segmentation, and mitigating noise. If the detected breast cancer is malignant, then emergency alerts go to the doctor, patient, and hospital. All records related to the categorizations of benign, malignant, ductal carcinoma, lobular carcinoma, mucinous carcinoma, and papillary carcinoma are stored in the database.

The proposed system model has two phases: training and validation, and is communicated through the cloud. In the training phase, the Internet of Medical Things (IoMT) is used to collect data for streamlined processes and patient convenience. IoMT devices provide more accurate data, decrease risk factors, efficient time management, remote monitoring, and better prediction. In the proposed model, IoMT enables devices to collect data for breast cancer detection. In the image data acquisition layer, the required data are obtained in images using different IoMT enabled devices. Then, in preprocessing, the images are resized and segmented, and the data noise is mitigated. The next step is to use the application layer to predict breast cancer and its stages, which is made up of two sublayers: the application layer and the performance layer.

The convolutional neural network technique is applied to the data in the application layer. The accuracy, miss rate, and other statistical parameters are quantified in the performance evaluation layer. If the trained model does not meet the required learning criteria (maximum number of epochs or achieves a higher accuracy rate than previously published accuracy), the application layer is retrained. However, the trained layer model is stored in the cloud to predict breast cancer and its stages. In the validation phase of the model, data are obtained from IoMT devices to predict breast cancer and its stages. In the preprocessing layer, images are resized and segmented, and the noise is mitigated. The proposed IPBCS-DL model imports data from the cloud to predict breast cancer and its stages. If breast cancer is not detected, then it is considered benign. However, if detected, then it is considered malignant. It is further classified into breast cancer stages, such as ductal carcinoma, lobular carcinoma, mucinous carcinoma, and papillary carcinoma. Ductal carcinoma is the most common form of breast cancer and is usually shown through a mammogram. Lobular carcinoma is the second most common form of breast cancer and contains 10%-15% of all breast cancers. Mucinous carcinoma is another form of cancer and occurs in the breast when an internal organ produces mucin. Papillary carcinoma mostly shows in women over the age of 60 years, and numerous papillary tumours are benign. The proposed system model assists medical experts in further treatment.

A. CONVOLUTIONAL NEURAL NETWORK

Deep learning (DL) is an extensive technique adopted in many fields for disease prediction, transportation, cultivation, aeronautics, etc. Deep learning has a high applicability rate due to its fast learning. The convolutional neural network (CNN) consists of two modules: the convolutional and pooling layers. The proposed IPBCS-DL utilizes a convolutional neural network layer and is used to predict breast cancer and classify its stages. A convolutional neural network consists of three layers: the input layer, the hidden layer, and the output layer.

The dimensions of the input images are reformed into $700 \times 460 \times 3$, where 700×460 is the input images' width and height, and 3 is the number of channels. The convolutional layer has potential because more computation tasks are performed in this layer. The primary purpose of this layer is to retrieve features by applying filters, preserve the spatial relationships between pixels, and apply a rectified linear unit (ReLU) activation function for nonlinearity.

Fig. 2 illustrates that the pooling layer decreases image dimensions and computation time by downsampling. Many pooling types, such as average pooling, max pooling, etc., give more accurate results in the proposed model.

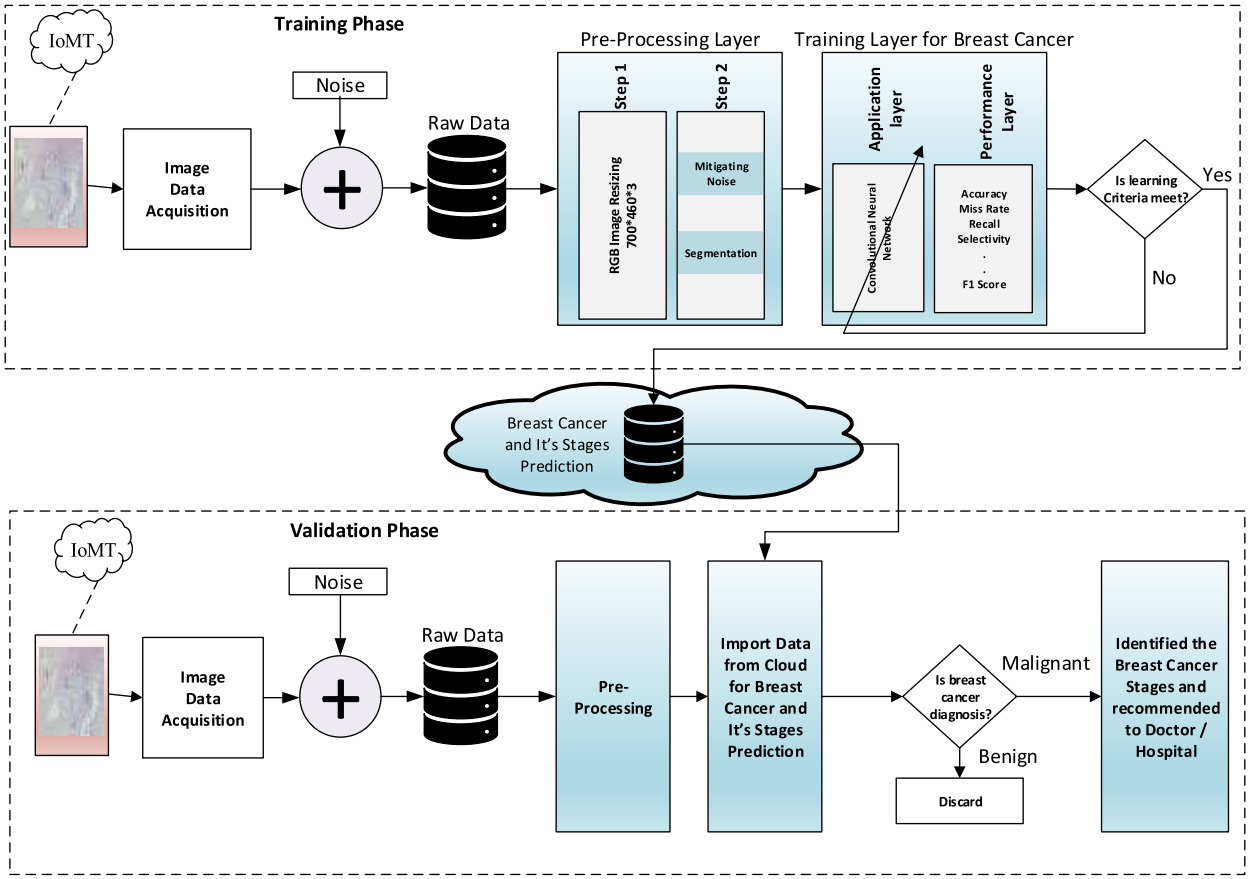

FIGURE 1. The proposed IPBCS-DL system model.

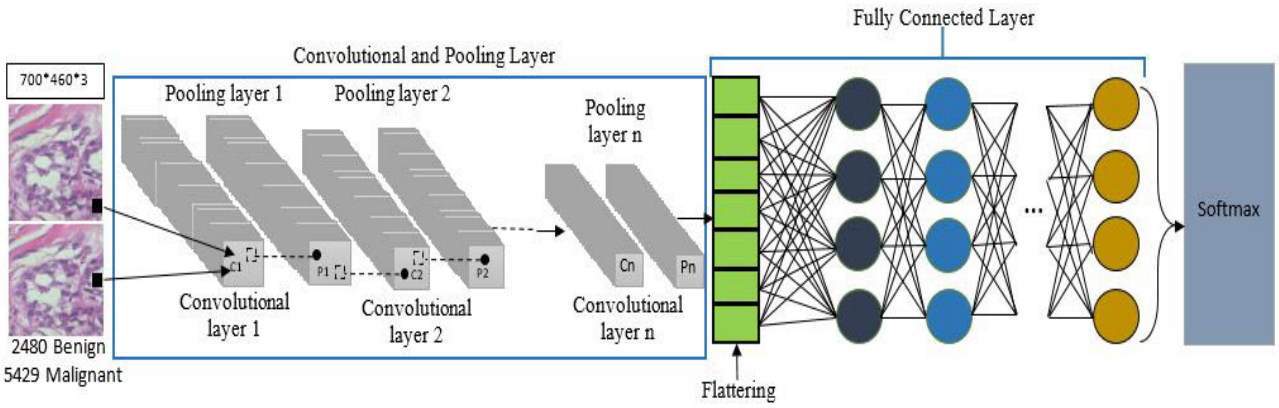

FIGURE 2. CNN Model for the proposed IPBCS-DL model.

The pooling layer's primary function is to preserve the specific image features captured during the CNN process. Weights are persistent in this layer because the pooling layer does not participate in the backpropagation procedure.

Furthermore, all inputs are interconnected in a fully connected layer. Extracted data from previous layers are compiled into a fully connected layer to obtain one final output. Ultimately, the convolutional layer transforms it into a single flattened length with a one-dimensional array before turning it into a fully connected layer. The softmax layer is used to convert logits into probabilities. In the final layer of the CNN model, the accuracy values are labeled as taken from the previous layer.

In the proposed mathematical model, the loss function can be written as

$$L = -\sum_{i=1}^{c} (Y_i \log(y_i)) \tag{1}$$

where c represents the total number of classes depending upon the application.

We use SoftMax transformation as shown in Eq. (2)

$$y_i = \frac{e^{Z_i}}{\sum_{j=1}^{n} e^{Z_K}} \tag{2}$$

where Z_i represents logits, and many logits transform into probabilities using softmax transformation.

$$Z_l = \sum_{j=1}^{noot} \left(W_{jl} * \mathrm{X}_j\right)$$

Z_l obtained by interconnected weights with the X_j

Here, we find loss with respect to weights based on two summations in Eq. (3). Then, we take the product of two derivatives (the dominators of the 1st and 2nd nominators are the same, and we apply the multiplication association rule, resulting in both being canceled).

$$\frac{\partial L}{\partial W_{j,l}} = \sum_{j=1}^{noot'} \sum_{l=1}^{c} \left(\frac{\partial L}{\partial Z_l} \frac{\partial Z_l}{\partial W_{j,l}}\right)$$
$$\frac{\partial y_i}{\partial Z_l} = softmax\ derivative \tag{3}$$

In Eq. (1), Loss having y_i as its parameter that is indirectly related to Z_i in terms of the following expression:

$$\mathrm{y}_i = \frac{e^{Z_i}}{\sum_{k=1}^{c} e^{Z_K}}$$
$$Z_l = \sum_{j=1}^{noot} \left(W_{jl} * \mathrm{X}_j\right)$$
$$Z_i = Z_l \tag{3a}$$

Two cases are important, where case 1: $\mathrm{I} = l$, and case 2: $\mathrm{i} \neq l$ when $\mathrm{i} = \mathrm{l}^{\mathrm{th}}$ unit. 'l' is the single neuron point of focus in softmax output neurons, and the '1' neuron has height values; the rest are close to zero.

case1 : $(\mathrm{i} = l)$

Taking the derivative of Eq. (2) through quotient rules

$$\frac{\partial y_i}{\partial Z_{(i=l)}} = \frac{e^{Z_i} \sum_{k=1}^{c} e^{Z_K} - e^{Z_i} e^{Z_l}}{\sum_{k=1}^{c} e^{Z_K} * \sum_{k=1}^{c} e^{Z_K}} \tag{4}$$

Taking common $\frac{e^{Z_i}}{\sum_{k=1}^{c} e^{Z_K}}$ from Eq. (4), we get the following:

$$\frac{\partial y_i}{\partial Z_l} = \frac{e^{Z_i}}{\sum_{k=1}^{c} e^{Z_K}} \left[\frac{\sum_{k=1}^{c} e^{Z_K} - e^{Z_l}}{\sum_{k=1}^{c} e^{Z_K}}\right]$$

By dividing, we get:

$$\frac{\partial y_i}{\partial Z_l} = \frac{e^{Z_i}}{\sum_{k=1}^{c} e^{Z_K}} \left[1 - \frac{e^{Z_i}}{\sum_{k=1}^{c} e^{Z_K}}\right] \{\because i = l\} \tag{5}$$

As we know

$$\mathrm{Y}_i = \frac{e^{Z_i}}{\sum_{j=1}^{n} e^{Z_K}}$$

Therefore, Eq. (5) can be further written as:

$$\frac{\partial y_i}{\partial Z_l} = y_i\left(1 - y_i\right) = y_i\left(1 - y_i\right) \quad for\ (i = l) \tag{6}$$

When $\mathrm{i}! = \mathrm{l}^{\mathrm{th}}$ unit, which has low probability where 'l' is the single neuron point of focus in softmax output neurons.

case2 $(\mathrm{i} \neq l)$:

Taking the derivative of Eq. (3) through quotient rules with respect to Z_l.

$$\frac{\partial y_i}{\partial Z_l} = \frac{\frac{\partial}{\partial Z_l} e^{Z_i} * \sum_{k=1}^{c} e^{Z_K} - e^{Z_i} \frac{\partial}{\partial Z_l} [\sum_{k=1}^{c} e^{Z_K}]}{\sum_{k=1}^{c} e^{Z_K} * \sum_{k=1}^{c} e^{Z_K}}$$

It can be written as:

$$\frac{\partial y_i}{\partial Z_l} = 0 - \frac{e^{Z_i} * e^{Z_l}}{\sum_{k=1}^{c} e^{Z_K} * \sum_{k=1}^{c} e^{Z_K}}$$
$$= -\frac{e^{Z_i}}{\sum_{k=1}^{c} e^{Z_K}} * \frac{e^{Z_l}}{\sum_{k=1}^{c} e^{Z_K}}$$

As we know that

$$y_i = \frac{e^{Z_i}}{\sum_{k=1}^{c} e^{Z_K}}$$

and

$$y_l = \frac{e^{Z_l}}{\sum_{k=1}^{c} e^{Z_K}}$$

Therefore, we can drive this equation as:

$$\frac{\partial y_i}{\partial Z_l} = -y_i y_l \quad for\ (i \neq l) \tag{7}$$

After summarizing Eq. (6) and Eq. (7)

$$\frac{\partial y_i}{\partial Z_l} = \begin{bmatrix} y_i\left(1 - y_i\right)\ for\ \ (i = l) \\ -y_i y_l \quad for\ (i \neq l) \end{bmatrix} \tag{8}$$

As we know that cross-entropy loss does not have any component of Z_l, we take the partial derivative of Z_l w.r.t. of this expression log (y_K)

$$\mathrm{L} = -\sum_{i=1}^{c} \left(Y_i * \log(y_i)\right)$$

After taking the derivative with respect to Z_l, it can be written as:

$$\frac{\partial L}{\partial Z_l} = -\sum_{k=1}^{c} \left(Y_K * \frac{\partial}{\partial Z_l} log(y_k)\right)$$
$$\frac{\partial L}{\partial Z_l} = -\sum_{k=1}^{c} Y_K \left(\frac{\partial}{\partial y_k} log(y_k)\right) \frac{\partial y_k}{\partial Z_l}$$
$$\frac{\partial L}{\partial Z_l} = -\sum\nolimits_{k=1}^{c} \frac{Y_K}{y_k} \frac{\partial y_k}{\partial Z_l} \tag{9}$$

$\frac{\partial y_k}{\partial Z_l}$ has already been calculated for the softmax gradient. Here we have two cases $i \neq l$ & $k \neq l$ as in Eq. (8). Now we have to divide Eq. (9) into two parts.

$$\frac{\partial L}{\partial Z_l} = -\frac{Y_k}{y_k} * y_k\left(1 - y_l\right) - \frac{\partial y_k}{\partial Z_l}$$

where,

$$\frac{\partial y_k}{\partial Z_l} = \begin{bmatrix} \sum\limits_{\mathrm{k} \neq \mathrm{l}}^{\mathrm{c}} \left(-\frac{\mathrm{Y_k}}{\mathrm{y_k}} * \mathrm{y_k y_l}\right) & for\ \ (\mathrm{k} \neq \mathrm{l}) \\ \frac{\mathrm{Y_k}}{\mathrm{y_k}} * \mathrm{y_k}\left(1 - \mathrm{y_l}\right) & for\ (\mathrm{k} = \mathrm{l}) \end{bmatrix}$$

It can be written as:

$$\frac{\partial L}{\partial Z_l} = -Y_k\,(1 - y_l) + \sum_{k \neq l}^{c} Y_k y_l$$

After further simplification, it can be written as:

$$\frac{\partial L}{\partial Z_l} = -Y_k + Y_k y_l + \sum_{k \neq l}^{c} Y_k y_l$$

$$\frac{\partial L}{\partial Z_l} = y_l \left(y_k + \sum_{k \neq l} Y_k \right) - y_k$$

where,
$\left(y_k + \sum_{k \neq l} Y_k\right) = 1$, then

$$\frac{\partial L}{\partial Z_l} = (y_l - Y_k)$$

$$\frac{\partial L}{\partial Z_l} = (y_l - Y_l) \quad \{\because k = l\}$$

$$\frac{\partial L}{\partial W_{j,l}} = \sum_{j=1}^{noot} \sum_{l=1}^{c} \left(\frac{\partial L}{\partial Z_l} \frac{\partial Z_l}{\partial W_{j,l}}\right) \tag{10}$$

where,

$$\frac{\partial Z_l}{\partial W_{j,l}} = x_j$$

x_j represent here as input weights.

After substituting the valves of $\frac{\partial L}{\partial Z_l}$ & $\frac{\partial Z_l}{\partial W_{j,l}}$ in Eq. (10), it can be written as:

$$\frac{\partial L}{\partial W_{j,l}} = \sum_{j=1}^{noot} \sum_{l=1}^{c} (y_l - Y_l) x_j \tag{11}$$

Eq. (11) represents the derivative of loss concerning weights for the fully connected layer.

IV. SIMULATION RESULTS AND DISCUSSIONS

This paper proposes an IoMT cloud-based intelligent prediction of breast cancer and its stages. MATLAB 2019a is utilized for simulation purposes. The proposed model is used to investigate 7909 images of the dataset [27]. The proposed IPBCS-DL is further divided into two phases: training and validation. The dataset is arbitrarily split into 70% for training (5537 samples) and 30% for validation (2372 samples). Furthermore, 5429 malignant images are used for breast cancer stage prediction; 70% (3801) is used for training, and 30% (1628) is used for validation purposes. Finally, the proposed model is compared with existing approaches with respect to various statistical evaluation parameters, such as accuracy, miss rate, true positive rate (TPR), recall, true negative rate (TNR), precision, false omission rate (FOR), false discovery rate (FDR), F0.5 Score, and F1Score.

Accuracy

$$= \frac{\frac{O_{Si}}{I_{Si}} + \frac{O_{Sk}}{I_{Sk}}}{\frac{O_{Si}}{I_{Si}} + \frac{\sum_{j=1}^{n} (O_{Sj,j \neq i})}{I_{Sj}} + \frac{O_{Sk}}{I_{Sk}} + \frac{\sum_{l=1}^{n} (O_{Sl,l \neq k})}{I_{Sk}}}$$

$$where, \quad i/j/k/l = 1, 2, 3, \ldots, n \tag{12}$$

Miss Rate

$$= \frac{\frac{\sum_{l=1}^{n} (O_{Sl,l \neq k})}{I_{Sk}}}{\frac{\sum_{l=1}^{n} (O_{Sl,l \neq k})}{I_{Sk}} + \frac{O_{Si}}{I_{Si}}} \quad where, \quad i/k/l = 1, 2, 3, \ldots, n \tag{13}$$

True Positive Rate/Recall

$$= \frac{\frac{O_{Si}}{I_{Si}}}{\frac{O_{Si}}{I_{Si}} + \frac{\sum_{l=1}^{n} (O_{Sl,l \neq k})}{I_{Sk}}} \quad where, \quad i/k/l = 1, 2, 3, \ldots, n \tag{14}$$

True Negative Rate/Selectivity

$$= \frac{\frac{O_{Sk}}{I_{Sk}}}{\frac{O_{Sk}}{I_{Sk}} + \frac{\sum_{j=1}^{n} (O_{Sj,j \neq i})}{I_{Sj}}} \quad where, \quad j/k = 1, 2, 3, \ldots, n \tag{15}$$

Precision

$$= \frac{\frac{O_{Si}}{I_{Si}}}{\frac{O_{Si}}{I_{Si}} + \frac{\sum_{j=1}^{n} (O_{Sj,j \neq i})}{I_{Sj}}} \quad where, \quad i/j = 1, 2, 3, \ldots, n \tag{16}$$

False Ommision Rate

$$= \frac{\frac{\sum_{l=1}^{n} (O_{Sl,l \neq k})}{I_{Sk}}}{\frac{\sum_{l=1}^{n} (O_{Sl,l \neq k})}{I_{Sk}} + \frac{O_{Sk}}{I_{Sk}}} \quad where, \quad k/l = 1, 2, 3, \ldots, n \tag{17}$$

False Discovery Rate

$$= \frac{\frac{\sum_{j=1}^{n} (O_{Sj,j \neq i})}{I_{Sj}}}{\frac{O_{Si}}{I_{Si}} + \frac{\sum_{j=1}^{n} (O_{Sj,j \neq i})}{I_{Sj}}} \quad where, \quad i/j = 1, 2, 3, \ldots, n \tag{18}$$

$$F_{0.5}Score = 1.25 \times Precision \times \frac{Recall}{0.25 \times Precision + Recall} \tag{19}$$

$$F_1Score = 2 \times Precision \times \frac{Recall}{Precision + Recall} \tag{20}$$

The proposed IPBCS-DL model predicts breast cancer. Malignancy indicates breast cancer, while benign indicates that breast cancer has not been identified. Table 1 shows the prediction of the proposed IPBCS-DL model during the training phase. A total of 5537 (70%) samples are used during the training phase. This is further divided into 3801 and 1736 malignant and benign samples, respectively. For malignant lesions, a total of 3801 samples are taken, out of which 3779 samples are correctly predicted as malignant, and 22 samples are incorrectly predicted as benign.

TABLE 1. Decision matrix for the proposed IPBC-DL model (training).

(70% of Samples for Training)			
No. of Samples (N=5537)		Output ($O_{malignant}$, O_{benign})	
		O_m Malignant	O_b Benign
Input	$I_{malignant}$= 3801	3779	22
	I_{benign}=1736	41	1695

TABLE 2. Decision matrix for the proposed IPBC-DL model (validation).

(70% of Samples for Validation)			
No. of Samples (N=2372)		Output ($O_{malignant}$, O_{benign})	
		O_m Malignant	O_b Benign
Input	$I_{malignant}$= 1628	1614	14
	I_{benign}=744	38	706

Similarly, 1695 samples are correctly predicted as benign, while 41 samples are incorrectly predicted as malignant.

Table 2 shows the prediction of the proposed IPBCS-DL model during the validation phase. 2372 (30%) are used during the training phase. This is further divided into 1628 and 744 malignant and benign samples, respectively. For malignant lesions, a total of 1628 samples are taken, out of which 1614 samples are correctly predicted as malignant, and 14 samples are incorrectly predicted as benign. Similarly, 706 samples are correctly predicted as benign, and 38 samples are incorrectly predicted as malignant.

Table 3 shows the classwise performance of the proposed IPBC-DL model in the training and validation phases. In training, the obtained accuracy and miss rate for the malignant class are 99.42% and 0.58%, respectively, while the accuracy and miss rate for the benign class are 97.64% and 2.36%, respectively. In the validation phase, the obtained accuracy and miss rate for the malignant class are 99.14% and 0.86%, respectively, while the accuracy and miss rate for the benign class are 94.89% and 5.11%, respectively.

Table 4 depicts the overall performance of the proposed IPBC-DL model in training and validation. In training, the obtained accuracy and miss rates were 98.86% and 1.14%, respectively. During validation, the obtained accuracy and miss rate are 97.81% and 2.19%, respectively.

Table 5 shows the capacity of the proposed IPBCS-DL model to predict breast cancer stages during the training phase. A total of 3801 (70%) samples are used during training; these samples are further divided into 2426, 438, 555, and 392 samples of malignant S1, S2, S3, and S4, respectively. For malignant S1, 2416 samples are taken, out of which 2414 samples are correctly predicted as malignant S1, and two samples are incorrectly predicted. For malignant S2, a total of 438 samples are taken, out of which 435 samples are correctly predicted as malignant S2, and the proposed model incorrectly predicts three samples. For malignant S3, a total of 555 samples are taken, out of which 551 samples are correctly predicted as malignant S3, and four samples are incorrectly predicted. Finally, for malignant S4, a total of 392 samples are taken, out of which 387 samples are correctly predicted as malignant S4, and five samples are incorrectly predicted.

TABLE 3. Classwise performance for the proposed IPBCS-DL model in training and validation.

Inputs	Training		Validation	
	Accuracy %	Miss rate %	Accuracy %	Miss rate %
$I_{malignant}$	99.42	0.58	99.14	0.86
I_{benign}	97.46	2.36	94.89	5.11

TABLE 4. Overall performance of the proposed IPBC-DL model.

Performance	Accuracy %	Miss rate %
Training	98.86	1.14
Validation	97.81	2.19

Table 6 shows the capacity of the proposed IPBCS-DL to predict breast cancer stages during the validation phase. A total of 1628 (30%) samples are used during validation and are further divided into 1034, 188, 237, and 168 malignant S1, S2, S3, and S4, respectively. For malignant S1, 1034 samples are taken, out of which 1031 samples are correctly predicted as malignant S1, and four samples are incorrectly predicted. For malignant S2, a total of 188 samples are taken, out of which 183 samples are correctly predicted as malignant S2, and the proposed model incorrectly predicts five samples. For malignant S3, 237 samples are taken, out of which 230 samples are correctly predicted as malignant S3, and four samples are incorrectly predicted. For malignant S4, 168 samples are taken, out of which 162 samples are correctly predicted as malignant S4, and six samples are incorrectly predicted.

Fig. 3 Presents the training phase performance of the proposed model with respect to accuracy, miss rate, recall, selectivity, precision, false omission rate, false discovery rate, F0.5 score, and F1 score. Ductal carcinoma S1 obtains an accuracy, miss rate, recall, selectivity, precision, false omission rate, false discovery rate, F0.5 score, and F1 score of 99.92%, 0.08%, 99.96%, 99.86%, 99.92%, 0.07%, 0.08%,

TABLE 5. Decision matrix for the proposed IPBCS-DL model (training).

(70% of Samples for Training)				
$I_{malignant}$=3801	$O_{malignant,S1}$	$O_{malignant,S2}$	$O_{malignant,S3}$	$O_{malignant,S4}$
$I_{malignant,S1}$=2416	2414	2	0	0
$I_{malignant,S2}$=438	1	435	2	0
$I_{malignant,S3}$=555	0	1	551	3
$I_{malignant,S4}$=392	0	0	5	387

TABLE 6. Decision matrix for the proposed IPBCS-DL model (validation).

(30% of Samples for validation)				
$I_{malignant}$=1628	$O_{malignant,S1}$	$O_{malignant,S2}$	$O_{malignant,S3}$	$O_{malignant,S4}$
$I_{malignant,S1}$=1035	1031	4	0	0
$I_{malignant,S2}$=188	1	183	4	0
$I_{malignant,S3}$=237	0	2	230	5
$I_{malignant,S4}$=168	0	0	6	162

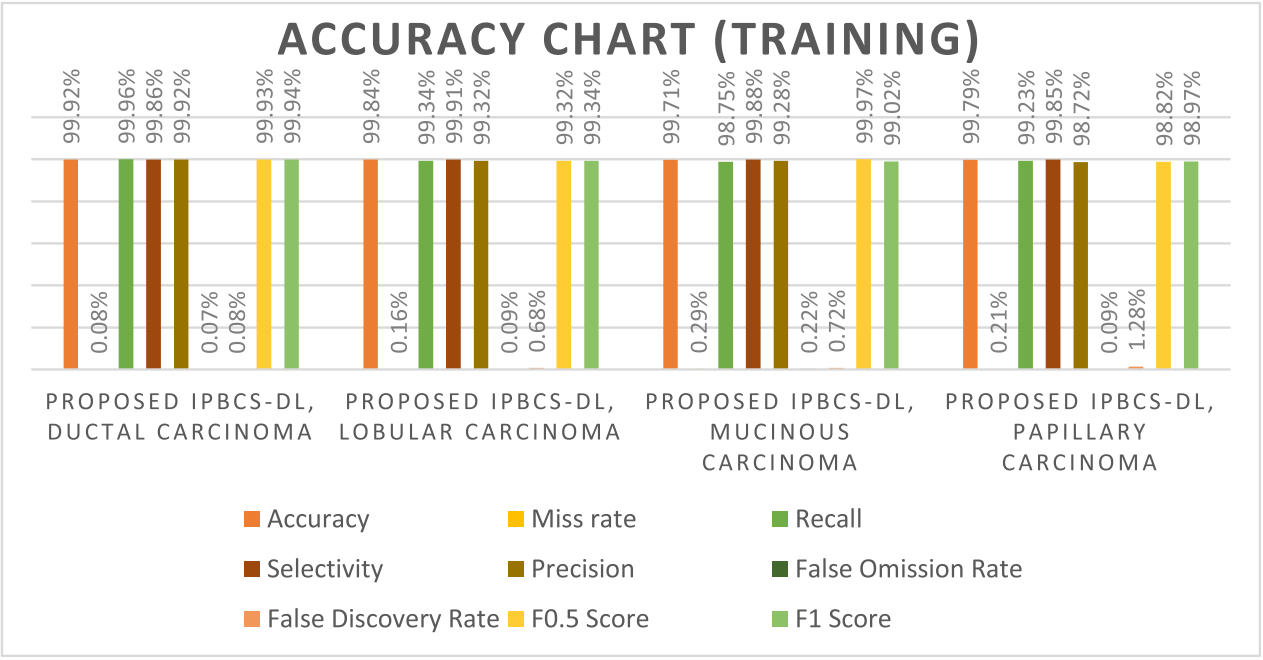

FIGURE 3. Accuracy chart of statistical measures for the proposed IPBCS-DL model (training).

99.93%, and 99.94%, respectively. Lobular carcinoma S2 obtains an accuracy, miss rate, recall, selectivity, precision, false omission rate, false discovery rate, F0.5 score, and F1 score of 99.84%, 0.16%, 99.34%, 99.91%, 99.32%, 0.09%, 0.68%, 99.32%, and 99.34%, respectively. Mucinous carcinoma S3 obtains an accuracy, miss rate, recall, selectivity, precision, false omission rate, false discovery rate, F0.5 score, and F1 score of 99.71%, 0.29%, 98.75%, 99.88%, 99.28%, 0.22%, 0.72%, 99.97%, and 99.02%, respectively. Finally, papillary carcinoma S4 obtains the accuracy, miss rate, recall, selectivity, precision, false omission rate, false discovery rate, F0.5 score, and F1 score of 99.79%, 0.21%, 99.23%, 99.85%, 98.72%, 0.09%, 1.28%, 98.82%, and 98.97%, respectively.

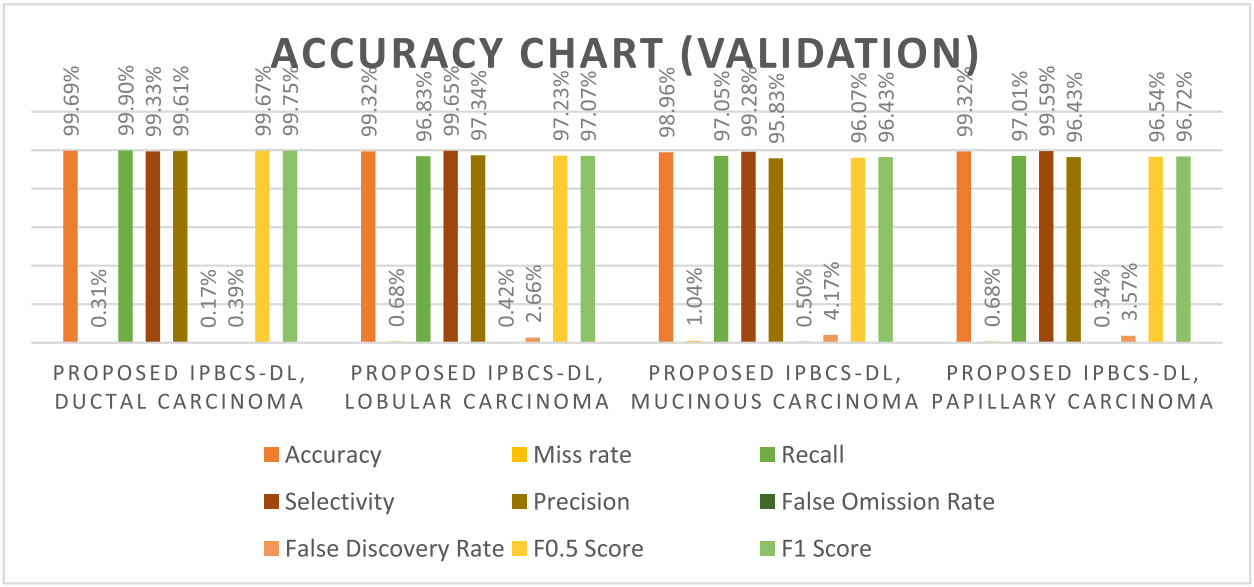

FIGURE 4. Accuracy chart of statistical measures for the proposed IPBCS-DL model (validation).

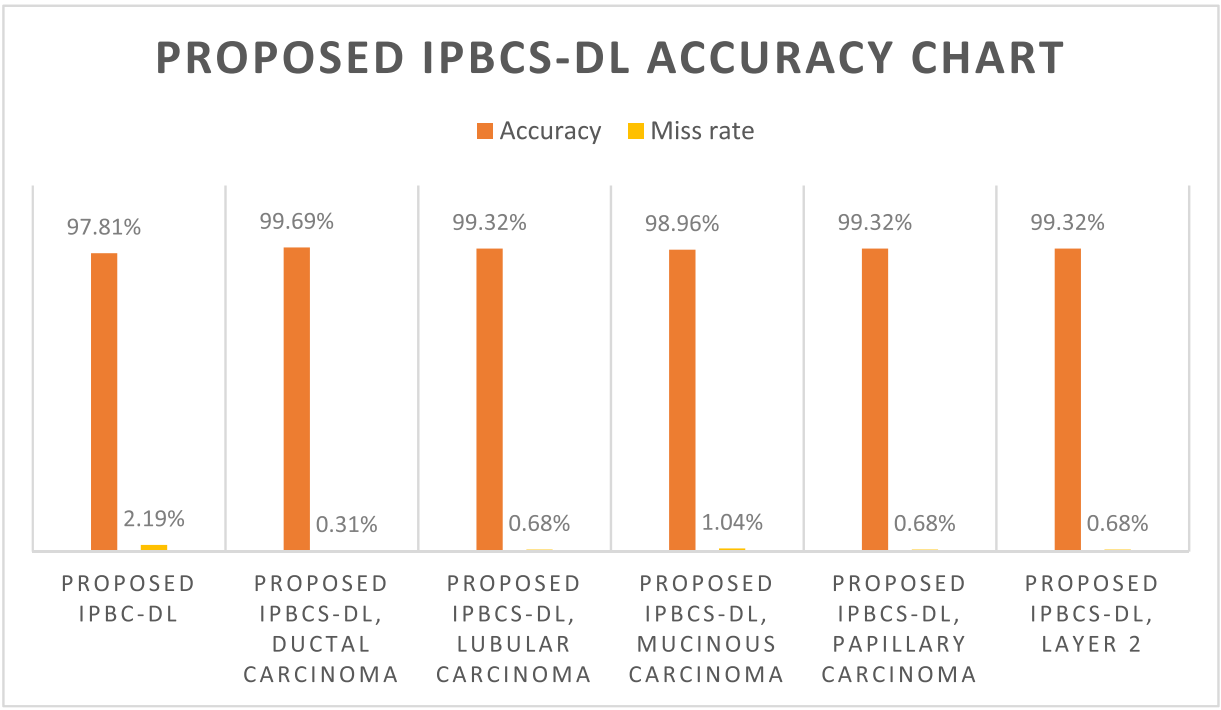

FIGURE 5. Overall accuracy chart for the proposed IPBCS-DL model.

Fig. 4 presents the validation phase performance of the proposed model with respect to the accuracy, miss rate, recall, selectivity, precision, false omission rate, false discovery rate, F0.5 score, and F1 score. Ductal carcinoma S1 obtains an accuracy, miss rate, recall, selectivity, precision, false omission rate, false discovery rate, F0.5 score, and F1 score of 99.69%, 0.31%, 99.90%, 99.33%, 99.61%, 0.17%, 0.39%, 99.67%, and 99.75%, respectively.

Lobular carcinoma S2 obtains an accuracy, miss rate, recall, selectivity, precision, false omission rate, false discovery rate, F0.5 score, and F1 score of 99.32%, 0.68%, 96.83%, 99.65%, 0.42%, 2.66%, 97.23%, and 97.07%, respectively. Mucinous carcinoma S3 obtains an accuracy, miss rate, recall, selectivity, precision, false omission rate, false discovery rate, F0.5 score, and F1 score of 98.96%, 1.04%, 97.05%, 99.28%, 95.83%, 0.50%, 4.17%, 96.07%, and 96.43%, respectively. Finally, papillary carcinoma S4 obtains the accuracy, miss rate, recall, selectivity, precision, false omission rate, false discovery rate, F0.5 score, and F1 score of 99.32%, 0.68%, 97.01%, 99.59%, 96.43%, 0.34%, 3.57%, 96.54%, and 96.72%, respectively.

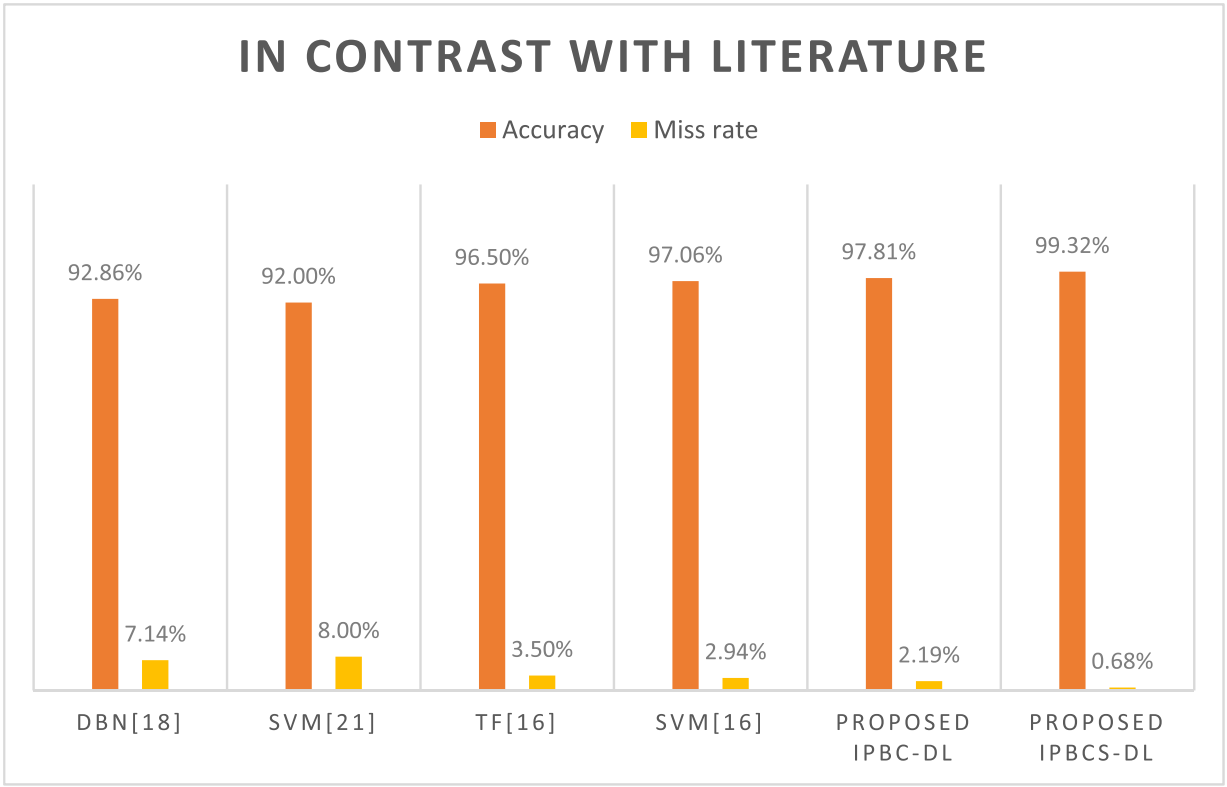

FIGURE 6. Accuracy chart in contrast with extant literature for the proposed IPBCS-DL model.

Fig. 5 presents the proposed IPBCS-DL model's overall accuracy for the validation phase. The proposed IPBCS-FH-DL model achieves an accuracy of 97.81% and a miss rate of 2.19%. The proposed IPBCS-FHDL model obtains 0.75%, 1.31%, 4.95%, and 5.81% more accurate predictions and minimized the miss rate by 0.75%, 1.31%, 4.95%, 5.81% and 0.75% compared to SVM [16], TF [16], DBN [18] and SVM [21], respectively. This accuracy is achieved because the proposed model does not use handcrafted features as other existing methods do. In ductal carcinoma (S1), the obtained accuracy and miss rate are 99.69% and 0.31%, respectively. In lobular carcinoma (S2), the accuracy and miss rate are 99.32% and 0.68%, respectively. In the case of mucinous carcinoma (S3), the obtained accuracy and miss rate are 98.96% and 1.04%, respectively. Finally, in the case of papillary carcinoma (S4), the accuracy and miss rate are 99.32% and 0.68%, respectively. Thus, the overall accuracy and miss rate are 99.32% and 0.68%, respectively. It is observed that ductal carcinoma achieved higher accuracy due to the large number of images used during training compared to the other classes.

Fig. 6 presents a comparison between the existing state-of-the-art approaches and the proposed IPBCS-DL model. The proposed model obtained an accuracy and miss rate of 97.81% and 0.68%, respectively, for breast cancer detection. These results indicate that this model is superior to existing approaches, such as TF [16], SVM [16], DBN [18], and SVM [21]. The performance of the proposed model is further evaluated by the medical experts of Inmol Cancer Hospital, Lahore, Pakistan. Furthermore, the proposed IPBCS-FH-DL model predicts breast cancer stages with an accuracy of 99.32% during the validation phase.

V. CONCLUSION

Breast cancer is a considerable risk to the lives of women worldwide. Mammography and biopsy are two different methods used to detect breast cancer and its different stages. The breast cancer images utilized for simulation are collected from various sources, and data fusion is applied to the dataset. The deep learning approach is used to detect breast cancer and its stages. The accuracy of the proposed model during training and validation is 98.86% and 97.81%, respectively. The overall accuracy of breast cancer stage prediction during training and validation is 99.82% and 99.32%, respectively. It is observed that the proposed IoMT cloud-based intelligent prediction of breast cancer and stages produce highly efficient and accurate results, even when compared to extant state-of-the-art methods.

VI. LIMITATIONS AND FUTURE WORK

The proposed IPBCS-DL model detects breast cancer and classifies it into four stages: ductal carcinoma, lobular carcinoma, mucinous carcinoma, and papillary carcinoma. These stages can be increased and improve the system performance. However, the IPBCS-DL model may increase the computational complexity of the system. In future work, other

computational intelligence approaches can be applied that may improve the system's accuracy.

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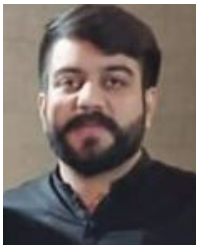

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