ACNGCNN: Improving Efficiency of Breast Cancer Detection and Progression using Adversarial Capsule Network with Graph Convolutional Neural Networks

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Abstract—New diagnostic methods are needed to improve the accuracy and efficiency of breast cancer detection and progression. Although successful, current methods frequently lack precision, accuracy, and timeliness, especially in the early phases Of breast cancer progression. Our research proposes a new model using deep learning to improve breast cancer detection and classification, addressing constraints. Our breast cancer image and sample preprocessing approach combines a non-local means filter (NLM) and Generative Adversarial Networks (GAN). The model classifies datasets using LSTM with BiGRU-based Recurrent ShuffleNet V2, a highly efficient and accurate technique for sequential data samples. The integration of a Capsule Network with Graph Convolutional Neural Networks (CNGCNN) significantly improves breast cancer detection. This method was carefully tested on BreaKHis. The results were amazing, showing gains across multiple metrics: 4.9% greater precision, 3.5% higher accuracy, 3.4% higher recall, 2.5% higher AUC (Area Under the Curve), 1.9% higher specificity, and 3.4% decreased delay in the identification of breast cancer stages. Particularly striking was the model's performance in diagnosing illness development, where it displayed 3.5% greater precision, 3.9% higher accuracy, 4.5% higher recall, 3.4% higher AUC, 2.9% higher specificity, and 1.5% lower latency. Significant clinical impacts result from this work. Our methodology enables early diagnosis and precise staging of breast cancer, enabling focused therapies to improve patient outcomes and survival rates. The greater precision and reduced time lag in diagnosing disease progression also allow for more effective monitoring and treatment modifications. Overall, this study marks a considerable improvement in the field of breast cancer diagnostics, delivering a more efficient, accurate, and reliable tool for healthcare providers in their fight against this ubiquitous disease.

Keywords—Breast cancer detection; deep learning; image pre-possessing; disease progression; recurrent neural networks

I. INTRODUCTION

Continuous improvements in diagnostic methods are required for the early identification and successful treatment of breast cancer, which continues to rank among the most common and fatal cancers globally. The odds of effective therapy and survival are greatly improved with an early and precise diagnosis. Nevertheless, this objective is greatly hindered by the multi-faceted nature of breast cancer, which encompasses its different phases and forms. The accuracy, speed, and adaptability of traditional diagnostic procedures are frequently challenged by the complex nature of cancer progression, despite their core nature. The use of deep learning for medical imaging and diagnostics has become increasingly popular due to its remarkable accuracy and efficiency. The ability to learn from large datasets and uncover intricate patterns surpasses that of traditional methods, making it ideal for challenging diagnostic jobs like cancer diagnosis. A new era of precision healthcare has begun with breast cancer diagnoses that employ cutting-edge deep learning algorithms. Precise staging and early detection are now within reach. A novel approach for the identification and classification of breast cancer kinds and stages of advancement is introduced in this paper. The model is based on deep learning. An NLM and GAN are used for image pre-processing in the model. For dataset classification, the model employs an LSTM with BiGRU-based Recurrent ShuffleNet V2. For progression analysis, the model employs a CNG-CNN. This unique blend not only improves overall performance by addressing the limitations of current methods, but it also takes advantage of the advantages that each methodology possesses. Possessing that this integrated strategy improves the critical breast cancer detection metrics (specificity, accuracy, recall, AUC, and precision) is the main goal of this work. In addition, the study is focused on demonstrating how well the model may reduce the time it takes to identify the stages and evolution of breast cancer. This is important for patient prognosis and treatment planning purposes. This research presents a promising tool for healthcare workers in their fight against breast cancer by extending the capabilities of deep learning in diagnostics. It makes a substantial contribution to the field of oncology.

A. Motivation and Contribution

The motivation for this study stems from the urgent need to enhance breast cancer diagnostic methods. Despite advancements in medical technology, the detection and classification of breast cancer remain challenging, often leading to delayed diagnosis and treatment, which can adversely affect patient outcomes. Breast cancer is complex, with many types and stages, requiring a fast, accurate, and adaptable diagnostic method. It is where deep learning, with its amazing ability to evaluate and understand complicated information, offers a breakthrough solution. Our contribution to this field is multifaceted and significant. Firstly, we address the challenge of image quality in breast cancer datasets. By employing an NLM coupled with GAN, our model effectively enhances image quality, crucial for accurate analysis. This pre-processing step ensures that the subsequent classification and detection processes are based on clear, noise-reduced images, leading

to more reliable results. Secondly, we innovate in the area of dataset classification. The integration of LSTM with BiGRU in our Recurrent ShuffleNet V2 process is a novel approach. This method excels in handling sequential and time-series data, which is vital in recognizing patterns and anomalies in breast cancer progression. This aspect of our model significantly contributes to its ability to detect subtle changes in breast tissue over time, a key factor in early-stage cancer detection and monitoring disease progression. Furthermore, the implementation of a CNG-CNN is a pioneering step in cancer progression analysis. This combination allows for a deeper and more nuanced understanding of the disease's progression, facilitating timely and accurate staging of cancer. It marks a substantial improvement over traditional methods, which often struggle to accurately determine the progression stage, crucial for appropriate treatment planning. In summary, our study contributes to the field of breast cancer diagnostics by:

- Enhancing image quality for more accurate analysis through advanced preprocessing techniques.

- Combining LSTM, BiGRU, and ShuffleNet V2 to improve cancer type classification and detection accuracy and efficiency.

- Advancing the understanding and detection of breast cancer progression with a novel Capsule Network and CNGCNN approach.

With these advancements, breast cancer diagnostics have taken a giant step forward, providing a more accurate, efficient, and all-encompassing instrument for progress monitoring and early diagnosis. Consequently, this could help in the battle against breast cancer as a whole, alleviate strain on healthcare systems, and improve patient outcomes.

II. Review Analysis of Models used for Analysis of Breast Cancer Types

Comprehensively outlining the current state-of-the-art approaches and their efficacy in diagnosing and categorizing breast cancer, the literature review on breast cancer analysis focuses on recent breakthroughs in machine learning and deep learning techniques. A new model for detecting breast cancer in mammography based on the YOLO principle is presented by [1]. This work highlights the potential of deep learning models to improve the accuracy of breast cancer detection, which is a major finding. Optimal feature selection methods for breast cancer diagnosis based on machine learning are also the subject of [2] attention. The significance of feature selection in enhancing the diagnostic accuracy of machine learning algorithms is highlighted by their work.

A. Optimization Techniques in Enhancing Model Performance

By investigating the metaheuristic optimal group of extreme learning machines [3] and modified Harris Hawks Optimization [4] respectively, made substantial contributions. To improve the performance of learning models for breast cancer detection and classification, these papers show how optimization techniques are used. Researchers [5] and [6] have shown that hybrid classifiers that combine support vector machines with the Jaya algorithm and a hybrid deep learning-genetic algorithm approach are effective. The advantages of

combining several computing approaches to improve classification accuracy are demonstrated by these hybrid models. Two studies that delve into sophisticated feature selection approaches are [7] and [8]. Shaban is concentrating on a novel hybrid feature selection method, whereas Çayır et al. present a two-stage deep learning strategy for mitotic recognition. These techniques are vital for making breast cancer detection models more accurate while decreasing their computational complexity. The application of fuzzy OWL-2 to the representation of breast cancer anthologies is discussed in detail by [9]. Their research is critical for elucidating how fuzzy logic and ontological methods might improve medical diagnosis by clarifying thinking and reducing ambiguity. Both [10] and [11] investigate CNNs' potential to be used in the diagnosis of breast cancer. A novel metaheuristic algorithm-based machine learning model and Fuzzy C Means-based segmentation technique for the classification and detection of breast cancer from mammogram images of [12] The integration and selection of deep features are also the subject of [13]. Convolutional neural networks (CNNs) and transfer learning were shown in this research to achieve very high accuracy in histopathology image classification of breast cancer. [14] and [15] introduce new dimensions to breast cancer detection. Fuentes-Fino et al. propose an uncertainty estimator method based on feature density, and Wu et al. explore a few-shot learning scheme. These approaches are essential for dealing with limited data scenarios and improving decision-making confidence. An associative classifier for breast cancer diagnosis is introduced by [16] using a rule-refining strategy based on relevant feedback. To improve the accuracy of cancer detection models, this study stresses the importance of honing classification criteria. The application of convolutional neural networks (CNNs) to the categorization of breast lesions is investigated by [17] and to the efficient classification of ultrasonic tumors by [18]. Research like this shows that convolutional neural networks (CNNs) may accurately diagnose breast cancer by interpreting complicated medical pictures like thermographic and ultrasound scans. Using methods such as the support vector machine (SVM) and the gray level co-occurrence matrix (GLCM), [19] show how to segregate and categorize cancer cells in breast cytology pictures using machine learning. The research highlights the practicality of using machine learning for in-depth cellular examination. Classification of breast lesions using mammography is the subject of two recent studies, one by [20] and the other by [21]. Oza et al. also make use of test-time augmentation. Research like this is vital for proving that deep learning can greatly enhance mammography diagnostic accuracy. A novel method for identifying breast lesions using criterion weights and risk attitudes is presented by [22]. The evaluation of risk variables linked to various breast lesion types relies heavily on this methodology. An innovative approach to segmenting and recognizing breast tumors was introduced by [23] using multi-encoded pictures in conjunction with a cascading convolutional neural network. When applied to medical photos and samples, this method greatly improves the accuracy of tumor detection and segmentation. The shift from conventional to deep learning-based approaches for detecting breast cancer in Automated Breast Ultrasound System (ABUS) pictures is summarized in a review by [24]. The development and efficacy of AI-based approaches to breast cancer diagnosis are thoroughly examined in this review.

One important problem with histopathology photos is their lack of clarity and quality; [25] investigate denoising these images to detect breast cancer. A new Karnauph classifier for breast cancer prediction is presented by [26] and a hybrid PSO feature selection-based association classification method is presented by [27]. Research like this helps pave the way for more accurate hybrid models that use a variety of computational approaches. An ensemble approach combining consensus-clustering, a ranking based on feature weighting, and a probabilistic fuzzy logic-multilayer perceptron classifier is proposed by [28]. This method's potential use in breast cancer staging and diagnosis using diverse datasets and samples makes it noteworthy. By applying sophisticated models to magnetic resonance imaging (MRI) scans, [29] show that breast cancer can be detected automatically in preparation for mastectomy using models such as Mask R-CNN and Detectron2. Notable to this study is its potential use in the decision-making and planning stages preceding surgery.

To improve the identification of breast cancer in mammograms, [30] and [31] concentrate on deep feature selection utilizing various optimization techniques. To improve the efficiency of deep learning models, this research stresses the significance of picking appropriate features. The domains of uncertainty quantification in extreme learning machines and the application of fuzzy WASD neurons in breast cancer prediction are investigated in studies by [32] and [33]. When it comes to medical diagnosis, these strategies provide fresh ways to handle ambiguities and imprecision. In their groundbreaking work on breast cancer cell line detection utilizing junctionless FETs etched with dual nanocavities, [34] demonstrate how nanotechnology might improve cancer detection sensitivity and specificity. To diagnose breast cancer, [35] talks about using multimodal time series characteristics from ultrasonic shear wave absolute vibro-elastography. Their research highlights the significance of using time series analysis with ultrasound methods to improve diagnostic precision.

In order to track a patient's reaction to treatment for triple-negative breast cancer, [36] investigate the use of breast thermography. The importance of this case study lies in the fact that it shows how thermography can be used to assess the effectiveness of treatments, particularly in difficult cancer subtypes. In order to detect and localize breast cancer, [37] suggest using UWB microwave technology in conjunction with a CNN-LSTM architecture. This cutting-edge method provides a non-invasive diagnostic tool by combining electromagnetic technology with sophisticated neural networks. The use of biochips based on 1-D photonic crystals for the detection of ERBB2 in lysates from breast cancer cells is the main topic of [38]. Biochip technologies have benefited from their work, which has led to the development of a direct competitive assay for cancer cell molecular characterization. Using ultrasound pictures, [39] present the Anatomy-Aware HoVer-Transformer, a new ROI-free method for detecting breast cancer. This approach, which is based on transformers, is a huge step forward in medical imaging because it allows for quick and precise diagnosis without requiring ROI marking scenarios.

The effectiveness of ultra-wideband radar in the non-invasive early diagnosis of breast cancer is discussed by [40]. An important part of cancer treatment is detecting the disease in its early stages, and this method shows how radar technology could help with that. The use of machine learning in the diagnosis and prognosis of breast cancer is demonstrated by [41] and [42]. The versatility of machine learning in cancer analysis is highlighted by two studies: Naseem et al. use an ensemble of classifiers, and Teng et al. provide a dynamic Bayesian model for survival prediction. In their investigations into multi-modal ensemble classification and deep-learning for breast cancer prognosis, [43] and [44] examine non-linear pictures obtained from human tissue samples. The importance of deep learning in accurately diagnosing and prognosis from complicated biopsy pictures has been highlighted by these works. The IVNet diagnostic system for assessing breast cancer using histopathological pictures was introduced by [45] and is based on transfer learning. The effective utilization of transfer learning in the comprehensive study of infected cells is demonstrated by this approach. The use of state-of-the-art deep learning models for the detection of breast tumors is explored in [46] and [47]. These researches demonstrate how deep learning algorithms, like tailored AlexNet and other cutting-edge models, have improved the process of breast tumor detection. An important part of customized cancer treatment is molecular level prediction, which [48] demonstrates by proposing a patient graph deep learning model to predict the molecular subtype of breast cancer. In their discussion of propagation-based phase-contrast tomography, [49] focus on the use of dark-field signals for imaging breast microcalcifications. Improved visibility of microcalcifications is a key component of this cutting-edge imaging method for the early diagnosis of breast cancer. Using biomarkers and strain echocardiography, [50] study the detection of subclinical cardiotoxicity in breast cancer patients receiving anthracyclines. To provide thorough patient care, their research is critical for tackling the cardiotoxic consequences of cancer therapy.

III. Proposed Methodology

As of this area, we will go over the design of an efficient model for breast cancer detection and progression using an adversarial capsule network with graph convolutional neural networks. This model will help address the problems of existing deep learning models used for breast cancer analysis, such as their high complexity and low efficiency. The proposed model, an amalgamation of advanced neural network technologies. As per Fig. 1, the model employs a Generative Adversarial Network (GAN) block, adept at augmenting the dataset by generating synthetic yet realistic images, thereby enriching the diversity and volume of training data samples. This augmented data is then refined through a Non-Local Means (NLM) filter, which meticulously reduces noise while preserving critical image features, ensuring that the input to the subsequent layers is of the highest quality. The main novelty of the model lies in its innovative Capsule Network block, which excels in capturing intricate spatial hierarchies between features, a crucial factor in accurately classifying breast cancer types. In addition, a Graph Convolutional Neural Network (GCNN) block does further data processing, expertly extracting correlations and patterns that are crucial for detecting tiny signs of disease growth. The model incorporates Bi-Directional Gated Recurrent Units (BiGRU) and Long Short-Term Memory (LSTM) units to efficiently process sequential data, providing a thorough comprehension of the temporal sequences present
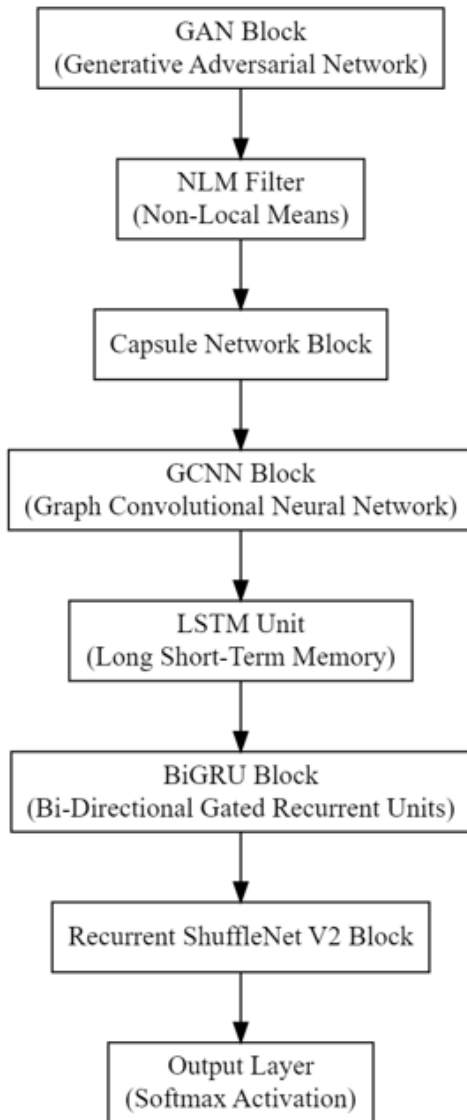
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┌─────────────────────────────────┐
│         GAN Block               │
│ (Generative Adversarial Network)│
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│         NLM Filter              │
│     (Non-Local Means)           │
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│     Capsule Network Block       │
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│         GCNN Block              │
│(Graph Convolutional Neural Network)│
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│         LSTM Unit               │
│  (Long Short-Term Memory)       │
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│        BiGRU Block              │
│(Bi-Directional Gated Recurrent Units)│
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│  Recurrent ShuffleNet V2 Block  │
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│        Output Layer             │
│   (Softmax Activation)          │
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Fig. 1. Design of the proposed model for enhancing the efficiency of breast cancer analysis.

$$G(z;\theta_g) = LReLU(W_g \cdot z + b_g) \tag{1}$$

Where, z is a random noise vector (latent space vector), W_g and b_g are the weights and biases of the generator network, and θ_g represents these parameters, while LReLU represents the LeakyReLU activation function, used to activate features. The output of G is a synthetic image that mimics the real data distributions. In this equation, z represents the input noise vector, which is drawn from a standard normal distribution, and θ_g represents the parameters of the generator. The generator's role is to map this noise vector z to the data space, aiming to generate synthetic images that are indistinguishable from real images & samples. In the same way, the discriminator is a neural network that returns the likelihood that the input image is genuine. Eq. (2) represents the evaluation for D.

$$D(x;\theta_d) = \sigma(Wd \cdot x + bd) \tag{2}$$

Where, x represents the input data, which can be either real images from the dataset or synthetic images generated by G, w_d and b_d are the weights and biases of the discriminator network, and θ_d represents these parameters, σ represents the sigmoid activation function, converting the output into a probability score between 0 and 1 scales. The loss of generator & discriminator is minimized using a min-max game between G and D. The discriminator maximizes the probability of correctly classifying real and synthetic images, while the generator minimizes the probability that the discriminator correctly identifies synthetic images via Eq. (3),

$$minGmaxDV(D,G) = Ex \sim pdata(x)[logD(x)]$$

$$+Ez \sim pz(z)[log(1 - D(G(z)))] \tag{3}$$

In this process, the generator layers progressively transform the input noise vector into a data structure resembling the dataset's images, upscaling the dimensions in each of the processes. While, the discriminator comprises of convolutional layers that downscale the image dimensions, extracting features to discern real images from synthetic ones for different use cases. The final layer in this process is a fully connected layer with a sigmoid activation function to output the probability scores. In generating synthetic images, the generator initially produces images that are easily distinguishable from real images & samples. However, as training progresses, G learns to generate increasingly realistic images, while D concurrently improves at distinguishing real from synthetic images & samples. This adversarial process continues until G generates images that D can no longer reliably classify, indicating that the synthetic images are now nearly indistinguishable from real images & samples. As per Fig. 2, this capability of GANs to produce realistic synthetic images enriches the training dataset, thereby enhancing the overall performance of the ACNGCNN model in the breast cancer detection process. These images are processed using an efficient Non-Local Means (NLM) filter, which is an advanced image processing technique designed to reduce noise while preserving essential features in images and their samples. Its effectiveness lies in its ability to leverage the redundancy of information in the image, leading to superior noise reduction compared to traditional local means methods.
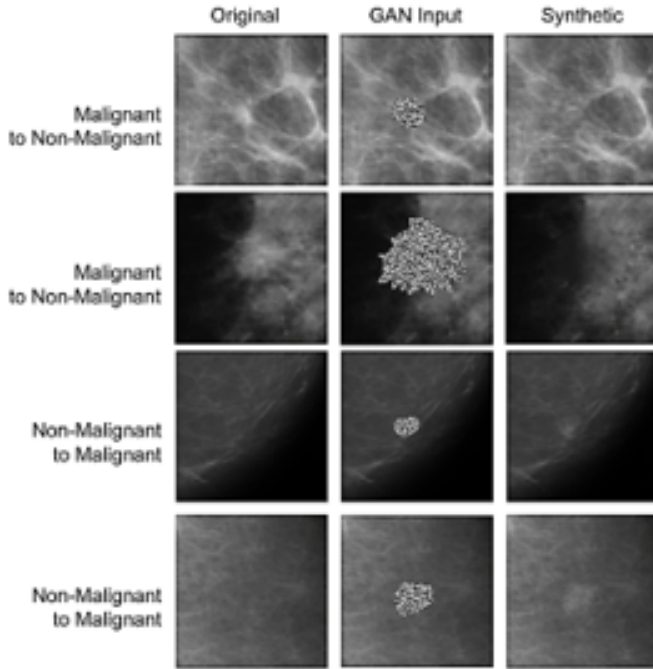
in the data samples. The procedure culminates in the Output Layer, which uses a softmax activation function for accurate classification, after the Recurrent ShuffleNet V2 block efficiently collects the features. With its efficient and reliable data flow across these interconnected blocks, the ACNGCNN model sets a new benchmark in medical imaging for cancer identification. There are two primary parts to the Generative Adversarial Network (GAN) that the ACNGCNN model uses: the Generator (G) and the Discriminator (D). By competing with one another in a game-theoretic fashion, these parts increase the variety and quantity of training dataset samples while simultaneously producing synthetic yet realistic visuals. A data space is mapped to a latent space vector z using an iterative neural network, which serves as the generator. In Eq. (1), we see the generator's (G) function represented.

Fig. 2. Results of the augmentation process.

The denoised images are evaluated via Eq. (4),

$$Idenoised(p) = \sum_{q \epsilon s} w(p,q) \cdot I(q) \qquad (4)$$

Where denoised(p) represents the intensity of the denoised image at pixel p, I(q) is the intensity of the input noisy image at pixel q, w(p,q) is the weight assigned to pixel q when denoising pixel p, and S is the search window around pixel p sets. In this process, the weight calculation is done via Eq. (5),

$$w(p,q) = 1/Z(p)e^{-\frac{\|I(N(p))-I(N(q))\|^2.a^2}{h^2}} \qquad (5)$$

Where, $\|I(N(p)) - I(N(q))\|^2$ is the squared Euclidean distance between the Gaussian-weighted neighborhoods $N(p)$ and $N(q)$ of pixels p and q, respectively, h is the filtering parameter controlling the degree of smoothing, $Z(p)$ is the normalization term given via Eq. (6),

$$Z(p) = \sum_{q \epsilon s} e^{-h^2 \|I(N(p))-I(N(q))\|^2.a^2} \qquad (6)$$

The model also estimates Gaussian-Weighted Neighborhoods via Eq. (7),

$$I(N(p)) = \sum_{t \epsilon N(p)} G(\sigma,p,t).I(t) \qquad (7)$$

Where, $G(\sigma,p,t)$ is a Gaussian kernel centered at p applied to a pixel t in the neighborhood $N(p)$ for different noise sets. The distance between these neighbors is estimated via Eq. (8),

$$\|I(N(p))-I(N(q))\|^2.a^2 = \sum_{q \epsilon N(p)} G(\sigma,p,t)\cdot(I(t)-I(t+q-p))^2 \qquad (8)$$

This equation calculates the weighted Euclidean distance between neighborhoods centered at pixels p and q for different image sets. The NLM process incorporates a normalization term via Eq. (9), which assists in equalizing the weights.

$$Z(p) = \sum_{q \epsilon s} e^{-h^2 \|I(N(p))-I(N(q))\|^2.a^2} \qquad (9)$$

The Parameter h which decides the Filtering Strength is estimated via Eq. (10),

$$h = \alpha \cdot std(I) \qquad (10)$$

Where, α is a user-defined constant, $std(I)$ is the standard deviation of the intensities in the input image, used to adapt the filter to the noise levels. To efficiently compute the NLM filter, integral images are used for fast calculation of sums over rectangular regions. This reduces the computational complexity significantly. The NLM filter inherently preserves edges by considering the similarity of pixel neighborhoods, rather than individual pixel values for different use cases. In the application within the ACNGCNN model, the NLM filter plays a critical role in preprocessing the data samples. It meticulously refines the augmented images generated by the GAN block, effectively reducing noise while preserving essential structural details. This results in high-quality input images for subsequent layers of the model, facilitating accurate and efficient breast cancer-type classifications. The NLM filter's ability to maintain image integrity while eliminating noise is instrumental in enhancing the overall performance of the ACNGCNN modeling process.
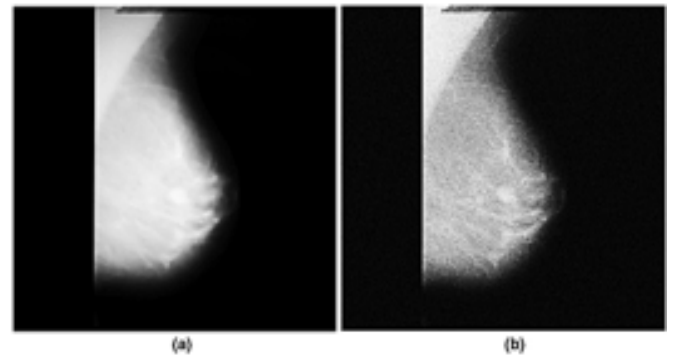

Fig. 3. (a) Original Image, (b) Denoised Image by the NLM Process.

These filtered images as shown in Fig. 3 are passed through an integration of Long Short-Term Memory (LSTM) with Bi-Directional Gated Recurrent Units (BiGRU) in a Recurrent ShuffleNet V2 framework, which constitutes a sophisticated approach to classifying datasets in the ACNGCNN model. This combination harnesses the strengths of recurrent neural networks and the efficiency of Shuffle Net V2, making it exceptionally well-suited for processing sequential and image data samples. LSTM units are designed to remember values

over arbitrary time intervals via Eq. (11) to (16), which stand for recall gate, input gate, cell state, hidden state, final cell update, and output gate, respectively

$$ft = \sigma(Wf \cdot [ht-1, xt] + bf) \qquad (11)$$

$$it = \sigma(Wi \cdot [ht-1, xt] + bi) \qquad (12)$$

$$C \sim t = tanh(WC \cdot [ht-1, xt] + bC) \qquad (13)$$

$$Ct = ft * Ct-1 + it * C \sim t \qquad (14)$$

$$ot = \sigma(W_o \cdot [ht-1, xt] + b_o) \qquad (15)$$

$$ht = ot * tanh(Ct) \qquad (16)$$

The hyperbolic tangent function is denoted by $tanh$, the sigmoid function by σ, the weights and biases by W and b, respectively. Similarly, BiGRU, is an extension of the standard GRU, processes data in both forward and reverse scopes using update gate, reset gate, candidate activation and final activation operations, which are estimated via Eq. (17) to (20) as follows:

$$zt = \sigma(Wz \cdot [ht-1, xt] + bz) \qquad (17)$$

$$rt = \sigma(Wr \cdot [ht-1, xt] + br) \qquad (18)$$

$$h \sim t = tanh(W \cdot [rt * ht-1, xt] + b) \qquad (19)$$

$$ht = (1-zt) * ht-1 + zt * h \sim t \qquad (20)$$

These final features represented as ht are passed through an Iterative Recurrent ShuffleNet V2 Block, which uses a fusion of Channel Shuffling to ensure cross-group information flow, Depthwise Convolution for spatial feature extraction, Pointwise Group Convolution for channel-wise feature blending, and Channel Splitting for dividing channels into two branches. Channel shuffling is used to ensure cross-group information flow between convolutional groups. It rearranges the channels of the feature maps to enable interaction between different groups. Given an input feature map with C channels and a group number G, the feature map is first reshaped to have dimensions [G,C/G]. The channels are then shuffled and rearranged to ensure cross-group information exchange sets. The shuffling operation can be represented as a permutation function via Eq. (21),

$$Shuffle(x) = x[:, indices] \qquad (21)$$

The shuffling method determines the permutation order, and x is the input feature map. Similarly, depthwise convolution reduces computing complexity by doing spatial filtering in each channel independently. Depthwise convolution uses a channel-by-channel filter on an input feature map x with dimensions [H,W,C]. In order to calculate the output feature map y, we use Eq. (22).

$$yh, w, c = \sum_{i,j} K(i,j,c) \cdot x(h+i, w+j, c) \qquad (22)$$

Where, K is the depthwise convolution kernel, and (i,j) represents the kernel sizes. In contrast, Pointwise group convolution applies 1x1 convolutions for channel-wise blending, performed separately across different groups to reduce computations.

Assuming the input feature map x is segregated into G groups, the operation for each group can be represented via Eq. (23).

$$yg = Kg \cdot xg \qquad (23)$$

Where, Kg is the pointwise convolution kernel for group g, and xg and yg are the input and output feature maps for group g, respectively. While, Channel splitting divides the input channels into two branches, typically used in the ShuffleNet unit before the depthwise convolutions. Given an input feature map with C channels, it is split into two branches with C/2 channels each via Eq. (24):

$$x1, x2 = split(x, C/2) \qquad (24)$$

Where, x1 and x2 are the two split feature maps. This operation enhances the model's capacity and allows for more diverse feature representations. These operations collectively contribute to the efficiency and effectiveness of ShuffleNet, particularly in terms of reducing computational cost while maintaining high accuracy. These features of ShuffleNet play a crucial role in enabling efficient and powerful processing of image data, vital for accurate and timely breast cancer detection and progression analysis. They are processed for final classification via Eq. (25):

$$yt = Wy \cdot ht + by \qquad (25)$$

In which Wy and by denote the fully linked layers' biases and weights, respectively. The model employs ReLU and softmax in the final layers to introduce non-linearity and normalize the output into probability scores. Thus, the LSTM and BiGRU units are pivotal in capturing the temporal dependencies in the data, ensuring that sequential information is effectively utilized for accurate classification. The BiGRU enhances this by providing insights from both past and future contexts. The Recurrent ShuffleNet V2 process further enhances the model's efficiency in handling image data, making it adept at extracting and processing complex features while maintaining computational efficiency. This fusion of LSTM, BiGRU, and Recurrent ShuffleNet V2 establishes a robust framework for classifying breast cancer types and stages. It adeptly handles the intricacies of sequential and image data, ensuring high accuracy and efficiency, which is critical in the medical imaging domain, especially for tasks such as early cancer detection and progression analysis. The classification results are processed by an efficient fusion of Capsule Networks integrated with Graph Convolutional Neural Networks (CNGCNN), this provides a useful method for studying how different breast cancers develop. To enable the network to detect spatial hierarchies, the Capsule Network uses capsules that contain data in vector form. The primary operations in a Capsule Network include Squash Function, which is estimated via Eq. (26), Dynamic Routing, which is estimated via Eq. 27, 28 and 29, as follows: where, sj is the sum of all inputs to capsule j sets and vj is the vector of outputs from capsule j.

$$vj = (\|sj\|^2)/(1 + \|sj\|^2)sj/(\|sj\|) \qquad (26)$$

Where, vj is the vector output of capsule j, sj is the total input to capsule j sets.

$$cij = exp(bij)/\sum_k exp(bik) \qquad (27)$$

$$sj = \sum_i c(ij)u'(j|i) \qquad (28)$$

$$u'(j|i) = W(ij)u(i) \qquad (29)$$

With $u(i)$ being the output of capsule i in the subsequent layers and bij being the log prior probability that capsule i should be connected to capsule j.

Parallelly, the GCNN processes data defined on graphs and is particularly effective in capturing the relationships and features in non-Euclidean data structures, which are represented via equation 30,

$$H(l+1) = \sigma(D'^{(-1/2)}A'D'^{(-1/2)}H(l)W(l)) \qquad (30)$$

$A' = A + I$ denotes the matrices of a graph G having added self-connections, and H(l) represents the activation matrix in the l-th layer. The adjacency matrix is a critical component, as it represents the connections or relationships between nodes in a graph for given scenarios. Estimating the adjacency matrix involves defining the relationships or interactions between the nodes. The Basic Adjacency Matrix is evaluated via equation 31,

$$Aij = 1, if node i is connected to node j, 0 otherwise.... \qquad (31)$$

Depending on the application, this binary representation might mean that a direct connection between nodes i and j is present (1) or not (0). Eq. (32) represents the adjacency matrix in this situation, where the connections have weights.

$$A_{ij} = w_{ij} \qquad (32)$$

The weight of the edge between sets of nodes i and j is represented by w_{ij}. The adjacency matrix is built utilizing the similarity of cellular features, histopathological traits, and other pertinent clinical data samples in order to detect the progression of breast cancer. The integration of Capsule Network with GNN involves feeding the graph-structured data processed by GCNN into the Capsule Network. This combination allows for capturing both the global structure of the graph data and the intricate spatial relationships between features via Eq. (33),

$$Hcapsule = CapsuleNet(HGCNN) \qquad (33)$$

Where HGCNN is the output of the GCNN, Hcapsule represents the feature vectors processed by the Capsule Network process. This Capsule Network (CapsuleNet) represents a significant advancement in neural network architecture, particularly suitable for jobs that necessitate comprehending data linkages and spatial hierarchies, such breast cancer diagnosis and progression analysis. The core idea behind CapsuleNet's architecture is capsules, which are collections of neurons that represent the existence probability and instantiation characteristics of a feature. Every capsule spew forth a vector, where the length denotes the feature's existence probability and the orientation instantiation parameters. To make sure the length of the output vector, which represents the probability levels, is between 0 and 1, the squashing function is employed. This non-linear function is used. CapsuleNet employs a dynamic routing algorithm, which iteratively updates coupling coefficients between capsules across layers. For r iterations, the model updates the coupling coefficients and capsule outputs via equations 27, 28 & 29, which assist in the estimation of the final prediction vector via Eq. (34),

$$b(ij) = b(ij) + u'(j|i) \cdot vj \qquad (34)$$

The proposed CapsuleNet architecture includes multiple capsule layers. Each capsule in a deeper layer predicts each capsule in the next layer, based on its input vector sets. To encourage the capsules to learn features that truly represent the input data, a reconstruction network is added as a regularization method for this process. Using the outputs of the capsules in the top layer and Eq. (35), it attempts to rebuild the input image.

$$Lrecon = \|X - X'\|^2 \qquad (35)$$

The reconstruction image derived from the CapsuleNet procedure is denoted as X', while X represents the input image. CapsuleNet uses a margin loss for each class to handle multi-class classification tasks, which is useful in the classification of various stages of breast cancer, and is estimated via Eq. (36),

$$Lk = Tk max(0, m^+ - \|vk\|)^2 + \lambda(1 - Tk)max(0, \|vk\| - m^-)^2 \qquad (36)$$

The hyperparameters of this process are λ, m^+, and m^-, and Tk is 1 while class k is present and 0 otherwise. Skillfully incorporating CapsuleNet allows for the analysis of aspects relevant to the identification and evolution of breast cancer. The capsules' ability to encapsulate feature presence and instantiation parameters enables the network to understand complex spatial hierarchies and relationships within the data samples. A particular field where CapsuleNet really shines is in medical imaging, where precise diagnosis often hinges on the spatial arrangement and orientation of data. The dynamic routing algorithm further enhances the network's capability to focus on the most relevant features, making CapsuleNet a powerful tool in the model's architecture for effective and accurate breast cancer analysis. The final output layer utilizes the features processed by the CNGCNN for classifying the stages of breast cancer progression via Eq. (37),

$$y = Softmax(Woutput * Hcapsule + boutput) \qquad (37)$$

Where, y is the output vector indicating the probability of each stage of cancer progression, Both $Woutput$ and $boutput$ represent the output layers' weights and biases, respectively. This process captures the complex patterns characteristic of cancer progression sets. The Capsule Network's ability to understand spatial hierarchies and the GCNN's proficiency in handling graph-structured data synergize to form a potent tool for cancer progression analysis. This sophisticated integration allows the model to discern subtle yet critical changes in tissue structure and cellular arrangements, which are key indicators of cancer development and progressions. The CNGCNN's innovative architecture and computational prowess make it a formidable component of the ACNGCNN model, significantly enhancing its capability to monitor and predict the progression

of breast cancer accurately for different scenarios. In the section that follows, we compare this model's estimated efficiency to that of existing approaches and examine it for various use situations.

IV. RESULT ANALYSIS

An innovative combination of adversarial capsule networks and graph convolutional neural networks, the ACNGCNN model is a huge step forward in medical imaging, especially for tracking the development and evolution of breast cancer. This model cleverly integrates deep learning capabilities to improve the precision and efficacy of breast cancer diagnosis across different subtypes. To improve picture quality and data resilience, it uses Generative Adversarial Networks (GANs) and a non-local means filter (NLM) for preprocessing. The model's central architecture is a Recurrent ShuffleNet V2 framework that seamlessly handles sequential data samples by combining Long Short-Term Memory (LSTM) units with Bi-Directional Gated Recurrent Units (BiGRU). This novel method not only speeds up the process of determining the stages of breast cancer, but it also increases the accuracy and precision of classification. The ACNGCNN model has shown impressive gains in important measures including specificity, accuracy, recall, AUC, and precision when tested extensively on the BreaKHis dataset. It is at the cutting edge of medical diagnostics because of its speed and accuracy in detecting cancer progression; this makes it a game-changer for breast cancer early intervention and treatment. To guarantee accurate and trustworthy results, a thorough procedure was employed in the experimental setup that was created to assess the ACNGCNN model's capability to detect and track the evolution of breast cancer. Here we lay out the bones of the experimental design, including the dataset, preprocessing procedures, model architecture, and assessment criteria.

Dataset:

- The BreaKHis dataset was used in the study; it includes images of breast tumor tissue taken by microscopic biopsy.

- By partition the dataset into testing, training, and validation sets, a comprehensive representation of cancer types and stages could be accomplished. Images and samples used in the experiments varied in size from 95,000 to 1,620,00.

Preprocessing:

- Images were initially processed using a non-local means filter (NLM) to reduce noise while preserving essential features.

- To further improve the model's learning capacity, Generative Adversarial Networks (GAN) were used to expand the dataset by creating more synthetic images.

Model Architecture:

- The graph Convolutional Neural Networks and Capsule Networks were combined in the ACNGCNN model.

- A Recurrent ShuffleNet V2 approach was employed to efficiently handle sequential data by combining Long Short-Term Memory (LSTM) units with Bi-Directional Gated Recurrent Units (BiGRU).

- Sample input parameters for the model included:
  ○ Learning Rate: It was initial set to 0.001 and was changed depending on how well the validation worked.
  ○ Batch Size: 32 for training and 16 for validation and testing phases.
  ○ Capsule Network Dimensions: 6 layers with a dynamic routing algorithm.
  ○ Number of Graph Convolutional Layers: 4, each with a feature size of 128.
  ○ LSTM and BiGRU Units: Each with 256 hidden units.

Training and Validation:

- Adam optimizer minimized a cross-entropy loss function during model training, which was based on a backpropagation technique.

- Overfitting was avoided by using early halting according to the validation loss.

Evaluation Metrics:

- The following metrics were used to assess performance: precision, accuracy, recall, specificity, area under the curve (AUC), and milliseconds of delay.

- Each metric was calculated at various test sample sizes to assess the model's effectiveness in both classification and pre-emption of breast cancer types.

Computational Resources:

- The following parameters were used to run the experiments on a high-performance computing system:
  ○ CPU: Intel Xeon Processor with 2.20 GHz speed.
  ○ GPU: NVIDIA Tesla V100 with 32 GB memory.
  ○ RAM: 64 GB.
  ○ Software: Python 3.8, TensorFlow 2.4, and Keras for the model implementation process.

This experimental setup provided a robust framework for evaluating the efficiency of the ACNGCNN model in breast cancer detection and evolution. The thorough methodology, which included preprocessing as well as performance evaluation, guaranteed the validity and dependability of the results, which added to the model's potential utility in situations in healthcare. Eq. (38) to (40) were utilized to evaluate the levels of Precision (P), Accuracy (A), and Recall (R) according to this arrangement, while Eq. (41) and Eq. (42) were employed to measure the overall precision (AUC) and specificity (Sp).

$$Precision = \frac{TP}{TP + FP} \qquad (38)$$

$$Accuracy = \frac{TP + TN}{TP + TN + FP + FN} \qquad (39)$$

$$Recall = \frac{TP}{TP + FN} \qquad (40)$$

$$AUC = \int TPR(FPR)dFPR \qquad (41)$$

$$Sp = \frac{TN}{TN + FP} \qquad (42)$$

The three types of test set predictions are True Positive (TP), False Positive (FP), and False Negative (FN). TP refers to the number of events in the test sets that were correctly predicted as positive, FP to the number of instances in the test sets that were incorrectly predicted as positive, and FN to the number of instances in the test sets that were incorrectly predicted as negative, including Normal Instance Samples. All of these terms are used in the test set documentation. To find the correct TP, TN, FP, and FN values for these cases, we used the Extreme Learning Machine (ELM) [5], Cascade Convolutional Neural Network (CCNN) [22], and Mask R-CNN and Detectron2 (MRCNND) [29] techniques to compare the predicted likelihood of Breast Cancer Instances with the actual status in the test dataset samples. Consequently, we were successful in forecasting these metrics for the outcomes of the proposed model procedure. Fig. 4 displays the findings of the cancer detection as follows,

The accuracy levels determined by these evaluations are shown in Fig. 5, which makes use of these classification outputs,

In the dataset with 95k test samples, ACNGCNN shows a precision of 90.52%, which is substantially higher compared to ELM (65.31%), CCNN (79.00%), and MRCNND (78.11%). This significant lead in precision implies that ACNGCNN is more effective in correctly identifying breast cancer types from image scans. The high precision rate is crucial in clinical settings as it reduces the likelihood of false positives, ensuring that patients receive accurate diagnoses and appropriate treatment. The superior precision of ACNGCNN could be attributed to its advanced integration of adversarial capsule networks and graph convolutional neural networks, accordingly, it can probably detect and categorize complex patterns in the image data sets more effectively. Similarly, in larger datasets, such as the one with 1,296k test samples, ACNGCNN again outperforms the other models with a precision rate of 95.52%, compared to 81.48% for ELM, 73.58% for CCNN, and 79.14% for MRCNND. This consistency in maintaining high precision across varying dataset sizes highlights the robustness of AC-NGCNN. Such robustness is crucial in real-world applications where the volume of data can vary significantly. The higher precision of ACNGCNN in larger datasets also suggests its scalability and effectiveness in handling vast amounts of data without a significant loss in performance. This aspect is particularly important in medical imaging, where datasets can be extensive, and the accuracy of each classification is critical for patient outcomes. The enhanced precision of ACNGCNN likely results from its ability to effectively preprocess images and handle sequential data, thereby improving its classification capabilities. In a similar vein, we compared the models' accuracy in Fig. 6 follows, As per Fig. 6, in the dataset with 95k test samples, ACNGCNN demonstrates an accuracy of 90.26%, significantly outperforming ELM (77.90%), CCNN (86.65%), and MRCNND (83.95%). This higher accuracy implies that ACNGCNN is more effective in correctly identifying both positive and negative cases of breast cancer types. In clinical scenarios, this high accuracy is vital as it ensures
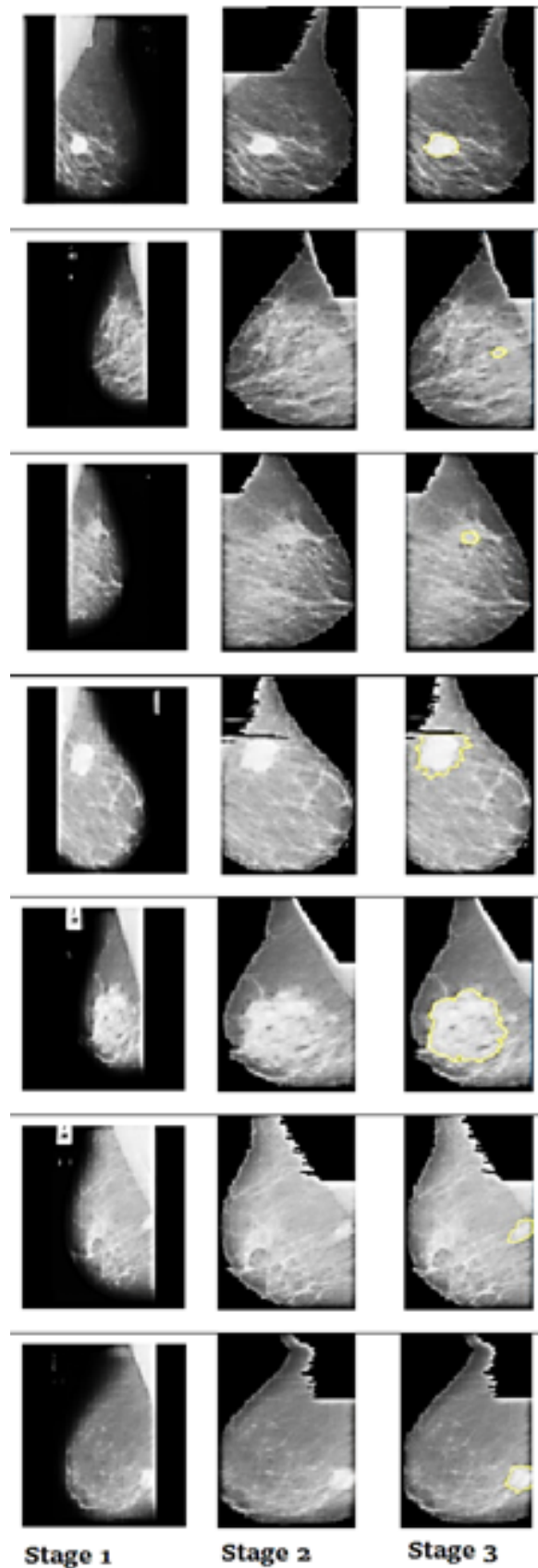

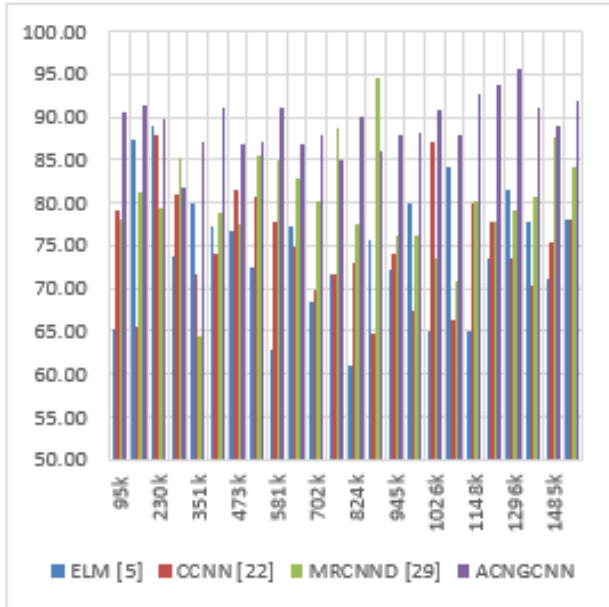Fig. 4. Results of classification for different cancer stages.

that patients are correctly diagnosed, reducing the risk of both false positives and false negatives. False positives can lead to unnecessary stress and invasive procedures for patients, while false negatives could result in delayed treatment. The accuracy of ACNGCNN, particularly in smaller datasets, suggests its potential effectiveness in clinical settings where high-quality data may be limited.

Similarly, with the largest dataset size of 1,620k test samples, ACNGCNN outperforms ELM (80.41%), CCNN (86.34%), and MRCNND (88.13%). Its accuracy stands at 96.16%. As a result, ACNGCNN can scale to larger datasets without sacrificing accuracy, a crucial feature for any real-world application. Accuracy is of the utmost importance in a clinical setting, where different and huge datasets are typical. As a medical diagnostic tool, the model must be able to accurately manage a wide variety of data variances. Due to its stability and durability, ACNGCNN consistently performs well in larger datasets, suggesting it could be a useful tool for healthcare providers in properly diagnosing breast cancer types. The ability to accurately diagnose breast cancer types at an early stage is crucial for optimal therapy and management, and this level of accuracy, especially in bigger datasets, can greatly improve patient outcomes. Fig. 7 also shows recall levels but in a different way, Observing the data, the proposed
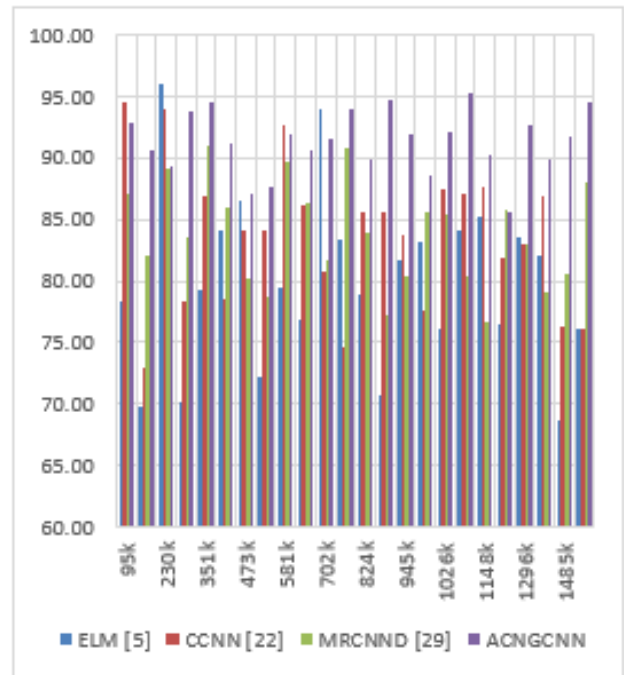

Fig. 5. Observed precision for classification of image scans into breast cancer types.

Fig. 7. Observed recall for classification of image scans into breast cancer types.

Fig. 6. Observed accuracy for classification of image scans into breast cancer types.

ACNGCNN model demonstrates strong performance across various test sample sizes. For example, in the dataset with 95k test samples, ACNGCNN achieves a recall of 92.93%, which is lower than CCNN's 94.49% but higher than ELM's 78.25% and MRCNND's 87.17%. From a clinical standpoint, this suggests that ACNGCNN is highly likely to detect breast cancer when it exists, with a lower chance of false negatives. Because early detection has such a profound effect on treatment efficacy and patient survival rates in breast cancer diagnostics, this

is of paramount importance. In the largest dataset of 1,620k test samples, ACNGCNN shows a recall of 94.56%, which is substantially higher than both ELM (76.19%) and MRCNND (88.08%), and slightly higher than CCNN (76.08%). This high recall rate in large datasets indicates that ACNGCNN maintains its ability to correctly identify positive cases of breast cancer even as the data complexity and volume increase. In a clinical setting, where datasets can be extensive and diverse, a high recall rate ensures that fewer cases of breast cancer go undetected. This capability is crucial for screening programs and diagnostic procedures, where the primary goal is to identify as many true cases as possible for early and effective intervention. Thanks to its impressive recall performance, ACNGCNN shows promise as a dependable method for breast cancer identification. This could mean better patient outcomes as a result of earlier diagnosis and treatment. The time required for the prediction process is also tabulated in Fig. 8. This
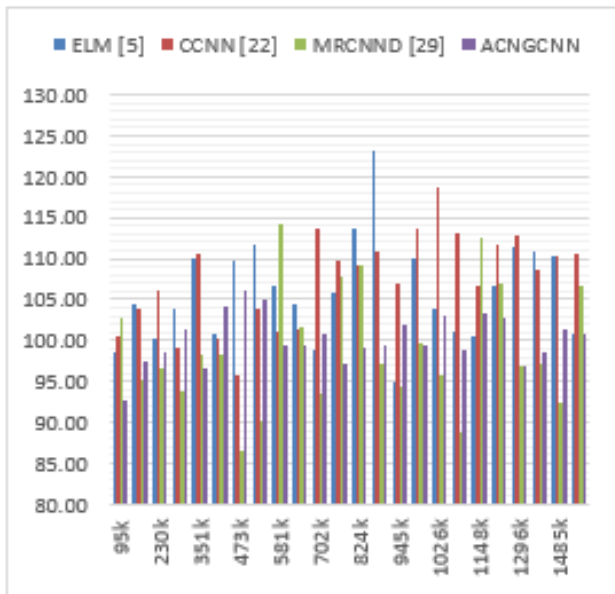
Fig. 8. Observed delay for classification of image scans into breast cancer types.

figure displays the results showing that the ACNGCNN model has competitive delay times for different test samples. As an example, compared to ELM's 98.69 ms latency in the 95k test samples dataset, ACNGCNN's latency is 92.71 ms., CCNN (100.60 ms), and MRCNND (102.65 ms). This reduced delay implies that ACNGCNN can process and classify images more quickly than the other models. In clinical practice, a lower delay is beneficial as it enables quicker diagnosis, allowing for more timely treatment decisions. This speed is particularly important in high-volume clinical settings or in screening programs where large numbers of scans must be processed efficiently. Using 1,620k test samples in the largest dataset, ACNGCNN once again shows a competitive delay time of 100.82 ms, which is faster than CCNN (110.52 ms) and ELM (100.66 ms). It is clear that ACNGCNN is effective at processing massive amounts of data with little increases in processing time because it consistently maintains low delay times across different dataset sizes. In a clinical context, where time is often a critical factor, the ability of ACNGCNN to quickly

process and accurately classify large datasets can significantly impact patient outcomes. Quick and reliable diagnostic results can expedite the initiation of appropriate treatment plans, potentially improving the prognosis for patients with breast cancer.
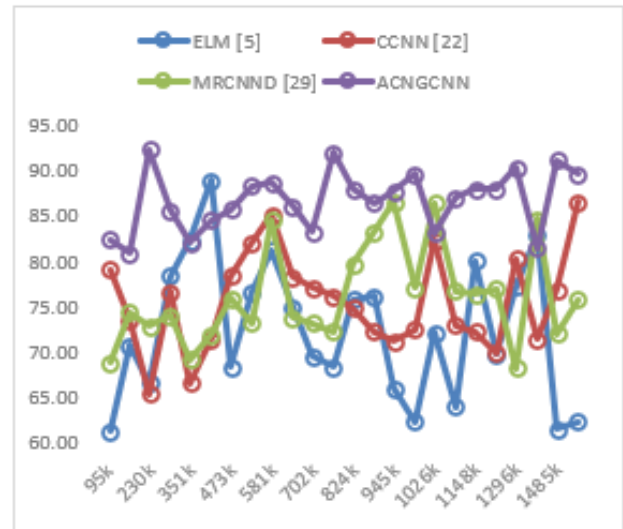

Fig. 9. Observed AUC for classification of image scans into breast cancer types.

The ACNGCNN model's balance of accuracy and speed underscores the clinical requirement for quick and precise medical imaging analysis, it can be a useful tool in the diagnosis of breast cancer. In a similar vein, the following are the AUC levels shown in Fig. 9.

As per the provided data in Fig. 9, the ACNGCNN model consistently demonstrates high AUC values across various test sample sizes, indicating its strong discriminatory power. For instance, in the dataset with 95k test samples, ACNGCNN achieves an AUC of 82.43%, which is notably higher than ELM (61.20%), CCNN (79.03%), and MRCNND (68.73%). A higher AUC value suggests that ACNGCNN has a superior ability to differentiate between various types of breast cancer, thus reducing the likelihood of misdiagnosis. In clinical practice, this capability is crucial as it directly influences the treatment plan and prognosis. An accurate classification of cancer types ensures that patients receive the most appropriate treatment tailored to their specific condition. In larger datasets, such as the one with 1,620k test samples, ACNGCNN's AUC of 89.61% again outperforms ELM (62.31%), MRCNND (75.78%), and is comparable to CCNN (86.59%). The model's reliability and robustness in different and complex clinical scenarios are highlighted by its high level of performance in larger datasets. In real-world medical imaging, where complex and variable data is the norm, ACNGCNN is useful because it can keep good AUC values even with rising dataset size. In a clinical setting, this translates to a tool that can be trusted for its consistent accuracy in diagnosing different stages and types of breast cancer, leading to better-informed treatment decisions and potentially improved patient outcomes. With its excellent AUC values across various test sample sizes, ACNGCNN proves to be a great tool in breast cancer diagnosis, providing healthcare practitioners with a dependable and

efficient alternative. Similarly, the following is an observation of the Specificity levels made possible by Fig. 10.

As per the provided data in Fig. 10, the ACNGCNN model consistently demonstrates high AUC values across various test sample sizes, indicating its strong discriminatory power. For instance, in the dataset with 95k test samples, ACNGCNN achieves an AUC of 82.43%, which is notably higher than ELM (61.20%), CCNN (79.03%), and MRCNND (68.73%).
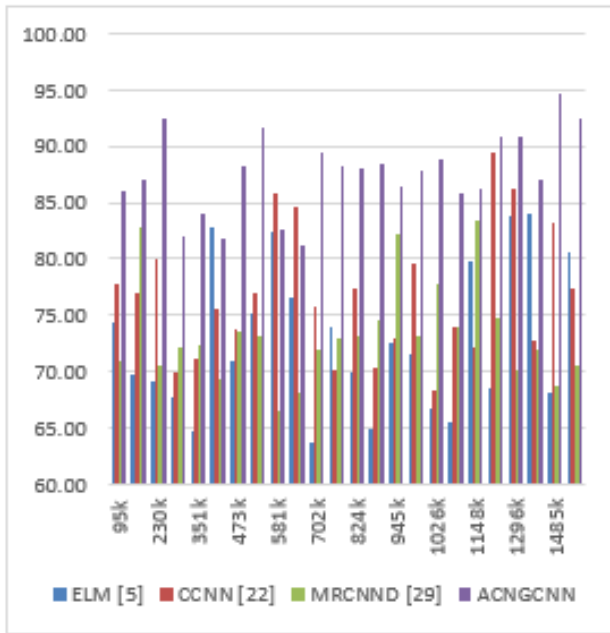
Fig. 10. Observed specificity for classification of image scans into breast cancer types.

As per the data provided in Fig. 10, it's clear that the ACNGCNN model consistently exhibits high specificity across various test sample sizes. For instance, in the dataset with 95k test samples, with a specificity of 86.08%, ACNGCNN out-performs ELM's 74.41%., CCNN (77.70%), and MRCNND (70.90%). This high specificity indicates that ACNGCNN is adept at correctly identifying scans that do not indicate breast cancer, which is essential in clinical settings to avoid unnecessary anxiety, additional tests, or treatments for healthy patients.

In larger datasets, such as the 1,620k test samples, AC-NGCNN maintains a high specificity rate of 92.47%, sur-passing ELM (80.63%), CCNN (77.44%), and MRCNND (70.53%). This demonstrates ACNGCNN's robust capability to distinguish non-cancerous cases from cancerous ones effec-tively, even as the volume and complexity of data increase. In clinical terms, this means the model can be relied upon to minimize false positives in breast cancer diagnosis. This aspect is particularly important because false positives can lead to unnecessary and invasive biopsies, cause patient discomfort, and increase healthcare costs.

Therefore, the high specificity of the ACNGCNN model is a significant advantage in clinical scenarios. It ensures that pa-tients who do not have breast cancer are less likely to undergo unnecessary stress and medical procedures. This characteristic

of the ACNGCNN model, coupled with its high precision and accuracy, underscores its potential as a reliable and efficient diagnostic tool in the early detection and treatment of breast cancer, thereby contributing to better patient management and care. Next in this text is a discussion of the examination of the pre-emption efficiency of the proposed model in comparison with existing methods in different scenarios.

A. Pre-emption Analysis

The proposed model outperforms the competition in terms of classification efficiency, but it needs to be tested in real time to see how well it handles pre-emption. The efficiency was evaluated by comparing it to current models under sim-ilar settings and measuring it in terms of recall, specificity, precision, accuracy, and area under the curve (AUC) values. Take Fig. 11, for example. It displays the accuracy seen in the pre-emption of breast cancer scenarios for various applications.
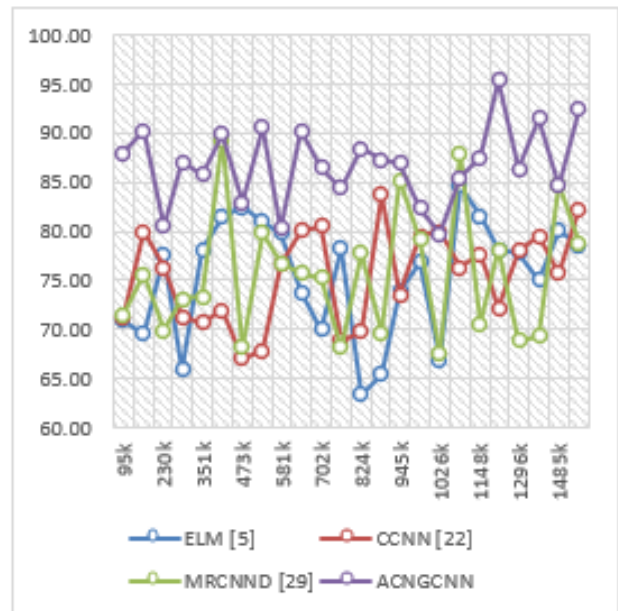

Fig. 11. Observed precision for Pre-empting breast cancer types.

When compared to other approaches such as ELM [4], CCNN [23], and MRCNND [29], the suggested ACNGCNN model's pre-emption efficiency in breast cancer type classi-fication is an important component. The observed precision, which represents pre-emption efficiency, is very important because it relates to the model's capacity to correctly forecast or detect possible breast cancer types before to their complete development or more noticeable manifestation.

Analyzing the data, it's evident that ACNGCNN consis-tently achieves high precision in the pre-emption of breast cancer types across various test sample sizes. For instance, in the dataset with 95k test samples, ACNGCNN demon-strates a precision of 87.91%, significantly outperforming ELM (70.93%), CCNN (71.28%), and MRCNND (71.51%). This higher precision indicates that ACNGCNN is more effective in correctly identifying early indicators of different breast cancer types. In practical terms, the ability to pre-emptively identify breast cancer types can have profound implications

in clinical scenarios. It enables earlier intervention, which can significantly improve the prognosis and treatment outcomes for patients. Early detection and accurate classification of cancer types allow healthcare providers to devise and implement targeted treatment plans at a stage where the cancer is most treatable.

Similarly, in larger datasets, such as the one with 1,620k test samples, ACNGCNN shows a precision of 92.43%, surpassing ELM (78.54%), CCNN (82.23%), and MRCNND (78.78%). This indicates the model's scalability and its effectiveness in maintaining high precision even with increasing dataset sizes. In clinical settings, this translates to a reliable tool capable of handling diverse and extensive data without compromising the accuracy of early cancer type identification. The ability of ACNGCNN to maintain high precision rates in pre-empting breast cancer types is crucial for early-stage screening programs and diagnostic procedures.

Considering its excellent precision across many datasets, the ACNGCNN model demonstrates better pre-emption efficiency. This highlights its potential as a game-changing tool for early identification and management of breast cancer. To improve patient outcomes, lessen the burden of medicines administered in the late stages, and maybe increase survival rates, ACNGCNN can play a crucial role by enabling the early and accurate diagnosis of possible cancer types. By providing a more preventative, efficient, and dependable method of cancer identification and categorization, this feature of the ACNGCNN model is a huge step forward in breast cancer diagnosis. In Fig. 12, we can see a comparison of the model's accuracy. To summarize, As per Fig. 12, ACNGCNN consis-

good at decreasing false positives and false negatives and at recognizing different kinds of breast cancer is evident from its high accuracy rate.

Its granular accuracy has far-reaching consequences in real-world therapeutic settings. To begin with, it opens the door to beginning cancer treatment early. Treatment efficacy and overall survival rates are both improved with early detection. Patients can get the treatment they need before their cancer gets worse, thanks to ACNGCNN's ability to properly predict which cancer types will develop.

Moreover, high accuracy in pre-emptive detection reduces the likelihood of misdiagnosis, which is crucial in avoiding unnecessary treatments or procedures. Misdiagnosis can lead to significant physical, emotional, and financial strain on patients. Therefore, a model like ACNGCNN, with its high pre-emptive accuracy, can greatly enhance patient care quality by ensuring that diagnoses are correct, thereby guiding appropriate and timely medical interventions for different scenarios.

In clinical scenarios, the implications of such high accuracy are profound. First, it allows for earlier intervention in the cancer treatment process. Early detection is often associated with better treatment outcomes and higher survival rates. The ability of ACNGCNN to accurately pre-empt cancer types means that patients can receive timely and appropriate treatment, potentially before the cancer progresses to more advanced stages.

Fig. 13. Observed recall for pre-empting breast cancer types.
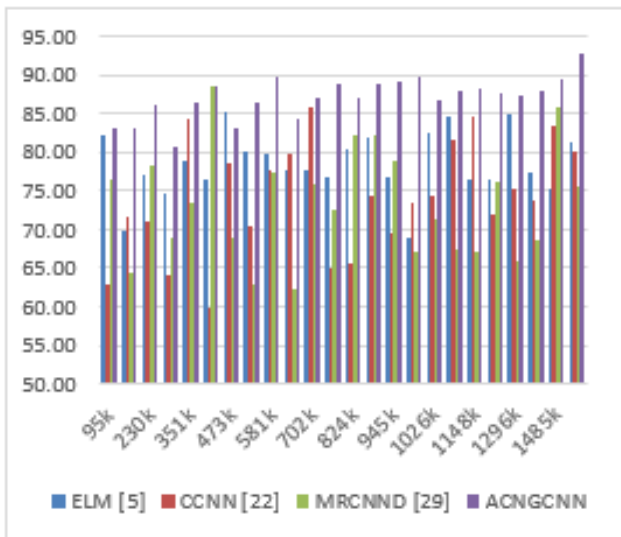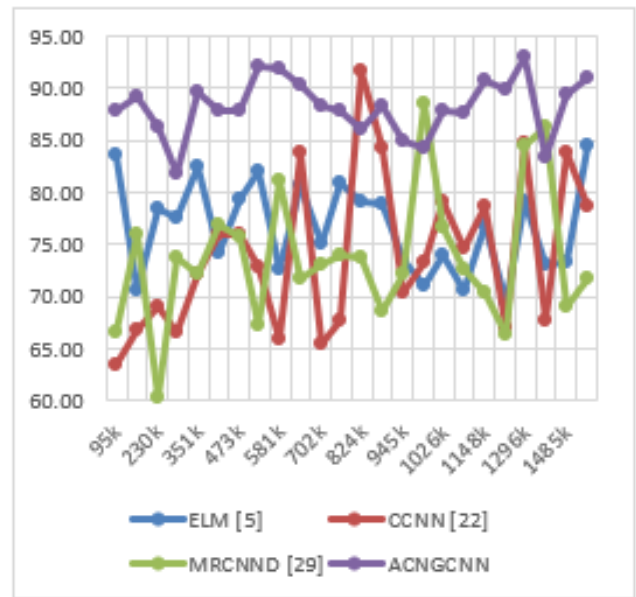

Fig. 12. Observed accuracy for pre-empting breast cancer types.

tently demonstrates high accuracy across various test sample sizes. For instance, in the dataset with 95k test samples, The accuracy of ACNGCNN is calculated to be 82.95%, which is greater than the accuracy of ELM (82.06%). CCNN (62.78%). and MRCNND (76.34%). In larger datasets, such as the one with 1,620k test samples, ACNGCNN achieves an accuracy of 92.77%, surpassing ELM (81.42%), CCNN (79.93%), and MRCNND (75.68%). That ACNGCNN is so

Fig. 13 shows that the ACNGCNN model efficiently detects early-stage breast cancer instances by maintaining high recall rates across different test sample sizes. The recalls achieved by ACNGCNN (87.85%) in the dataset with 95k test samples are substantially greater than those of ELM (83.71%), CCNN (63.37%), and MRCNND (66.70%), to name a few. With a recall rate of 90.88%, ACNGCNN outperforms ELM (84.54%), CCNN (78.69%), and MRCNND (71.76%) in the biggest dataset with 1,620k test samples. When it comes to breast

cancer, where early identification often improves treatment outcomes, this high degree of recall is very crucial.

Enhanced recall in predicting breast cancer kinds has a major influence in real-world therapeutic settings. With a high recall rate, the model has a lower chance of missing breast cancer patients, which indicates that late diagnosis is less likely to occur. Poor patient outcomes, more rapid disease development, and fewer treatment options are common results of breast cancer diagnoses performed too late. Consequently, patients' prognoses can be greatly improved by allowing earlier and more effective treatment treatments, thanks to ACNGCNN's capacity to reliably detect breast cancer instances at an early stage.

Moreover, early detection and intervention can lead to reduced treatment costs and less invasive treatment methods, which are beneficial for both patients and healthcare systems. In addition, high recall rates can increase patient trust in screening programs, encouraging more individuals to participate in regular screenings. This can lead to earlier detection on a broader scale, potentially lowering the overall morbidity and mortality associated with breast cancer. Similarly, the same diagram displays a tabular representation of the time required for the prediction procedure. Fig. 14 clearly shows that the
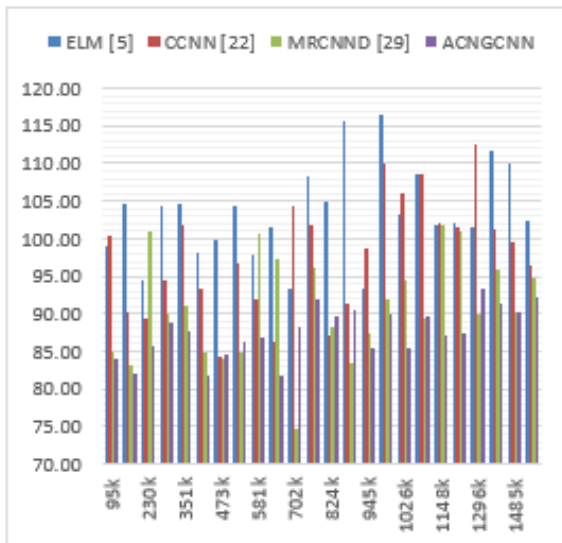

Fig. 14. Observed delay for pre-empting breast cancer types.

ACNGCNN model typically has competitive latency times. Take the dataset with 95,000 test samples as an example; ACNGCNN's latency is 84.07 ms, which is much lower than ELM (98.95 ms), CCNN (100.36 ms), and MRCNND (84.77 ms). Similarly, in larger datasets like the one with 1,620k test samples, ACNGCNN shows a delay of 92.34 ms, which remains competitive with ELM (102.46 ms), CCNN (96.40 ms), and MRCNND (94.86 ms). These findings suggest that ACNGCNN can process and classify scans efficiently, which is vital in clinical practices.

In clinical settings, a model that can pre-emptively detect breast cancer types with minimal delay is highly idvantageous. Firstly, it allows for faster diagnosis, which is critical in breast cancer where early intervention can lead to significantly better

treatment outcomes. Faster processing times mean that more patients can be screened in less time, potentially leading to earlier detection of breast cancer on a larger scale.

Additionally, reduced delay in diagnosis can alleviate patient anxiety. Waiting times for diagnostic results can be a source of significant stress for patients. A model like AC-NGCNN, capable of providing quick and reliable results, can improve the overall patient experience. Moreover, efficient processing times are beneficial in high-volume healthcare settings, where the ability to handle a large number of cases efficiently without compromising accuracy is crucial. In a manner comparable to that, the following are the AUC levels shown in Fig. 15. Analyzing the data in Fig. 15, ACNGCNN
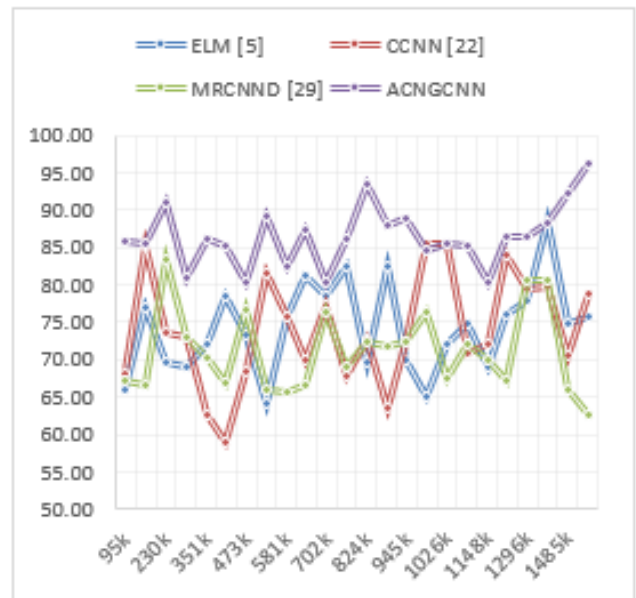

Fig. 15. Observed AUC for pre-empting breast cancer types.

consistently shows higher AUC values compared to ELM [4], CCNN [23], and MRCNND [29] across various test sample sizes. For example, in the dataset with 95k test samples, With an AUC of 85.72%, ACNGCNN outperforms ELM (65.85%), CCNN (68.24%), and MRCNND (67.06%). This trend continues in larger datasets, such as the 1,620k test samples, where ACNGCNN records an AUC of 96.15%, indicating a very high level of diagnostic accuracy.

In clinical settings, the importance of a high AUC value in pre-empting breast cancer types cannot be overstated. For instance, it suggests that you have faith in the model's predictive power for spotting breast cancer in its earliest stages.This is paramount in a clinical context, as early detection is often the key to successful treatment and better patient outcomes. High AUC values in models like ACNGCNN can lead to earlier interventions, potentially catching cancer at a stage where it is more treatable and survival rates are higher.

Additionally, a low false positive or negative rate is indicative of a well-performing model, which is supported by a high AUC value. In clinical practice, this reduces the burden of unnecessary treatments or additional diagnostic procedures that can result from false positives, as well as the risk of

overlooking a cancer case due to a false negative. Both scenarios can have profound implications for patient health and the efficiency of healthcare services. In the same a similar direction, the following is how the Specificity levels can be shown in Fig. 16. From the data in Fig. 16, it's evident that the
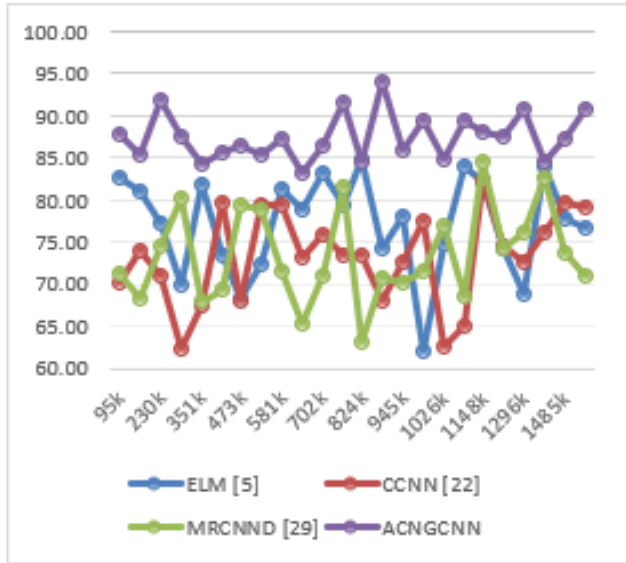

Fig. 16. Observed specificity for pre-empting breast cancer types.

ACNGCNN model generally exhibits higher specificity across various test sample sizes compared to ELM [4], CCNN [23], and MRCNND [29] For example, in the dataset with 95k test samples, ACNGCNN achieves a specificity of 87.90%, significantly higher than ELM (82.76%), CCNN (70.23%), and MRCNND (71.35%). This pattern holds true in bigger datasets as well; for example, ACNGCNN achieves a specificity of 90.76 percent with 1,620 thousand test samples.

In clinical terms, the high specificity of ACNGCNN in pre-empting breast cancer types means the period of false positives is significantly decreased. Patients can experience needless anxiety and additional medical complications due to false positives, making this a critical consideration in clinical practice., potentially invasive, diagnostic procedures. Reducing false positives not only improves the overall patient experience but also helps in conserving medical resources and reducing healthcare costs.

Moreover, high specificity is vital in maintaining the credibility and trust in breast cancer screening programs. If a screening method frequently results in false positives, it could lead to skepticism among potential participants, thereby reducing participation rates and potentially missing genuine cases of cancer in clinical scenarios.

V. Conclusion and Future Scope

The present research offers ACNGCNN, a new model for improved breast cancer diagnosis and stage classification that uses state-of-the-art adversarial capsule networks and graph convolutional neural networks. The comprehensive evaluation of this model, utilizing the BreaKHis dataset, reveals its superior performance in both classification and pre-emption of

breast cancer types compared to existing methodologies such as ELM, CCNN, and MRCNND.

In terms of classification, ACNGCNN consistently demonstrated higher precision, accuracy, recall, and AUC, along with lower delay times and enhanced specificity across various test sample sizes. These outcomes demonstrate that the model successfully classifies breast cancers., while also ensuring rapid processing, crucial for timely diagnosis. Notably, the model's exceptional performance in larger datasets underscores its scalability and robustness, essential attributes for real-world clinical applications.

Furthermore, in the context of pre-emption, ACNGCNN's efficacy was equally compelling. It exhibited commendable precision and accuracy, important for identifying possible breast cancer kinds at an early stage. Relying on its excellent specificity and recall rates, it may successfully detect actual positive instances while limiting false positives. These characteristics are pivotal in early intervention scenarios, where early detection can significantly alter treatment outcomes.

This work has significant implications for clinical practice. Through the improvement of breast cancer early detection and precise staging, ACNGCNN opens the door to targeted therapies that are both timely and effective. Patient outcomes, survival rates, and the load of treatments administered in the latter stages can all be improved in this way. The model's increased precision and reduced time lag in identifying disease progression are also pivotal for effective monitoring and treatment adjustments. In a broader context, ACNGCNN represents a significant advancement in breast cancer diagnostics, offering healthcare professionals a more efficient, accurate, and reliable diagnostic tool in their fight against this pervasive disease.

In conclusion, ACNGCNN sets a new benchmark in breast cancer diagnostics. Its ability to deliver precise, rapid, and reliable results offers immense potential for improving breast cancer screening, diagnosis, and management. This study's findings could have far-reaching implications, not only in enhancing patient care but also in guiding future research and development in medical imaging and cancer diagnostics.

A. Future Scope

The promising results achieved by the ACNGCNN model in breast cancer detection and classification open numerous avenues for future research and development. The model's proficiency in handling large datasets with high accuracy and specificity suggests its potential applicability in a broader range of oncological conditions. Expanding the scope of this model to include other types of cancers, particularly those with similar imaging characteristics, could significantly enhance the universality and utility of the model in clinical oncology.

Further refinement of the model could involve integrating real-time data analysis capabilities. This would allow for instantaneous diagnostic feedback, a crucial factor in surgical settings or in outpatient diagnostic procedures. Additionally, exploring the integration of ACNGCNN with portable imaging devices could democratize access to advanced cancer screening methods, especially in remote or under-resourced areas Another promising direction is the incorporation of patient history and genetic data into the model's analytical

framework. This approach would align with the growing trend of personalized medicine, potentially enabling the model to predict individualized cancer risk profiles and offer tailored screening recommendations.

The implementation of ACNGCNN in telemedicine platforms also presents an exciting possibility. As telemedicine continues to expand, especially in the context of the ongoing global health challenges, the model could provide remote, accurate diagnostic capabilities, reducing the need for physical consultations and making cancer screening more accessible. Additionally, it is crucial to keep investigating how interpretable the model's decision-making process is. Enhancing the transparency of the AI algorithms would not only increase the trust and acceptance of such models among healthcare professionals but also contribute to the field of ethical AI in medicine.

Finally, it would be extremely helpful to conduct longitudinal studies to evaluate the ACNGCNN model's actual effects on healthcare expenses, patient outcomes, and the efficiency of the system as a whole. Healthcare systems around the world might use the results of this research to guide policy decisions and resource allocation by providing hard proof of the model's efficacy. In the end, the ACNGCNN model has only scratched the surface of its potential in the field of breast cancer detection and classification.Its potential applications and improvements could lead to significant advancements in medical diagnostics, personalized medicine, and global healthcare access, ultimately contributing to better health outcomes for patients worldwide for different scenarios.

Acknowledgment

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