Clinics in Oncology

Research Article
Published: 27 Sep, 2024

Enhancing TNM Staging in Breast Cancer: A Hybrid Approach with CNN, Edge Detection, and Self-Organizing Maps for Improved Accuracy

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Abstract

Breast cancer remains a leading cause of mortality among women globally, underscoring the urgent need for improved diagnostic and staging techniques to enhance patient outcomes. This study aims to automate the TNM staging of breast cancer using a hybrid approach that integrates Convolutional Neural Networks (CNNs), edge detection methods, and Self-Organizing Maps (SOMs). Utilizing the Duke Breast Cancer MRI dataset, which provides detailed MRI scans crucial for accurate tumor characterization, the research addresses the limitations of traditional TNM staging, which often relies on manual interpretation by radiologists and can lead to inconsistencies and inaccuracies. Our approach combines CNNs with advanced edge detection algorithms and SOMs to automate and enhance the accuracy of breast cancer staging. The hybrid model effectively identifies and delineates tumor boundaries and critical anatomical features, offering a more reliable and objective evaluation. Notably, this method improves accuracy from 93% with conventional CNN models to 98%, representing a significant advancement in precision. This improvement not only provides more accurate diagnoses but also enables more personalized and effective treatment plans. For patients, this enhanced accuracy translates to better prognostic assessments and tailored treatments, potentially leading to improved outcomes and reduced likelihood of overtreatment or under treatment. For medical staff, the improved accuracy reduces the likelihood of misdiagnoses and enhances workflow efficiency by minimizing manual interpretation, thus alleviating some of the burdens associated with cancer staging. The model's performance is optimized through various testing methods and statistical evaluations, validating its stability and reliability. The integration of edge detection and SOMs captures comprehensive information, prevents overfitting, and provides valuable insights into data clustering. This combined approach supports personalized medicine by ensuring treatments are customized to individual patient characteristics, ultimately contributing to better survival rates and quality of life for patients.

Keywords: Breast cancer staging; Hybrid Convolutional Neural Network (CNN); Self-organizing map; Edge detection; Medical imaging; Duke breast cancer MRI dataset

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Received Date: *24 Jul 2024*
Accepted Date: *13 Sep 2024*
Published Date: *27 Sep 2024*

Citation:
Ajlouni N, Özyavaş A, Ajlouni F, Takaoğlu F, Takaoğlu M. Enhancing TNM Staging in Breast Cancer: A Hybrid Approach with CNN, Edge Detection, and Self-Organizing Maps for Improved Accuracy. Clin Oncol. 2024; 9: 2109.

ISSN: 2474-1663

Introduction

Breast Cancer (BC) remains one of the most prevalent and deadly cancers affecting women globally, second only to lung cancer in mortality rates [1]. Accurate staging of breast cancer, particularly through the TNM (Tumor, Node, Metastasis) system, is critical for determining appropriate treatment strategies and prognostic outcomes. Medical advancements have led to a decline in cancer mortality rates. Yet, follow-up studies reveal a recurring issue: Many cancer survivors develop new primary malignant tumors, whether in the same organ or elsewhere in the body [2,3].

BC is a common and serious condition affecting women worldwide, with high rates of incidence, morbidity, and mortality. There are two main types: Benign, which do not spread and are less dangerous, and malignant, which spread to other parts of the body and are highly dangerous. Malignant tumors arise from uncontrolled cell growth and can be fatal if not treated early. According to 2022 estimates by the World Health Organization (WHO), early detection and treatment are crucial for improving survival rates and outcomes in breast cancer patients. Breast cancer caused

approximately 670,000 deaths globally in 2022, highlighting its significant impact. The American Cancer Society notes a decline in overall cancer mortality rates but raises concern about increasing incidence rates for certain cancers, including breast cancer. Early detection through techniques like mammography, ultrasound, and MRI scans is crucial for improving treatment outcomes and survival rates, underscoring the importance of early diagnosis in reducing breast cancer-related fatalities.

The WHO suggests mammography screening for breast cancer in developed countries with adequate resources and health awareness, particularly for educated women aged 50 to 69. However, mammography is less effective and feasible in underdeveloped nations with limited resources and poorer health conditions [4]. Awareness of these disparities can aid in early breast tumor diagnosis. The most common types of breast cancer are invasive ductal carcinoma, ductal carcinoma in situ, and invasive lobular carcinoma.

Advancements in medical oncology [5], along with efforts in prevention and early diagnosis [6], play a crucial role in combating malignant tumors. Staging is a method used to describe the tumors' location, size, type, involvement of lymph nodes, and the presence of metastases. It serves as a universal nomenclature for the anatomical stage of a disease [7]. Among the various staging systems, the TNM system is widely recognized. The TNM system aims to help patients understand their disease, enhance communication among specialists, assist in treatment selection and evaluation, and improve patient prognosis [7,8].

Machine learning explores methods for developing algorithms that learn from data and make predictions [9]. These algorithms utilize computer models and information derived from past data to support classification and forecasting processes [10]. Data extraction technologies enable the detection of dependencies in medical data, facilitating the creation of predictive models.

Related Work

Breast cancer is a significant cause of cancer-related deaths among women globally, emphasizing the importance of early detection for better outcomes. Deep learning models, including attention-based models, Convolutional Neural Networks (CNNs) with small SE blocks, and multi-task learning, show promise in detecting and classifying breast cancer from mammography and histopathological images [11]. Studies have demonstrated high accuracy in classifying benign and malignant cases [11]. Another study highlighted accurate segmentation of breast ultrasound images [12]. CNN models have been effective in classifying breast cancer cases, surpassing traditional machine learning methods [13].

Combining feature selection and extraction techniques with deep learning improves prediction accuracy [4,14]. Deep learning models outperform traditional methods in detecting and classifying breast cancer, aided by larger datasets, transfer learning, and data augmentation [4,14]. Attention mechanisms in CNNs help identify significant regions in mammography, potentially reducing false positives [15]. Residual networks and multi-task learning strategies have also shown superior performance in breast cancer classification [16,17].

Meta-learning frameworks for CNN models enhance breast cancer classification by optimizing weight initialization [18]. Ensemble learning techniques combining multiple CNN models have achieved high classification accuracy [19-21]. Dual-branch CNN architectures effectively extract global and local features from breast cancer histopathology images [22].

Deep learning approaches in mammography analysis have outperformed traditional methods, highlighting the need for larger datasets and model interpretability [23]. Ensemble CNN models like BOF-CNNs excel in classifying mammograms as cancerous or benign [24]. Multiple kernel learning combined with CNNs improves feature integration and classification performance [25].

Integration of deep learning with feature selection and extraction methods enhances the prediction of breast cancer outcomes [26]. Deep CNNs with transfer learning have been effective in classifying medical images for accurate diagnosis [27-29]. Various studies continue to explore novel deep learning architectures and techniques to advance breast cancer diagnosis and treatment [30-43].

TNM Staging

The TNM staging system is a standardized method used by healthcare professionals to classify the extent of cancer in a patient's body, specifically in breast cancer cases. It consists of three key components: Tumor (T), Node (N), and Metastasis (M). Each component provides critical information about the size and spread of the cancer, guiding treatment decisions and predicting prognosis.

The Tumor (T) category assesses the size and extent of the primary tumor within the breast tissue. The staging ranges from T0, indicating no evidence of a primary tumor, to T4, indicating a large tumor size or extensive spread to nearby tissues. For instance, Tis (Carcinoma *in situ*) describes abnormal cells that are present but confined to the original site without invading nearby tissues.

The Node (N) category evaluates whether cancer has spread to nearby lymph nodes, which act as filters trapping and destroying harmful substances, including cancer cells. The N classification ranges from N0, indicating no cancer spread to nearby lymph nodes, to N3, indicating extensive involvement of nearby lymph nodes.

The Metastasis (M) category indicates whether cancer has spread to distant organs or tissues beyond the primary site. A classification of M0 signifies no distant metastasis, whereas M1 indicates the presence of distant metastasis, significantly influencing treatment decisions and prognosis. For example, a staging designation such as T2N1M0 would indicate a moderately sized primary tumor (T2) with cancer spread to nearby lymph nodes (N1) but no evidence of distant metastasis (M0). This staging provides clinicians with critical information to tailor treatment plans, predict patient outcomes, and monitor disease progression over time.

Stages of breast cancer

Breast cancer is categorized into five stages, numbered from 0 to IV. These stages help determine how far the cancer has spread and guide treatment decisions. The higher the stage number, the more advanced the cancer. Staging is done at the time of diagnosis and remains crucial for determining prognosis and appropriate treatment options. Figure 1 illustrates the four stages of the breast cancer and their expected location [44].

Stage 0: Known as carcinoma *in situ*, stage 0 breast cancer is non-invasive, meaning the cancer cells are confined to the ducts or lobules of the breast and have not spread to surrounding tissues. An example is Ductal Carcinoma *in situ* (DCIS).

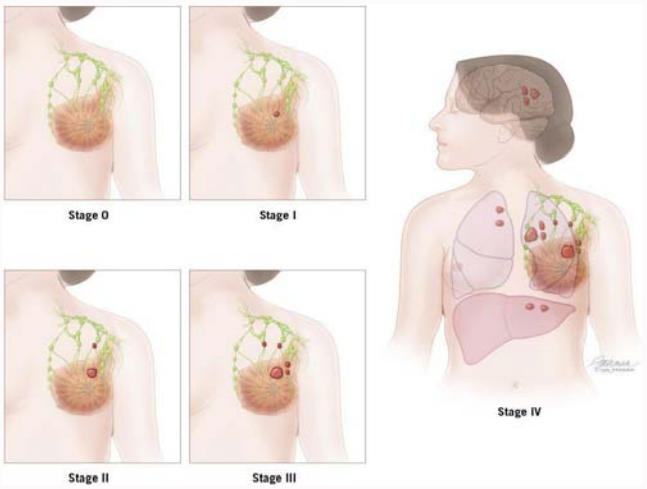

Figure 1: An illustration of the breast cancer stages.

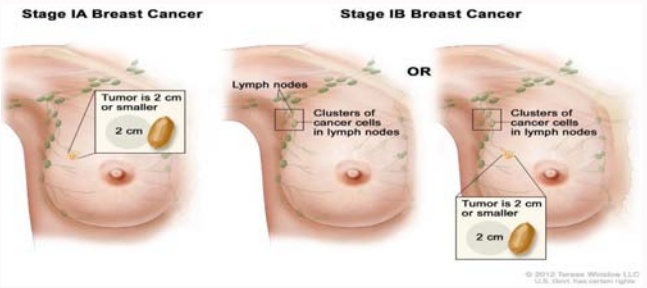

Figure 2: Stage IA & IB breast cancer with tumor size.

Stage I: This stage represents early-stage invasive breast cancer. The tumor measures up to 2 centimeters, and there is no spread to the lymph nodes (Stage IA) or there is a tiny amount of cancer in a few nearby lymph nodes (Stage IB). Figure 2 illustrates stage IA and IB breast cancer stages [45].

Stage II: In this stage, the cancer is growing but still contained within the breast or nearby lymph nodes. The tumor size ranges from 2 cm to 5 cm (Stage IIA), or the tumor is larger than 5 cm without lymph node involvement or smaller with more extensive lymph node involvement (Stage IIB).

Stage III: This is more advanced cancer that has spread to more lymph nodes or other areas near the breast. It includes larger tumors (greater than 5 centimeters) and/or significant lymph node involvement (Stages IIIA, IIIB, and IIIC), but it has not spread to distant organs.

Stage IV: Known as metastatic breast cancer, this stage indicates that the cancer has spread to distant organs such as the bones, liver, lungs, or brain. Regardless of the size of the tumor or lymph node involvement, any spread to distant organs categorizes the cancer as stage IV.

TNM System

The TNM system is another detailed way to describe the extent of breast cancer using three parameters, the T (Tumor Size) parameter is defined as:

- T0: No evidence of a primary tumor.
- Tis: Carcinoma in situ (confined to the ducts or lobules).
- T1: Tumor is 2 centimeters or smaller.
- T2: Tumor is larger than 2 centimeters but not larger than 5 centimeters.
- T3: Tumor is larger than 5 centimeters.
- T4: Tumor of any size growing into the chest wall or skin.

The N (Node Involvement) are defined as:

- N0: No cancer in nearby lymph nodes.
- N1: Cancer has spread to 1-3 nearby lymph nodes.
- N2: Cancer has spread to 4-9 nearby lymph nodes.
- N3: Cancer has spread to 10 or more lymph nodes or to lymph nodes near the collarbone or internal mammary nodes.

The M (Metastasis) is defined as:

- M0: No distant spread.
- M1: Cancer has spread to distant organs.

This means that the staging of T2N1M0 means the tumor is between 2 and 5 centimeters in size, cancer has spread to 1 to 3 nearby lymph nodes, and there is no distant metastasis.

Artificial Intelligent Algorithms

Artificial Intelligence (AI) encompasses a broad range of algorithms and techniques designed to enable machines to perform tasks that typically require human intelligence. These tasks include learning, reasoning, problem-solving, perception, and language understanding. AI algorithms can be categorized into several key areas, each with its specific methods and applications.

Machine Learning (ML) is one of the most prominent areas within AI. It includes supervised learning algorithms like linear regression, which predicts continuous outputs based on input features [46], and logistic regression, used for binary classification problems [47]. Support Vector Machines (SVM) find the hyperplane that best separates classes in the feature space [48], while decision trees create a tree- like model of decisions and their possible consequences [49]. Random forests, an ensemble of decision trees, improve prediction accuracy and control over-fitting [50]. Other notable supervised learning algorithms include *k*-Nearest Neighbors (k-NN) [51], neural networks [52], and Gradient Boosting Machines (GBM) [53].

Unsupervised learning techniques, such as *k*-means clustering [54], hierarchical clustering [55], and Principal Component Analysis (PCA) [56], help identify patterns and structures in data without labeled outputs. Self-Organizing Maps (SOMs), another important unsupervised learning algorithm, are used for clustering and visualization by projecting high-dimensional data into lower-dimensional (often two- dimensional) maps while preserving topological properties [57]. SOMs are particularly useful for visualizing complex relationships in data and identifying clusters.

Autoencoders, a type of neural network, are used for dimensionality reduction by learning efficient coding's of data [58]. In reinforcement learning, algorithms like Q-learning [59] and Deep Q-Networks (DQN) enable agents to learn optimal actions through rewards [60], while policy gradient methods directly learn the policy to maximize cumulative rewards [61].

Deep learning, a subset of ML, involves algorithms such as

Convolutional Neural Networks (CNNs), which are specialized for processing structured grid data like images [62], and Recurrent Neural Networks (RNNs), suitable for sequential data [63]. Long Short-Term Memory (LSTM) networks address long-term dependencies in sequences [64], and generative adversarial networks (GANs) create realistic synthetic data by pitting two networks against each other [65]. Transformers, advanced models designed for sequence-to-sequence tasks, excel in natural language processing [66].

Evolutionary algorithms, including Genetic Algorithms (GAs) and Genetic Programming (GP), mimic natural selection processes to evolve solutions and computer programs [67]. Differential Evolution (DE) iteratively improves candidate solutions for optimization problems [68]. Bayesian algorithms, like Naive Bayes [69] and Bayesian networks [70], provide probabilistic models to represent and reason about uncertainty. Fuzzy logic algorithms use fuzzy set theory to model imprecise information [71], while swarm intelligence algorithms, such as Ant Colony Optimization (ACO) [72] and Particle Swarm Optimization (PSO) [73], model collective behavior to solve optimization problems.

Ensemble learning algorithms combine predictions from multiple models to improve accuracy and robustness. Bagging, such as in random forests, reduces variance [74], while boosting, including AdaBoost and XGBoost [75].

Proposed Method

The proposed method aims to improve the breast cancer staging process by systematically preparing and analyzing a dataset of DICOM images using various machine learning techniques. This research addresses the critical need for accurate and efficient cancer staging, which is vital for optimal treatment planning and patient outcomes in oncology. Accurate staging directly impacts treatment decisions, prognosis, and overall patient management, yet current methods can be time-consuming and prone to variability. By introducing advanced machine learning techniques, this research seeks to provide more precise and reliable staging.

To achieve this, the dataset is first extracted to make it accessible for further processing. The DICOM images are then loaded from the specified directory and resized to a uniform size of 128 × 128 pixels. Each image is labeled based on its folder name (Cancer Stage), ensuring a consistent format suitable for model training. This preprocessing step involves reading the images, resizing them, and assigning appropriate labels. Subsequently, the Canny Edge detection algorithm is applied to the preprocessed images to enhance their features by detecting edges, crucial for highlighting significant structures in medical images. The resulting edge-detected images form an additional dataset for training and evaluation.

A Convolutional Neural Network (CNN) model is then constructed and trained using the preprocessed images. CNNs are selected for their robust feature extraction and classification capabilities, making them ideal for predicting cancer stages based on image data. The architecture of the CNN typically includes convolutional layers, pooling layers, and fully connected layers.

Following this, a second CNN model is trained specifically on the edge-detected images to determine whether the edge-enhanced images provide superior classification performance compared to the original images. The performance of this model is compared with the original CNN to assess the impact of edge detection on classification accuracy.

The image data is then flattened, and a Self-Organizing Map (SOM) is trained for clustering. SOMs employ unsupervised learning to identify patterns in the data, which can enhance classification when combined with CNN results. The SOM assists in visualizing data clustering and uncovering underlying patterns that may not be apparent in the original images.

Finally, both CNN models (with and without edge detection) are evaluated, and their results are potentially combined with SOM predictions for comprehensive classification. This approach leverages multiple techniques to improve overall accuracy by utilizing their complementary strengths. The combination of supervised learning (CNN) and unsupervised clustering (SOM) aims to enhance the robustness and generalization ability of the classification system.

Edge detection highlights important structures and boundaries in medical images, facilitating the CNN's ability to learn relevant features, significantly enhancing model performance. Combining CNNs and SOMs leverages the strengths of both methods, capturing more information from the data and potentially leading to more robust models. Training different models on both original and edge-detected images enables the system to learn from multiple perspectives, helping to avoid overfitting and improving the model's generalization to new data. Additionally, SOMs provide visual insights into data clustering, useful for understanding underlying patterns and relationships, guiding further improvements and refinements in the model. Employing a combined approach that evaluates models on different versions of the data (original and edge-detected) and incorporates unsupervised clustering increases the system's robustness to variations and noise in the data, ensuring the final model is more reliable and effective in real-world scenarios.

Improving the breast cancer staging process has significant implications for oncology. Enhanced staging accuracy can lead to better diagnostic precision, allowing for more tailored and effective treatment plans. This can improve patient outcomes, reduce the likelihood of overtreatment or under treatment, and optimize the use of healthcare resources. Furthermore, advancements in staging can contribute to more personalized medicine approaches, where treatments are specifically tailored to the individual characteristics of each patient's cancer. This research, therefore, has the potential to make a substantial impact on both the diagnostic and treatment aspects of breast cancer care, ultimately contributing to improved survival rates and quality of life for patients.

Edge detection methods

The Canny edge detection algorithm, introduced by John F. Canny in 1986, is designed to detect a wide range of edges in images while minimizing noise and false positives. The process begins with noise reduction, which is crucial for accurate edge detection. This is achieved by applying a Gaussian filter to smooth the image. The Gaussian function $G(x, y)$ is defined as

$$G(x,y)=\frac{1}{2\pi\sigma^2}\exp\left(-\frac{x^2+y^2}{2\sigma^2}\right) \quad (1)$$

where σ controls the amount of smoothing. This Gaussian blur helps in reducing the impact of noise on edge detection.

Following noise reduction, the algorithm moves on to gradient calculation. This step determines the intensity and direction of edges by calculating the gradient of the image. The gradients are computed using Sobel operators, specifically G_x and G_y:

$$G_x = \begin{bmatrix} -1 & 0 & 1 \\ -2 & 0 & 2 \\ -1 & 0 & 1 \end{bmatrix} \quad (2)$$

$$G_y = \begin{bmatrix} -1 & -2 & -1 \\ 0 & 0 & 0 \\ 1 & 2 & 1 \end{bmatrix} \quad (3)$$

which are convolution kernels that detect changes in the x and y directions, respectively. The gradient magnitude M and direction θ are calculated using

$$M = \sqrt{G_x^2 + G_y^2} \quad (4)$$

and

$$\theta = \arctan\left(\frac{G_y}{G_x}\right) \quad (5)$$

This information is essential for identifying where the edges lie and their orientation.

The next stage is non-maximum suppression, which serves to thin out the edges. In this step, each pixel in the gradient image is compared to its neighbors along the gradient direction. If the pixel's gradient magnitude is not greater than the magnitudes of its neighbors, it is suppressed. This process helps in retaining only the most significant edges, leading to a clearer representation of the edges in the image. After non-maximum suppression, the algorithm employs double thresholding to further refine the edge detection. Two thresholds are used: A high threshold T_{high} and a low threshold T_{low}. Pixels with gradient magnitudes above the high threshold are classified as strong edges, while those below the low threshold are considered non-edges. Pixels with gradient magnitudes falling between these two thresholds are classified as weak edges. This classification helps in distinguishing between strong and weak edges.

Finally, edge tracking by hysteresis is applied to finalize the edge detection process. This step involves linking weak edges to strong edges. If a weak edge pixel is connected to a strong edge pixel, it is included in the final edge map. This process helps in ensuring that only continuous and significant edges are retained, while isolated weak edges are discarded.

Applying canny edge detection to breast MRI images: When applying Canny edge detection to breast MRI images, the objective is to accurately identify the boundaries of the breast tissue. This process involves several essential steps, beginning with preprocessing. Applying Contrast Limited Adaptive Histogram Equalization (CLAHE) enhances contrast, which improves edge detection. Following this, noise reduction is performed since breast MRI images can contain noise from various sources, such as the imaging process and patient movement. A Gaussian blur is applied to smooth the image, mitigating the impact of this noise on subsequent edge detection steps.

Next, gradient calculation identifies regions with significant intensity changes, which typically correspond to tissue boundaries. This is especially useful for highlighting the edges of the breast tissue. Non-maximum suppression is then used to preserve only the local maxima of the gradient magnitudes, ensuring that the detected edges are thin and well-defined. This is crucial for accurately delineating the breast boundaries.

Adaptive Canny edge detection is employed next, with dynamically adjusted thresholds to suit the image's contrast. This is followed by contour detection, which includes dilation to close gaps in detected edges, ensuring a more complete detection of the breast boundaries. Once contours are identified, bounding rectangles are drawn around the filtered contours to highlight the detected breast cups.

To improve the process, parameter tuning is carried out. This involves adjusting the parameters for contour area filtering and dilation size based on the selected dataset to better capture the breast cups. Additional morphological operations, such as erosion and closing, are applied to refine the contours and reduce false detections, maintaining the integrity of the detected edges. Finally, manual validation of results is conducted to ensure accuracy, especially when dealing with diverse MRI images. Figure 3 illustrates the results of this process, demonstrating that the Canny method successfully detected and boxed the breast cups in a selected image from the dataset.

The process is further improved to achieve orientation robustness. Data augmentation techniques such as rotations, flipping, and scaling are used during training. Including augmented images with various rotations ensures the model learns to detect breast boundaries regardless of orientation. Horizontal and vertical flips, as well as scaling transformations, further enhance the robustness of the model. Implementing feature-based alignment methods, such as using key point detectors (*e.g.*, SIFT, SURF) and matching techniques, helps align images to a standard orientation before applying edge detection, reducing the variability introduced by different orientations.

Convolutional Neural Networks (CNN)

CNNs are a class of deep learning algorithms commonly used for analyzing visual data. CNNs are designed to automatically and adaptively learn spatial hierarchies of features from input images, making them particularly powerful for tasks such as image recognition, object detection, and image segmentation [62]. Figure 4 illustrates the CNN structure.

Architecture of CNNs: A typical CNN architecture consists of multiple layers, each performing specific operations to transform the input data into a form suitable for the desired task. The main types of layers in CNNs include:

1. **Convolutional Layers:** These layers apply convolutional filters (kernels) to the input image. A convolutional layer consists of several filters, each of which detects a specific feature such as edges, textures, or patterns in the image. Mathematically, the convolution operation is defined as:

$$(f \times g)(t) = \int_{-\infty}^{\infty} f(\tau)\, g \times (t-\tau) d\tau \quad (6)$$

In discrete terms for image processing, it simplifies to:

$$(f \times g)(n) = \sum_a \sum_b f[a,b]\, g[n-a, n-b] \quad (7)$$

where f is the input image, and g is the filter [76].

2. **Pooling Layers:** These layers perform down sampling operations, reducing the spatial dimensions (width and height) of the input volume. Pooling helps to reduce the computational load and control overfitting. The most common type of pooling is max pooling [77], which takes the maximum value from a set of values within a specified window. If X is the input and p is the pooling size:

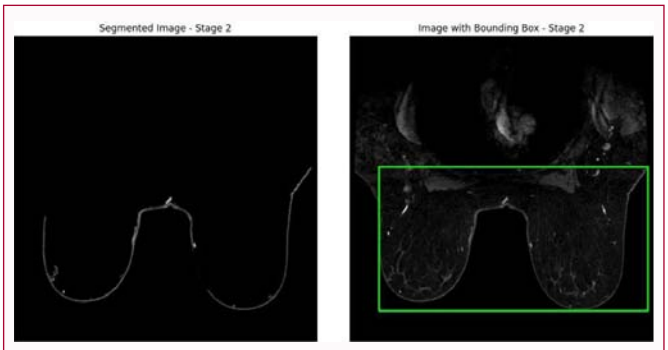

Figure 3: Illustration of the Cany edge detected image section located within a box.

$$Y_{i,j} = \max\left(X_{m,n}\right) for\left(m,n\right) \in pooling \text{ window} \quad (8)$$

3. **Fully Connected Layers:** These layers are similar to the dense layers in traditional neural networks, where each neuron is connected to every neuron in the previous layer. These layers are typically used towards the end of the network to perform classification based on the features extracted by the convolutional and pooling layers [78].

Training CNNs: The training process of CNNs involves forward propagation and backpropagation. During forward propagation, the input image passes through the network, layer by layer, and predictions are made. The loss is then calculated using a loss function (*e.g.*, cross-entropy loss for classification). Backpropagation is used to compute the gradients of the loss with respect to each parameter in the network, and these gradients are used to update the parameters using an optimization algorithm like Stochastic Gradient Descent (SGD) [79,80].

CNNs have revolutionized various fields, primarily computer vision. Some notable applications include:

Image Classification: Classifying images into predefined categories. Prominent datasets like ImageNet have been used to train CNNs, achieving human-like performance [81,82].

Object Detection: Identifying and localizing objects within an image. Techniques like Region-Based CNN (R-CNN) and You Only Look Once (YOLO) have made significant advancements in real-time object detection [83].

Image Segmentation: Dividing an image into segments based on object boundaries. Fully Convolutional Networks (FCNs) and U-Net are popular architectures for semantic segmentation [82,84].

Medical Image Analysis: Detecting anomalies in medical images, such as tumors in MRI scans or lung nodules in CT scans. CNNs have shown great promise in improving diagnostic accuracy [85-88].

Duke breast dataset

The duke breast cancer dataset [89], consists of Breast MRI images used to assess the extent of disease in breast cancer patients. It is a single-institutional, retrospective collection of data from 922 biopsy- confirmed invasive breast cancer patients over a decade. This data has supported numerous published papers on radio-genomics, outcomes prediction, and other areas. Additionally, it features pre-operative Dynamic Contrast-Enhanced (DCE)-MRI images, de-identified for The Cancer Imaging Archive (TCIA) release. These MRI images, acquired using 1.5T or 3T scanners in the prone position, include a non-fat saturated T1-weighted sequence, a fat-saturated gradient echo T1-weighted pre-contrast sequence, and typically three to four post-contrast sequences in DICOM format. Radiologists have annotated the locations of lesions in the DCE-MRI images, and the dataset includes 529 computer-extracted imaging features representing various characteristics such as size, shape, texture, and enhancement of the tumor and surrounding tissue, incorporating both commonly published features and those developed in-house. The dataset is publicly available at https://www.cancerimagingarchive.net/collection/duke-breast- cancer-mri/. A sample of the dataset images is illustrated in Figure 5.

Self-Organizing Map (SOM)

Self-Organizing Maps (SOM), also known as Kohonen maps, are a type of artificial neural network designed for unsupervised learning. They are widely used for tasks such as clustering, visualization of high-dimensional data, and dimensionality reduction [90-94]. The SOM network structure consists of a grid of neurons arranged typically in one or two dimensions. Each neuron j in the grid is characterized by a weight vector $w_j = (w_{j1}, w_{j2}, \ldots, w_{jd})$, where d is the dimensionality of the input data. Neurons in SOMs are organized such that neighboring neurons respond to similar input patterns. The learning process of SOMs involves two main phases: Initialization and training. During initialization, the weight vectors w_j are usually initialized randomly or using techniques like Principal Component Analysis (PCA) to align with the principal axes of the input data distribution. In the training phase, each input vector x is presented to the SOM. The network identifies the Best Matching Unit (BMU), which is the neuron j with the weight vector w_j most similar to x, based on measures such as Euclidean distance [95].

After identifying the BMU, SOM updates the weights of the BMU and its neighboring neurons to move closer to x. This update rule is governed by:

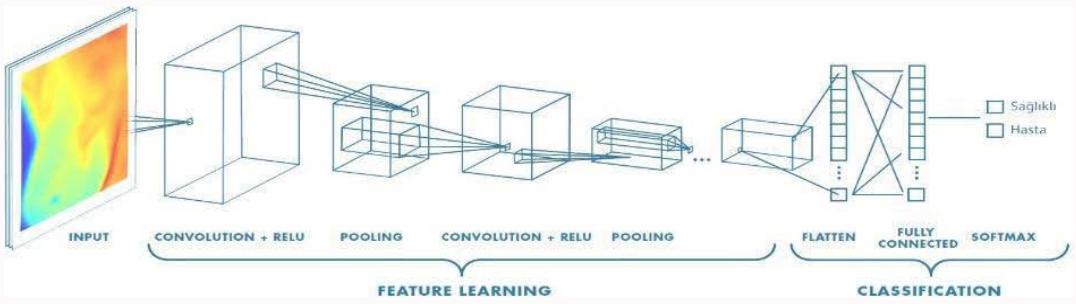

Figure 4: Illustration of conventional CNN structure.

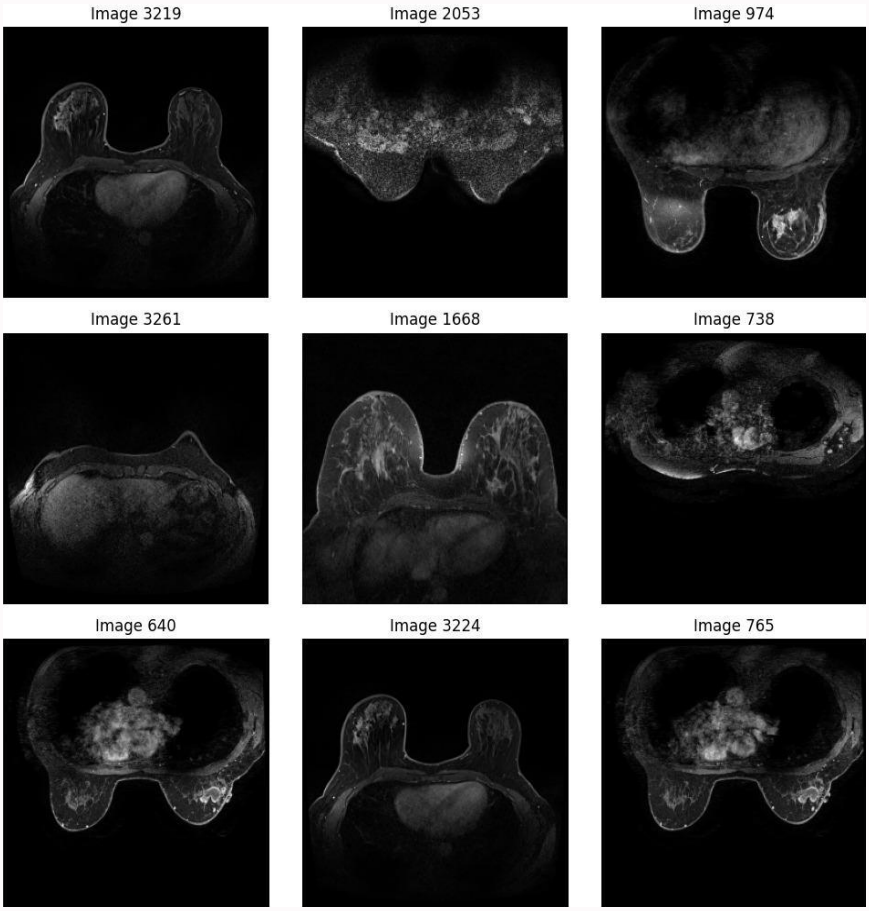

Figure 5: Illustration a sample of dataset 'd cm' images.

$$w_j(t+1) = w_j(t) + \eta(t) \cdot h_{ji}(t) \cdot \left(x - w_j(t)\right) \quad (9)$$

where $w_j(t)$ is the weight vector of neuron j at iteration t, $\eta(t)$ is the learning rate at iteration t, and $h_{ji}(t)$ is the neighborhood function that decreases with the distance between neurons j and i.

SOMs preserve the topological properties of the input data in the output map, meaning that similar input vectors are mapped to nearby neurons in the SOM grid. This property facilitates visualization and interpretation of complex data structures. Applications of SOMs include clustering to identify natural groupings within data, dimensionality reduction for visualizing high-dimensional data in lower dimensions, and data visualization to represent data distributions in an intuitive manner.

Since SOMs consist of a grid of neurons, typically arranged in one or two dimensions. Each neuron j in the grid is associated with a weight vector $w_j = (w_{j1}, w_{j2}, \ldots, w_jd)$, where d is the dimensionality of the input data. Neurons in SOMs are spatially organized, meaning neighboring neurons in the grid respond to similar input patterns. The mathematical representation of SOM process is as follows:

1. **Network Structure:** SOMs consist of a grid of neurons arranged in one or two dimensions. Each neuron j in the grid is associated with a weight vector $w_j = (w_{j1}, w_{j2}, \ldots, w_jd)$, where d is the dimensionality of the input data.

2. **Learning Process:** SOMs learn iteratively through a competitive learning process:

- **Initialization:** Initialize the weight vectors w_j randomly or using some initialization method.

- **Training:** For each input vector x, find the neuron j whose weight vector w_j is closest to x in terms of Euclidean distance:

$$j = \arg\min_j \| x - w_j \| \quad (10)$$

This neuron j is the Best Matching Unit (BMU).

- **Weight Update:** Adjust the weights of the BMU and its neighboring neurons to move closer to x:

$$w_j(t+1) = w_j(t) + \eta(t) \cdot h_{ji}(t) \cdot \left(x - w_j(t)\right) \quad (11)$$

where $\eta(t)$ is the learning rate at iteration t, and $h_{ji}(t)$ is the neighborhood function that decreases with distance from the BMU.

3. **Topological Organization:** SOMs preserve the topological properties of the input data in the output map. Neurons that are close to each other in the grid respond to similar input patterns, allowing SOMs to capture and visualize the underlying structure and relationships within the data.

Research contribution

This study makes several significant contributions to the field of medical imaging and oncology, particularly in the automated TNM staging of breast cancer using advanced machine learning techniques. The main contributions are as follows:

1. **Development of a Hybrid Diagnostic Model:** The research introduces a novel hybrid approach that integrates Convolutional Neural Networks (CNNs), edge detection methods, and Self-Organizing Maps (SOMs) for the automated staging of breast cancer. This model leverages the strengths of both supervised learning (CNNs) and unsupervised clustering (SOMs) to enhance the accuracy and reliability of TNM staging in oncology.

2. **Improved Staging Accuracy:** By combining CNNs with edge detection and SOMs, the proposed method achieves a significant improvement in staging accuracy, increasing it from 93% with conventional CNNs to 98%. This represents a notable advancement in the precision of breast cancer diagnostics, which is crucial for effective treatment planning and patient management in oncology.

3. **Automation of the Staging Process:** The study addresses the limitations of traditional manual interpretation of medical images, which can be inconsistent and prone to errors. The automated hybrid model reduces the need for manual intervention, thus minimizing the risk of misdiagnosis and improving the efficiency of the diagnostic process in oncology.

4. **Comprehensive Evaluation and Validation:** The performance of the hybrid model is thoroughly evaluated through various statistical methods, including paired *t*-tests, Wilcoxon signed-rank tests, ANOVA, and the Friedman test. These analyses confirm the model's superior performance and robustness, validating its ability to generalize well to new data in the field of oncology.

5. **Utilization of Advanced Edge Detection Techniques:** The research highlights the importance of edge detection in medical imaging, demonstrating that edge-enhanced images significantly improve the accuracy of CNNs. This contribution underscores the potential of combining image processing techniques with machine learning for better feature extraction and classification in oncology.

6. **Integration of SOMs for Enhanced Clustering:** By incorporating SOMs into the hybrid model, the study provides a novel approach to data clustering and pattern recognition in medical images. SOMs enhance the model's ability to uncover underlying patterns and relationships in the data, contributing to more accurate and reliable staging in oncology.

7. **Support for Personalized Medicine:** The hybrid model's improved accuracy and automation support the shift towards personalized medicine in oncology. By providing precise and reliable diagnostic information, the model enables more tailored and effective treatment plans, improving patient outcomes and quality of life.

8. **Potential for Broader Applications:** While focused on breast cancer, the hybrid approach developed in this study has the potential to be adapted and applied to other types of cancer and medical conditions in oncology. This contribution opens avenues for future research and the development of similar diagnostic models for a wide range of applications.

Experimental setup

The process begins by uploading the zip file containing the dataset and extracting it. This ensures that the dataset is readily available for further processing and model training.

Following this, it is crucial to install the necessary libraries, such as 'Pydicom', 'Tensorflow', 'Minisom', and 'Opencv-python-headless'. These libraries are essential for processing DICOM images, building Convolutional Neural Networks (CNNs), and applying Self-Organizing Maps (SOMs).

Once the libraries are installed, the next step is to load the DICOM images from the specified dataset directory and resize them to a uniform size of 128 × 128 pixels. The images should also be labelled based on their folder names. This pre-processing step ensures the dataset is in a consistent format, making it suitable for model training.

The Canny edge detection algorithm is then applied to the preprocessed images. This step enhances the image features by detecting edges, which is particularly useful for highlighting significant structures in medical images.

Subsequently, a Convolutional Neural Network (CNN) model is built and trained using the preprocessed images. CNNs are known for their powerful feature extraction and classification capabilities, making them ideal for predicting cancer stages based on image data.

A second CNN model is then trained specifically on the edge-detected images. This step aims to assess whether the edge-enhanced images provide better classification performance compared to the original images.

The image data is then flattened, and a Self-Organizing Map (SOM) is trained for clustering. SOMs utilize unsupervised learning to discover patterns in the data, which can potentially enhance classification when combined with CNN results.

The final step involves evaluating both CNN models (with and without edge detection) and potentially combining their results with SOM predictions for comprehensive classification. This approach leverages multiple techniques to improve accuracy by utilizing their complementary strengths.

In terms of advantages over using only a CNN, edge detection highlights important structures and boundaries in medical images, facilitating the CNN's learning of relevant features and potentially improving model performance, especially in medical imaging where edges and shapes are critical. Combining CNNs and SOMs leverages the strengths of both methods-CNNs excel in supervised learning, while SOMs are effective for unsupervised clustering and pattern discovery. This combination captures more information from the data, potentially leading to better and more robust models. Training different models on both original and edge-detected images allows the system to learn from multiple perspectives, helping to avoid overfitting and improving the model's generalization to new data. Additionally, SOMs provide visual insights into data clustering, which can be useful for understanding underlying patterns and relationships, guiding further improvements and refinements in the model. Using a combined approach that evaluates models on different versions of the data (original and edge-detected) and incorporates unsupervised clustering increases the system's robustness to variations and noise in the data, ensuring the final model is more reliable and effective in real-world scenarios.

Results and Discussion

The results of the conventional convolutional plus edge detection, and proposed methods are presented below in Table 1. All the tests utilize a fully adaptive optimizer for guaranteed fast convergence [80,87,88]. The tables contain the validation accuracy of conventional CNN, conventional CNN plus edge detection, and the proposed method.

Table 1: The Validation accuracy of CNN, CNN_Edge_Det, Proposed Method.

Iteration	CNN_Val_Acc	CNN_ED_Val_Acc	Proposed Method_ Val_Acc
1	22.11	25.35	29.89
10	29.3	34.68	42.98
20	47.97	57.88	65.91
30	55.17	73.67	79.53
40	68.62	8396	87.19
50	76.69	86.91	92.16
60	81.81	9242	95.67
70	89.94	93.89	97.84
80	90.84	94.89	98.32
90	91.85	95.25	99.47
100	92.96	96.89	99.71

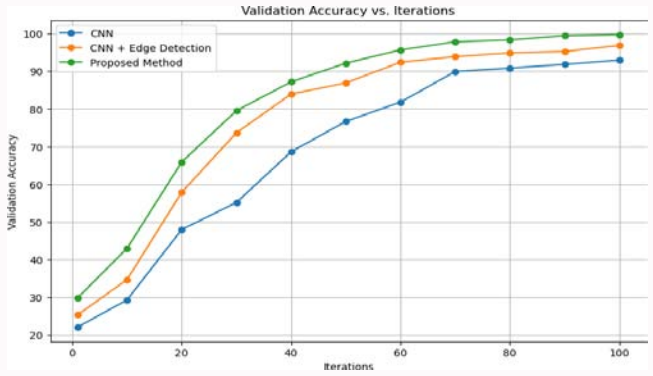

Figure 6: An illustration of validation accuracy for the three tested methods.

Table 1 presents the results for the conventional Convolutional Neural Network (CNN), the CNN combined with edge detection, and the proposed method. All tests employed a fully adaptive optimizer to ensure rapid convergence [80,87,88]. The table includes validation accuracy metrics for the conventional CNN, the conventional CNN with edge detection, and the proposed method.

Figure 6 illustrates the plot of the validation accuracies per iteration for the three models.

Figure 6 compares the validation accuracy of three methods-conventional CNN, CNN with Edge Detection, and the Proposed Method-over 100 iterations. From Table 1 and Figure 6, it is evident that the conventional CNN starts with an accuracy of 22.11% in the first iteration and shows a steady improvement over time. By the 100th iteration, its accuracy reaches 92.96%. While this method demonstrates significant progress, it converges at a slightly lower accuracy compared to the other methods.

In contrast, the CNN with Edge Detection begins with an accuracy of 25.35%, which also improves with each iteration. Although the improvement is noticeable, it does not reach the performance levels of the proposed method. By the end of the 100 iterations, this method achieves an accuracy of 96.89%. The inclusion of edge detection enhances the conventional CNN's accuracy but still falls short of the performance seen with the proposed method.

The Proposed Method starts with an initial accuracy of 29.89%, surpassing both the Conventional CNN and CNN with Edge Detection. It shows the most substantial improvement over the iterations, reaching an accuracy of 99.71% by the 100th iteration. This method consistently outperforms the other two, with a notable increase in accuracy over time.

The test results reveal the effectiveness of the proposed method in enhancing breast cancer diagnostics. The proposed method demonstrates the highest validation accuracy across all iterations, reflecting its superior performance in learning and generalizing from the training data. This rapid improvement and elevated accuracy suggest that the proposed method integrates advanced techniques or optimizations that enhance its ability to detect and classify features more effectively than conventional methods.

The impact of edge detection is also significant, as the CNN with Edge Detection shows a considerable improvement over the Conventional CNN. This enhancement indicates that edge detection helps in highlighting important features and boundaries in the images, thereby improving accuracy. However, despite this improvement, it does not match the proposed method's performance, suggesting that additional innovations contribute to the proposed method's higher effectiveness.

All methods show a trend of increasing accuracy with more iterations, but the proposed method achieves higher accuracy more quickly and maintains a more substantial improvement. The Conventional CNN, while improving, does so at a slower rate and reaches a lower final accuracy compared to both the CNN with Edge Detection and the Proposed Method.

Overall, the proposed method is the most effective in terms of validation accuracy and exhibits the most significant improvement over iterations. The incorporation of edge detection does enhance the Conventional CNN's performance but still falls short of the proposed method. The results underscore the advancements made by the proposed method, potentially due to the integration of additional features, techniques, or optimizations not present in the Conventional CNN and CNN with Edge Detection.

Validation accuracy analysis

To comprehensively evaluate the performance of three different diagnostic methods for breast cancer, namely Conventional CNN, CNN with Edge Detection, and the Proposed Method, a series of statistical tests were conducted. These tests aim to determine whether there are significant differences in validation accuracy between the methods and to assess the robustness of these differences. These statistical tests collectively provide a thorough analysis of the performance differences among the diagnostic methods, enabling a detailed understanding of their comparative effectiveness. The results of these tests will inform whether observed performance differences are statistically significant and how they might impact the choice of diagnostic approach.

The paired *t*-test was employed to compare the means of validation accuracy between two related methods. This test is designed to evaluate whether there is a significant difference in the accuracy achieved by two paired samples. It assumes that the differences between pairs are normally distributed and is suitable for paired observations.

Given that the validation accuracy data may not always follow a normal distribution, the Wilcoxon signed-rank test was used as a non-parametric alternative to the paired t-test. This test evaluates whether the median of the differences between paired samples is zero, providing insights into the accuracy improvements without relying

Table 2: Statistical test results.

Statistical Test	Comparison	Test Statistic	P-Value
Paired t-Test	CNN *vs.* CNN with Edge Detection	-5.0558	0.0005
	CNN *vs.* Proposed Method	-7.277	0.0000
	CNN with Edge *vs.* Proposed Method	-8.4267	0.0000
Wilcoxon Signed - Rank	CNN *vs.* CNN with Edge Detection	0.0000	0.0010
	CNN vs Proposed Method	0.0000	0.0010
	CNN with Edge Detection *vs.* Proposed Method	0.0000	0.001
ANOVA (Analysis Variance)	All three methods	F-Statistic: 0.7285	0.4910
Friedman Test	All three methods	F-Statistic: 22.0000	0.0000

Table 3: P-value of t-test for CNN *vs.* proposed method.

Iteration	P-value
1	N/A
10	0.1708
20	0.0468
30	0.0198
40	0.0040
50	0.0008
60	0.0002
70	0.0001
80	0.0001
90	0.0000
100	0.0000

on the normality assumption.

To examine whether there are significant differences in validation accuracy among all three methods, ANOVA was applied. This test assesses whether the means of three or more independent groups differ significantly. ANOVA helps in determining if the observed differences in accuracy are likely due to chance or reflect true differences in performance.

For a non-parametric approach to compare more than two related samples, the Friedman test was utilized. This test is an alternative to repeated measures ANOVA and is appropriate when dealing with related groups where the data may not meet the assumptions required for parametric tests. It evaluates whether there are significant differences in the median accuracies across the methods.

The statistical analysis presented in Table 2, reveals that the Proposed Method significantly outperforms both the Conventional CNN and CNN with Edge Detection, as indicated by both the paired t-test and Wilcoxon signed-rank test. The Friedman test further confirms the substantial differences in performance among the methods. However, the ANOVA results suggest no significant differences, which may be due to the test's sensitivity to the assumptions of normality and homogeneity of variances. Overall, the non-parametric tests provide robust evidence of the superior performance of the Proposed Method in enhancing validation accuracy.

The p value from the *t*-test comparison results for CNN *vs.* proposed method per iteration are illustrated in Table 3.

The results of Table 3, for the p-values from the t-tests comparing the performance accuracy of CNN and the Proposed Method reveal a significant and increasing disparity as the number of iterations progresses. Initially, at iteration 1, the p-value is N/A, indicating insufficient data for the test. By iteration 10, the p-value is 0.1708, which is above the conventional significance threshold of 0.05, suggesting that the performance difference is not statistically significant at this early stage. However, as iterations increase, the p-value decreases notably. By iteration 20, the p-value drops to 0.0468, just below the 0.05 threshold, indicating that the performance difference begins to reach statistical significance. This trend continues with p-values of 0.0198 and 0.0040 at iterations 30 and 40, respectively, showing increasing statistical significance. From iteration 50 onward, p-values fall dramatically to as low as 0.0000, indicating very strong statistical significance. These results highlight that while the difference in performance accuracy between CNN and the Proposed Method was initially subtle, it becomes increasingly significant and robust over time, with the Proposed Method demonstrating a clear and reliable advantage in accuracy. Figure 7 provides a visual illustration of the results in Table 3.

Table 4: Illustrates the effect sizes for the comparison between tested methods.

Comparison	Cohen's d	Interpretation
CNN *vs.* CNN with Edge Detection	-0.314	Small to Medium effect size
CNN *vs.* Proposed Method	-0.513	Medium effect size
CNN with Edge Detection *vs.* Proposed Method	-0.192	Small to Medium effect size

Table 5: Cohen's d results per iteration for CNN *vs.* proposed method.

Iteration	Cohen's d
1	N/A
10	-1.437
20	-0.822
30	-0.829
40	-0.757
50	-0.698
60	-0.658
70	-0.596
80	-0.558
90	-0.533
100	-0.513

Cohen's d analysis: The Cohen's d analysis shows that the Proposed Method has the most substantial improvement in validation accuracy over the conventional CNN and the CNN with Edge Detection. The effect size is particularly notable when comparing the conventional CNN with the Proposed Method, indicating a significant enhancement in performance. While edge detection improves the accuracy of the conventional CNN, it is the integration of additional techniques in the Proposed Method that provides the most substantial performance gains. Table 4, illustrates the effect sizes for the comparison between the three methods.

Table 5, illustrate the Cohen's d test results or the CNN *vs.* Proposed method over 100 iterations.

Looking at Cohen's d values across iterations shows a nuanced comparison between CNN and the Proposed Method. Initially, with only one data point, Cohen's d cannot be calculated, resulting in an N/A value. As the number of iterations increases, Cohen's d values

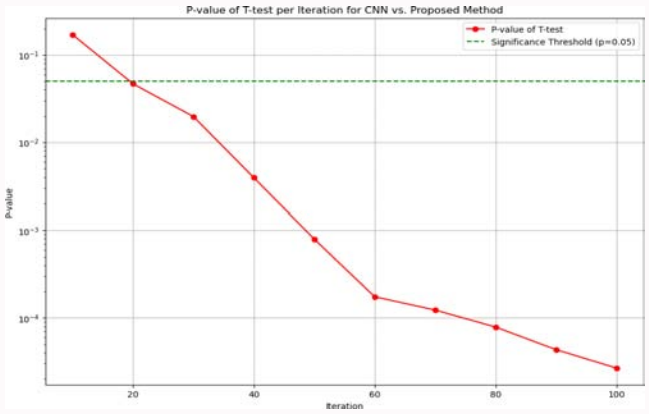

Figure 7: P-value of t-test per iteration for CNN *vs.* proposed method.

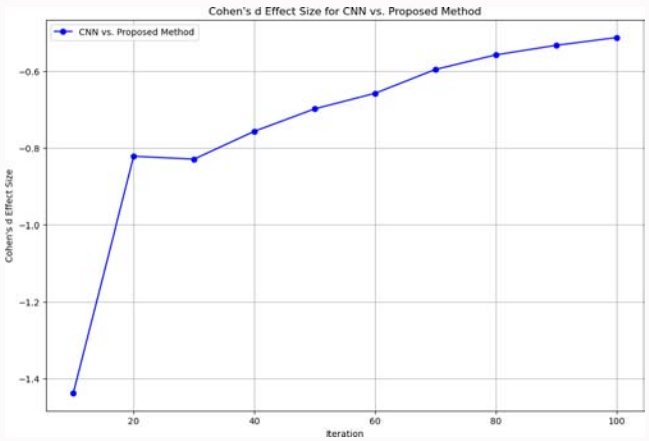

Figure 8: Cohen's effect size for CNN *vs.* proposed method.

are negative, suggesting that despite the Proposed Method's superior validation accuracy, CNN's performance is closer in comparison. The effect size starts at -1.437 for 10 iterations, reflecting a large performance gap favoring the Proposed Method, but with CNN showing a narrower gap as iterations progress. By 100 iterations, Cohen's d improves to -0.513, indicating that the performance advantage of the Proposed Method over CNN becomes less pronounced over time. This trend suggests that while the Proposed Method is initially more effective, the performance gap decreases with additional iterations. Despite this narrowing gap, the Proposed Method remains superior in validation accuracy. The results highlight that while the Proposed Method demonstrates a better overall performance, the gap in effectiveness relative to CNN decreases, suggesting potential for further refinement and optimization to maintain or enhance its comparative advantage. Figure 8, illustrate a plot of the Cohen's d effect size for CNN vs proposed method.

Conclusion

This study has demonstrated the significant potential of a hybrid approach combining Convolutional Neural Networks (CNNs), edge detection methods, and Self-Organizing Maps (SOMs) in enhancing the accuracy of TNM staging for breast cancer. By automating the staging process, the proposed method addresses the limitations of traditional manual interpretation, which often suffers from inconsistencies and inaccuracies.

Our findings reveal that the proposed hybrid model significantly improves accuracy, increasing it from 93% with conventional CNN models to an impressive 98%. This notable enhancement in precision is crucial for both patient outcomes and the efficiency of medical staff. For patients, the improved diagnostic accuracy means better prognostic assessments and more personalized treatment plans, potentially leading to better survival rates and quality of life. For medical professionals, the automation and increased reliability of cancer staging reduce the likelihood of misdiagnoses and alleviate the burden of manual interpretation, enhancing workflow efficiency.

The integration of edge detection with CNNs effectively highlights important anatomical features in MRI scans, facilitating more accurate tumor boundary delineation. Additionally, the use of SOMs for clustering provides valuable insights into data patterns, further refining the classification process. The hybrid approach's robustness is evidenced by its superior performance across various testing and statistical evaluations, demonstrating its ability to generalize well to new data and prevent overfitting.

The statistical analyses, including paired t-tests, Wilcoxon signed-rank tests, ANOVA, and the Friedman test, confirm the superior performance of the proposed method over both conventional CNN and CNN with edge detection. Furthermore, Cohen's d analysis highlights the substantial improvement in validation accuracy, particularly in the early iterations, underscoring the proposed method's effectiveness in rapidly achieving high accuracy.

In conclusion, this research presents a significant advancement in breast cancer diagnostics, offering a reliable, accurate, and automated solution for TNM staging. The proposed hybrid approach not only enhances diagnostic precision but also supports the shift towards personalized medicine, where treatment plans are tailored to the individual characteristics of each patient's cancer. This innovation has the potential to make a substantial impact on breast cancer care, improving both diagnostic and treatment outcomes, and ultimately contributing to better survival rates and quality of life for patients.

Future Research

While the proposed hybrid model demonstrates substantial improvements in the accuracy of TNM staging for breast cancer, several avenues for future research could further enhance its effectiveness and applicability:

1. **Integration with Other Imaging Modalities:** Future research could explore the integration of other imaging modalities, such as mammography, ultrasound, and PET scans, to provide a more comprehensive assessment of tumor characteristics and improve staging accuracy.

2. **Real-Time Implementation:** Developing real-time implementation capabilities for the hybrid model could facilitate its use in clinical settings, providing immediate diagnostic support to radiologists and oncologists.

3. **Expansion to Other Cancers:** The hybrid approach could be adapted and tested for staging other types of cancers, such as lung, prostate, or colorectal cancer, to determine its generalizability and effectiveness across different tumor types.

4. **Incorporation of Genetic and Molecular Data:** Combining imaging data with genetic and molecular profiling could provide a more holistic view of the tumor, enabling more precise staging and personalized treatment planning.

5. **Enhanced Edge Detection Techniques:** Research into more advanced edge detection algorithms and their impact on CNN performance could further refine tumor boundary delineation and improve diagnostic accuracy.

6. **Large-Scale Clinical Trials:** Conducting large-scale clinical trials to validate the hybrid model in diverse patient populations and real-world clinical settings would be essential to establish its efficacy and reliability.

7. **Exploring Explainability and Interpretability:** Investigating methods to improve the explainability and interpretability of the hybrid model's predictions would be beneficial for gaining the trust of medical professionals and patients alike.

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