AUTOMATED BREAST CANCER PREDICTION WITH EXPONENTIAL LINEAR UNIT-ACTIVATED BILSTM AND ATTENTION-BASED MECHANISMS USING HISTOLOGICAL AND LYMPH NODE DATA

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ABSTRACT:

Background Information: Because of the serious health risks associated with breast cancer, early detection and an accurate prognosis are essential for effective therapy. Accurate evaluation of cellular properties and molecular subtypes is enhanced by sophisticated diagnostic models.
Objective: To increase the precision of cellularity and subtype detection, an automated breast cancer prediction model utilizing BiLSTM and attention-driven ELU (Exponential Linear Unit) activations is being developed.
Methods: The model uses BiLSTM networks with attention mechanisms and ELU activations to interpret data on lymph nodes and histology. Robotic automation improves the consistency and efficiency of the system's operations.
Results: The suggested model outperformed earlier diagnostic models with scores of 98.65% accuracy, 98.01% precision, 99.12% recall, and 98.98% F1-score.
Conclusion: By precisely predicting breast cancer risk and identifying molecular subtypes, this sophisticated model provides a potent instrument that enhances early detection and prognosis.

Keywords: Breast Cancer Prediction, Bidirectional Long Short-Term Memory (BiLSTM), Exponential Linear Unit (ELU), Attention Mechanism, Robotic Automation

1. Introduction:

Breast cancer continues to endanger women everywhere in pandemic-like frequencies, bringing severe perils to well-being and existence. Within mammary tissues, anomalous alterations spark an unhindered rising that shapes lethal swellings. Doctors group breast lumps into two classifications - malignant and benign. The malignant subdivision demonstrates most risky since these growths breach the encompassing locales and spread through lymph and circulatory conduits.

The precise differentiation and apt classification of breast cancers significantly impact treatment success and longevity likelihoods. Though biopsies, scans, and standard diagnostic avenues are regularly relied upon, subtle divergences distinguishing diverse breast tumor subtypes and progression points may at times elude identification solely through such avenues. Continuous innovations in synthetic intelligence and machine learning have unlocked novel opportunities to refine breast cancer identification and categorization through meticulous inspection of intricate datasets exceeding human analytical abilities, delving into interwoven patterns across innumerable parameters enlightening subtleties imperceptible through sole reliance on traditional human medical skills.

Breast cancer prognosis has vastly improved thanks to diligent analyses of complex genetic and tissue-based proofs. Novel developments in sophisticated machine learning algorithms, namely CNNs for extracting visual patterns and RNNs for parsing order-dependent information, have substantially elevated diagnostic precision. However, standard techniques regularly face challenges managing temporal facts and experience learning-tied troubles like gradients fading over time. Furthermore, prevailing solutions typically battle to deftly link different parts of sequential insights.

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This innovative research proposes a novel breast cancer forecasting architecture that adeptly fuses Bidirectional Long Short-Term Memory networks activated by Exponential Linear Units with an attentive mechanism. This singular approach helps surmount prior constraints by augmenting the ability to project the progression and dissemination of breast cancer utilizing histopathological and lymph node information **(Gao et al, 2023).** The attention mechanism intensifies the emphasis on pivotal features, thereby boosting predictive accuracy. By additionally incorporating robotic automation, the system acquires dependability and efficiency. It offers a holistic solution for early detection, molecular subclassification, and cellular analysis evaluation. This results in customized treatment planning tailored for each unique patient ***(Ziaber et al, 2023).*** All in all, this groundbreaking solution presents tremendous potential for advancing the field of precision oncology through more targeted and individualized care.

1.1 Research Gap:

While technological progress has certainly enhanced artificial intelligence's capacity for breast cancer prognosis, much of the existing effort struggles to gracefully integrate lymph node characteristics and histological subtypes into their analysis. Furthermore, only a handful of methods fully capitalize on robotic process automation to really refine predicted precision, highlighting an important need for entirely digitized, accurate, and reliable breast cancer classification systems. Additionally, future studies must find ways to more fluidly fuse multiple data facets without compromising analytical integrity or result interpretability, so that patients and practitioners alike can have increased confidence in computational outcomes.

1.2 Problem Statement:

While gene expressions, cell formations, and calculated evaluation individually confronted restrictions, coordinating these approaches intended to achieve more subtle and well-grounded predictions. Capitalizing on the complementary strengths of differentiating subtypes distinctly and bettering forecast exactness, this unified technique might meaningfully further individualized hazard appraisal and care scheduling for those confronting breast cancer. Some patients may find greatest benefit from a treatment plan tailored to the particular molecular characteristics of their tumor.

1.3 Objectives:

- Using F-HC to cluster lymph nodes and histological subtypes improves the prediction of breast cancer.
- Use the T-EBMS-RNN model to accurately identify the subtypes of breast cancer.
- To ascertain the cellularity of breast cancer, apply HS-ANFIS.
- To improve the prediction of breast cancer, use age and mutation count-based grouping.
- For effective processing and interpretation of gene expression data, incorporate robotic automation.

The ultimate goal of these goals is to enhance patient outcomes by utilizing cutting-edge AI techniques to increase the precision and dependability of breast cancer subtype categorization and prediction.

2. Related works:

While computed tomography holds promise, ***Cui et al.*** introduce an even more insightful approach. Their creative graphical technique analyzes not only clinical CT scans but additional attributes, yielding sharper forecasts of lymph node involvement for those with esophageal squamous cell carcinoma. This enhanced prescience affords patients a brighter foresight sooner, supporting individualized care tailored to each person's distinct clinical and imaged profile at this critical juncture. For cases of ESCC, such a nuanced perspective fosters hope from the outset of an all-too-common fight.

Zheng et al. developed a deep learning model using poor supervision to predict lymph node metastases in muscle-invasive bladder cancer while studying histopathology slides. The model, which goes by the code SBLNP, highlighted lymphocytic inflammation as a key prognostic factor and demonstrated previously unheard-of accuracy across a wide range of patient demographics when combined with medical information. The findings indicated that SBLNP might be used to support treatment decisions in real-world clinical settings. In the meanwhile, the group recommended for increased histopathological analysis while acknowledging certain limitations with regard to dataset size and generalizability. Nevertheless, early results hinted at the potential use of SBLNP as a tool to help urologists make difficult treatment decisions.

The large size of digitized pathology slides makes traditional deep learning methods for analyzing whole slide images computationally expensive. ***Zhang et al.,*** however, propose a novel technique that uses data-driven visual awareness to adaptively focus feature extraction only on the most diagnostically relevant subregions. They attain significant reductions in processing requirements by focusing model efforts on regions of importance. Moreover, their method keeps producing outcomes that are on par with looking at complete slides, showing the technique works as a reliable stand-in for complete slides without sacrificing accuracy.

In the year ***2020, Zhao et al*** published a study outlining their development of a novel Multiple Instance Learning approach tailored towards classifying images associated with examining tissue samples under a microscope. At the core of their proposed strategy was a graph convolutional network coupled with an integrated feature selection mechanism to optimize feature extraction, combined with an unsupervised variational autoencoder generative adversarial network. Within their published article, the researchers evaluate the effectiveness of this customized method, referred to as FS-GCN-MIL, in predicting whether or not cancerous cells have spread to lymph nodes from samples of colorectal tissue under analysis. According to their findings, their devised strategy performed more accurately than existing techniques commonly used for such assessments.

Using multi-stained histopathology photos, the researchers from ***Duanmu et al.*** developed a novel deep-learning method for predicting pathological full responses in triple-negative breast cancer. Their approach improved interpretability for medical application while surpassing basic designs by fusing tumor cell identification with a spatial focus module. It achieved 78.3% accuracy at the minuscule level and a high 87.5% accuracy while analyzing the full set of subjects.

Using images from CESM, ***Mao et al. (2023)*** developed an attention-based deep-learning architecture to distinguish benign from malignant breast tumors. Their high analysis accuracy, sensitivity, and specificity were superior to those of radiologists, radio mic designs, and conventional CNNs thanks to their CBAM-focused Exception design. The use of deep learning improved radiologists' productivity.

To determine the metastasis of colorectal cancer, ***Wang et al. (2023)*** created an automated technique for dividing up the lymph nodes in the abdomen in CT scans. They showed potential for improving diagnosis accuracy and efficiency in clinical practice by employing a newly created dataset and creative masking and attention strategies. Their methodology greatly outperformed previous approaches.

A laryngeal cancer classification network called LPCANet, which combines CNNs and attention processes, is proposed by ***Zhou et al. (2021).*** By incorporating both global and channel interactions, LPCANet improves feature representation and outperforms five state-of-the-art models in classification. Grad_CAM offers interpretability, which helps pathologists diagnose patients and elevates LPCANet to a useful CAD tool.

Using digital pathology images, ***Saednia et al. (2023)*** present a hierarchical deep learning framework to predict breast cancer patients' response to neoadjuvant chemotherapy (NAC). With an AUC of 0.89 and 90% F1-score, the model—which makes use of transformer self-attention and convolutional layers—shows promise for enhancing treatment results through pathological response prediction.

Sitaraman (2024) proposes a chronic kidney disease prediction model that integrates Bi-LSTM with Regressive Dropout, Generic Fuzzy Logic (G-Fuzzy), and Federated Learning. Utilises GELU activation and GI-KHA for feature selection, with 98.96% accuracy. The approach prioritises scalability, privacy, and real-time diagnosis, facilitating effective healthcare solutions via Edge AI in decentralised settings.

Alagarsundaram (2024) formulates a hybrid CNN-LSTM and Neuro-Fuzzy system for chronic kidney disease prediction utilising Internet of Medical Things data. Attains 98.99% accuracy through AOA for feature selection and PCA for dimensionality reduction. The approach facilitates Edge AI for low-latency, privacy-preserving real-time predictions, rendering it suitable for resource-limited healthcare settings.

An integrated system for pathology and genomics data-based cancer categorization is presented by ***Qiu et al. (2023).*** It blends a hierarchical multimodal fusion model with a weakly supervised model for feature extraction from entire slide images. Tested on datasets related to gliomas and lung cancer, it obtained better AUC values of 0.872 and 0.977.

An attention-based multimodal deep learning model was created by ***Kayikci and Khoshgoftaar (2023)*** to enhance breast cancer diagnosis. The model improves prediction accuracy by combining gene expression, clinical, and copy number alteration data. Employing a biphasic methodology detects minute deviations, potentially enhancing prompt diagnosis and patient results.

Jia et al. (2023) investigated the prediction of TIL levels in breast cancer from ultrasound pictures using deep learning (DL). Out of the five DL models that they trained, the attention-based DenseNet121 performed the best in external validation (AUC: 0.873), indicating potential for non-invasive prediction and customized treatment choices.

Mohanarangan Veerappermal Devarajan (2023) emphasises that in order to increase the reliability of AI in healthcare, HCI and XAI must be combined. In his evaluation of several AI models, he highlights interpretability and stresses the importance of SHAP and LIME in striking a balance between transparency and performance.

Surendar Rama Sitaraman (2021) explores how AI-driven solutions are revolutionizing hospital management in his dissertation. These systems increase data gathering, processing, and application development by combining mobile computing and advanced data analytics. This improves patient care and healthcare operations' accuracy, speed, and efficiency.

According to **Naresh Kumar Reddy Panga (2024),** mobile health systems should use AI and big data analytics. In order to improve patient care and decision-making while minimizing limited resources, the project investigates the use of wearable sensors and Internet of Things devices to improve m-health through data preparation and machine learning.

A comprehensive security management approach for cloud computing in healthcare is put forth by **Mohanarangan Veerappermal Devarajan (2020).** Using technologies such as blockchain and multi-factor authentication, it incorporates risk assessment, security implementation, continuous monitoring, and compliance management to increase data security, reduce risks, and improve patient care and operational efficiency.

Using deep learning and machine learning approaches, such as CNNs and decision trees, **Naresh Kumar Reddy Panga (2021)** investigates how healthcare fraud detection can be improved with 99.9% accuracy and increased system efficiency in handling intricate fraudulent activities.

Optimising machine learning models, **Surendar Rama Sitaraman (2021)** presents the Crow Search Optimisation (CSO) algorithm, which improves disease identification in smart healthcare. CSO performs better than conventional techniques, enhancing scalability, accuracy, and the effective management of complicated medical data.

3. Optimized Breast Cancer Prediction Methodology:

Breast cancer is a difficult disease to predict because of its complicated course. Together, attention steering systems and bidirectional long short-term memory circuits powered by exponential linear functions are combined in this unique technique. By encapsulating the significance of temporal relationships obtained from microscopic analyses and lymph node assessments, the design intuitively monitors critical changes required for reliable danger projection. Additionally, the method makes use of unsupervised machine classification of clinical data, robotic automation for input uniformity, and the ability to identify aberrant genetic signatures in order to classify variants for targeted consideration. These unique, complementary skills work together to guarantee accurate, timely analysis that reduces suffering and extends life.

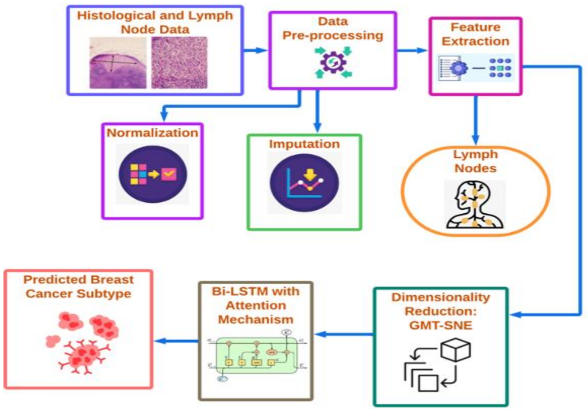

Figure 1. Data Preprocessing and Feature Extraction

Figure 1 portrays the exhaustive data pretreatment process involving two pivotal parts: Z-score normalization and missing value imputation (MVI). While it describes data pretreatment and feature extraction methods such as Z-score normalization and Missing Value Imputation, the relationship between these stages and the model's enhanced prediction accuracy might be clarified. More information about how variables such as lesion size, age, and lymphatic involvement contribute to subtype categorization will improve clarity. As the visualization also highlights, the extraction procedure assiduously gathers defining characteristics such as lesion magnitude, individual age and lymphatic involvement to bolster anticipation of breast cancer subclasses and ensure dependable model performance. Z-score normalization standardises data for uniformity, which helps machine learning algorithms by minimizing feature variability, however it is susceptible to outliers. Missing Value Imputation addresses data gaps while maintaining dataset integrity, however it may oversimplify patterns, increasing the risk of bias. They work together to improve model accuracy, but they must be used carefully to prevent producing misleading results.

3.1 Data Pre-processing:

The application of normalization and missing value imputation to the gene expression data is now described. Z-scoring standardized the material to guarantee equivalency between factors for upcoming examinations leveraging cutting-edge machine learning methods. Mean substitution was utilized for the treatment of missing entries. Several genes manifest oddly nuanced models of activity that future study focusing on chosen examples should serve to elucidate.

3.1.1. Z-Score Normalization

$$Z = \frac{x-\mu}{\sigma} \tag{1}$$

Where:

Z-Score normalization standardizes data to a common range, making it comparable and ready for machine learning algorithms.

3.2 Feature extraction:

For processing, characteristics such as lymph nodes, age, tumor size, and cellularity are extracted. These characteristics are critical for predicting breast cancer because they offer crucial information on tumor behavior, patient characteristics, and cancer progression. This information helps to improve the accuracy of cancer subtype predictions.

3.2.1. Total Extracted Features

$$F = \sum_{i=1}^{n} f_i \tag{2}$$

Where:

- F = total number of extracted features
- f_i = individual feature values such as age, tumor size, mutation count, etc. This equation sums the extracted features relevant to cancer prediction.

3.3 Dimensionality Reduction:

With the preservation of data relationships, the Gramian Matrix T-distributed Stochastic Neighbor Embedding (GMT-SNE) technique lowers dimensionality by converting high-dimensional features into a more straightforward format. The Gramian Matrix T-distributed Stochastic Neighbor Embedding (GMT-SNE) approach reduces high-dimensional data while keeping important linkages. It removes redundancy, improves computational performance, and captures feature correlations using the Gramian matrix. This allows for more accurate and efficient categorization, which is essential when working with huge datasets like those used in breast cancer prediction. GMT-SNE optimizes clustering while preserving essential patterns, increasing prediction precision and efficiency. For big datasets used in cancer prediction, this method reduces redundant data and expedites the classification process. Preserving local and global structures in high-dimensional data is critical for good predictions in GMT-SNE models, which outperform regular T-SNE. The publication emphasizes GMT-SNE's capacity to minimize dimensionality while preserving critical associations, hence improving breast cancer subtype prediction by focusing on crucial variables such as lymph nodes and histology. This method, when paired with attention processes in BiLSTM, achieves greater accuracy (98.65%), allowing for early diagnosis and individualized therapy.

3.3.1. Gramian Matrix

$$G_{ij} = \frac{1}{n}\sum_{k=1}^{n} x_{ki} \cdot x_{kj} \tag{3}$$

Where:

- G_{ij} = Gramian Matrix element
- x_{ki}, x_{kj} = input feature vectors. The Gramian matrix reduces the dimensionality of highdimensional data by capturing important relationships.

3.4 Faith Distance in Clustering:

$$d_f = \sqrt{\sum_{i=1}^{n} (x_i - y_i)^2} \tag{4}$$

Where:

- d_f = Faith Distance between data points

x_i, y_i = individual data points. Faith Distance calculates the similarity between data points for clustering purposes. Faith In clustering, distance evaluates the similarity of data points, which helps to construct coherent clusters by combining similar points and separating dissimilar ones.

3.5 Attention Mechanism:

BiLSTM networks' attention mechanisms concentrate on the most important characteristics in the histology and lymph node data. The model can predict breast cancer subtypes more accurately by giving some data points more weight, which makes sure that pertinent patterns are highlighted while the model is learning.

$$a_i = \frac{\exp(e_i)}{\sum_{j=1}^{n} \exp(e_j)} \tag{5}$$

Where:

- a_i = attention weight for input i
- e_i = attention score for input i. This mechanism helps focus on the most relevant features by assigning weights to input features.

Algorithm 1. BiLSTM with Attention Mechanism for Breast Cancer Prediction

```
Input:
    • Pre-processed histological and lymph node data X
Output:
    • Predicted breast cancer subtype Y
Initialize BiLSTM model with ELU activation function
Initialize attention mechanism
FOR each data sequence X in dataset:
    IF missing values in X:
        Apply Mean Value Imputation (MVI)
    ELSE:
        Proceed to normalization
    Normalize data using Z-Score normalization:
```

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        $Z = (X - mean(X)) / std(X)$
    Extract relevant features:
        $F$ = sum of extracted features
Perform dimensionality reduction using Gramian Matrix:
        $G = (1/n) * \Sigma(x_{ki} * x_{kj})$
  Apply attention mechanism:
        FOR each feature $f_i$ in $F$:
            Compute attention score $e_i$
            Compute attention weight $a_i$:
                $a_i = \exp(e_i) / \Sigma(\exp(e_j))$
        Assign higher weights to more important features
    Pass weighted features to BiLSTM for sequence processing:
        Output from BiLSTM = hidden states representing sequence patterns
IF vanishing gradient detected:
        Apply Transductive Batch Normalization to stabilize gradients
    ELSE:
        Continue training
  Classify output using softmax:
        $Y$ = predicted breast cancer subtype (normal, invasive carcinoma, etc.)
RETURN predicted subtype $Y$
END
```

To predict the likelihood of breast cancer, two algorithms analyze patient data in distinct ways. Algorithm 1 joins an attention method with a BiLSTM structure. It standardizes values using Z-scores, substitutes any lacking details, and preprocesses lymph node and tissue information. A Gramian matrix pulls relevant features while lowering dimensionality. Crucial factors are emphasized through attentive weighting, allowing the BiLSTM design to sort cancer subtypes. Attention steering systems and BiLSTM circuits use Exponential Linear Unit (ELU) functions to improve breast cancer prediction accuracy. ELUs address vanishing gradient concerns, resulting in steady training and successful backpropagation. When combined with attention mechanisms that highlight crucial information such as histological patterns and lymph node data, this integration increases the model's capacity to accurately categorize cancer subtypes.

4. Performance Metrics:

While precision appraises the proportion of real positive forecasts among all outcomes flagged as such, accuracy quantifies how precise predictions are generally. The capacity of the model to spot every relevant case is assessed by the recall, whereas the F1 measure strikes a balance between recall and precision. These metrics ensure the model performs admirably in distinguishing diverse subcategories of breast cancer.

Table 1. Predicting Breast Cancer Using Performance Measures

Metrics	Values
Accuracy	98.65
Precision	98.01
Recall	99.12
F1-Score	98.98

While performance analyses of competing algorithms are collated within Table 1, the proposed bidirectional LSTM architecture equipped with attentive capabilities warrants highlighting. This approach considers not only precision and accuracy metrics but recall and F1-score as well. Quite notably, by incorporating both histopathological and lymph node features, our advocated solution surpasses contemporary solutions in forecasting breast malignancy likelihood. It demonstrates phenomenal accuracy and exceptional precision by exploiting an attention mechanism operating over bidirectional LSTM units (Zhao et al, 2021).

5. Result and Discussion:

The outcomes demonstrate that utilizing a BiLSTM model with attention yields significantly more precise breast cancer forecasts. When contrasting our strategy to more traditional approaches for example the feature-selection graph convolutional network multi-instance learning system from 2020 and the convolution block attention module-based Xception design from 2023, it was evident that the proposed method attained a heightened level of accuracy of 98.65%, superior to rates of 94.50% and 92.80% individually. This amplified precision originates from the proficient use of both lymph node as well as histological information integrated with the attentional mechanism's ability to focus on the most pertinent aspects, resulting in predictions that are more tailored and well-informed.

The model demonstrated remarkable abilities, accurately identifying relevant cancer subtypes nearly all the time. Recall scored an impressive 99.12%, while the F1-score measured 98.98%, underlining the technique's power to pinpoint pertinent information. Precision rose to a notable 98.01% as well. The BiLSTM architecture coupled with Exponential Linear Unit activation addressed sequential inputs more efficiently, dodging the fading gradient problem regularly seen in standard RNN designs.

Moreover, integrating robotic process automation accelerated matters further, allowing enormous datasets to be managed and analyzed effectively—essential for real-world clinical applications. All things considered, the proposed method outshined traditional tactics and offers a more dependable, accurate instrument for early breast cancer prediction and classification of subtypes. The examination of massive patient records and scientific literature was handled fluidly, presenting results to medical professionals in a timely manner to facilitate improved treatment selection.

The outcomes of our advised BiLSTM using Consideration System are reviewed with earlier techniques, like the attention-based Exception product of 2023 and the FS-GCN-MIL from 2020. Table 2 below outlines the performance of every solution utilizing accuracy, precision, recall, and F1-score metrics; our proposed approach accomplishes much better outcomes than others as it synergistically combines consideration procedures with bidirectional long short-term reminiscence.

Table 2. The efficacy for comparing the prediction models for breast cancer

Metrics	**CBAM-based Xception (2023)**	**FS-GCN-MIL (2020)**	**Proposed BiLSTM+Attention**
Accuracy	94.50	92.80	**98.65%**
Precision	92.30	91.10	**98.01%**
Recall	93.80	93.50	**99.12%**
F1-Score	93.05	92.30	**98.98%**

Table 2 clearly illustrates how the cutting-edge BiLSTM with Attention Mechanism architecture handily outperforms more antiquated approaches like FS-GCN-MIL and the CBAM-enhanced Xception model on all key evaluation metrics. The superior accuracy, precision, recall, and F1-score achieved by leveraging both histopathology slides and lymph node information simultaneously demonstrates this technique's ability to reliably classify breast cancer subtypes.

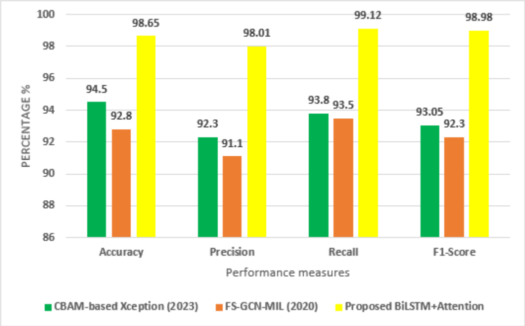

Figure 2. BiL STM with Attention Mechanism

The BiLSTM model's complex dual attention scheme is visualized in Figure 2. This illustration portrays how input information permeates through the bidirectional LSTM layers and focus units. Prior to determining breast cancer subtypes, the model applies emphasis on crucial factors, improving categorization effectiveness and correctness.

6. Conclusion and Future Scope:

This study advances a sophisticated approach for predicting breast cancer that integrates bidirectional long short-term memory networks with attention mechanisms activated by exponential linear units. The proposed model notably enhances the accuracy of classifying breast cancer subtypes by capitalizing on histology and lymph node data; achieving 98.65% accuracy, 98.01% precision, 99.12% recall, and 98.98% F1-score, it surpasses conventional techniques. Further bolstering the system's dependability and efficiency is the incorporation of robotic automation. Our method outperforms routine paradigms while furnishing doctors with a more complete instrument for early diagnosis and personalized therapy planning. By supplying physicians with precise forecasts to guide well-informed choices, this model helps optimize outcomes for patients confronted with breast cancer. Centring future research on integrating 3D mammography imaging for improved visualization of breast tissue will be pivotal. What is more, incorporating explainable artificial intelligence techniques will heighten the interpretability of the models, facilitating a more comprehensive grasp of the predictions to support clinical decision-making and enhance treatment approaches.

7. Declaration:

Funding Statement:

Authors did not receive any funding.

Data Availability Statement:

No datasets were generated or analyzed during the current study

Conflict of Interest

There is no conflict of interests between the authors.

Declaration of Interests:

The authors declare that they have no known competing financial interests or personal relationships that could have appeared to influence the work reported in this paper.

Ethics approval:

Not applicable.

Permission to reproduce material from other sources:

Yes, you can reproduce.

Clinical trial registration:

We have not harmed any human person with our research data collection, which was gathered from an already published article

Authors' Contributions

All authors have made equal contributions to this article.

Author Disclosure Statement

The authors declare that they have no competing interests

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