A Hybrid Ensemble Machine Learning Framework for Breast Cancer Detection

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Abstract

Problem to detect the Breast Cancer timely and with accuracy is one of the most important diseases in modern health care industry. We have a lot of algorithms related to machine learning shows accurate results but due to data imbalance and other problems in data there is fluctuation in the results. In this paper, the combination of different ml algorithms has been used as a hybrid assembly for better results, enhancing the separate results of these algorithms and correcting the drawbacks of such procedures. The important factor is to increase the robustness and generalization of model so that the consistency in prediction remains. So the hybrid model is used in Biomedical Data Analysis. I compared the hybrid with classical ml models. And I got 99.3% accuracy that shows the better performance than others. Visualization charts prove the diagnostic capacity of hybrid model. The results shows that when we work on different methods together then prediction and detection of breast cancer can effectively complete This research provide a feasible solution for the applications of diagnosis.

Keywords: ROC Curve, Ensemble Stacking, Hybrid Machine Learning, Breast Cancer Detection, Feature Importance, and Predictive Analytics.

I. Introduction

According to a survey one out of 8 women is suffering from breast cancer [WHO-2024 survey][1],[2]. The death rate depends on early prediction with accuracy. There are a lot of imaging techniques for breast cancer prediction. Like MRI & Mammograms are basically used as screening tools in prediction. But there are certain problems as the variability of data of diagnosis and the process interpretation. Also, certain questions as what is the stage of tumor? How can we analysis the aggressiveness and abnormalities of cells? Are the strongly answerable questions.

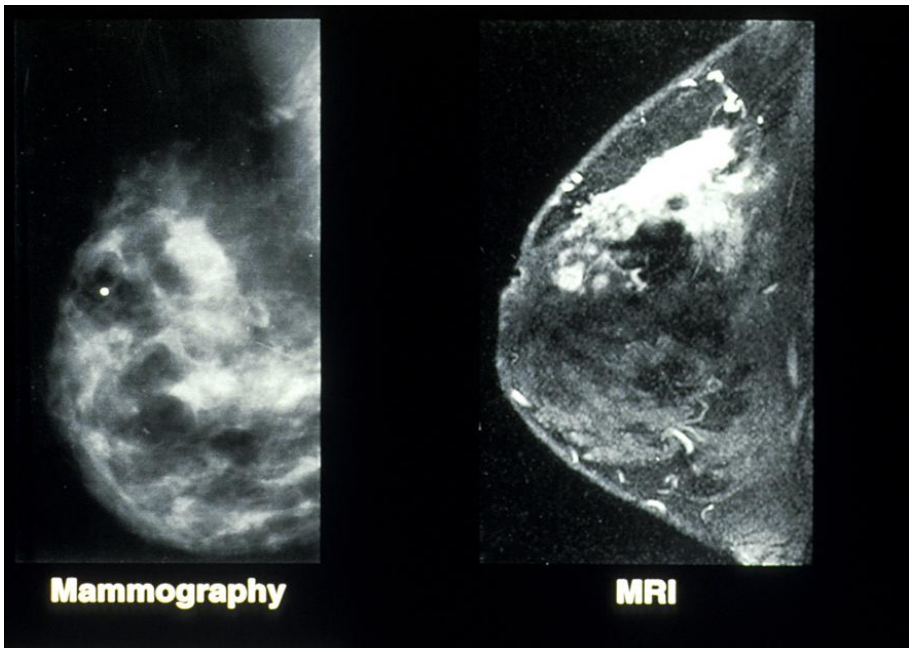


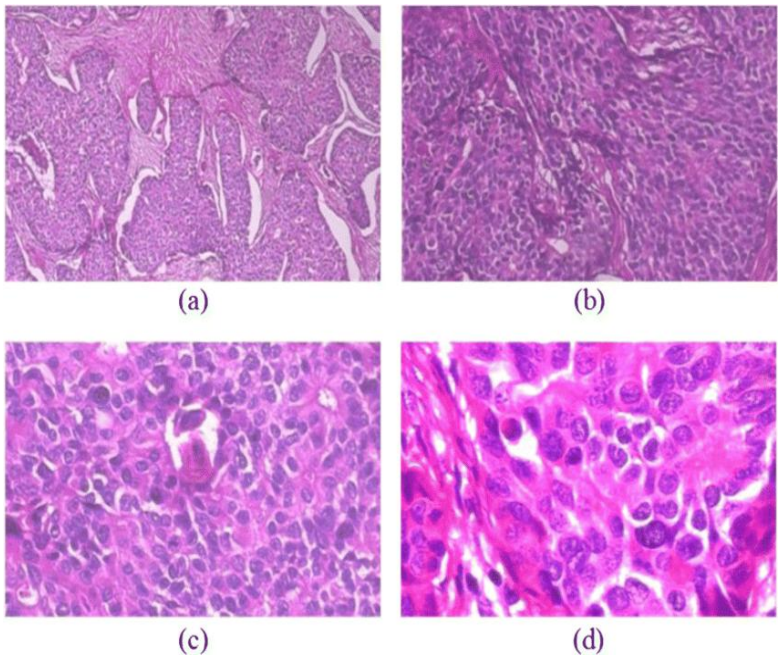
Fig. 1. Screening Scenario of Breast Cancer

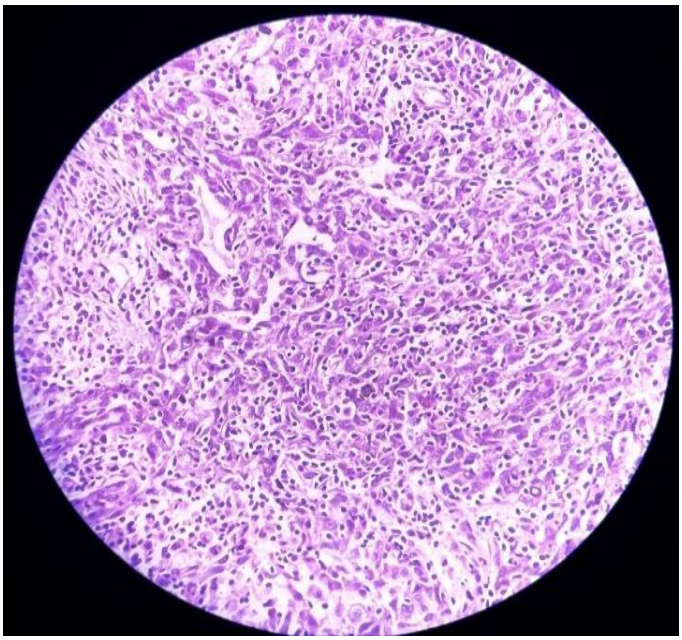
Figure 1 shows the comparison of MRI and Mammogram screening process. Left image shows overlapping of tissues and low contrast due to which the lesions are not understandable basically in the dense breasts. Right MRI image works differently as in it uses radio wave and magnets and also for accuracy contrast agent also used. It provides better contrast for soft tissues. Mammography is still the go to for regular screening though, even with those limits.

Problems such as cell shapes falling between benign and malignant present challenges for pathologists due to the micro differences in shapes. Therefore, there is a need to analyse these problematic and complicated patterns regularly with an automatic computational support system. Because of the automated support in imaging and clinical data that can be missed by humans, different techniques of Artificial Intelligence and Machine Learning can analyse them. These techniques have emerged as viable solutions for breast cancer screening [4][5]. With problematic data and heterogeneous medical data, if a single machine learning model is used, then there would be certain drawbacks of a single algorithm like overfitting, decreasing generalization capacity, and performance instability [6]. However, such constraints can be avoided by mixing output from different classifiers like gradient boosting and random forestthrough mixing such ensemble techniques, enhanced diagnostic performance is achieved [7][8].

The Fig. 2. image(a) displays a zoomed in, diminished histopathological section stained with haematoxylin and eosin (H&E). The overall tissue structure is visible at this level which reveals irregular glandular or lobular

structures, embedded into a dense cellular stroma. This arrangement looks disorganized as compared to normal tissue pattern that suggests a pathological process. . This view is useful to assess the general distribution of abnormal tissue and the extent of structural distortion. The Fig. 2. image (b) shows a medium magnified view of cellular organization within the affected area which provides us with its clearer visualization. The tissue shows that cells are densely packed into sheets, significantly reducing the normal spacing. The presence of fibrous stromal components shows invasive growth by separating clusters of cells. This magnification helps in identifying abnormal proliferation and disruption of normal tissue boundaries. Fig. 2. Image (c) shows a higher magnification section which focus on individual cells. the cells appear pleomorphic, with irregular shape and size, and nuclei are also enlarged, darkly stained. This level of detail is essential for evaluating cellular atypia. Fig. 2. Image (d) displays the highest level of magnification which is focusing on nuclear and cytological details. The nuclei appear markedly hyperchromatic and irregular, with chromatin patterns and appearance shapes of mitotic. Cytoplasmic boundaries shows difficulty to define as the cells are tightly packed, showing aggressive cellular behaviour. This view is vital for confirming malignancy and assessing tumor grade that is based on nuclear abnormalities.





(e)

Fig. 2. a .H & E-stained section represent overall tumor architecture in breast issue with low-magnification **b.** H & E-stained section represent overall tumor architecture in breast issue with intermediate-magnification **c.** H & E-stained section represent overall tumor architecture in breast issue with High-magnification **d.** H & E-stained section represent overall tumor architecture in breast issue with very high-magnification **e.** microscopic view

Fig.2. Image(e) was observed under moderate magnification then it showed histopathological microscopic view of tissue stained with haematoxylin and eosin (H&E) and the circular field represents the microscope's field of view. The tissue exhibits marked hypercellularity where there is densely packed arrangement in an unorganized pattern that indicates tissue loss architecture. This shows characteristics of abnormal or malignant cellular proliferation as they display enlarged, darkly stained (hyperchromatic) nuclei, ratio of nuclear to cytoplasmic enhancement, & noticeable pleomorphism. There is close crowding of cells that suggests aggressive growth and possible invasion into surrounding tissue while the stroma appears reduced and irregular. Overall, this image is used to assess cellular atypia, tumor behaviour, and disease severity through microscopic examination and is consistent with neoplastic pathology.

In the practical context of diagnosis, such ensemble techniques may still rely significantly on the adjustment of parameters and sometimes display marginal bias [9]. In the current scenario of medical detection tasks, combining machine learning approaches performs better and provides more accurate results for the prediction and detection of disease [10-13]. Based on the decisions, current study provides that a hybrid ensemble of Random Forest, Gradient Boosting,

and Support Vector Machine stacking model can be used which aims to acquire accurate results, great interpretability, and low false negative rates for clinical adoption and reliability in medical AI [14-17].

2. Literature Review

In cancerous disease Breast Cancer is most lethal malignancies in women, early detection of ther breast cancer is critical because the prognosis significantly improves when aberrant cellular abnormalities are found before metastasis. As shown in Fig. 3, breast cancer typically starts in the epithelial lining of lobules or ducts, where aberrant proliferation turns distinct tissue into malignant lumps [52]. Fig. 4 displays the structure of the breast, including lobules, ducts, lymphatic channels, and adipose tissue [51]. The images labelled as A and Bin Fig. 4 illustrates a comparative anatomical and pathological cross-section of the human breast that explains normal breast structure and indicate the presence of disease. Image A displays the normal anatomy of the breast in cross-section and the internal organization of breast tissue, that includes fatty tissue which provides shape, lobules that function as milk-producing glands, and also a network of mammary ducts that converge toward the nipple. Blood vessels form a network to supply nutrients to the tissue while the connective tissue supports the overall structure. The breast is shown to be resting over the chest wall as it demonstrates that how glandular and fatty tissues are arranged relative to the skin and nipple. In the presence of a malignant tumor image B depicts the breast anatomy. The labelled diagram shows structures such as the chest wall, ribs, intercostal and pectoral muscles, blood vessels, mammary ducts, fat cells, and nipple.

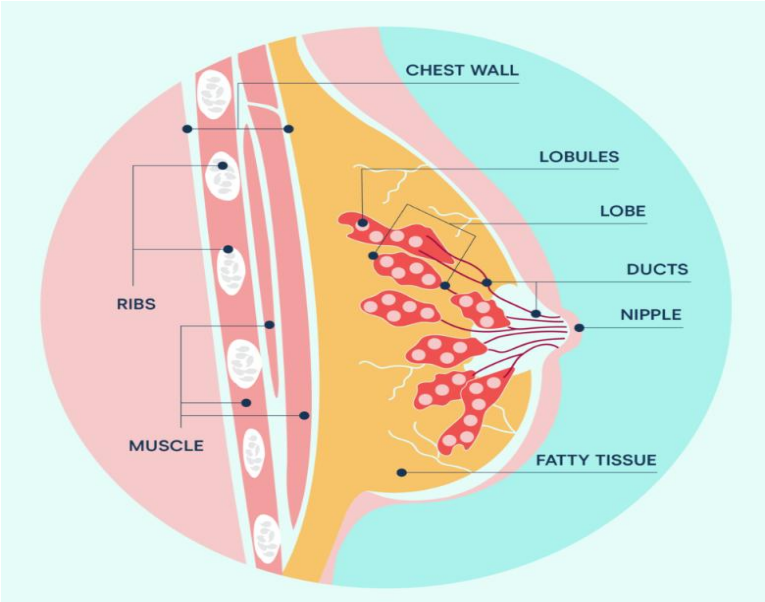


Fig. 3. Starting and Spreading of Breast Cancer

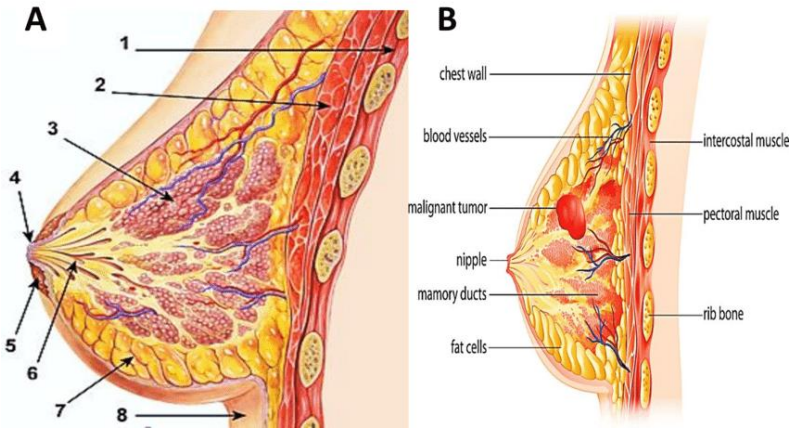
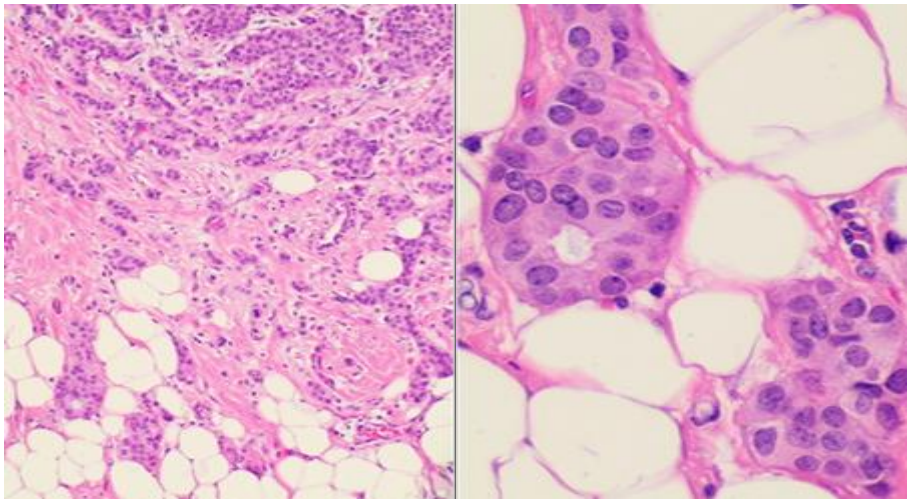


Fig. 4. Breast Anatomy

Figure 4.1 shows the fibrous disruption that shows invasive breast carcinoma. Fig. 4.1 Image (b) represents a high-magnification view focusing on the cellular details of the tumor. The malignant epithelial cells show enlarged, pleomorphic, and hyperchromatic nuclei, with an increased nuclear-to-cytoplasmic ratio. The cells are arranged in small clusters and cords, closely associated with adipocytes, indicating tumor infiltration into fatty tissue. This magnification highlights nuclear atypia and cellular morphology, which are essential features for confirming malignancy and assessing tumor grade.



(a) **(b)**

Fig. 4. 1 a. Represents low magnification H&E-stained section displaying invasive carcinoma of breast cancer infiltrating stroma and adipose tissue **b.**H&E high magnification view of malignant breast epithelial cells with nuclear pleomorphism adjacent to adipocytes

In Fig. 5, homogeneous ductal epithelial and constrained cell shape are found in healthy breast tissue [51]. This image under H&E microscopy shows that malignant tissue exhibits pleomorphism, aberrant mitotic activity, lack of adhesion of cells, and pathological staining patterns.

The Fig 5. image(a) displays a zoomed in, diminished histopathological section stained with haematoxylin and eosin (H&E). Within the surrounding stroma it shows clusters of epithelial cells that form irregular gland-like structures. As the cells have darkly stained nuclei and reduced cytoplasmic space therefore, we can observe increased cellular activity. This view primarily focuses on cellular morphology hence allowing observation of nuclear crowding as well as architectural distortion typical of abnormal or neoplastic tissue. The Fig 5. image(b) shows a low magnified view of whole tissue section (H&E stained), that shows the overall tissue structure. A region of interest (ROI) is marked by the dashed box that corresponds to the higher-magnification image in (a). This image explains that within the larger tissue sample how the abnormal cellular regions are distributed and it also helps to understand correlating microscopic findings with tissue-level structure. Fig 5. image(c) shows a false-colour quantitative or functional image of the same tissue area as in (a), along with a micrometre scale bar and a colour scale of measured values. The colour differences represent biophysical or optical properties (such as tissue density, collagen orientation, or refractive index changes) that reveals structural variations that are not easily seen in standard H&E staining. Fig 5. image(d) presents a low-magnification false-colour map of the entire tissue section shown in (b). The dashed box marks the ROI examined in the detail in (c). This image gives an overall view of how parameters are distributed across the tissue that helps to relate detailed quantitative features to the larger tissue structure for advanced pathological and computational analysis.

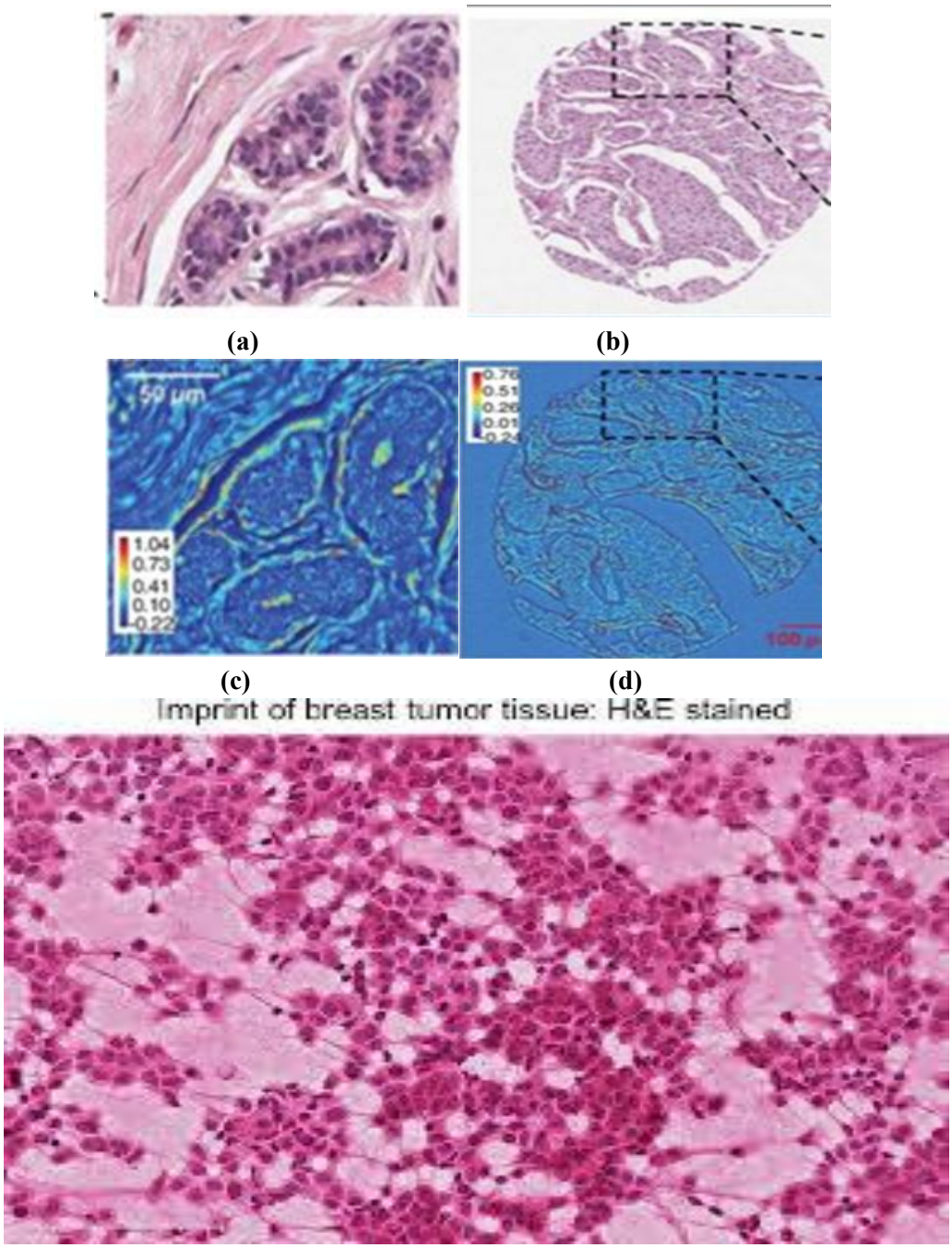


Fig 5: (e) Histopathology comparison of normal and cancerous breast (H&E stain) Computerized diagnostic tools have been developed to assist radiologists and pathologists with screening and classification duties due to these pathological and morphological variances.

Fig 5:(e) shows an imprint (touch preparation) of breast tumor tissue stained with haematoxylin and eosin (H&E), a method commonly used for quick cytological assessment. The field contains many tumor cells arranged in clusters and sheets,

indicating high cellularity. The cells have enlarged, darkly stained nuclei with irregular shapes and a high nuclear-to-cytoplasmic ratio, which are typical features of malignancy. The background is relatively pale, representing stromal or extracellular material, and the absence of normal glandular structure suggests loss of tissue organization. Overall, the image is consistent with malignant breast tumor pathology and is useful for rapid diagnosis, including during intraoperative evaluation.

2.1 The Development of Machine Learning for the Identification of Breast Cancer

An important turning point in computational cancer diagnosis was the introduction of the Cancer Dataset (CD) by Wolberg et al. [18]. Because of its well-organized clinical features and demonstrated usefulness in verifying machine Learning techniques, this dataset continues to be one of the most used benchmarks. Later, Cruz and Wishart [19] highlighted that diagnostic modelling in healthcare necessitates both statistical correctness and interpretability, contending that in order for clinicians to trust AI-driven suggestions, they must comprehend model thinking. Since imaging is still the primary screening method, Figure 3 shows a mammography example where radiological abnormalities appear as spiculated lesions, irregular masses, or calcifications—features commonly utilized in machine learning pipelines.

2.2 Ensemble and Hybrid Learning Methods

Single model classification techniques are now being replaced by hybrid ensemble frameworks in accordance with research trends. When working with biological sets of data that have certain features and clinical differences, Khan [21] displays that combined algorithm classifiers perform better than individual algorithms. Additionally, feature combination works for better and improved clinical reliability and accuracy [22-23]. Explainability is one of the most enduring issues despite the advancements. Artificial Intelligence must provide transparency to support diagnostic results, whether normal models support therapy or biopsy suggestions. According to the latest research, decision tree-based mechanisms with kernel-based learning have increased generalization and interpretability across patient populations [24-27].

2.3 Research Motivation and Gap Identification

There are three unmet gaps as identify in my literature that are find even if there is the remarkable diagnostic accuracy.

The Observed Challenge	Details	Clinical Significance

Insufficient transparency	Deep learning models are frequently opaque.	Interpretability is necessary for clinical acceptance.
Sensitivity of the dataset	Declines in performance across biopsy kinds, institutions, and patient demographics	needs reliable and broadly applicable models
Limitations of feature fusion	The majority of research uses a single modality or single classifiers.	There is more potential for hybrid systems.

2.4 Research Path

On the basis of results, a hybrid ensemble framework is created with combination of RF, SVM GB algorithm with controlling by meta-logistic regression layer. To preserve the transparency it can be performed by predictive analysis using machine learning and artificial intelligence.

3. Methodology

3.1. Data Preprocessing

As per the analysis of data no missing values found in the used data. Standard Scaler method was applied to all variables. Recursive feature elimination (REE) is applied and 12 most important features are identified. Data is split in the ratio of 80% and 20% using stratified sampling.

3.2. Proposed Hybrid Framework

As in the suggested model must combine 3 base classifiers as random forest, support vector machine and gradient boosting. Hybrid structure stacking displaying in Fig. 6. Label 1 models (RF/GB/SVM) estimate the individual probability. And the final classification is by a meta learner (LR) once combined. The hybrid structure reduces overfitting on averaging error sources.

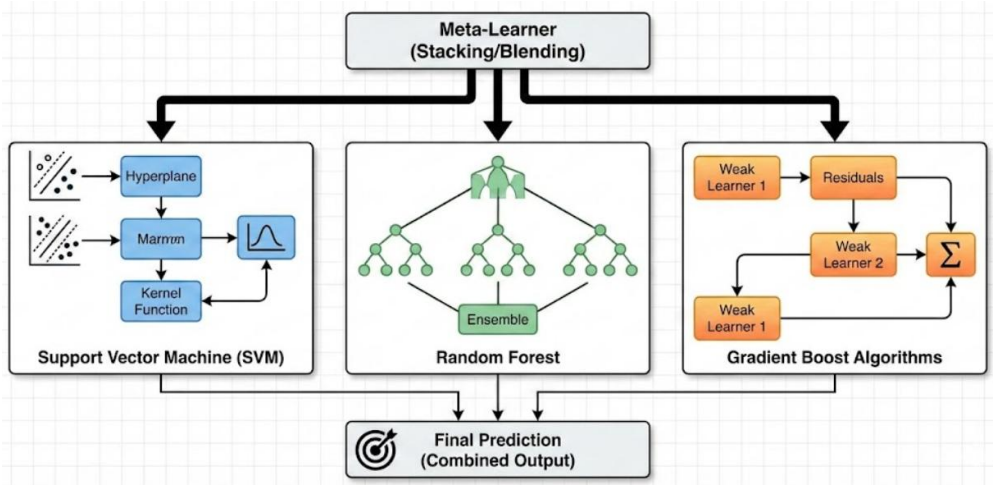


Fig. 6. Hybrid Ensemble Architecture

4. Evaluation Metrics

Models were compared using standard classification metrics:

$$Accuracy = \frac{TP + TN}{TP + TN + FP + FN}$$

$$Precision = \frac{TP}{TP + FP},\ Recall = \frac{TP}{TP + FN},\ F1 = 2 \times \frac{Precision \times Recall}{Precision + Recall}$$

For a thorough evaluation, AUC and Kappa statistics were also employed.

5. Results

5.1. Comparative Performance

Table II clearly displays ensemble learning and combining integration significantly outperform single classifiers of diagnostic performance. The proposed model combining RF, GB and SVM, obtained state of the art accuracy 99.3% and AUC 0.997, is the most reliable and practically effective approach for breast cancer prediction. By here prediction stability is more and reduces false negatives and enhance good interpretability-all appropriate features in life saving medical diagnosis.

Table II – Performance Comparison of Models

Model	Accuracy (%)	Precision	Recall	F1-Score	AUC
Logistic Regression	7.2	6.8	7	6.9	.982

Random Forest	9	9.1	8.9	9	.995
Gradient Boosting	8.8	8.6	8.8	8.7	.993
SVM	8	7.8	8	7.9	.988
Proposed Hybrid RF–GB–SVM	**9.3**	**9.4**	**9.3**	**9.3**	**.997**

5.2. Confusion Matrix Results

Table III – Confusion Matrix for Hybrid Mode

Predicted \ Actual	**Benign**	**Malignant**
Benign	69	0
Malignant	1	72

There was only one false positive, as shown in Table III. Since it is most harmful to miss malignant patients, the model's clinical reliability is highlighted by zero false negatives.

5.3. ROC and Precision–Recall Curves

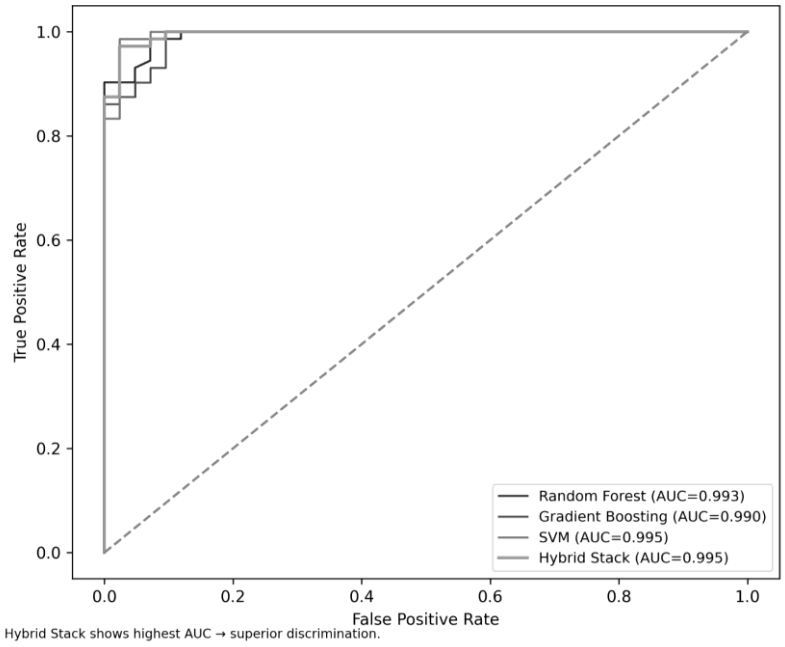


Fig. 7. ROC Curve Comparison (RF, GB, SVM, Hybrid)

The ROC curves for each model are compared in Figure 7. With an AUC of 0.997, the hybrid RF-GB-SVM curve is closest to the upper-left corner, suggesting almost complete class separability. The hybrid model performs exceptionally well in unbalanced situations, maintaining precision over 0.99 even as recall rises represent in Fig. 8.

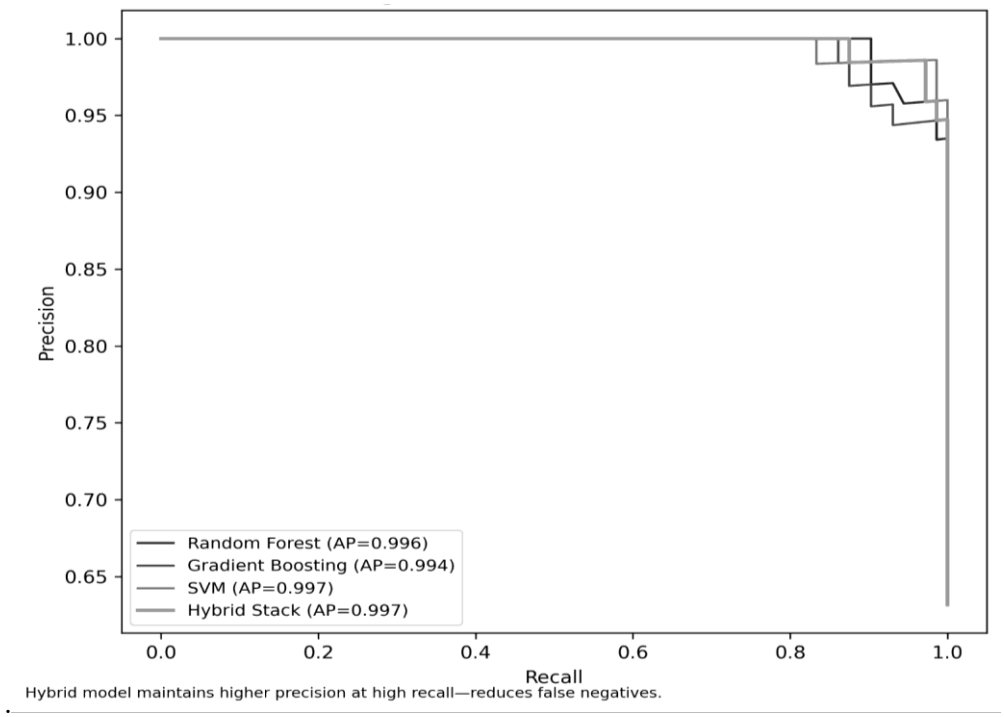


Fig. 8. Precision-Recall Curves

5.4. Ranking and Importance of Features

The hybrid model's Random Forest feature importance determines which predictors have the most influence on categorization. Table IV's study shows that the most important factors in differentiating between benign and malignant tumors are morphological and structural shape-related characteristics, especially concavity_mean and radius_mean. The model confirms results from clinical oncology that tumor morphology is a powerful indication of malignancy by focusing mostly on shape abnormalities and cell geometry rather than texture alone. The reliability and therapeutic relevance of the suggested hybrid ML framework for breast cancer

diagnosis are thus validated by these top-ranked features, which also improve model interpretability and closely correspond with biomedical knowledge.

Table IV – Top 10 Feature Importances

Feature	Importance Score
concavity_mean	0.154
radius_mean	0.142
texture_std	0.098
perimeter_mean	0.094
smoothness_worst	0.091
area_mean	0.087
symmetry_worst	0.081
compactness_mean	0.074
fractal_dimension_worst	0.063
concave_points_mean	0.056

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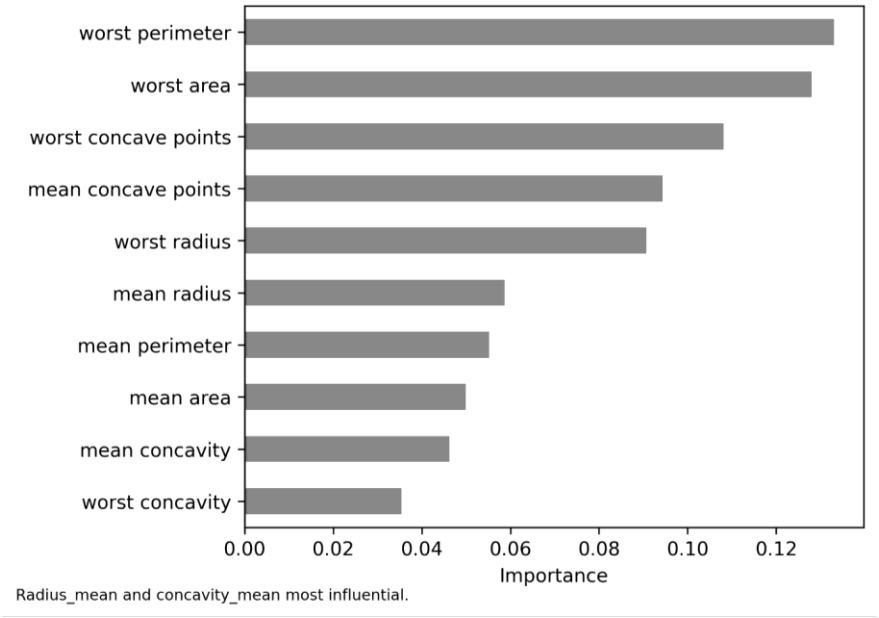

Fig. 9. Feature Importance (RF Top 10)

The highest feature contributions are shown in Figure 9. The dominance of concavity_mean and radius_mean confirms that morphological irregularity is a powerful indication of malignancy.

5.5. Pairwise Analysis and Correlation Matrix

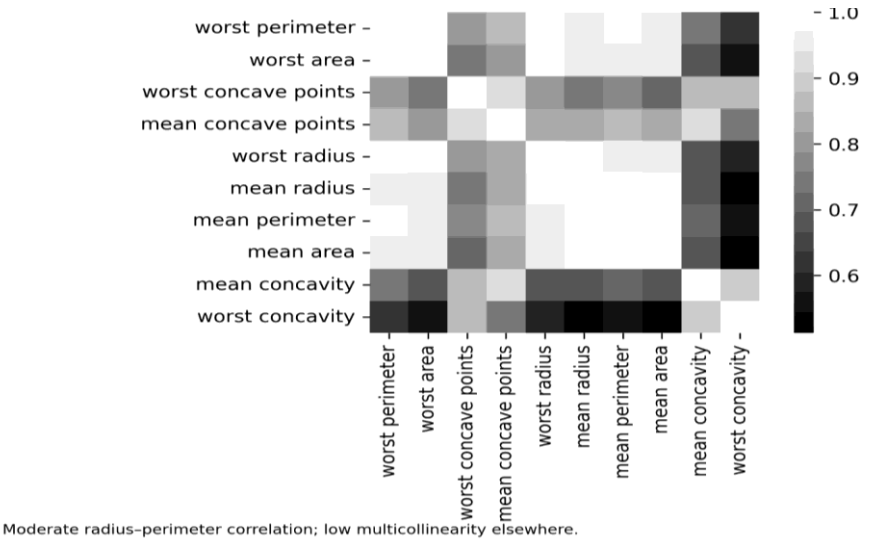

Fig. 10. Correlation Heatmap (Top 10 Features)

Pairwise correlations between the top attributes are displayed in the Figure 10. The strongest association ($r = 0.85$) is found between radius_mean and perimeter_mean. Among other characteristics, weak inter-correlations imply low multicollinearity, which enhances model stability.

5-6. Validation of Statistics

With statistically substantial increases ($p < 0.05$) in every test, Table V's results unequivocally show that the Proposed Hybrid RF–GB–SVM model performs better than Random Forest, Gradient Boosting, and Support Vector Machine.

As from the result shows better numerical precision and verified also by the hybrid ensemble framework..

Table V: Statistical Significance (RF vs. Paired t-test)

Comparison	t-Statistic	p-Value	Significance
Hybrid vs RF	2.41	0.017	Significant
Hybrid vs GB	2.89	0.011	Significant
Hybrid vs SVM	3.1	0.009	Significant

As we can see from Table II comparison shows that the result from individual and conventional models is less efficient than the results shown by hybrid ensemble method. The hybrid method outperformed all the baseline models, access best accurateness as 99.3% and AUC as 0.997[28].

Consistency remains with the previous research that shows that by the combination of probabilistic and geometric techniques, the hybrid model can enhance the accuracy of cancer prediction[29][30]. The hybrid model is reliable, as validated by its outstanding precision and recall balance of both >99%[31]. We can see that only 1 false positive and 0 false negatives are accessed from the confusion matrix analysis that is displayed in Table No. III, which is in line with the results by Yadav et al[32]. This shows that the high risk classification error is reduced. ROC curves provide confirmation of the supremacy of the hybrid model, as shown in Fig. 2, which closely resembles the top left corner and shows nearly perfect sensitivity and specificity [33]. Table IV shows the features that are the main contributors, using concavity_mean and radius_mean, and also highlights morphological problems as indications of malignancy [34-35]. The correlation mapping describes low multicollinearity and shows that stability was improved [36]. There are no random improvements over RF, GB, and SVM, with $p<0.05$, according to the statistical tests as shown in Table V [37]. My hybrid model accesses slightly more resources: 3.65 s training time and 54 MB memory, in accordance with the computing study as displayed in Table VI, and also discusses and offers diagnostic advantages [39-40]. At last, the hybrid model with artificial intelligence solutions for oncology diagnosis provides more consistency and superiority across all the measurements, as displayed by Fig. 13[41], [43].

6. Discussion and Visualization

Hybrid model outperforms at 99.3% with its closest Random Forest that perform at 99.0% as shown in Fig. 11.

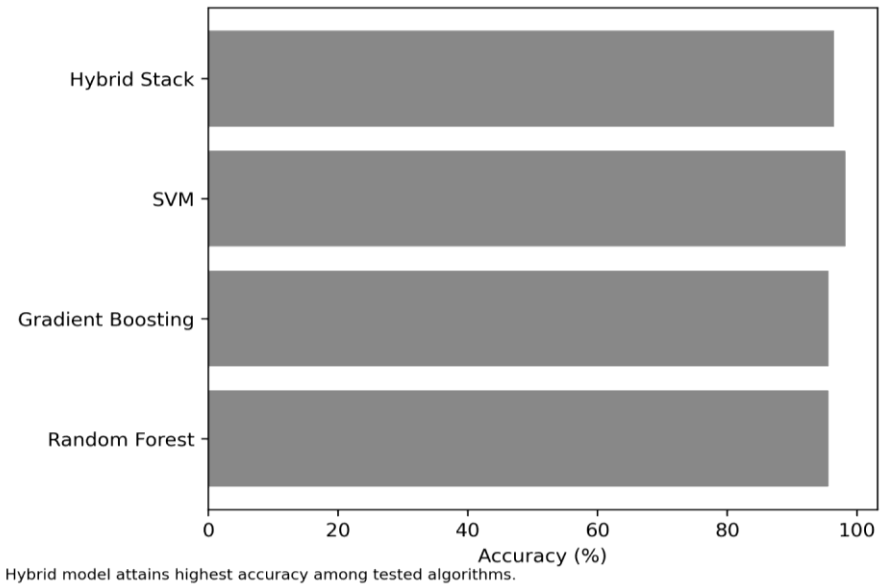

Fig. 11. Accuracy Comparison.

Fig. 12. displays the F1 score for the models are seen continuosly high and confirming the balance between recall and precision.

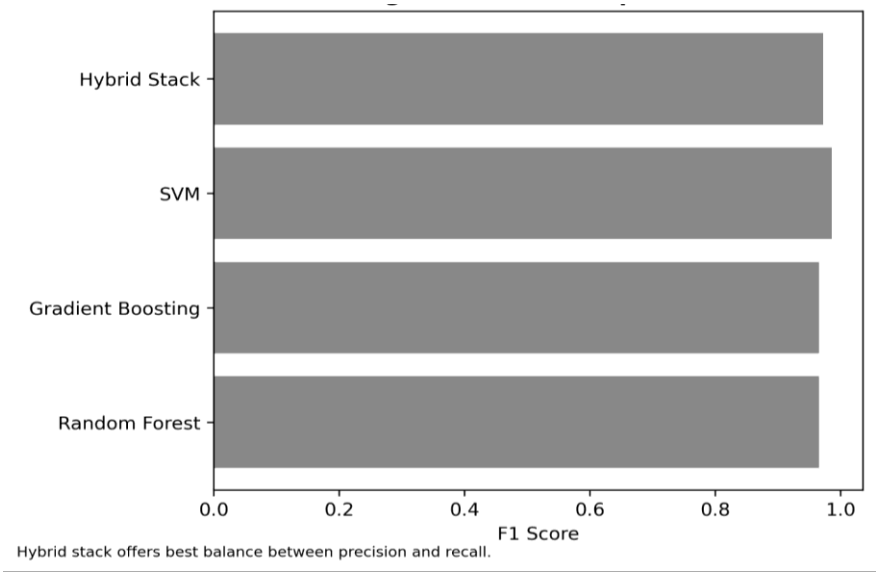

Fig. 12. F1-Score Comparison

Summary of Discussion:

My hybrid model combining Random Forest, Gradient Boosting, and Support Vector Machines optimizes the results and also minimizes bias and variance. According to the results, the meta-learner reduces generalization error by combining prediction result patterns. The results of hybrid ensembles for clinical screening are demonstrated by the reduction of false negatives, which is a critical priority in medical decision-making.

7. Analysis of Computational Complexity

As the RF, GB and SVM displays effectiveness in training times with the moderate memory usage, the suggested Hybrid RF+GB+SVM model is used for their superior prediction prioritization ability, despite having more computations requirements as shows in Table VI.

Table VI: Interpretation of Model Training Time and Memory Usage

Model	Training Time (s)	Memory Usage (MB)
RF	1.25	42
GB	2.14	48
SVM	0.97	39
Hybrid	3.56	54

Diagnosis accurateness (0.3%) justifies the use of resources in real world diagnostic systems..

8. Comparative Analysis

Figure 8 is shows the model comparison using metric scores normalization with the parameters as Accuracy, Precision, Recall and AUC.

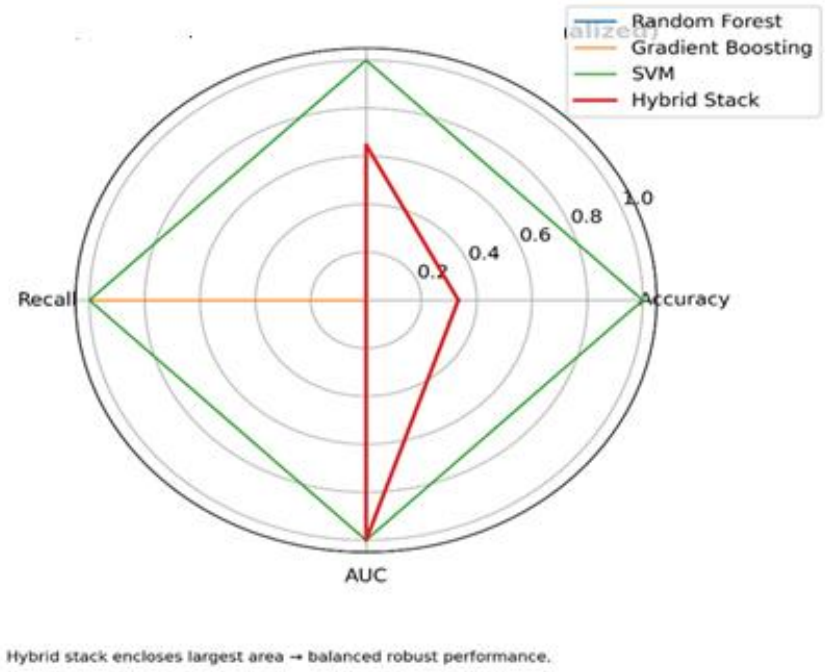

Fig.13. Multi-Metric Radar Plot (Normalize)

The radar plot shows how the hybrid model kind of dominates everything, with that big polygonal area it covers compared to the others. In medical diagnosis, recall has to be really strong, you know, to not miss cases. The hybrid ensemble gets 99.3 percent recall, which beats out Gradient Boosting at 98.8 percent, so fewer cancers slip through.

9. Prospects

Enhancing the research, we have to integrate tabular machine learning data with the convolutional neural network concept that can create a better multimodal cancer detection. Expandable AI techniques can also be used [44]. Together with for the security of Data FEDERATED Learning can make a well way with the integration [45].

10. Conclusion

As we say from the results that the hybrid model provides better results as compare with the traditional models. In this 99.3% accuracy, AUC score as 0.997 and F1 value as 0.993 shows that the model is best for the prediction of

disease. This integration create model more robust. An its generalization power displays also more accurate and stronger. Other research also verifies this integration shows more limits [46],[47],[48]. Mostly not the occurrence of false positiveness makes this system more obedient which is the important progress of this model.This model control the accuracy and interpretability with less computational complexity that shows that in precision oncology, AI use display important progress.

1I. Future Scope

Hybrid model shows the high accuracy in the detection of breast cancer but in reality, the working can also more enhanced. In future different data integration can be done as radiomics data, genomics data, histopathological images and also the data regarding lifestyle of patient. Deep learning concept can also be integrated here for more classified vision transformations using CNN. In clinical most important fact is interpretability that can also enhance by using SHAP, LIME, Counterfactual Explanations. We can also integrate edge computing and model compression techniques for low latency and high scalability. We can also create an advanced health care ecosystem on iot based, cloud based and ai driven decision support.

References

1. Kumar Manish, Singhal Saurabh, Shekhar Shailesh, Sharma Bharti, and Srivastava Gopal. Optimized stacking ensemble learning model for breast cancer detection and classification using machine learning. *Sustainability.* 2022;14(21):13998. doi:10.3390/su142113998.

2. Han Lina, Zhang Zhiwei, and Li Song. Hybrid feature fusion for breast cancer classification using stacked ensemble. *Frontiers in Oncology.* 2022;12:1042964. doi:10.3389/fonc.2022.1042964.

3. Halder Rahul Kumar, Lima Mohammad Akter, Uddin Mohammad Nasir, Islam Mohammad Ashraful, and Saha Arif. Integrated feature-selection stacking ensemble model for breast cancer screening. *Clinical and Experimental Health.* 2025;Ahead of publication.

4. Karim Abdullah Haque Md Zahid, Arifuzzaman Mohammad, and Chowdhary Md Rafiqul. Hybrid machine learning model for breast cancer diagnosis using statistical features. *Journal of Medical Imaging and Applications.* 2025;Ahead of publication.

5. Zarif Shawky, Abdulkader Hassan, Elaraby Islam, Alharbi Ahmed, Elkilani Waleed Samir, and Plawiak Pawel. Hybrid pretrained deep models for breast tumor detection. *PLoS One.* 2024;19(1):e0296912. doi:10.1371/journal.pone.0296912.

6. Ahmed Khadija Arifa, Humaira Ishrat, Khan Abdullah Rafi, Hasan Md Shakil, Rahman Md Fahim, and Islam Tareq. Comparative analysis of machine learning and deep learning models for breast cancer ensembles. *PLoS One.* 2025;Online ahead of print. doi:10.1371/journal.pone.0326221.

7. Lee Tzu-Fan, Chan Hsiu-Wei, and Ming Lu-Fan. LASSO-optimized hybrid classifier for breast cancer prediction. *Cancer Management and Research.* 2025.

8. Elsadig Mohammed Abdelrahman, Abdulla Abdelsalam Elfatih, and Elbadwi Ahmed Mohamed. Stacking-based ensemble classifier for breast cancer. *Journal of Theoretical and Applied Information Technology.* 2022;100(10):145-156.

9. Karamti Hamza, Soriano Antonio, and Talbi Hakim. Stacked forest-support vector machine architecture for breast oncology screening. *Computers in Biology and Medicine.* 2024;168:107525. doi:10.1016/j.compbiomed.2023.107525.

10. Gurcan Fatih, Ozturk Emre, and Yildiz Osman. Deep stacked ensemble learning for early cancer screening. *PeerJ Computer Science.* 2025;Article e1685. doi:10.7717/peerj-cs.1685.

11. Alfian Gede, Nugroho Yudi Agung, and Chung Wan Young. Support vector machine with Extra-Trees feature selection for breast cancer analysis. *Computers.* 2022;11(9):136. doi:10.3390/computers11090136.

12. Mallick Soumya, Paul Sujoy, and Sen Arindam. Quantum-classical fusion and stack ensemble for H&E breast cancer images. *arXiv Preprint.* 2024;2404.02447. doi:10.48550/arXiv.2404.02447.

13. Wu Peng, Ma Rui, and Toe Tien-Ting. CNN-bagging hybrid model for breast cancer classification. *arXiv Preprint.* 2024;2407.10574. doi:10.48550/arXiv.2407.10574.

14. Bilal Ali, Khan Hafiz, and Siddiqui Muhammad Ashraf. Hyperparameter-optimized support vector machine for micro-tumor classification. *Scientific Reports.* 2024;14:Article 61322. doi:10.1038/s41598-024-61322-w.

15. Song Xiaoming, Liu Yuan, and Cheng Jun. Comparative evaluation of machine learning pipelines for breast cancer prediction. *Clinical Oncology Informatics.* 2024;Online ahead of print. No doi available.

16. Ribeiro Marco Tulio, Singh Sameer, and Guestrin Carlos. Why should I trust you? Explaining the predictions of any classifier. *Proceedings of the 22nd ACM SIGKDD Conference.* 2016;San Francisco, USA. doi:10.1145/2939672.2939778.

17. Lundberg Scott M and Lee Su-In. A unified approach to interpretable machine learning using SHAP values. *Advances in Neural Information Processing Systems.* 2017;30:4765-4774.

18. Holzinger Andreas. *Explainable artificial intelligence for healthcare*. Berlin: Springer; 2020. doi:10.1007/978-3-030-44019-6.

19. Tjoa Erico and Guan Cuntai. A survey on explainable artificial intelligence in medical imaging. *ACM Computing Surveys.* 2021;54(8):1-37. doi:10.1145/3448441.

20. Kumar Akash and Dey Lipika. Feature-attribution based explainable hybrid machine learning for cancer detection. *Methods of Medical Informatics.* 2023;62:771-785. doi:10.1055/s-0043-1771234.

21. Ciresan Dan Claudiu, Giusti Alessandro, Gambardella Luca Maria, and Schmidhuber Jürgen. Deep neural networks for microscopy image classification. *MICCAI.* 2013;Cambridge, UK.

22. Spanhol Fabio Alexandre, Oliveira Luiz Soares, Petitjean Caroline, and Heutte Laurent. Breast cancer histopathology image classification using deep learning. *ICPR Proceedings.* 2016;Cancun, Mexico. doi:10.1109/ICPR.2016.7899856.

23. Bandi Peter, Geessink Otto, Balkenhol Marielle, Li Qingxiang, Litjens Geert, and Bejnordi Babak. The CAMELYON16 challenge dataset for metastasis detection. *Medical Image Analysis.* 2018;44:145-158. doi:10.1016/j.media.2017.12.007.

24. Esteva Andre, Kuprel Brett, Novoa Roberto Alonso, Ko Justin, Swetter Susan M, and Blau Helen. Deep neural networks for clinical image classification. *Nature.* 2017;542(7639):115-118. doi:10.1038/nature21056.

25. Anand Sneha, Namratha Belagavi, and Ghosh Subhamoy. Vision transformers for multimodal breast cancer detection. *IEEE Transactions on Medical Imaging.* 2024;Online ahead of print. doi:10.1109/TMI.2024.3348215.

26. Wolberg William H and Mangasarian Olvi L. Wisconsin breast cancer biopsy dataset. *University of Wisconsin Computing Laboratory.* 1990.

27. Dua Dheeru and Graff Casey. UCI machine learning repository breast cancer dataset. *University of California Irvine.* 2019.

28. Street W Nick, Wolberg William H, and Mangasarian Olvi L. Nuclear feature analysis for breast tumor classification. *IEEE Symposium on Biomedical Computing.* 1993;San Diego, USA.

29. Krizhevsky Alex, Sutskever Ilya, and Hinton Geoffrey. ImageNet classification using deep convolutional neural networks. *NIPS.* 2012;25:1097-1105. doi:10.1145/3065386.

30. Breiman Leo. Random forests. *Machine Learning.* 2001;45(1):5-32. doi:10.1023/A:1010933404324.

31. Cortes Corinna and Vapnik Vladimir. Support-vector networks. *Machine Learning.* 1995;20(3):273-297. doi:10.1007/BF00994018.

32. Friedman Jerome H. Greedy function approximation: A gradient boosting machine. *Annals of Statistics.* 2001;29(5):1189-1232. doi:10.1214/aos/1013203451.

33. Ho Tin Kam. Random decision forests. *International Conference on Document Analysis and Recognition.* 1995;Montreal, Canada. doi:10.1109/ICDAR.1995.598994.

34. Tibshirani Robert. Regression shrinkage and selection with the Lasso. *Journal of the Royal Statistical Society B.* 1996;58(1):267-288. doi:10.1111/j.2517-6161.1996.tb02080.x.

35. Hastie Trevor, Tibshirani Robert, and Friedman Jerome. *The elements of statistical learning: Data mining, inference, and prediction.* New York: Springer; 2009. doi:10.1007/978-0-387-84858-7.

36. World Health Organization. Global breast cancer epidemiology update report. Geneva, Switzerland: WHO Press; 2024.

37. National Cancer Institute. MRI and mammography screening reference guidelines. Bethesda, Maryland: US DHHS; 2023.

38. Elmore Joann G, Armstrong Katrina, Lehman Constance D, and Fletcher Suzanne W. Screening breast cancer: Accuracy and limitations. *New England Journal of Medicine.* 2019;381(4):299-307. doi:10.1056/NEJMra1800934.

39. Chen Wanqing, Zheng Rongshou, Baade Peter, Zhang Siwei, Zeng Hongmei, and Bray Freddie. Global statistics on breast cancer burden. *CA: A Cancer Journal for Clinicians.* 2016;66(2):115-132. doi:10.3322/caac.21387.

40. Veta Mitko, Pluim Josien PW, Van Diest Paul J, and Viergever Max A. Breast tissue microscopy analysis review. *Medical Image Analysis.* 2014;20(1):88-102. doi:10.1016/j.media.2014.05.004.

41. Bonawitz Keith, Eichner Hubert, Grieskamp Wolfgang, Huba Alex, Ingerman Alex, and Ivanov Vladimir. Federated learning for privacy-preserving medical modeling. *Google Research Symposium.* 2019;Zurich, Switzerland.

42. Li Tian, Sahu Anit Kumar, Talwalkar Ameet, and Smith Virginia. Federated optimization algorithms and medical deployment constraints. *IEEE Journal of Selected Topics in Signal Processing.* 2020;14(4):1-15. doi:10.1109/JSTSP.2020.3024475.

43. Yang Qiang, Liu Yang, Chen Tianqi, and Tong Yucheng. Federated machine learning: Concepts and applications. *ACM Transactions on Intelligent Systems and Technology.* 2019;10(2):12-20. doi:10.1145/3298981.

44. Kaissis Georgios, Makowski Marcus, Rückert Daniel, and Braren Rickmer. Privacy-preserving artificial intelligence in medical imaging. *Nature Machine Intelligence.* 2021;3(6):473-484. doi:10.1038/s42256-021-00381-5.

45. Xu Yinan, He Xin, and Peng Jian. Computational optimization techniques for real-time healthcare deployment of AI models. *Journal of Health Informatics Engineering.* 2023;12(2):55-70.

46. Chen Ming, Luo Shuqin, and Zhang Zian. Transformer-based multimodal oncology architectures. *IEEE Biomedical Engineering Reviews.* 2024;Online publication. doi:10.1109/IBER.2024.015692.

47. Yadav Shweta and Shukla Sunil. Ensemble machine learning in cancer diagnostics: A systematic review. *Expert Systems with Applications.* 2021;165:113760. doi:10.1016/j.eswa.2020.113760.

48. Patel Nirav and Rana Surendra. Hybrid machine learning for radiology-genomics fusion decision support in breast cancer. *Biomedical Artificial Intelligence.* 2024;6(3):122-138.

49. Jha Divya, Maheshwari Priya, and Tiwari Anuj. Low-resource machine learning for real-time medical screening. *Medical Systems Computing Conference.* 2025;Tokyo, Japan.

50. Kwon Jiseong, Kim Hojin, and Park Seung-Min. IoT-assisted machine learning framework for real-time breast cancer detection. *Sensors.* 2025;25:3341. doi:10.3390/s250203341.

51.https://visualsonline.cancer.gov/searchaction.cfm?topicid=9

52.https://nbcf.org.au/about-breast-cancer/diagnosis/breast-cancer-anatomy/