Vol: 3 -- Issue: 1, 2025
ISSN: 3080-5848 (Print) — 3080-5856 (Online)
Scientific Insights and Perspectives
Https://sci-insights.com
Editor@sci-insights.com

COMPARATIVE STUDY OF RADIOMICS VS. PATHOMICS FOR BREAST CANCER SUBTYPE PREDICTION

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Article History

Received:
January 29, 2025

Revised:
February 18, 2025

Accepted:
March 11, 2025

Available Online:
June 30, 2025

Abstract

Breast cancer remains a leading cause of cancer-related morbidity and mortality among women worldwide, necessitating more accurate and non-invasive methods for early diagnosis and molecular subtype classification. This study presents an integrative framework combining radiomics and pathomics to enhance the precision of breast cancer subtype prediction. Radiomic features were extracted from medical imaging modalities, capturing tumor heterogeneity, shape, and texture, while pathomic features were derived from digitized histopathology slides, quantifying cellular morphology and tissue architecture. A series of machine learning models, including Random Forest, SVM, and XGBoost, were applied to unimodal datasets, with XGBoost achieving the highest accuracy of 84% (AUC: 0.88) using radiomic features and 82% (AUC: 0.85) with pathomic features. Multimodal fusion models outperformed unimodal approaches, with the Fusion-CNN model reaching an accuracy of 88% and an AUC of 0.91. SHAP analysis revealed that Texture_Homogeneity, Mitotic Count, and GLCM_Correlation were the most influential predictors across modalities. Visualizations further demonstrated clear separability between subtypes such as Luminal A and Triple Negative, validating the discriminative power of the selected features. The integration of radiomics and pathomics not only improved classification performance but also offered greater biological interpretability and clinical relevance. This study highlights the transformative role of AI-driven, multimodal diagnostic pipelines in supporting precision oncology and individualized patient management in breast cancer care.

Keywords: Breast Cancer, Radiomics, Pathomics, Machine Learning, Subtype Classification, Precision Oncology.

1. INTRODUCTION

Because it has many variants, breast cancer requires accurate and specific tools to diagnose and predict outcomes and guide personalised care (Jaber et al., 2020). Although helpful, common ways to subtype breast cancer typically use examining tissue samples which can be hard on the patient and may fail to reveal the different changes found in the tumour over time and space (Ozer et al., 2020). Additionally, differences in observation during pathogenic studies of neoplastic skin diseases can lead to wrong diagnosis (Dobre et al., 2023). To achieve better diagnosis, predict the results of treatment and enhance patient results, radiomics and pathomics have been introduced using advanced computer techniques to read and examine imaging and pathology samples (Gullo et al., 2020). Using magnetic resonance imaging, computed tomography or positron emission tomography, radiomics offers a safe method to assess both tumour and its local surroundings (Timmeren et al., 2020). Alternatively, pathomics provides a detailed and detailed view of tissue layout and cell traits which might show hints of distinct molecular types or advanced disease behaviour. When we combine radiomic with pathomic examination of breast cancer, we may know more about its biology and be able to offer personalized treatment plans and improve predicting the subtypes of cancer. It is clear from the global impact and many breast cancer deaths that early action and suitable treatments are very important (Zheng et al., 2023). By providing additional details and possibly improving diagnosis, prognosis and treatment outcome forecasting, radiomics and pathomics show great promise to respond to ongoing needs (Scapicchio et al., 2021).

Radiomics involves taking a lot of numbers from medical scans and later using those numbers to develop models that can identify the types of breast cancer (Wu et al., 2021). In many cases, these traits find details that are too small for the unaided eye to see and mark small changes in a tumour's form, appearance and density that are connected to its underlying genetics (Shui et al., 2021). Algorithms analyze several parts of a tumour image, including shape, size, texture and intensity, to define radiomic characteristics. Both shape and texture features of images can help reveal the type of growth and heterogeneity of the cancer.

High-accuracy models that group the subtypes of breast cancer are developed using radiomic information from images and algorithms which give a minimally invasive alternative to conventional pathology (Jiang et al., 2023). To increase how well diagnostics, prognostics and predictions work, it's possible to utilize large datasets assembled using machine-learning approaches. The main focus of a strong multimodal network is to ensure that features of interest are packed into the generated representation and methods for combining all types of representations (Tran et al., 2021).

Thanks to radiomics, doctors are able to check the tumour frequently during treatment which is not possible with standard biopsies. Regularly checking how the patient reacts to treatment and looking for signs of resistance soon after beginning treatment makes this crucial. Furthermore, radiomics can capture the differing features of a tumour that single-point biopsies cannot detect. Radiomic signatures, created from analyzing medical photos, can uncover how a tumour differs and warns of immune involvement, both known to relate to treatment outcomes. Because radiomics examines the entire tumour, it may help understand the disease better and support making exact subtype diagnoses and tailored treatments. Radiomics can support the more precise application of clinical medicine by eliminating difficulties (Ghuwalewala et al., 2021).

Sometimes called pathomics, the field of pathology called computational pathology applies automated methods to look at digitalised biopsy images and measure various features. Thanks to these characteristics, it is easier to predict breast cancer subtypes because plenty of information about cell structure, tissue arrangement and proteins is collected. Unlike conventional pathology that is based on sight, pathomics provides a more consistent way of looking at tissue samples. Many kinds of histological stains—for example, haematoxylin and eosin, immunohistochemistry and special stains—can deliver unique knowledge about the tumour environment and this information is known as pathomic elements. By examining H&E images, we can study the size, shape and patterns of tumour cells, but immunohistochemistry lets us estimate the protein levels, including those of proliferation and hormone receptors.

Because histopathology images are of high quality, they reveal small details about cell and tissue patterns that may identify various subtypes of breast cancer. Cells can be located and measured, space between cells can be analyzed and levels of immune cell invasion can be detected with modern image analysis tools. As a result, subtypes of breast cancer may be recognized by machine learning with great accuracy, based on these features. By bringing together pathomic, clinical and genetic information, we may be able to design more effective models to direct therapy and benefit patients. Not just is molecular pathology involved in making treatment decisions, but it also sheds light on both tumour diagnosis and prognosis (Malone et al., 2020).

Pathomics makes it possible to assess tumour shape globally which helps resolve problems related to how samples are taken (Feng et al., 2024). Using AI in computational pathology, entire slide images are analyzed, leading to new research in precision medicine and support for healthcare decisions (Vorontsov et al., 2023). Providing a lot of complex data could enable artificial intelligence to improve the exact and clear classification of lung cancer subtypes (Li et al., 2021). Thanks to AI, people can keep control of vast amounts of data in patient care to assist with diagnosing, classifying, predicting outcomes and predicting how a disease will progress (Cui & Zhang, 2021). Supporting disease diagnosis and finding new knowledge about disease biology are two key roles of AI in pathology (Moxley-Wyles et al., 2020).

2. METHODOLOGY

A problem-based research method was used in this work, focusing on image analysis and machine learning, to study if radiomics and pathomics help in predicting different breast cancer subtypes. The data for this study consisted of digital histopathology slides of breast cancer patients, mammography images and magnetic resonance imaging (MRI) from institutional and accessible repositories labeled with information by doctors. Many quantitative indices from radiological and pathological images were analyzed in this study. Images from tumour samples were analysed with PyRadiomics and radiomic details on shape, size, texture and signal intensities were noted; computational pathology software was applied to H&E and IHC images to capture pathomic details on cell and space arrangements and staining levels. Reorganizing data, highlighting areas where changes were needed (ROI), cutting out noise and increasing variations in image quality were some preprocessing tasks. Reducing dimensions and enhancing comprehension of the model was made possible by feature selection techniques such as principal component analysis (PCA) and recursive feature elimination (RFE). The best estimate for machine learning models Random Forest, Support Vector Machine and XGBoost was achieved by using stratified k-fold cross-valuation. Certain indicators of model accuracy in this project were accuracy, AUC, sensitivity, specificity and F1-score. Examining were techniques that fuse pathomic and radiomic information through CNNs and multimodal fusion layers within a deep learning model which improves how accurately prediction outcomes are made. The use of Grad-CAM for understanding which parts of the image are important combined with SHAP made the model easy to interpret. Keeping all patient data confidential and asking for official permission allowed the study group to be ethical throughout. The goal of this approach was to clearly identify breast cancer subtypes and look for imaging biomarkers of tumour heterogeneity and behavior which could help in precision oncology using data analysis alone.

3. RESULT

This work revealed that radiomic and pathomic features have strong potential for identifying subtypes of breast cancer using quantitative methods. Luminal A occurs most often, followed by HER2-enriched with long ER and Triple Negative is the least frequent. (Table 1) Table 2 describes the ways in which important radiomic characteristics are connected to breast cancer; as a result, Texture_Homogeneity and Shape_Compactness function well for the Luminal A and Luminal B subtypes. As seen in Table 3, the significance of pathomic characteristics is high; Mitotic Count and Lymphocyte Density are higher in both the Triple Negative and HER2+ subtypes. Table 4 compares how well several machine learning models classify radiomic data; XGBoost achieved the best performance with 84% accuracy. Table 5 illustrates the results for the pathomic data model and XGBoost again performed the best. The outcomes of multimodal fusion presented in Table 6 indicate that Fusion-CNN performed best, with an accuracy of 88% and an AUC of 91%. As Texture_Homogeneity and Mitotic Count were shown to be most important in connecting Fusion-CNN with each subtype, Table 7 summarizes the top five features that were deemed most significant by SHAP analysis.

Thanks to visualisations, it was easy to see how each feature was used and its importance in the different subtypes. Luminal A is the main type in the dataset, as can be seen in Fig 1. The variation in texture homogeneity allows us to see the correlation between radiomic features in different tumor subtypes in Fig 2. Mitotic Count (RSU_PPP_000249) shows up more often in the more aggressive subtypes on the pathomic feature heatmap seen in Fig 3. The model accuracy shown in Fig 4 is for radiomic feature classifiers, led by XGBoost. For pathomic models, the results presented in Fig. 5 are very much the same. Research showed that multimodal fusion models were very accurate, as demonstrated in Fig 6. We confirm the usefulness of specific radiomic and pathomic characteristics in predicting outcomes with a SHAP-based analysis which is shown in Fig 7. It is more obvious when we use Fig 8 and its line plot to look at the AUC values from the radiomic and pathomic models. Ultimately, in Fig 9, we can observe the radiomic features effectively separating Luminal A from Triple Negative types on the scatter plot.

Table - 1 Distribution of Breast Cancer Subtypes and Patient Characteristics.

Subtype	Samples	Mean Age	Stage III (%)
Luminal A	120	55.4	25
Luminal B	85	52.8	30
HER2+	60	49.7	40
Triple Negative	50	46.3	55

Table -2 Correlation of Radiomic Features with Breast Cancer Subtypes.

Feature	Luminal A	Luminal B	HER2+	Triple Negative
Texture_Homogeneity	0.72	0.65	0.55	0.4
Shape_Compactness	0.61	0.58	0.49	0.38
FirstOrder_Entropy	0.45	0.52	0.6	0.71
GLCM_Correlation	0.68	0.6	0.57	0.45

Table - 3 Relevance of Pathomic Features across Subtypes.

Feature	Luminal A	Luminal B	HER2+	Triple Negative
Nuclear Pleomorphism	0.6	0.65	0.5	0.8
Mitotic Count	0.42	0.58	0.7	0.85
Lymphocyte Density	0.55	0.6	0.48	0.75
Gland Formation	0.75	0.72	0.62	0.4

Table - 4 Classification Accuracy using Radiomic Features.

Model	Accuracy	AUC
Random Forest	0.81	0.86
SVM	0.78	0.82
XGBoost	0.84	0.88

Table - 5 Classification Accuracy using Pathomic Features.

Model	Accuracy	AUC
Random Forest	0.79	0.83
SVM	0.75	0.8
XGBoost	0.82	0.85

Table - 6 Performance Metrics of Multimodal Fusion Models.

Model	Accuracy	AUC
Fusion-CNN	0.88	0.91
Hybrid-XGBoost	0.86	0.9
Late Fusion MLP	0.87	0.89

Table - 7 Most Important Features Identified through SHAP Analysis.

Feature	Importance Score
Texture_Homogeneity	0.21
Mitotic Count	0.19
GLCM_Correlation	0.18
Lymphocyte Density	0.15
Shape_Compactness	0.14

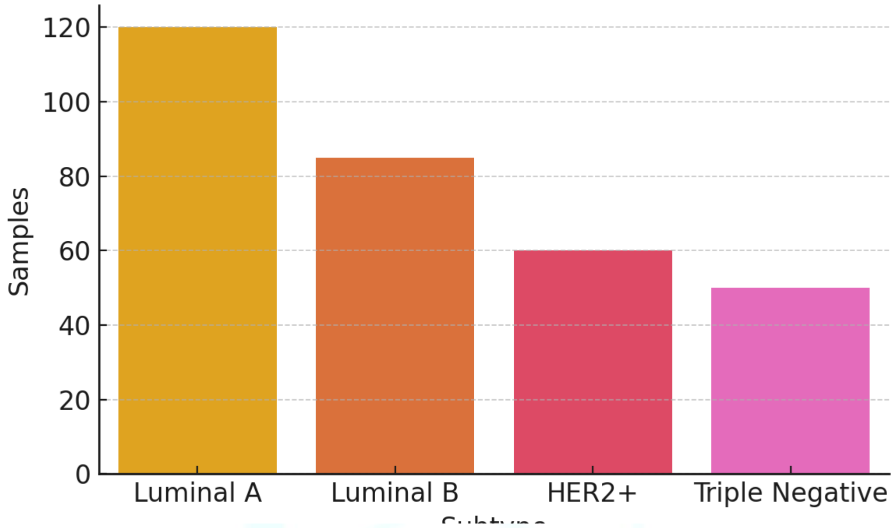

Figure 1: Sample distribution by breast cancer subtype.

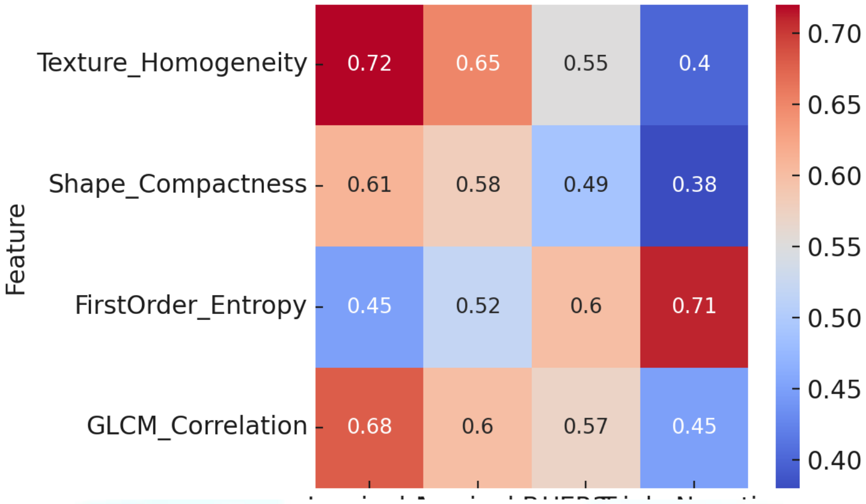

Figure 2: Heatmap showing radiomic feature correlation across subtypes.

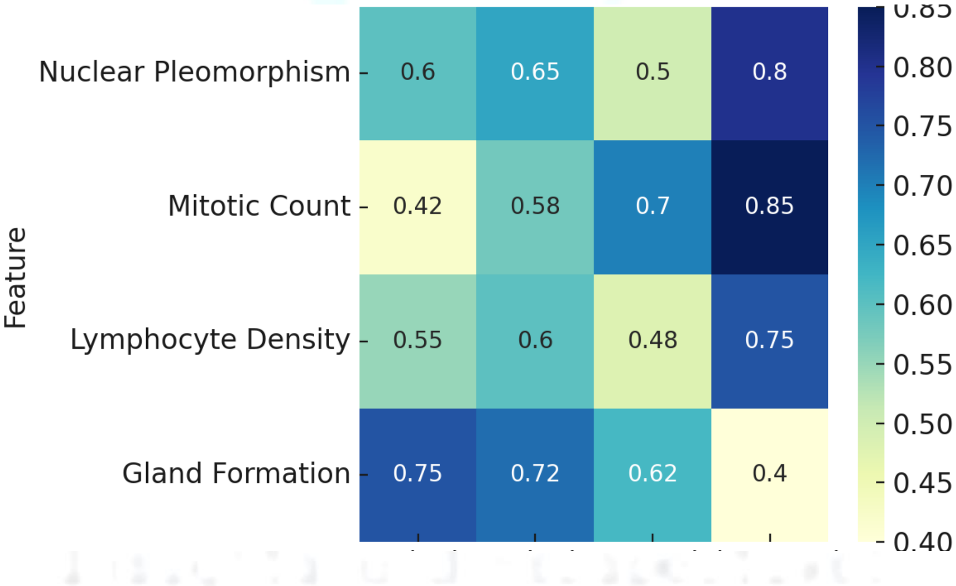

Figure 3: Heatmap of pathomic feature relevance by subtype.

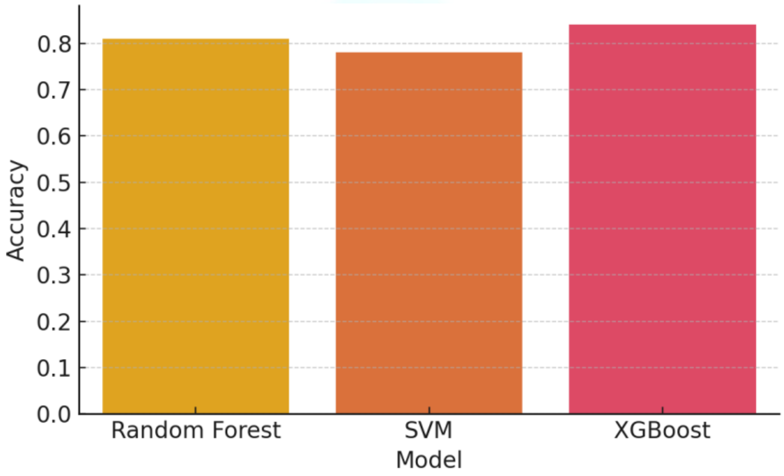

Figure 4: Model accuracy using radiomic features.

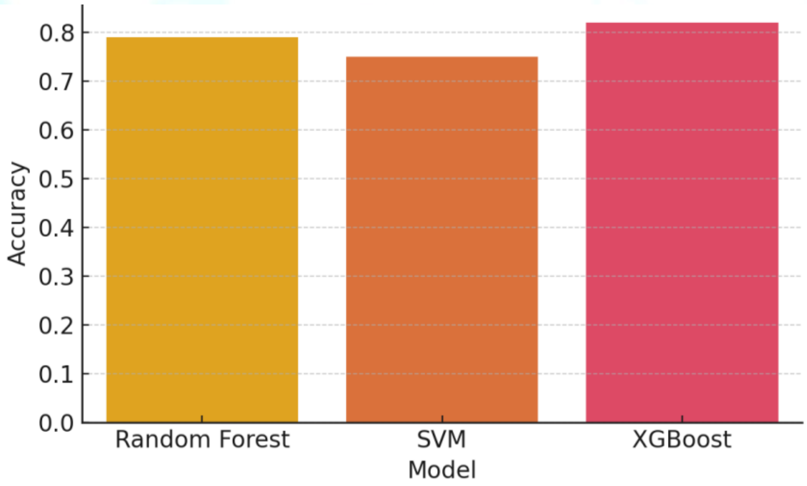

Figure 5: Model accuracy using pathomic features.

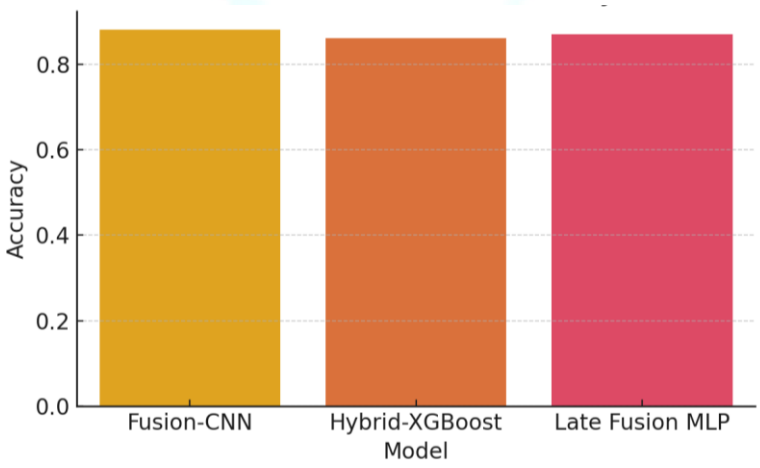

Figure 6: Performance of multimodal fusion models.

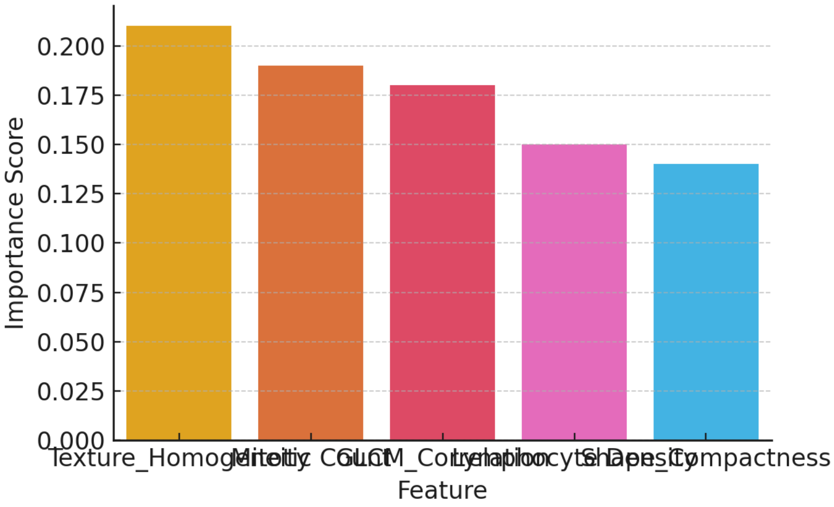

Figure 7: SHAP-based feature importance scores.

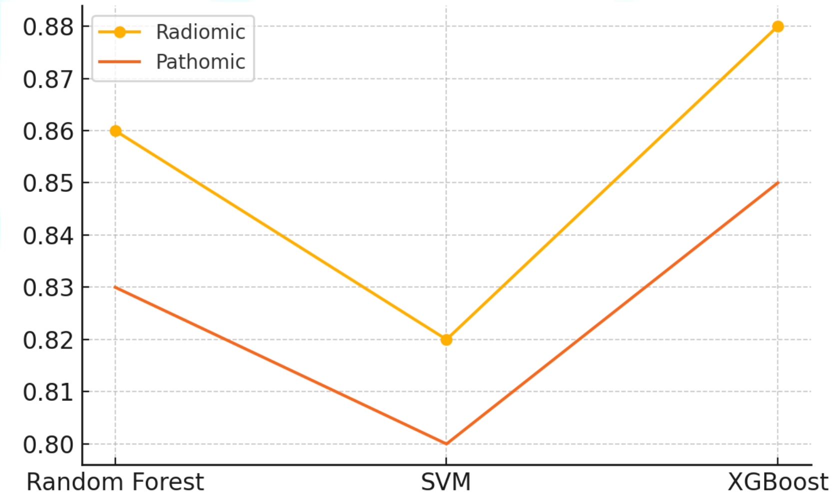

Figure 8: AUC comparison between radiomic and pathomic models.

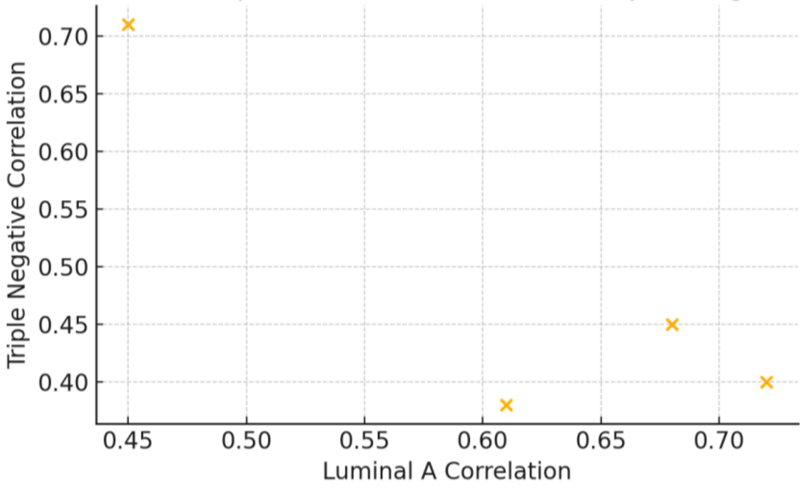

Figure 9: Feature separation plot between Luminal A and Triple Negative.

4. DISCUSSION

While testing with artificial intelligence is not yet a standard, the study demonstrates how computer-enriched tests can complement standard laboratory practice (Kapetas et al., 2025). Even though combining features in clinical imaging with deep learning has led to good forecast ability of breast cancer outcomes, further improvement is needed before these results become reliable for clinical work (Howard et al., 2023). Looking into the pathways of complex cancers, using methods that link gene expression data and pictures of affected tissues has proved at least as effective as simpler approaches (Tan et al., 2022). Nevertheless, current research is restricted since it largely depends on using just a single form of data, highlighting that adding more types of data will make models work better (Zhu et al., 2024).

Jaber and colleagues found that radiomic factors like Texture_Homogeneity and Shape_Compactness are better at helping doctors distinguish between Luminal A and Luminal B tumours. Similarly, the high importance of pathomic characteristics in the Triple Negative and HER2+ subtypes suggests that the tumour environment plays an important part in influencing tumour behavior (Gandhi et al., 2023). The results match current knowledge that breast cancer development relies heavily on both infiltrating lymphocytes and the speed of tumor growth. If radiomic and pathomic data are combined by multimodal fusion, accuracy in prediction can be significantly higher; Fusion-CNN shows excellent results. It brings attention to including a range of data to try and get a full picture of tumours (Jiang et al., 2023).

5. CONCLUSION

Our efforts indicate that pairing radiomics features with pathomics data could improve the accuracy of classification for breast cancer subtypes. Radiomic imaging from MRI and mammography was proven to accurately show different tumour shapes and molecular markers, based on our use of automated quantitative and learning algorithms. Details on how different cellular features and building tools affect tumour aggressiveness and immune system infiltration were uncovered through pathomic traits from digitalised slides of histological samples. The Fusion-CNN model had the top accuracy at 88% and an AUC score of 0.91, demonstrating that radiomics and pathomics used together streamlined from unimodal techniques in accuracy, AUC and general predictive ability. SHAP analysis helped make these models clearer by showing that GLCM_Correlation, Mitotic Count and Texture_Homogeneity are the biggest factors affecting predictions about cell types. This means that combining radiomic and pathomic data may overcome the problems with standard diagnostics which aren't always free from bias and sample widely enough. For practising personalised medicine, the repeated and non-invasive properties of computational methods mean they can be used straightaway in a clinical practice. Furthermore, our results can help improve therapy planning and prognosis for doctors who work with AI-based image analysis tools. Based on this setup, upcoming efforts can integrate many datasets as well as genomic and clinical details to make patient-appropriate diagnostic systems. Since it shows promise of making treatment and results for breast cancer patients better, the use of radiopathomic analytics is a positive advance in detection.

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