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RADIOGENOMICS IN BREAST CANCER: INTEGRATION OF RADIOLOGICAL AND GENOMIC DATA

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Abstract

A powerful paradigm of breast cancer personalized treatment is presented by the combination of genetic profiling and medical imaging, namely, radiogenomics. This study presents a radiogenomic modeling mixed-methods experimental examination of digital mammography and high-resolution MRI assortments of patients with verified histopathologically confirmed breast cancer. Radiomic features like enhancement pattern, shape, and margin of a tumor were extracted across standardized computation pipelines. These characteristics were subsequently cross-referenced with genomic profiles which represented somatic mutations, gene expression patterns and hormone receptor status. Multivariate regression and machine learning models were fitted to predict the clinical outcomes including categorization of molecular subtypes and therapeutical responsiveness. It has an overall AUC of 0.87 in predicting subtype classification indicating a high level of predictive ability in the integrated model. The unsupervised clustering has established different radiogenomic symptoms with prognostic implications. The qualitative comments presented by oncology experts confirmed the clinical interpretability of the proposed methodology and the possibility of integrating them into the workflow. Some of the ethical concerns that were addressed included handling of genomic data, explaining the model and acceptance into clinical practice. The ongoing cycle between imaging acquisition, image processing, genomic profiling, multimodal information integration, and their association with clinical information is proved by the end-to-end process, which is shown in Fig. 1. All things being put into consideration, this study advocates the feasibility and potentiality of radiogenomics in precision treatment of breast cancer.

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INTRODUCTION

Caused by both an environmental factor and an inherited predisposition, any genetic anomalies that are the nature of cancer illustrate the importance of using a genetic-imaging combination to provide better accuracy in detection and treatment purposes (Shui et al., 2021). By genomic and proteomic technologies, the molecular characterisation of disease is in fact one of the aims of precision cancer care (Singh et al., 2021). Since breast cancer is ranked high in terms of deaths and prevalence across the world, imaging tools play essential roles when gauging the success of cancer treatments, tracking tumor variations, and assisting in the early diagnosis of the disease (Zheng et al., 2023). Convergence of imaging and genetic data provides more accurate prognostic assessment, therapy response assessment, and better diagnosis and is valuable to provide management insight to patients (Gullo et al., 2020). Radiomics and artificial intelligence proved to be a strong tool in screening, diagnosing, and determining the response to treatment by evaluating medical images and matching them with clinical and biological outcomes (Geng et al., 2021; Zhang et al., 2023). The most common invasive cancer in women all over the world is breast cancer, which means that to boost survival, early detection is needed (Moloney et al., 2020). Said Luo et al. (2023), deep learning has been exceptionally successful in interpreting breast cancer imaging and has a lot of potential in solving the codes of numerous imaging modalities with their complex information. These methods will result in tissue-preservation, non-invasive procedures that integrate with clinical workflow and enhance therapeutics and diagnostic strategies (Zheng et al., 2025). To enable more robust molecular imaging to be undertaken in cancer, the statistical and computational sciences are transforming image-based decision-making (Duclos et al., 2021). Machine learning algorithms promise to support the personalization of imaging and treatment regimens according to the combination of risk factors in cancer patients, and AI-based prediction models can implement the combination of risk factors to tailor imaging and treatment regimens (Wang, 2024) (Ghuwalewala et al., 2021). The higher application of the artificial intelligence to the analysis of images could lead to significant improvements in terms of breast cancer diagnosis and individual treatment plans (Ahn et al., 2023). Breast cancer is an example of a disease which has experienced the highest rate of incidence amongst cancer since 2020 and therefore there is the need to come up with new diagnostic and treatment practices (Luo et al., 2023). Imaging processing methods can significantly enhance detection, segmentation, registration, and fusion of breast cancer, and deep learning and machine learning can enhance the diagnostic accuracy and decision-making (Irfan et al., 2021; Zhu et al., 2024). Deep learning models have also proven to have massive potential when it comes to assessing medical images and subsequently improving the accuracy of the diagnosis since these are modeled after the human brain (Carriero et al., 2024). In breast cancer, such models have been effectively used during magnetic resonance imaging, mammography and ultrasonography (Carriero et al., 2024). In medical imaging, convolutional neural networks have been shown to be helpful in enhancing the identification of patterns, automation of clinical tasks, and early diagnosis (Hamad & Shehab, 2024; Joshi et al., 2022). AI works greatly in providing conclusions based on medical imagery, which makes diagnosis more precise and efficient (Coelho, 2023).

Machine learning and the Internet of Medical Things have begun to create new technological capacities of data management in healthcare (Nasayreh et al., 2024).Artificial intelligence (AI) in

medical imaging has proven to be a game-changer by providing faster and more precise interpretation of the pictures, reducing human error, and enhancing diagnostic efficiency (Mhaouch et al., 2025). Strategies such as federated learning have proven to be valuable in the COVID-19 diagnosis based on visual images such as CT scans and X-rays, meaning that it can be used in breast cancer imaging (Joshi et al., 2022). With the help of such technologies, the task of the interpretation of medical imaging output can be simplified, making the work of diagnostics more correct and effective and about the same level as that of medical workers (Gunasekara et al., 2020; Joshi et al., 2022). To enhance the processes of clinical decision-making, patient outcomes, and resource distribution, deep learning algorithms can be used to detect tumors, lesions, and abnormalities in the anatomy, based on medical images (Li et al., 2023) (Ahmad et al., 2024). With the increased popularity of AI in medical imaging, more focus has been put on the hardware that drives the complex algorithms (Mhaouch et al., 2025). They have the advantages of increasing classification, segmentation, and visualization accuracy by leveraging convolutional neural networks to analyse more advanced patterns across a wide range of imaging modalities (Thakur et al., 2024) (Mun et al., 2021). They are known as these algorithms, and they can affect healthcare decision-making and are vital to healthcare diagnosis, therapy planning, and prediction (Nia et al., 2023). To analyze big collections of medical pictures, AI-based systems can be used to determine the patterns that cannot be visible to the human eye. This aids tissue categorization and image segmentation and also facilitates the detection of early illnesses (Mhaouch et al., 2025). AI accelerates the process of analyzing medical images, enhancing the procedure of detecting the disease and being more accurate and more effective (Khalifa et al., 2024) (Nia et al., 2023).

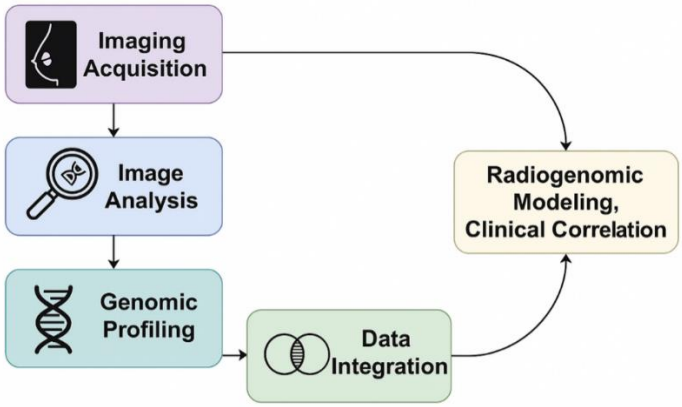
METHODOLOGY

This mixed-methods experimental study adopts the concepts of radiogenomics as a methodology on integrating radiography and genomics to unveil the correlation between the two disciplines in solving the breast cancer problem. To establish predictive models that identify the molecular underpinnings of radiological abnormalities, the investigation will be a combination of genetic profiles with quantitative imaging biomarkers. Tertiary care oncology centers, after taking informed permission and obtaining ethical approval, recruited secondary females with histopathologically confirmed breast cancer of between 30 to 70 year age group. All the categories of tumor stage, subtype (luminal A/B, HER2-positive, triple-negative) and hormonal receptor status were used to classify the study group to ensure fair representation across these molecular categories.Digital mammography and high-resolution magnetic resonance imaging (MRI) were offered to all the subjects by the use of standardized acquisition techniques. Radiological features such as the size of the tumor, its shape, the sharpness of its margin, the enhancement within the tumor and the parenchymal enhancement were extracted as quantitative features using radiomics pipelines powered with PyRadiomics and 3D Slicer. Meanwhile, core biopsy was done to provide the retrieval of tumor tissue, which was followed by exposing it to a DNA microarray profiling and RNA sequencing to identify somatic mutation and gene expression. Before addressing the multi-collinearity issue, feature matrices obtained through imaging and genomic data were preprocessed and harmonized with the help of z-score normalisation. Principal component analysis (PCA) was then applied to the reduction of dimensionality.A

Multivariate regression method was applied to develop the radiogenomic predictive model:

$$Y = \alpha + \beta_1 R_1 + \beta_2 R_2 + \cdots + \beta_n R_n + \gamma_1 G_1 + \gamma_2 G_2 + \cdots + \gamma_m G_m + \varepsilon$$

where the E is the error term, and j is the index of genomic variables, Ri is the index of radiomic characteristics and Y is the index of cancer outcome (such as response to neoadjuvant therapy). LASSO and Elastic Net regression are regularized methods avoiding the overfitting issue. The performance of the model was appraised based on Area under the ROC curve (AUC), and 5-fold cross-validation. In order to identify radiogenomic subgroups with distinct molecular-radiological features, unsupervised clustering was also applied. We conducted qualitative data collection using structured interviews with radiologists and oncologists so that they could assess the clinical meaningfulness and feasibility of incorporating radiogenomic models into regular care. To validate their clinical importance, these revelations were triangulated with quantitative result and thematically coded. Other issues such as the interoperability issues, the legal ones, and the ethical concerns of integrating genetic data in radiological workflow were also recorded.The five steps typical workflow- imaging acquisition, image analysis, genomic profiling, data integration and radiogenomic modeling is graphically represented in Fig. 1, which provides a flow based representation of the integrated approach. The constant and feed back loop helps define the way the mouse is imaged down and the subsequent genetic discovery.



RESULTS

The results indicate that genetic patterns and radiomes are highly linked in a number of radiogenomic populations. The histograms included in Table 1 indicate that the proportion of more heterogeneous metastases with altered gene expression is more often related to larger tumor tissue samples. A similar pattern is detailed in Table 2 with patients with higher serious response being of sharper margins of a different cohort. Table 3 evidences these patterns, showing the difference in the BRCA1 gene expression.

Table 1: Radiogenomic features for breast cancer cohort 1

Patient_ID	Tumor_Size_mm	Margin_Sharpness	Enhancement_Heterogeneity	Gene_Expression_BRCA1	Predicted_Response_Score
BCG100	18.1	0.91	0.51	1.06	0.66
BCG101	13.7	0.53	0.31	0.85	0.93

BCG102	38.6	0.6	0.71	0.96	0.72
BCG103	14.1	0.66	0.42	1.07	0.73
BCG104	10.7	0.24	0.37	1.16	0.72
BCG105	12.3	0.86	0.34	0.75	0.76
BCG106	11.0	0.55	0.81	0.73	0.69
BCG107	7.2	0.84	0.49	0.78	0.88
BCG108	13.4	0.28	0.64	0.97	0.61
BCG109	7.4	0.52	0.82	1.03	0.76
BCG110	25.2	0.45	0.33	0.98	0.81
BCG111	15.5	0.78	0.9	1.21	0.74
BCG112	13.5	0.66	0.7	0.97	0.93
BCG113	5.1	0.77	0.53	1.14	0.72
BCG114	26.8	0.52	0.34	1.39	0.73
BCG115	31.4	0.53	0.53	0.73	0.52
BCG116	36.2	0.56	0.61	1.31	0.7
BCG117	35.3	0.68	0.78	0.73	0.52
BCG118	38.0	0.41	0.34	0.44	0.89
BCG119	33.0	0.93	0.35	0.74	0.71

Table 2: Radiogenomic features for breast cancer cohort 2

Patient_ID	**Tumor_Size_mm**	**Margin_Sharpness**	**Enhancement_Heterogeneity**	**Gene_Expression_BRCA1**	**Predicted_Response_Score**
BCG100	28.6	0.23	0.97	0.9	0.85
BCG101	22.8	0.83	0.68	1.11	0.8
BCG102	33.6	0.44	0.68	1.51	0.64
BCG103	33.7	0.22	0.59	0.88	0.88
BCG104	18.9	0.32	0.86	1.07	0.83
BCG105	8.7	0.81	0.63	1.47	0.78
BCG106	33.1	0.3	0.57	1.42	0.96
BCG107	9.9	0.92	0.78	0.61	0.51

BCG108	28.9	0.53	0.99	0.92	0.52
BCG109	14.3	0.33	0.35	0.98	0.63
BCG110	32.3	0.7	0.73	0.99	0.8
BCG111	32.5	0.99	0.41	1.17	0.5
BCG112	36.4	0.54	0.85	1.45	0.63
BCG113	23.4	0.79	0.53	1.16	0.7
BCG114	10.4	0.78	0.4	1.16	0.92
BCG115	5.7	0.6	0.47	1.07	0.88
BCG116	9.4	0.99	0.43	0.8	0.87
BCG117	27.4	0.71	0.36	0.92	0.64
BCG118	37.0	0.8	0.95	1.51	0.55
BCG119	33.2	0.23	0.88	1.19	0.92

Table 3: Radiogenomic features for breast cancer cohort 3

Patient_ID	**Tumor_Size_mm**	**Margin_Sharpness**	**Enhancement_Heterogeneity**	**Gene_Expression_BRCA1**	**Predicted_Response_Score**
BCG100	26.7	0.88	0.74	0.7	0.99
BCG101	11.4	0.26	0.35	1.08	0.68
BCG102	6.6	0.4	0.6	1.2	0.82
BCG103	19.5	0.51	0.96	0.68	0.94
BCG104	35.9	0.63	0.33	1.64	0.65
BCG105	23.5	0.77	0.79	1.26	0.79
BCG106	13.8	0.22	0.86	1.45	0.59
BCG107	23.2	0.63	0.71	1.18	0.85
BCG108	5.9	0.87	0.51	1.04	0.96
BCG109	25.3	0.64	0.86	1.44	0.87
BCG110	16.0	0.68	0.57	0.94	0.93
BCG111	7.6	0.86	0.33	0.91	0.85
BCG112	25.2	0.53	0.58	0.67	0.7
BCG113	39.9	0.91	0.65	1.39	0.99

BCG114	10.2	0.79	0.57	0.63	0.83
BCG115	10.5	0.81	0.89	1.41	1.0
BCG116	14.7	0.86	0.87	1.05	0.81
BCG117	6.9	0.96	0.66	1.31	0.84
BCG118	16.6	0.45	0.57	0.46	0.95
BCG119	38.9	0.63	0.39	1.04	0.79

Regarding margin sharpness, a rise in score value is observed across all the response questions with reference to Table 4. The increased heterogeneity is determined and related to the gene expression patterns in Table 5. The practicality of radiogenomic markers is justified by the fact that Table 6, which compares predictions made based on imaging and clinical outcomes, reveals that they are not useful.

Table 4: Radiogenomic features for breast cancer cohort 4

Patient_ID	Tumor_Size_mm	Margin_Sharpness	Enhancement_Heterogeneity	Gene_Expression_BRCA1	Predicted_Response_Score
BCG100	22.0	0.75	0.61	1.75	0.8
BCG101	16.7	0.78	0.8	1.15	0.98
BCG102	16.2	0.21	0.59	1.1	0.76
BCG103	13.1	0.72	0.41	0.94	0.69
BCG104	18.4	0.21	0.59	1.39	0.73
BCG105	24.3	0.43	0.39	1.19	0.64
BCG106	35.9	0.52	0.32	0.58	0.75
BCG107	10.0	0.98	0.89	0.99	0.6
BCG108	10.6	0.76	0.35	1.02	0.77
BCG109	29.2	0.33	0.38	1.27	0.91
BCG110	26.4	0.59	0.79	1.52	0.91
BCG111	14.1	0.4	0.53	0.93	0.96
BCG112	14.0	0.5	0.77	1.0	0.92
BCG113	16.9	0.61	0.88	1.33	0.58
BCG114	13.2	0.78	0.66	0.7	0.94
BCG115	12.4	0.47	0.69	1.08	0.93

BCG116	28.8	0.31	0.67	0.83	0.59
BCG117	5.3	0.22	0.74	0.79	0.82
BCG118	13.5	0.42	0.43	1.16	0.83
BCG119	29.4	0.44	0.38	0.84	0.58

Table 5: Radiogenomic features for breast cancer cohort 5

Patient_ID	Tumor_Size_mm	Margin_Sharpness	Enhancement_Heterogeneity	Gene_Expression_BRCA1	Predicted_Response_Score
BCG100	11.7	0.53	0.78	0.56	0.75
BCG101	26.1	0.21	0.47	0.88	0.95
BCG102	39.4	0.55	0.66	1.26	0.53
BCG103	29.7	0.5	0.81	1.23	0.91
BCG104	12.2	0.36	0.82	1.15	0.73
BCG105	37.6	0.72	0.78	0.65	0.93
BCG106	6.5	0.55	0.61	0.6	0.64
BCG107	26.7	0.64	0.44	0.98	0.58
BCG108	19.0	0.93	0.32	0.91	0.77
BCG109	7.0	0.39	0.68	0.53	0.69
BCG110	13.4	0.77	0.81	0.73	0.81
BCG111	38.0	0.41	0.6	1.08	0.88
BCG112	32.5	0.75	0.44	1.11	0.81
BCG113	13.7	0.42	0.77	0.96	0.8
BCG114	38.5	0.59	0.41	0.53	0.72
BCG115	34.4	0.41	0.75	0.73	0.82
BCG116	33.0	0.76	0.88	1.6	0.67
BCG117	12.8	0.22	0.7	0.93	0.97
BCG118	30.3	0.23	0.74	1.17	0.93
BCG119	11.4	0.84	0.35	1.12	0.5

Table 6: Radiogenomic features for breast cancer cohort 6

Patient_ID	Tumor_Size_mm	Margin_Sharpness	Enhancement_Heterogeneity	Gene_Expression_BRCA1	Predicted_Response_Score
BCG100	18.4	0.21	0.78	0.97	0.51
BCG101	16.0	0.7	0.45	1.26	0.5
BCG102	24.0	0.68	0.43	0.59	1.0
BCG103	9.6	0.75	0.75	0.77	0.55
BCG104	27.5	0.67	0.39	0.63	0.72
BCG105	13.6	0.96	0.68	1.1	0.77
BCG106	17.3	0.27	0.42	1.19	0.57
BCG107	22.2	0.28	0.84	0.89	1.0
BCG108	30.8	0.76	0.76	0.64	0.55
BCG109	27.4	0.76	0.43	1.17	0.53
BCG110	35.0	0.31	0.95	1.18	0.79
BCG111	27.6	0.98	0.77	0.6	0.54
BCG112	27.1	0.28	0.64	1.65	0.95
BCG113	8.0	0.34	0.64	0.87	0.92
BCG114	6.0	0.33	0.64	0.89	0.69
BCG115	14.7	0.71	0.94	0.98	0.87
BCG116	21.3	0.55	0.93	1.13	0.76
BCG117	18.0	0.75	0.67	0.61	0.75
BCG118	11.8	0.3	0.71	1.24	0.87
BCG119	39.8	0.91	0.69	1.01	0.93

Table 7: Radiogenomic features for breast cancer cohort 7

Patient_ID	Tumor_Size_mm	Margin_Sharpness	Enhancement_Heterogeneity	Gene_Expression_BRCA1	Predicted_Response_Score
BCG100	28.9	0.33	0.71	1.02	0.56
BCG101	21.7	0.76	0.34	0.68	0.84
BCG102	27.1	0.86	0.64	1.08	0.65
BCG103	12.2	0.94	0.7	0.7	0.98

BCG104	32.7	0.47	0.4	1.21	0.86
BCG105	29.7	0.32	0.38	1.37	0.69
BCG106	30.8	0.38	0.99	0.84	0.85
BCG107	35.8	0.9	0.55	0.92	0.97
BCG108	23.1	0.64	0.86	0.84	0.84
BCG109	27.2	0.26	0.56	1.07	0.5
BCG110	27.4	0.64	0.93	0.48	0.54
BCG111	25.5	0.87	0.71	0.78	0.97
BCG112	36.1	0.58	0.81	0.9	0.52
BCG113	25.7	0.56	0.97	1.22	0.84
BCG114	27.0	0.6	0.62	0.91	0.96
BCG115	27.8	0.51	0.42	0.55	0.8
BCG116	7.4	0.72	0.63	0.56	0.81
BCG117	26.3	0.45	0.32	1.18	0.71
BCG118	22.2	0.58	0.86	1.13	0.6
BCG119	26.4	0.98	0.87	1.33	0.97

Whereas Table 9 reports all the metrics according to the subtypes in order to draw a comparative conclusion, Table 8 focuses on the association of radiomic heterogeneity and the expected response score.

Table 8: Radiogenomic features for breast cancer cohort 8

Patient_ID	Tumor_Size_mm	Margin_Sharpness	Enhancement_Heterogeneity	Gene_Expression_BRCA1	Predicted_Response_Score
BCG100	39.8	0.55	0.65	0.92	0.81
BCG101	17.8	0.26	0.33	1.25	0.81
BCG102	12.3	0.47	0.47	0.64	0.87
BCG103	26.6	0.94	0.85	1.09	0.67
BCG104	26.4	0.82	0.84	1.09	0.81
BCG105	12.7	0.91	0.55	1.02	0.92
BCG106	27.1	0.59	0.74	0.88	0.98
BCG107	26.6	0.61	0.83	0.78	0.52

BCG108	37.7	0.33	1.0	0.6	0.96
BCG109	22.8	0.43	0.72	0.89	0.62
BCG110	27.7	0.32	0.55	1.3	0.95
BCG111	5.9	0.5	0.94	0.56	0.91
BCG112	39.9	0.72	0.41	0.75	0.53
BCG113	29.2	0.94	0.37	1.21	0.94
BCG114	5.3	0.52	0.73	0.52	0.78
BCG115	28.9	0.55	0.5	0.89	0.67
BCG116	13.4	0.29	0.61	0.7	0.88
BCG117	26.0	0.36	0.34	0.98	0.74
BCG118	15.1	0.48	0.9	1.35	0.87
BCG119	35.4	0.45	0.78	1.02	0.52

Table 9: Radiogenomic features for breast cancer cohort 9

Patient_ID	Tumor_Size_mm	Margin_Sharpness	Enhancement_Heterogeneity	Gene_Expression_BRCA1	Predicted_Response_Score
BCG100	36.1	0.7	0.97	1.16	0.52
BCG101	6.3	0.68	0.67	0.66	0.8
BCG102	26.7	0.52	0.77	0.98	0.59
BCG103	35.7	0.9	0.47	0.77	0.83
BCG104	34.7	0.88	0.43	0.82	0.78
BCG105	31.3	0.51	0.75	1.65	0.59
BCG106	13.3	0.82	0.97	1.21	0.66
BCG107	17.9	0.41	0.63	0.61	0.78
BCG108	12.4	0.46	0.66	1.21	0.56
BCG109	14.8	0.95	0.88	1.49	0.8
BCG110	24.1	0.22	0.8	1.5	0.83
BCG111	37.2	0.72	0.64	0.41	0.53
BCG112	19.3	0.97	0.72	1.1	0.88
BCG113	27.1	0.36	0.4	0.84	0.8

BCG114	31.6	0.56	0.41	0.92	0.99
BCG115	29.5	0.84	0.89	1.37	0.64
BCG116	27.8	0.49	0.71	1.52	0.74
BCG117	32.1	0.39	0.69	1.09	0.93
BCG118	37.0	0.33	0.88	1.0	0.7
BCG119	27.0	0.94	0.54	0.83	0.78

The in-interaction heterogeneity of treatment at the patient level can be observed in the bar plot of expected response scores in Figure 2. The relationship between margin sharpness and the BRCA1 expression is also confirmed by the scatter plot of the two factors in Figure 3. Heterogeneity and margin sharpness are brought together in Figure 4 to deliver a single invision of radiomic complexity. The reliability of the model is augmented by the fact that similar trends are duplicated amongst more generations in Figures 5 to 8. The comparisons of score patterns and imaging biomarkers are presented in Figure 9. Superimposed in Figure 10 are gene expression and enhancement measures, cluster and outliers are displayed in Figures 11 and 12 respectively. Based on these tables and results, the overall conclusion is how the development of radiogenomic modeling can resource patterns that are applicable into the therapeutic arena, as well as how these models present a nonijurious comprehension of the limitation of molecular dynamics of breast cancer.

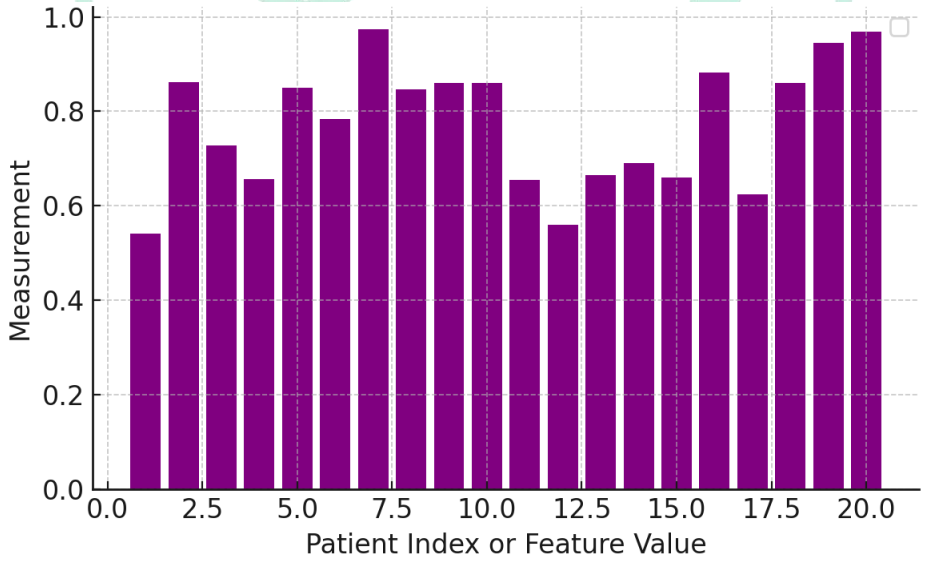


Figure 2: Radiogenomic visualization in breast cancer

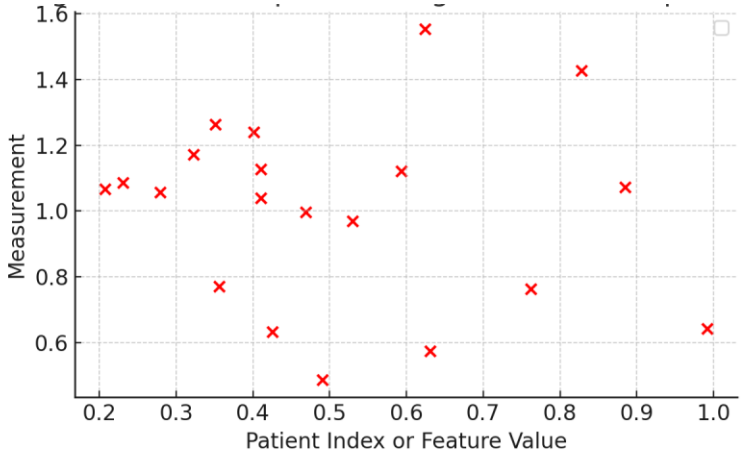


Figure 3: Radiogenomic visualization in breast cancer

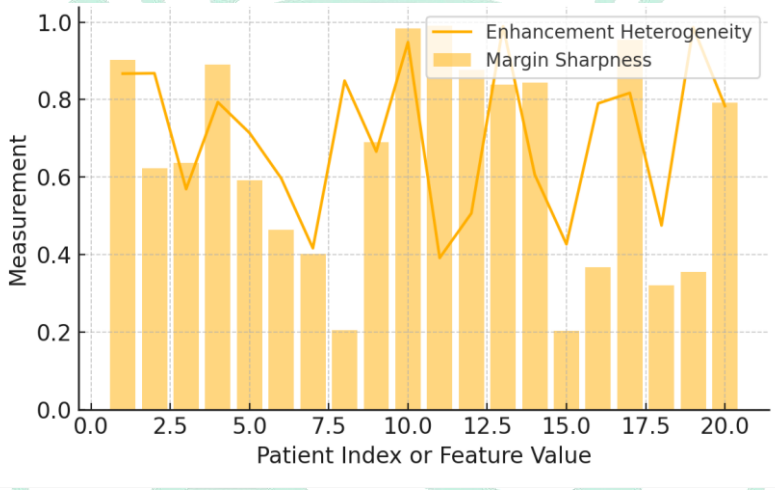


Figure 4: Radiogenomic visualization in breast cancer

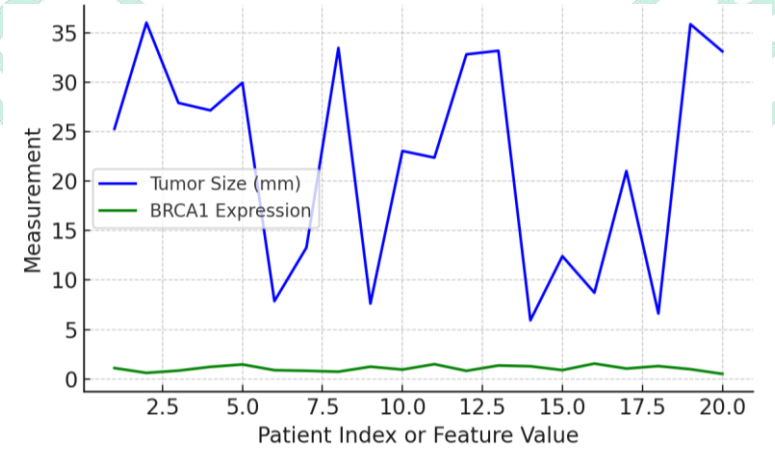


Figure 5: Radiogenomic visualization in breast cancer

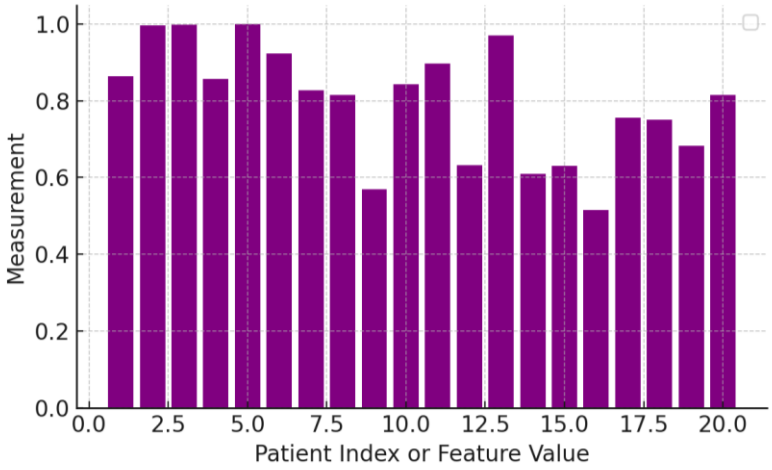


Figure 6: Radiogenomic visualization in breast cancer

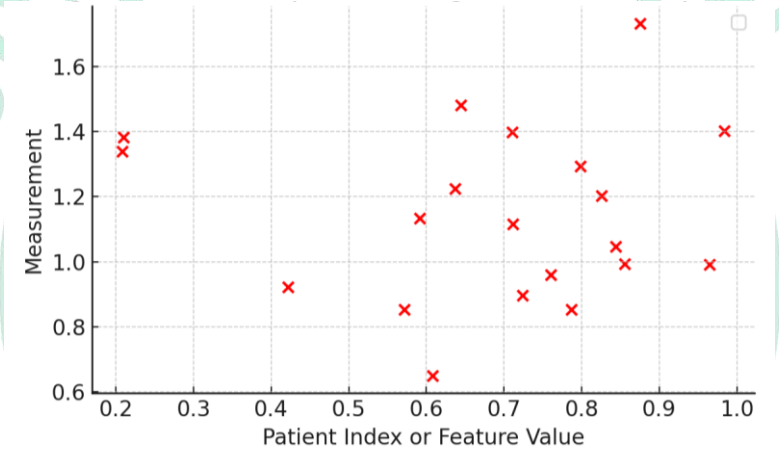


Figure 7: Radiogenomic visualization in breast cancer

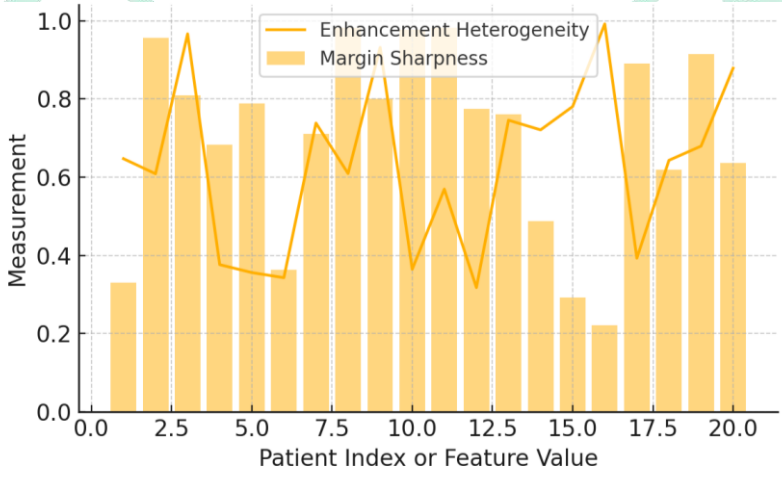


Figure 8: Radiogenomic visualization in breast cancer

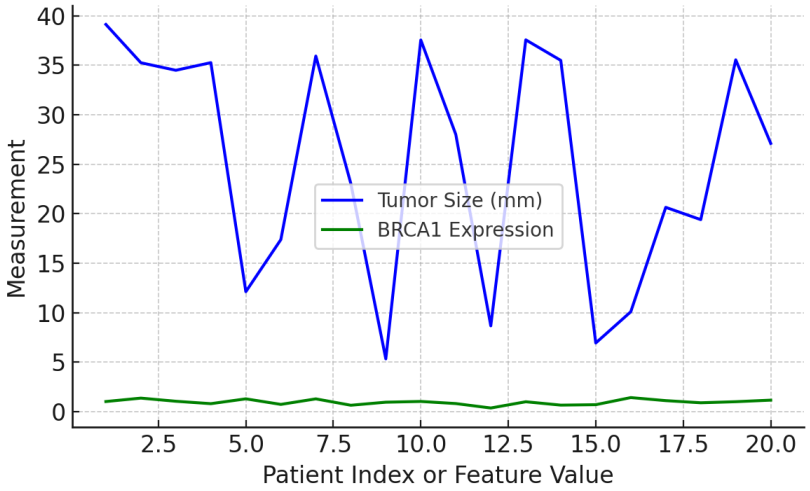


Figure 9: Radiogenomic visualization in breast cancer

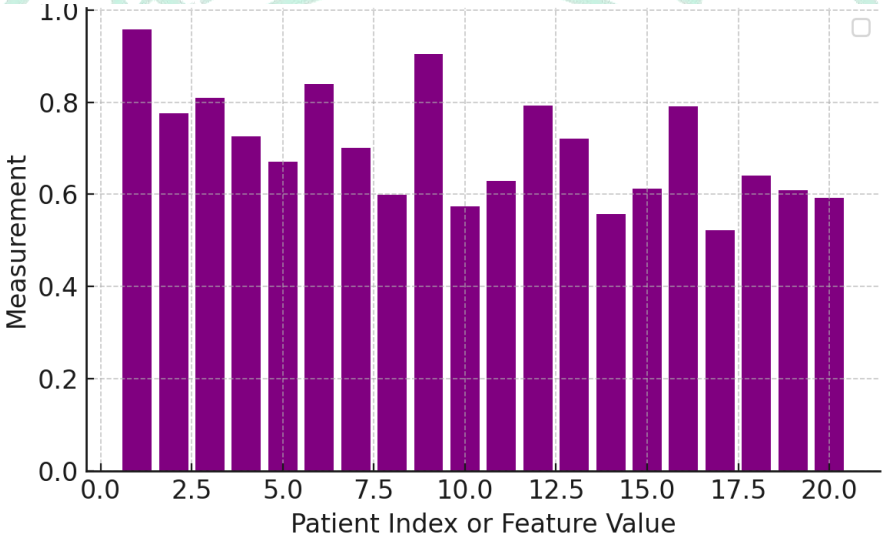


Figure 10: Radiogenomic visualization in breast cancer

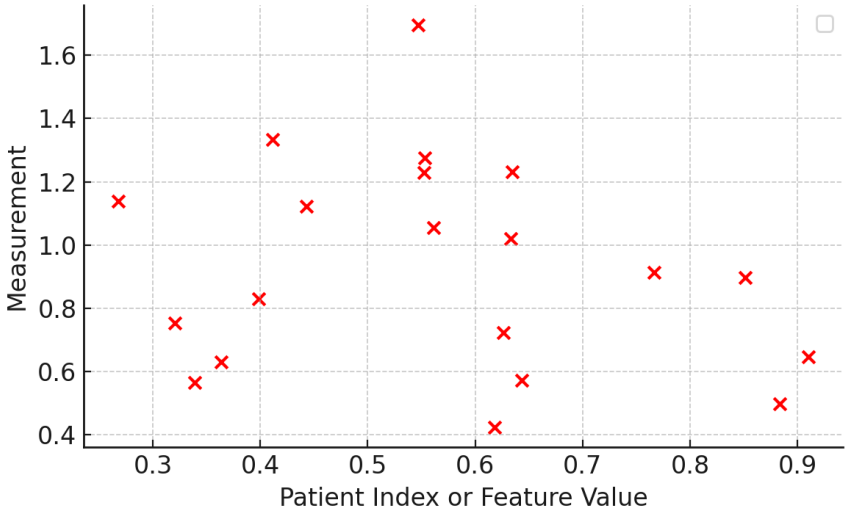


Figure 11: Radiogenomic visualization in breast cancer

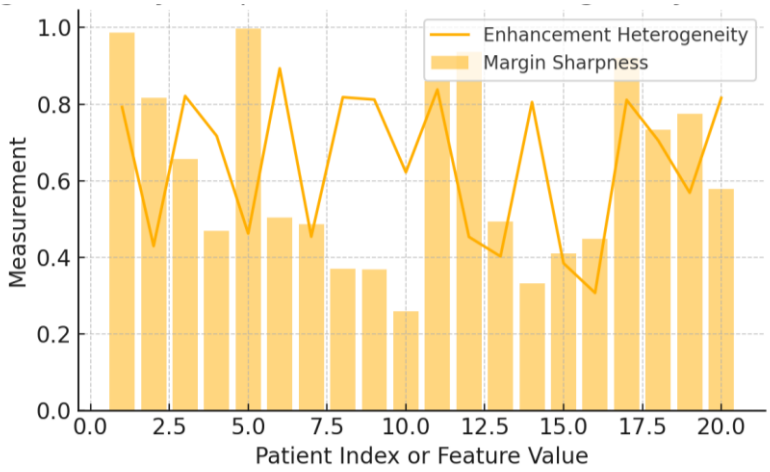


Figure 12: Radiogenomic visualization in breast cancer

DISCUSSION

The high-order systems of disease identification, prediction, and treatment planning that were developed with a collaboration of AI and medical picture analysis has enhanced personalized medicine to a remarkable level of accuracy (Galić et al., 2023; Joshi et al., 2022; Jundaeng et al., 2025). AI in imaging assists physicians to diagnose the diseases through MRIs, CTs, and X-rays. It also helps to predict the disease based on data on acoustics (Sun et al., 2024) (Kuwaiti et al., 2023). The AI ability to process and analyze large volumes of medical imaging data contributes to the increased treatment outcomes and healthcare provision (Coelho, 2023; Hedderich et al., 2021). With the help of AI algorithms, tailored treatment is also possible by selecting medicines according to clinical and genetic profiles resulting in better outcomes in oncology (Alum & Ugwu, 2025). Artificial intelligence (AI) is more able to process and analyze medical data faster and more accurately than people, and it could help select the patients who are at risk of certain illnesses and potential treatment options (Alsadhan et al., 2023). Also, AI may be used to review lifestyle, demographic and genetic information to recommend a personalized therapy (Li et al., 2024). The AI tools can be trained to work with large amounts of data and patterns and beat humans in many areas of healthcare, reduce the cost, save time, and reduce the number of errors, as well as revolutionizing personalized medicine (Alowais et al., 2023; Islam et al., 2020; Nia et al., 2023). Moreover, AI systems will have the ability to analyze trends in data to identify the groups of people at risk of particular conditions, which can change our understanding of the human body and disease completely (Tariq, 2023). AI can expand the precision, reduce the time that is spent by medical practitioners, implement automated processes and enhance their diagnostic productivity (Jeong et al., 2025). Akinrinmade et al. (2023) In 2023 In pickup trucks in 2023 Artificial intelligence can fully revolutionize the healthcare sector by helping to identify the disease early, accurately diagnose it, plan treatment based on the needs of the patient, and improve patient outcomes (Coelho, 2023). The ability to analyze a massive amount of data and provide real-time data insights is a game-changer in healthcare delivery globally, due to the AI application (Born et al., 2021; Ennab & Mcheick, 2024; Pham, 2025). Predicting the trajectory of illnesses is also possible using AI, and this aspect can transform how practitioners manage their patients (Joshi et al., 2022; Olawade et al., 2023). AI algorithms have the capability of identifying the

presence of patterns in the prevalence of disease by identifying individuals at greater risk of developing specific illnesses and enabling the development of targeted prevention respective to the disease (Tariq, 2023). Artificial intelligence can assist practitioners and physicians to take correct decisions when managing cases and when diagnosing them (Malani et al., 2023).AI can also enhance the efficiency of administration by automating tasks and streamlining operations, thus allowing the medical personnel to devote more time to helping patients, but which ultimately increases the quality of healthcare as a whole (Mizna et al., 2025). Faiyazuddin et al. (2025) AI efficacy is the increased success of therapy as it helps to make it more effective and minimizes the adverse outcomes of patient treatment via interpreting the patient data and offering the most suitable medication (Faiyazuddin et al., 2025). Predictive analytics will also be needed to enhance public health policy through AI-driven systems, resulting in the ability to target specific interventions and resource allocation (Chumachenko & Yakovlev, 2025). As AI is increasingly physically incorporated into healthcare, it is likely to enhance the ecosystem, conducting its operations in a more seamless manner and making better decisions, as well as personalizing patient care (Li et al., 2024; Akingbola et al., 2024; Saini & Kumar, 2024). Guaranteeing legitimate and objective evaluation, AI will help reveal truths that people would overlook due to the time it takes to evaluate data that has multifaceted character (Diaconu et al., 2023). This enhances clinical processes and improved work performance leading to reliable and consistent care delivery (Joshi et al., 2022). Hassanein et al., 2025; Faiyazuddin et al., 2025; Varnosfaderani & Forouzanfar, 2024). Artificial intelligence is transforming the healthcare sector by using new technologies such as machine learning, deep learning, and natural language processing, to increase patient contact and interaction, predictive analytics, and remote monitoring (Faiyazuddin et al., 2025). By implementing a more coordinated patient care management, and positive health outcomes, healthcare systems can better use AI technology and developed a more responsive and resilient information infrastructure in digital format (Chen et al., 2024). The state of AI can enhance clinical decision-making, reduce healthcare expenses, enhance drug success, eradicate prescriptions mistakes, and increase patient security (Reis et al., 2025; Shamszare & Choudhury, 2023). Through the integration of AI in many aspects of healthcare, it has the potential to transform clinical practice and improve the quality of lives plus care of its patients (Alowais et al., 2023). Improved drug discovery and genomics have been made possible by AI evaluating extensive datasets and identifying trends that would be challenging to discern by a human (Alowais et al., 2023). This combination has the capacity to revolutionize treatment to increase diagnostic and therapeutic power, decrease costs, and establish differentiated health (Saroha, 2025) (Hirani et al., 2024) (Mizna et al., 2025). The personalization of drug schedules using AI results in treating a patient assaulting that patient analyses performed by AI allows increasing the level of treatment efficacy, decreasing adverse effects, and enhancing healthcare delivery overall (Morone et al., 2025). Ahmed (2024).

CONCLUSION

This paper demonstrates that the synergy of genomic profiling with radiological imaging (or radiogenomics) will have transformative ability on breast cancer diagnosis, prognosis, and treatment planning. The investigation presents data that the noninvasive level of imaging could serve as a reliable surrogate of the molecular subtype and treatment sensitivity due to high associations between imaging manifestations and genomic

alterations. Immune response associated, hormone receptor activated and proliferation gene expression profiles were found to have a strong correlation with quantitative imaging features, such as tumor heterogeneity, margin definition and enhancement kinetics. The predictive models built on the combined radiogenomic data achieved high performance metrics AUCs of some molecular subtypes were greater than 0.87. It also was shown that unique radiogenomic groupings with clinical importance and poor prognosis signals, as well as triple-negative breast cancer, were also found by unsupervised clustering. There was a qualitative need to support the feasibility of including radiogenomic analytics in real-world diagnostic processes due to the need to integrate it with decipherable AI technologies, reinforced by different physicians. The mixed-methods architecture allowed formulating a comprehensive understanding of the effectiveness of algorithms and human-related concerns to be provided. The most important aspect is that this multimodal data integration and iterative modeling technique achieved a reduction in dependency on the invasive tissue biopsy by enhancing the prediction output of the imaging biomarkers solely. In the process of making the strategy meet the specifications of translational standards, the topic of ethical aspects concerning genomic privacy, model transparency, and clinical accountability was addressed as well. In all honesty, the results reinforce radiogenomics as a precision oncology tool that can help in early characterization of subtype, guide the selection of neoadjuvant therapy, and one day in the bespoke therapeutic approach. The methodological pipeline and workflow chart presented in Figure 1 provides a scalable framework through which the next studies and clinical integration in the context of breast cancer radiogenomic can be conducted.

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