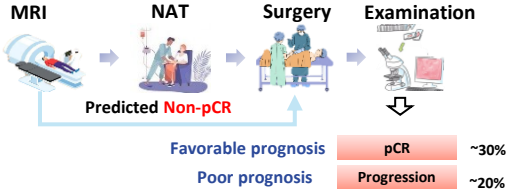
Early Prediction of Pathologic Complete Response in Breast Cancer via Graph Network Modeling of Intratumoral and Peritumoral Dynamics on DCE-MRI

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Motivation

- According to the International Agency for Research on Cancer[1], breast cancer is the most common cancer with the highest mortality among women.
- Neoadjuvant chemotherapy is the first-line treatment for patients with locally advanced breast cancer. Pathological complete response(pCR) is an important marker associated with outcomes. However, due to tumor heterogeneity, only about 30 percent of patients achieve pCR[2].



- Moreover, pCR is confirmed only after surgery through pathological examination, making it difficult to assess treatment efficacy early and adjust therapy in time. Therefore, it is necessary to modelling intratumoral and peritumoral dynamics to predict pCR in early stage.

Method

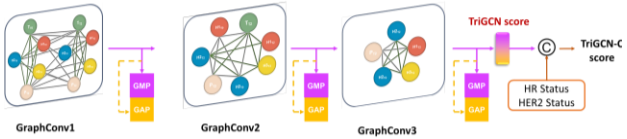
Habitat Geneartion

1. Preprocessing by N4 bias correction, resampling to 1mm and z-score standardization. Segmented the tumor and expanded by 5 mm to define the peritumoral regions.
2. To capture intratumoral information, tumor was partitioned into 100 superpixels using Simple Linear Iterative Clustering, and were categorize into three habitats using k-means clustering.



Model development

1. Constructed graph with ten nodes—tumor, peritumoral region, and three habitats at both pre-treatment and one-cycle.
2. A three-layer Graph Convolutional Network (TriGCN) was employed to model node interactions.



Experiments & Results

Model development

- Integrated model demonstrated superior performance, achieving AUCs of 0.85, 0.81 and 0.79 in the training, internal testing, and external testing set. These results outperformed the clinical model (AUC: 0.69–0.75), as well as the single-timepoint models (AUC: 0.66–0.76) in the testing sets.

AUC comparison of different models

Models	Training set	Internal test set	External test set
Clinical	0.75	0.72	0.69
TriGCN(T_0+T_1)	0.77	0.74	0.73
TriGCN-C(T_0+T_1)	**0.85**	**0.81**	**0.79**
TriGCN-C(T_0)	0.91	0.73	0.66
TriGCN-C(T_1)	0.93	0.76	0.71

- Although the single-timepoint models outperformed the integrated model in the training set, they suffered from overfitting in the testing sets. In contrast, the integrated model captured the dynamic changes of the tumor during treatment, enabling better generalization and demonstrating robust prediction.

References
[1] Int J Cancer, 2025, 156(7): 1336-1346.
[2] Radiology, 2023, 308(1): e222830.

Conclusion

This study shows that DCE-MRI from pre-NAC and early-NAC can predict pCR, assisting in early adjustments of therapeutic strategies. Graph-based models have proven effective in capturing the interactions among different tumor nodes. These findings emphasize the model's promise for predicting treatment response in clinical practice.