

RadioabTrace: A Radiomic–Protein Trajectory Model for Early Lung Adenocarcinoma Progression



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BACKGROUND

Management of early lung adenocarcinoma (LUAD) remains challenging because current pathology provides a static diagnosis, whereas clinical decision-making requires a continuous assessment of progression risk across the adenocarcinoma in situ (AIS), microinvasive adenocarcinoma (MIA), and invasive adenocarcinoma (IAC) spectrum. We aimed to develop an interpretable multimodal model integrating radiomic features and a seven-antibody protein panel to reconstruct the progression trajectory of LUAD and identify patients with potentially indolent versus high-risk disease.

METHODS

This retrospective cohort study included 307 patients diagnosed with LUAD between 2020 and 2022. RadioabTrace integrated CT radiomics and a seven-antibody protein panel from pathologically confirmed early lung adenocarcinoma. After feature preprocessing and normalization, multimodal features were embedded into a topology-guided trajectory space anchored by AIS, MIA, and IAC labels. Each tumor was assigned a pseudotime score along the AIS-MIA-IAC progression axis, and invasive cases received a branch score reflecting divergence toward low- or high-risk phenotypes. Model performance was assessed using ROC/PR analyses, and feature contributions were evaluated by correlation, regularized regression, permutation importance, and bootstrap stability.

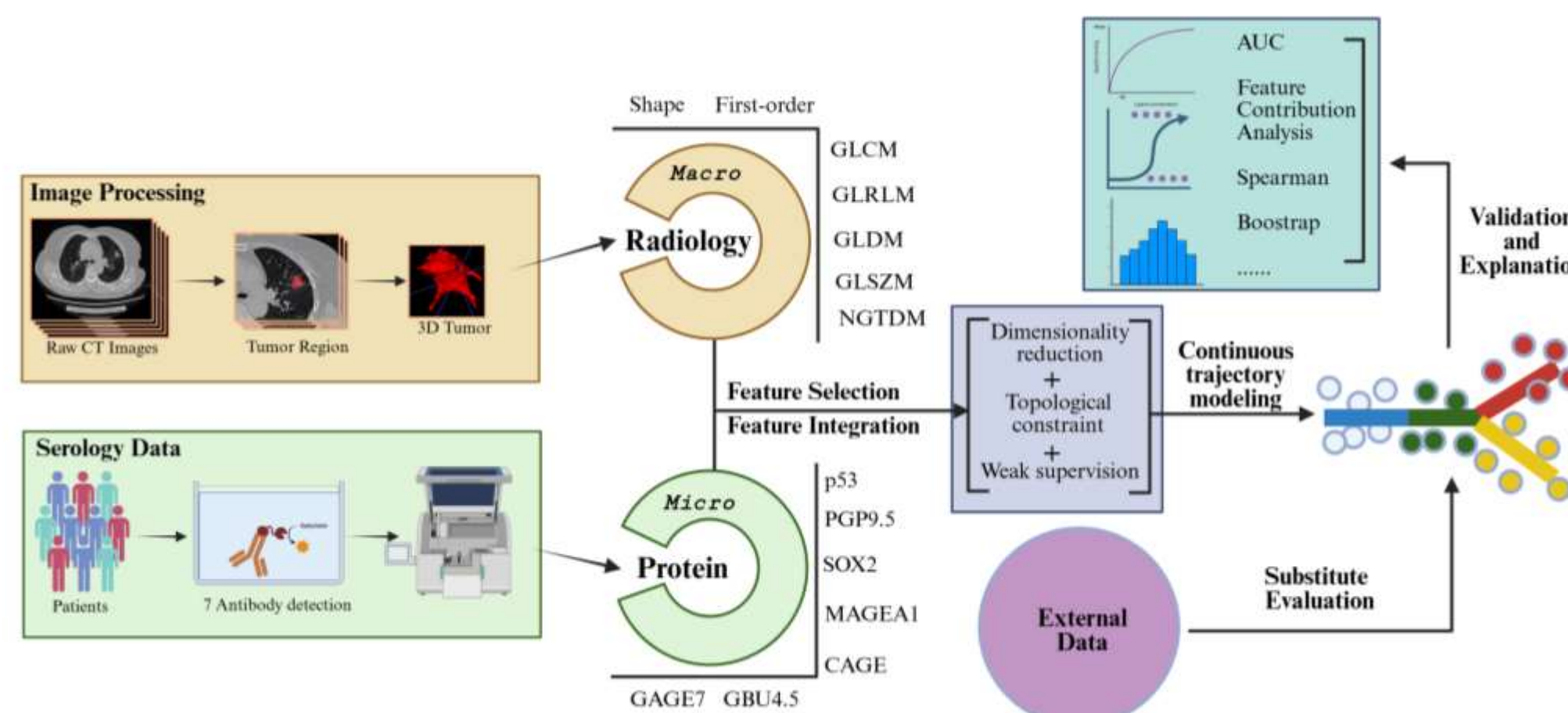


Figure 1. Workflow of RadioabTrace.

RESULTS & CONCLUSION

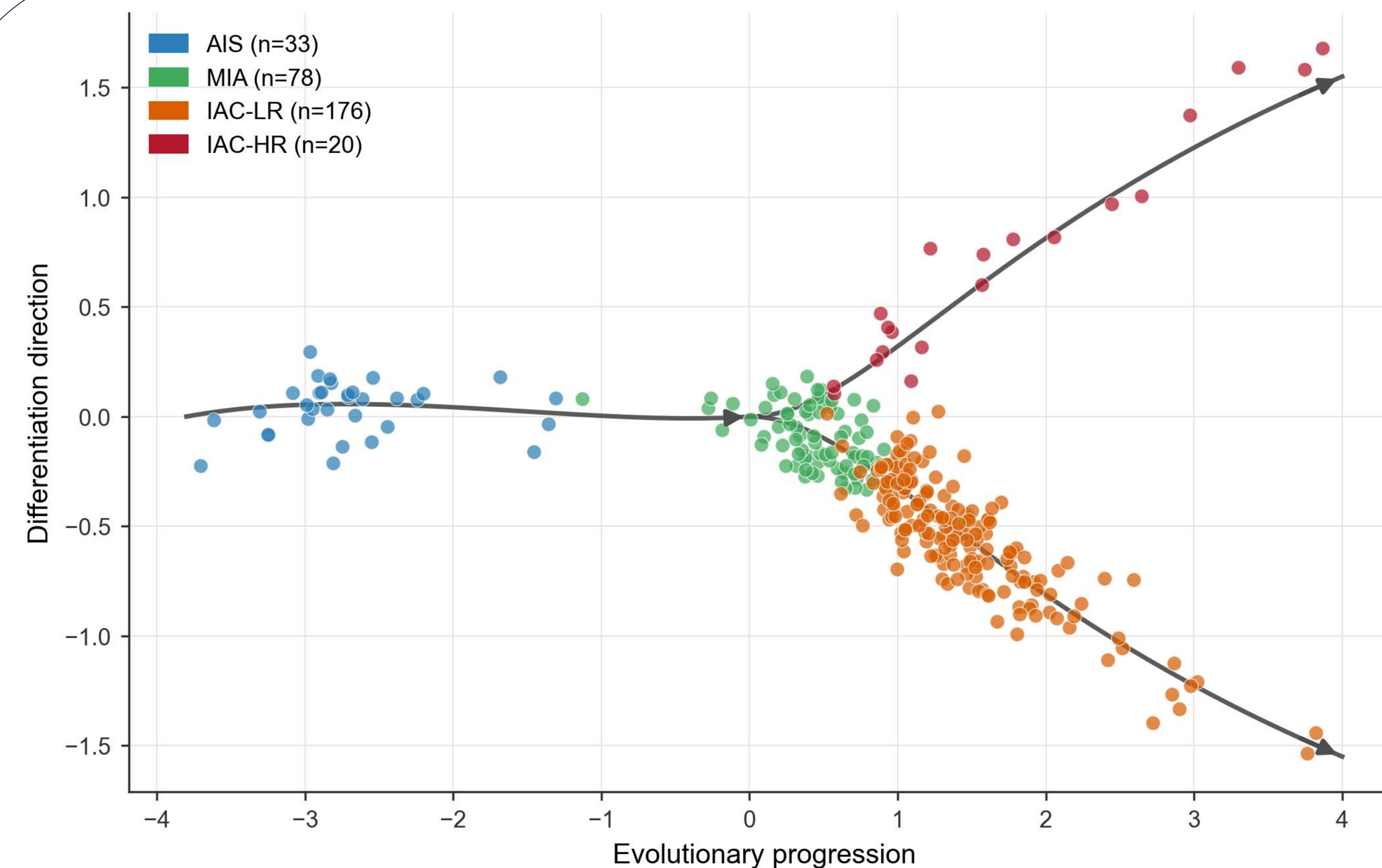


Figure 2. RadioabTrace reconstructs AIS-MIA-IAC progression as a continuous branching trajectory.

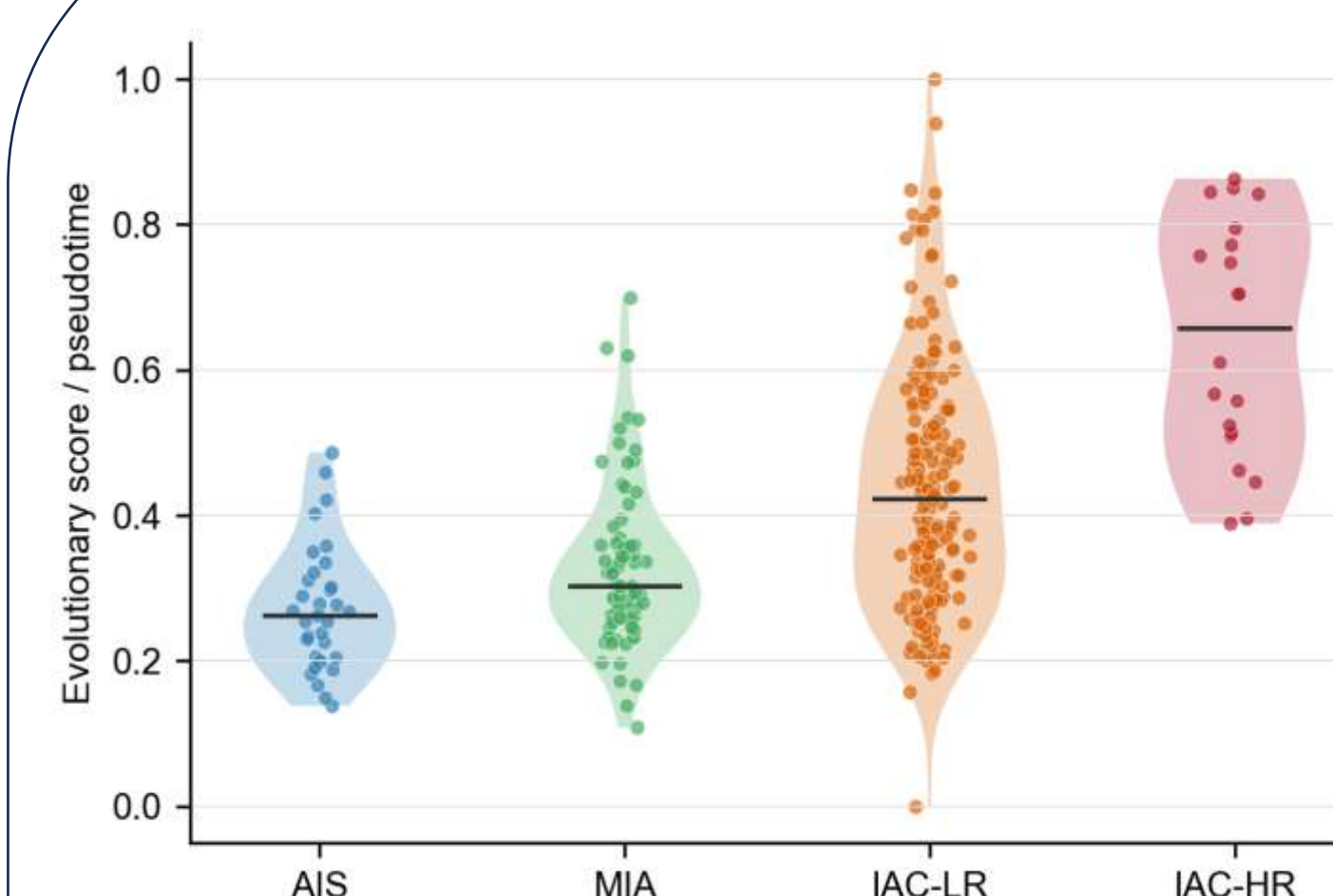


Figure 3. Pseudotime score of four pathological stages.

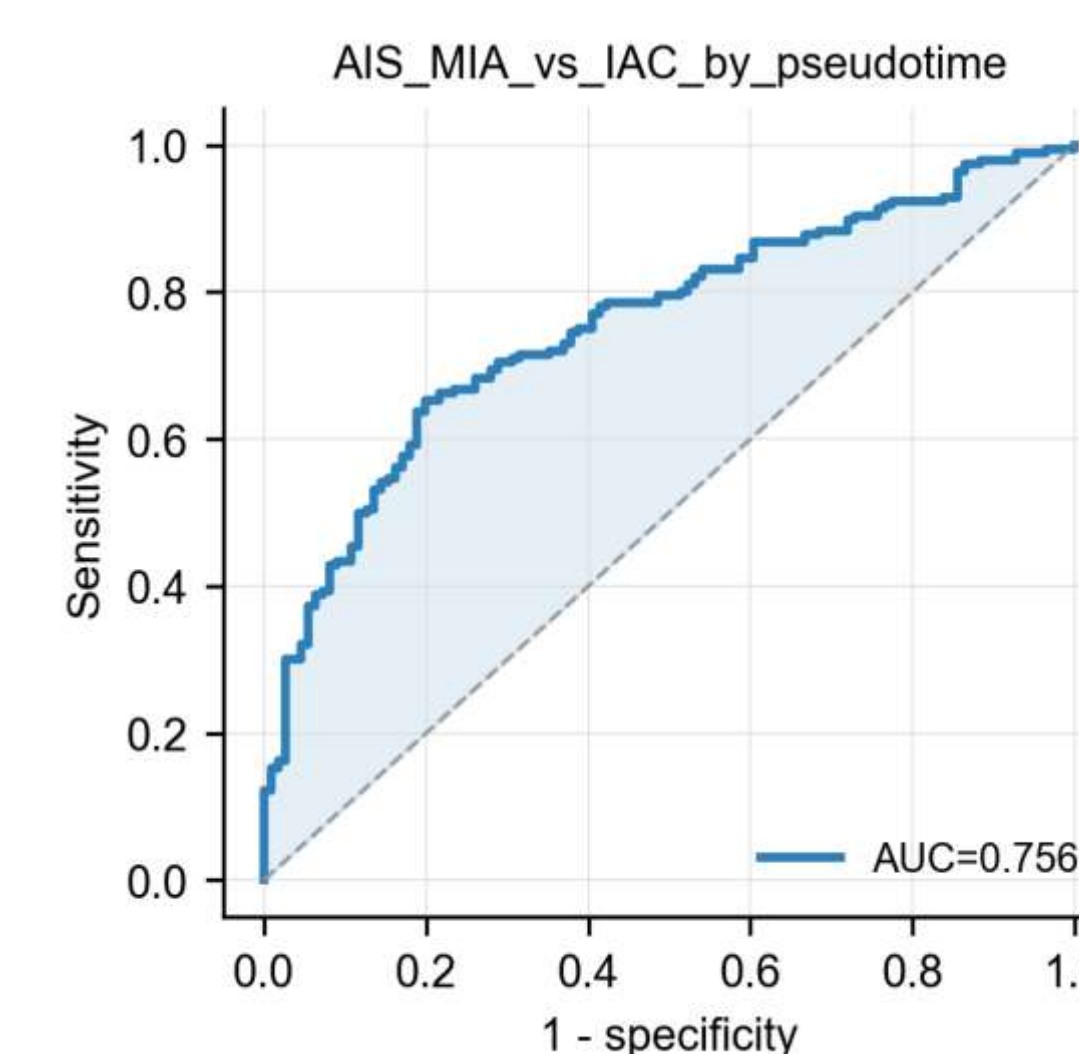


Figure 4. AUC of pseudotime trajectory model.

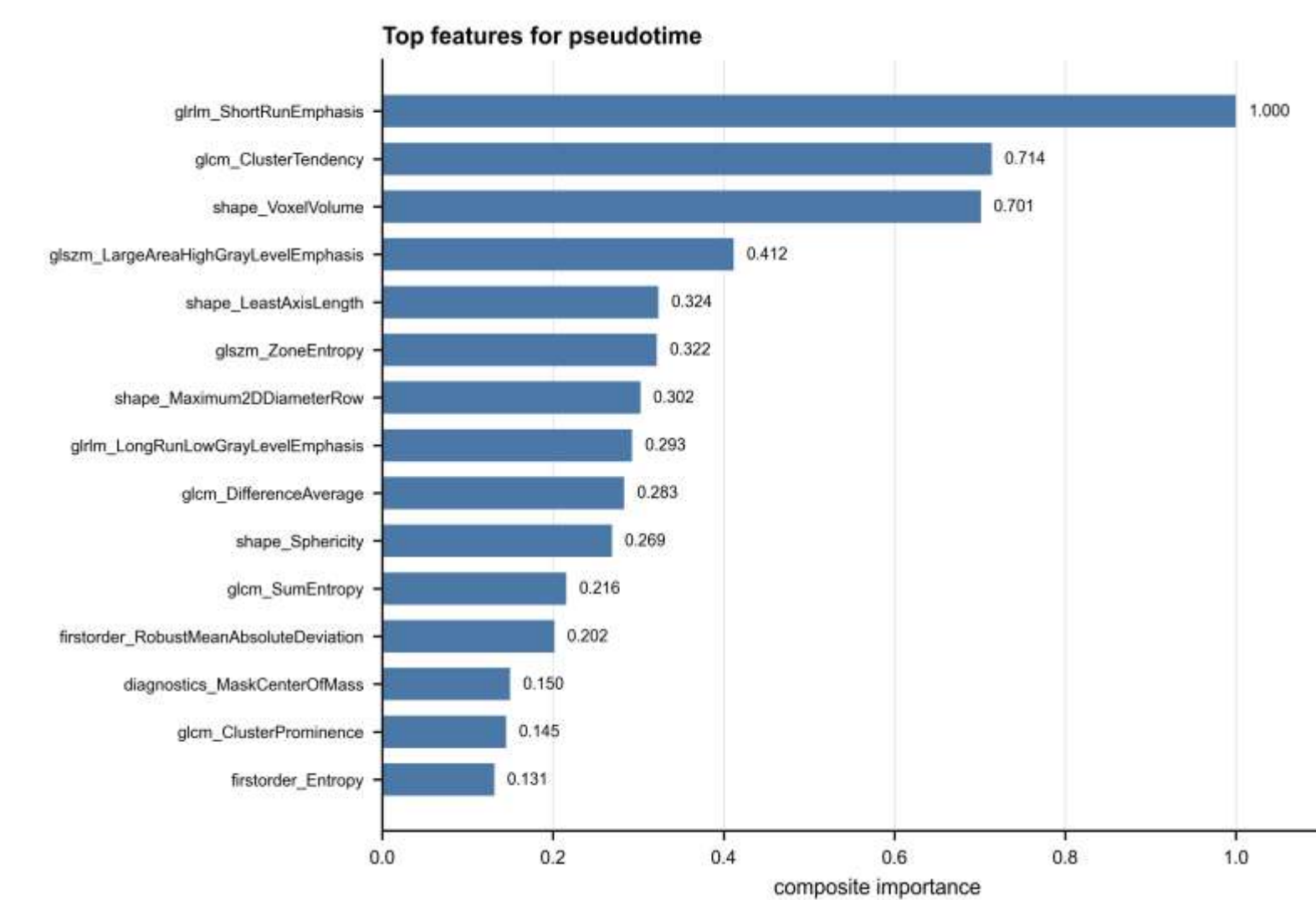


Figure 5. The main drivers of trajectory progression.

RadioabTrace reconstructed a continuous AIS-MIA-IAC trajectory, with MIA located at the transitional zone and IAC diverging into low- and high-risk branches. Pseudotime increased with pathological progression and distinguished invasive transformation. Branch score further separated high-risk IAC from low-risk IAC. Feature contribution analysis highlighted texture and shape features as major drivers of trajectory progression.

TAKE HOME MESSAGES

- 1 RadioabTrace models AIS–MIA–IAC progression as a continuous trajectory.
- 2 Pseudotime increases along pathological progression and separates AIS/MIA from IAC
- 3 Radiomic texture, tumor morphology, and protein phenotypes jointly contribute to invasive-risk divergence..

AI USE / ACKNOWLEDGEMENTS

AI USE STATEMENT

OpenAI Codex was used only for code refinement and data-processing efficiency. All analyses, interpretations, and conclusions were conducted and verified by the authors.

ACKNOWLEDGEMENTS

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