Annotation-free whole coronary radiomics for prediction of major adverse cardiovascular events

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Aims: Accurate prediction of major adverse cardiovascular events (MACE) from coronary CT angiography (CCTA) remains limited by approaches relying on manual plaque localization and lesion-level vulnerability analysis. We propose a fully automated framework for MACE prediction based on whole-coronary radiomics that eliminates the need for plaque annotation and provides a scalable approach to risk assessment.

Materials and methods: Coronary lumen and vessel wall geometries from 95 subjects (278 vessels) were reconstructed from CCTA using QAngioCT, and radiomic features were extracted from the volume enclosed between wall and lumen. Feature stability was assessed using morphological perturbations, and only robust features (ICC > 0.75) were retained. Multiple machine learning pipelines were evaluated via cross-validation. The best model was selected based on balanced accuracy and validated on an independent test set.

Results: The optimal pipeline combined correlation filtering, Mann–Whitney U test, and Minimum Redundancy Maximum Relevance with a LightGBM classifier achieving an accuracy of 0.85 and sensitivity of 0.88 on the independent test set. Four GLCM-based radiomic features were employed in the final model. SHAP analysis (see Figure 1) demonstrated that more organized and complex tissue patterns (high Imc and CS) may underlie lower-risk phenotypes while locally homogeneous patterns (high Corr) were associated with increased risk, potentially capturing more uniform tissue characteristics consistent with lipidic/necrotic components.

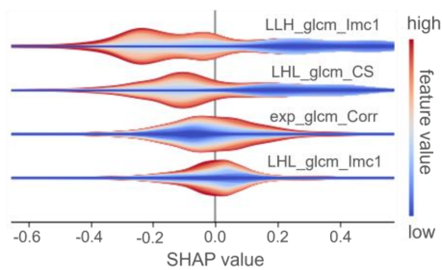

Figure 1. SHAP analysis.

Conclusion: This study introduces an annotation-free, whole-coronary radiomic framework for patient-level MACE prediction from CCTA. By leveraging the full coronary anatomy and explainable machine learning, the method enables automated, reproducible risk stratification without lesion annotation.