A Genotype-Guided Radiomics Signature Framework for Recurrence Prediction of Non-Small Cell Lung Cancer

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Non-small cell lung cancer (NSCLC), which accounts for about 80%-85% of lung cancer, is one of the malignant tumors with the highest morbidity and mortality. The postoperative recurrence rate in patients with NSCLC is high, which directly endangers the lives of patients. In recent years, recurrence prediction of NSCLC has largely focused on learning representations from computed tomography (CT) images. It has been shown that recurrence states can better characterized by gene. However, gene acquisition is expensive and invasive, and cannot meet the recurrence prediction requirements of all patients. In this study, we propose a genotype-guided end-to-end method that leverages rich gene knowledge to improve prediction results from CT images. In our method, a Residual Multilayer Perceptron (ResMLP)-based network is used to learn representations of genes that is most reflective of the recurrence, serving as a gene model (teacher model). Meanwhile, radiomics and a deep learning model are applied to extract features from CT images as a CT model (student model). A recalibration module employing Bidirectional Feature Alignment (BFA) loss is designed to align gene features and CT image features, transferring useful gene features to guide the student model trained from CT images. In the testing phase, NSCLC recurrence prediction can be achieved with only CT images. According to the experiment on the publicly available NSCLC radiogenomics dataset from the Open Research Cancer Imaging Archive (TCIA), the proposed method reached the state-of-the-art performance on all measurement indicators (accuracy 89.36, area under curve 0.86, specificity 0.91, sensitivity 0.89). These results can provide objective guidance for clinicians to formulate individualized treatment plans for NSCLC patients, effectively assist clinical decision-making, and significantly improve the survival rate of patients.