Variance in Segmentation of Lung Tumors: Creating Robust Radiomics Models in Lung Cancer

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Radiomics is a method for mining quantitative features from medical images. These texture features can be used to identify disease characteristics with better accuracy and efficiency than traditional screening methods. However, recent evidence suggests these features vary across different manual contouring methods, resulting in unreliable models. This experiment studied the impact of variability in manual contouring of lung nodules of CT scans on texture analysis. We compared three delineations across three datasets for a series of classification problems: (1) diagnosis of adenocarcinoma (n=51); (2) prediction of response to pemetrexed chemotherapy (n=95); (3) prognosis for patients undergoing tri-modality therapy (n=31). A series of experiments were performed measuring the stability of three different contours. Dice and Jaccard similarity indices returned mean values of 0.799 and 0.707, indicating high levels of similarity. Intratumoral and peritumoral texture features were extracted from each delineation, resulting in a concordance correlation coefficient of 0.754. The top four features were selected using the mRMR algorithm. Across all datasets and segmentations, the top feature belonged to the Laws level or the Laws edge family. Using the top selected features, simple LDA and QDA models were constructed for each segmentation, resulting in a standard deviation of 0.0423 for AUC and 0.0242 for ACC across different delineations. All models outperformed traditional screening methods. These results indicate that while variability in manual contouring leads to a certain amount of general feature variability during extraction, specific features are unaffected and can be used to create robust radiomics models with low variability and high accuracy.

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