

Comparisons and Validation of the Three Pulmonary Nodule Malignancy Risk Models (Brock, Radiomics, Deep Learning): A Secondary Analysis of Data from the National Lung Screening Trial

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Abstract: Lung cancer is the leading cause of cancer death worldwide each year. Non-invasive medical image technologies are becoming routine in screening high-risk populations for lung cancer patients. Different from the traditional radiological imaging analysis (e.g., manually interpreted by radiologists), the rapid progress of computational methods and artificial intelligence is leading to the extensive implementation of radiomics and/or deep learning in the medical image analysis. In particular, radiomics is the high-throughput extraction and analysis of the quantitative features from advanced medical images with the assistance from computer science to provide a comprehensive quantification of tumor phenotype for cancer patients, and deep learning generally refers to the application of deep neural networks (e.g., CNNs) to process and analyze medical images. In the past we have developed a panel of radiomic features to classify the benign from malignant lung nodules to reduce the unnecessary diagnostic interventions. In this study, we further analyzed the clinical and imaging data from the National Lung Screening Trial and constructed three risk models for discrimination of lung nodule malignancy: the Brock model built from the semantic features, our radiomic model built from the radiomic features, and the deep learning model built from transfer learning. The performance of the three models was thoroughly assessed and compared. In addition, external validation of using an independent cohort has been conducted to evaluate the accuracy of our models.