Lung Cancer Decision Support System: Novel Automated Noninvasive Tumor Malignancy and Patient Outcomes Prediction Modelling through Radiomics Phenotype Feature Quantification

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Lung cancer is the leading cause of cancer related deaths in the world. Despite therapeutic advances, the overall five year survival rate remains low, near 16%. Prediction of patient outcomes and tumor metastases suffers despite advancements in big data solutions. Medical imaging, through computed tomography (CT) scanning, provides routine, noninvasive phenotype tumor classification, but leaves clinical decisions to human intervention. Radiologists have a false negative rate of 7% and false positive rate of 66% in diagnosis. Characterization through genomics has been explored, however spatial and individual cell differentiation with institution technique variation limits success. The invasive procedures used reduce quality of life for already high risk patients. My research proposes a Lung Cancer Decision Support System (LCDSS) using quantitative automated phenotypical approach. Utilizing the emerging field of high-throughput, quantitative feature extraction, radiomics, LCDSS consists of a novel pipeline for prediction of malignancy, patient survival, and tumor metastases. Innovative EPEC image processing, contouring, and feature extraction methodology was developed to detect solitary pulmonary regions (SNRs) from 3-dimensional DICOM CT images. LCDSS was tested using 4682 biopsy-confirmed, CT scan slices from 61 patients. The accuracy of the tool was 96.1%, exceeding the hypothesis, with sensitivity and specificity of 94.4%, 97.0%. The LCDSS thus allows accurate, consistent, noninvasive, and efficient analysis of lung cancer with high accuracy in prediction, paving path towards personalized treatment. Future work will focus on deep learning for novel feature creation and retrospective clinical trials to further improve accuracy and better understand tumor development.