A Matter of Life and Breath: Early Lung Cancer Detection via Deep Learning CT Scan Analysis and DNA Methylation/exRNA Sequencing

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The American Cancer Society projects that over 135,000 Americans will die from lung cancer in 2020. It is recognized that the earlier lung cancer is detected, the higher the survival rate and the lower the treatment cost. However, current detection methods, such as human-interpreted imaging tests and tissue biopsies, can be inaccurate, dangerous, and costly. The purpose of this project is to identify lung cancer earlier and more accurately through a minimally invasive blood-based liquid biopsy test using epigenetic signatures of DNA methylation in lung cancer, extracellular RNA sequencing, and deep learning CT scan analysis. A novel application of targeted bisulfite padlock probing for DNA methylation sequencing was applied to 43 plasma samples total, 23 with NSCLC lung cancer. 8 samples were first tested as a pilot study. For RNA sequencing, cDNA synthesis was performed and the cDNA were prepared for sequencing. Several deep learning architectures and parameter modifications were tested on various datasets and preprocessing methods for the lung cancer nodule classification task. Using Keras and convolutional neural networks, an average accuracy of 93% and AUC of 0.98 were achieved for nodule classification. RNA sequencing prep did not work but significant improvements were shown in RNA/cDNA quality after modifications. DNA methylation sequencing results showed high separation between cancer and control and many statistically significant methylation signature differences were identified between lung cancer and control samples, especially for lung adenocarcinoma in particular.

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