A Deep Learning Method for Tumor Region Identification and Tumor Proportion Score Estimation for PD-L1 Expression in Non-Small Cell Lung Carcinoma

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Overview

PD-L1 (Programmed Death Ligand 1) protein expression has emerged as an important predictive biomarker for identifying patients with advanced lung cancer most likely to respond to immunotherapy.

We propose a computational technique using Deep Learning for detecting the cancer regions and calculating the Tumor Proportion Score (TPS) for PD-L1 expression, in immunohistochemically stained sections from Non-Small Cell Lung Carcinoma (NSCLC).

Methods

Tumor Proportion Score is the ratio between the PD-L1 positive tumor cells to the total tumor cell count. Thus, our proposed approach uses a two stage setup that first segments the tumor region from the tissue, followed by tumour cell instance segmentation.

Tumor Region segmentation is performed using DeepLabV3+ [1] architecture. This eliminates regions including benign epithelium, lymphocytes, and necrosis, from the calculation of the TPS.

At the second stage, we deploy a modified HoverNet [2] nuclei instance segmentation model that uses dual encoder with input at two different resolutions for greater context. The model categorises nuclei into PD-L1 positive, PD-L1 negative tumour cells, and lymphocytes, with the former two used for final scoring.

Results

Our proposed approach achieved a sensitivity of 90.1% and specificity of 96.9% in cancer region segmentation.

We evaluated the performance of the proposed dual stage approach at WSI level by comparing the TPS calculated by our computational method and that determined by an expert pathologist.

We observed a Pearson’s Coefficient of 0.91 that signifies a strong correlation between observations of the computational method and the pathologist.

Dataset

The Deep Learning models were trained using anonymised, de-identified Whole Slide Images (WSI) from 41 patients of NSCLC with varying PD-L1 scores. Anonymised, de-identified WSIs from another 57 patients were used as test data for pathological validation.

WSIs with tumor region as well as nuclei boundaries, marked by expert pathologists, were used to train the Deep Learning models.

Conclusion

We demonstrate the application of Deep Learning algorithms for rapid determination of PD-L1 expression on IHC stained Whole Slide Images of NSCLC, showing a high correlation with Tumor Proportion Score determined by expert pathologists (Pearson’s Coefficient of 0.91).

References