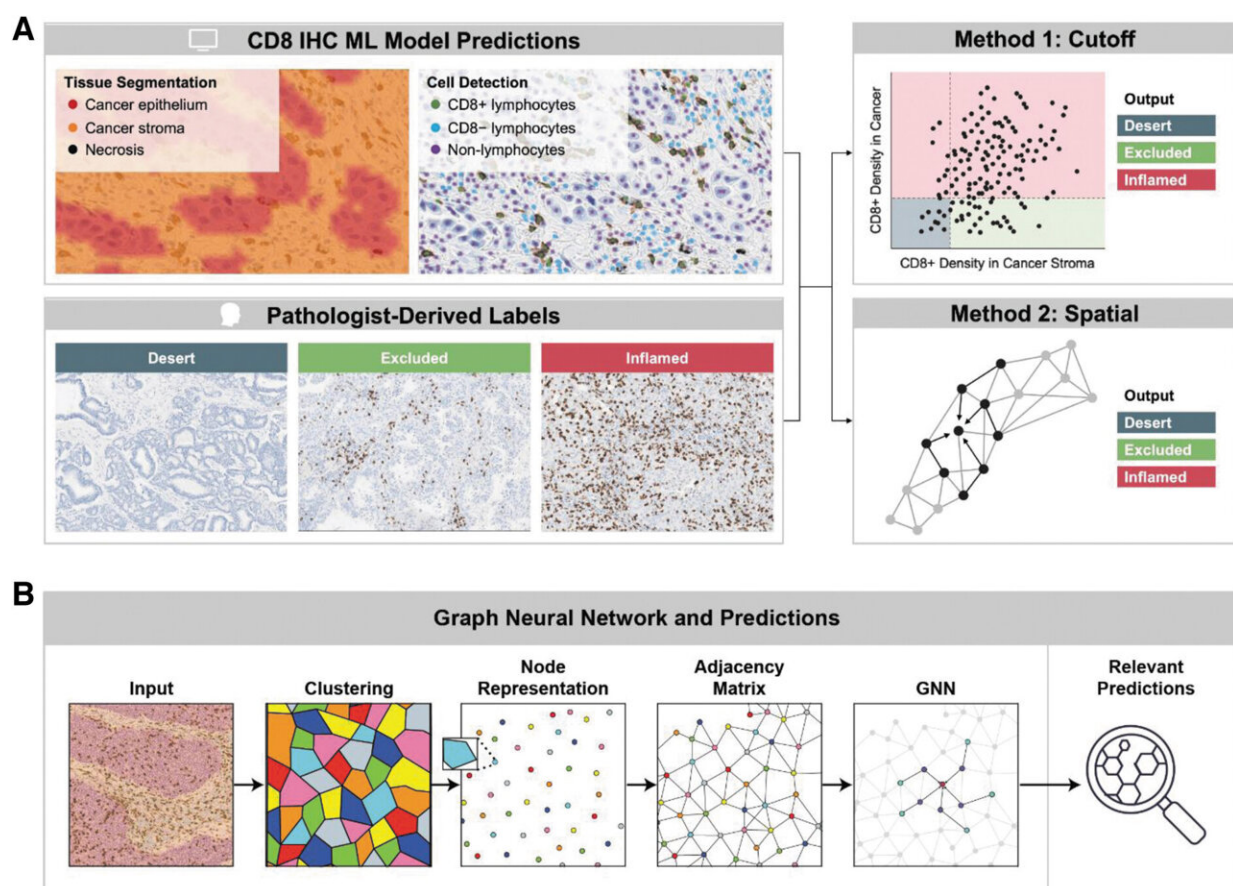# Using machine learning to identify patients with cancer that would benefit from immunotherapy

April 16 2024, by Kathryn Ryan

Digital pathology approaches to immune phenotyping. **(A)** Two ML models were developed using digitized WSIs to classify tissue regions (e.g., cancer epithelium, stroma, and necrosis) and cell types (e.g., CD8$^+$, CD8$^-$, and nonlymphocytes). In the first approach (Method 1), data-driven cutoffs were applied to model-generated HIFs of CD8$^+$ lymphocyte count proportion within the cancer

epithelium and stroma to classify samples as desert, excluded, or inflamed. In the second approach (Method 2), all tissue and cell model predictions were used to train a GNN to classify samples as desert, excluded, or inflamed. **(B)** For the spatial model, an unsupervised GNN was applied to CD8 IHC WSI. This GNN was trained to discover tissue patterns defined by the spatial arrangement of CD8$^+$ cells and other cell types relative to cancer epithelium and stroma. GNN, graphical neural network; HIFs, human interpretable features; IHC, immunohistochemistry; ML, machine learning; WSIs, whole slide images. Credit: *AI in Precision Oncology* (2024). DOI: 10.1089/aipo.2023.0008

A new study examines the development of two machine learning models to classify the immunophenotype of a cancer specimen.

The digital pathology approach presented can characterize and classify cancer immunophenotypes in a reproducible and scalable fashion, holding promise for the application of such a. method to identify patients that may benefit from immunotherapy in non-small cell lung cancer (NSCLC), according to the study published in *AI in Precision Oncology*.

The cellular composition of the tumor immune microenvironment is a key contributor to the response of the tumor to immunotherapy. TGF-ß signaling is known to promote immune exclusion, where CD8$^+$ T cells are in the surrounding stromal tissue but not within the tumor itself.

To better identify patients who are immune-excluded, Rui Wang, from Sanofi, and co-authors developed two machine learning models to quantify CD8$^+$ cell positivity and classify the immunophenotype of a cancer specimen in patients with NSCLC.

"Our results support the potential use of machine learning-predicted cancer immunophenotypes to identify patients that may benefit from

immunotherapy and TGF-ß blockage in NSCLC," concluded the investigators.

"This research points towards improvements in patient identification for drug candidacy, utilizing AI and machine learning to pinpoint precise biomarkers for immunotherapy in NSCLC. It signifies progress towards personalized medicine, promising treatments tailored to individual patient profiles for greater effectiveness and minimized side effects."

"Essentially, it emphasizes the importance of directing new treatments to the right patients, paving the way for a new era of precision in cancer care," says Douglas Flora, MD, Editor-in-Chief of *AI in Precision Oncology*.

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