

Precision Histopathology: Automated Cell Classification on H&E-stained Images for Personalized Medicine

Stanford researchers have developed an innovative approach for accurate and automated cell classification on H&E-stained images using multiplexed immunofluorescence (mIF) imaging, eliminating human annotations, and enhancing biological interpretability in histopathology.

Accurate and reliable cell classification using Hematoxylin and Eosin (H&E) staining is crucial for disease diagnosis, yet challenges persist using current methods which rely on error-prone and time-consuming manual annotations. Moreover, existing AI approaches lack interpretability and struggle with spatial resolution limitations, hindering precise analysis of cell types. Hence, prior efforts at automation have been hampered by inefficient manual annotation processes, limiting analysis to few cell types, and yielding suboptimal results.

To address these challenges, Stanford researchers have developed an innovative method using mIF imaging to accurately classify cells in H&E-stained images, providing a robust ground truth based on protein markers. This approach enables the identification of diverse cell types with higher accuracy and generates extensive data for training deep learning models. By training on this ground truth, deep learning models outperform existing methods, facilitating precise cell type identification for personalized treatment decisions in precision medicine. In summary, this automated cell classification approach not only eliminates manual annotations but also ensures reliable, accurate and biologically interpretable results, marking a significant advancement in histopathology.

Stage of Development

Software Prototype. Next steps involve validating model in lung tumors and expanding to different tumor types. Future steps also involve spatial analysis to

predict patient outcomes, paving the way for companion diagnostics in immunotherapy.

Applications

- Discovery of novel predictive biomarkers for personalized cancer therapy.
- Biomarker discovery for predicting immunotherapy response in cancer patients.
- Companion diagnostics in cancer immunotherapy.
- Discovery of novel spatial biomarkers within the tumor microenvironment at single-cell level.

Advantages

- Accurate classification of cell types on H&E images, without human annotations.
- Granular due to reliance on protein markers, identifying diverse cell types.
- Scalable across diverse patient populations with potential for personalized medicine.
- Generates vast amounts of data for training advanced deep learning models.
- Allows to generate a single-cell map from histopathology images with high cellular resolution.
- Provides biologically interpretable results, when compared to black-box models.

Innovators

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