PathAI

Oncology Publications

Advancing the understanding of Cancer through Digital Pathology

Manuscripts

2024

Spatial mapping of immunosuppressive cancer-associated fibroblast gene signatures in H&E-stained images using additive multiple instance learning
Markey and Kim et al., *bioRxiv*

AI powered quantification of nuclear morphology in cancers enables prediction of genome instability and prognosis
Abel et al., *npj Precision Oncology*

Adjuvant Trastuzumab Emtansine Versus Paclitaxel Plus Trastuzumab for Stage I Human Epidermal Growth Factor Receptor 2-Positive Breast Cancer: 5-Year Results and Correlative Analyses From ATEMPT
Tarantino et al., *Journal of Clinical Oncology*

Scoring PD-L1 Expression in Urothelial Carcinoma: An International Multi-Institutional Study on Comparison of Manual and Artificial Intelligence Measurement Model (AIM-PD-L1) Pathology Assessments
Rüschoff et al., *Virchows Archiv*

Spatial Architecture of Myeloid and T Cells Orchestrates Immune Evasion and Clinical Outcome in Lung Cancer
Enfield et al., *Cancer Discovery*

Classification of the Tumor Immune Microenvironment Using Machine-Learning-Based CD8 Immunophenotyping as a Potential Biomarker for Immunotherapy and TGF-β Blockade in Nonsmall Cell Lung Cancer
Pomponio et al., *AI in Precision Oncology*

2023

Artificial intelligence–powered assessment of pathologic response to neoadjuvant atezolizumab in patients with non-small cell lung cancer: results from the LCMC3 study
Dacic et al., *Journal of Thoracic Oncology*

Manuscripts

2022

Association of artificial intelligence-powered and manual quantification of programmed death-ligand 1 (PD-L1) expression with outcomes in patients treated with nivolumab ± ipilimumab
Baxi et al., *Modern Pathology*

Distinct hepatic immunological patterns are associated with the progression or inhibition of hepatocellular carcinoma
Mirshahi et al., *Cell Reports*

2021

Human Interpretable Features Derived from Densely Mapped Cancer Pathology Slides Predicts Diverse Molecular Phenotypes
Diao et al., *Nature Communications*

Oral Presentations

2023

Comparison of digital vs. manual PD-L1 tumour scoring on SP263-stained whole imaging slides from Impower110
Herbst et al., *World Congress on Lung Cancer*

Digital pathology-based prognostic & predictive biomarkers in metastatic non-small cell lung cancer
Qamra et al., *AACR Annual Meeting*

2021

Artificial intelligence (AI) powered pathologic response assessment of resection specimens after neoadjuvant atezolizumab in patients with non-small cell lung cancer: results from LCMC3 study
Dacic et al., *ASCO Annual Meeting*

2020

Clinical/biomarker data for neoadjuvant atezolizumab in resectable stage IB-IIIB NSCLC: primary analysis in the LCMC3 study
Carbone et al., *World Congress on Lung Cancer*

The role of AI-based digital pathology tools in immune-oncology programs at Bristol-Myers Squibb (BMS)
Baxi et al., *Pathology Visions*

2019

Artificial intelligence-powered retrospective analysis of PD-L1 expression in nivolumab trials of advanced non-small cell lung cancer
Baxi et al., *SITC Annual Meeting*

Posters

2024

Immune phenotypes derived from H&E-stained whole slide images correlate with prognosis and response to checkpoint inhibitors in NSCLC
Le et al., *ASCO Annual Meeting*

Association of machine learning (ML)-derived histological features with transcriptomic molecular subtypes in advanced renal cell carcinoma (RCC)
Beig et al., *ASCO Annual Meeting*

Correlation between machine learning-based characterization of HER2 protein expression by immunohistochemistry and response to neoadjuvant treatment in HER2+ breast cancer
Kurt et al., *USCAP Annual Meeting*

Machine learning (ML)-spatial quantification of the tumor microenvironment (TME) identifies differences associated with response to bintrafusp alfa (BA) vs pembrolizumab (PEM) treatment in the Phase 3 INTR@PID Lung 037 study
Abel et al., *AACR Annual Meeting*

Spatial markers of immune response and distribution reveal heterogeneity within immune-phenotype subgroups
Le et al., *AACR Annual Meeting*

Unsupervised detection of stromal phenotypes with distinct fibrogenic and inflamed properties in NSCLC
Patel et al., *AACR Annual Meeting*

Foundation AI models predict molecular measurements of tumor purity
Gerardin et al., *AACR Annual Meeting*

2023

Accurate quantification of slide-level HER2 scores in breast cancer using a machine-learning model, AIM-HER2 Breast Cancer
Shanis et al., *San Antonio Breast Cancer Symposium*

Posters

Digital Pathology Models reveal Case-Specific Characteristics of the Tumor Microenvironment
Gerardin et al., *San Antonio Breast Cancer Symposium*

Prediction of PAM50 molecular subtypes from H&E-stained breast cancer specimens using tumor microenvironment features and additive multiple instance learning models
Guramare et al., *San Antonio Breast Cancer Symposium*

Artificial Intelligence-Based Prediction of Oncotype DX Score from whole slide images using human-interpretable features and breast biomarkers
Le et al., *San Antonio Breast Cancer Symposium*

Deep learning models identify key tumor microenvironment features associated with genetic signatures of UV mutagenesis and alkylating agent treatment in melanoma
Nofallah et al., *SITC Annual Meeting*

Quantification of tumor infiltrating lymphocytes (TILs) from pathology slides reflects molecular immune phenotypes
Shen et al., *SITC Annual Meeting*

Quantifying the effect of microsatellite instability and mismatch repair deficiency on the tumor microenvironment
Conway et al., *SITC Annual Meeting*

Clinical Validation of an Artificial Intelligence (AI) Algorithm for PD-L1 Quantification in Non-Small Cell Lung Cancer (NSCLC)
Walk et al., *CAP Annual Meeting*

Machine-learning enabled quantification of colocalized multiplex IHC signals with spectral overlap
Tahir et al., *AACR-NCI-EORTC Molecular Targets and Cancer Therapeutics*

Artificial Intelligence (AI) Analysis of Histological Images Accurately Identified Luminal Subtypes Urothelial Carcinomas Characterized by High Proliferator-Activated Receptor Gamma (PPARG) Expression
Kirov and Parmar et al., *AACR-NCI-EORTC Molecular Targets and Cancer Therapeutics*

Posters

Spatially-resolved prediction of gene expression signatures associated with LRRC15+ cancer-associated fibroblasts in H&E whole slide images using additive multiple instance learning models
Markey and Kim et al., *AACR-NCI-EORTC Molecular Targets and Cancer Therapeutics*

Cell type identification using multiplex immunofluorescence (mIF)-guided machine learning in DLBCL
Chhor et al., *EHA Annual Meeting*

Artificial intelligence (AI)-based classification of stromal subtypes reveals associations between stromal composition and prognosis in NSCLC
Najdawi et al., *AACR Annual Meeting*

Development of a high-throughput image processing pipeline for multiplex immunofluorescence whole slide images at scale
Tahir et al., *AACR Annual Meeting*

Digital SP263 PD-L1 tumor cell scoring in non-small cell lung cancer achieves comparable outcome prediction to manual pathology scoring
Prizant and Shamshoian et al., *AACR Annual Meeting*

Machine Learning Models Identify Key Histological Features of Renal Cell Carcinoma Subtypes
Vilchez et al., *AACR Annual Meeting*

Comparison of an Artificial Intelligence Measurement Model (AIMM) versus Manual Scoring in Gastric Cancer (GC) Samples Stained with Programmed Death Ligand 1 (PD-L1) Immunohistochemistry (IHC) pharmDx 28-8 and 22C3 Assays
Kumar and Badve et al., *USCAP Annual Meeting*

Comparison of an Artificial Intelligence Measurement Model (AIMM) versus Manual Scoring by Pathologists in Bladder Cancer (BC) Samples Stained with Programmed Death Ligand 1 (PD-L1) Immunohistochemistry (IHC) pharmDx 28-8 and 22C3 Assays
Kumar and Badve et al., *USCAP Annual Meeting*

Posters

Development of Machine Learning Powered Models for Prostate Cancer HRD Prediction
Nercessian et al., *ASCO Genitourinary Cancers Symposium*

2022

A Sensitive Machine Learning-Based Approach to Assess Multiple Myeloma t(11;14) Genetic Subtype From Histopathology Images
Stanford-Moore et al., *ASH Annual Meeting*

Quantitative analysis of fiber-level collagen features in H&E whole-slide images predicts neoadjuvant therapy response in patients with HER2+ BC
Nguyen et al., *San Antonio Breast Cancer Symposium*

AI-based quantitation of cancer cell and fibroblast nuclear morphology reflects transcriptomic heterogeneity and correlates with survival in breast cancer
Abel et al., *San Antonio Breast Cancer Symposium*

Machine learning-based characterization of the breast cancer tumor microenvironment for assessment of neoadjuvant-treatment response
Kirkup et al., *San Antonio Breast Cancer Symposium*

Identification of clinically relevant spatial phenotypes in large-scale multiplex immunofluorescence data via unsupervised graph learning in non-small cell lung cancer
Egger et al., *SITC Annual Meeting*

Concordance analysis of AI-powered CD8 quantification and automated CD8 topology with manual histopathological assessment across seven solid tumor types
Guramare et al., *SITC Annual Meeting*

Characteristics of the tumor microenvironment in IDH1-mutated cholangiocarcinoma patients from ClarIDHy trial
Saatcioglu et al., *SITC Annual Meeting*

Posters

A multi-tumor machine learning model to identify tertiary lymphoid structures (TLS) in histopathological H&E images as a potential clinical biomarker
Matos-Cruz et al., *SITC Annual Meeting*

Artificial intelligence–powered immune phenotyping of advanced or metastatic urothelial carcinoma clinical trial samples from hematoxylin and eosin–stained whole slide images
Conway et al., *SITC Annual Meeting*

Generation of an atlas characterizing the tumor immune microenvironment via AI-based histologic mapping of multiple cancer types at scale
Conway et al., *Pathology Visions*

AI-powered analysis of nuclear morphology associated with prognosis in high-grade serous carcinoma
Michener et al., *EMSO Annual Meeting*

Digital Pathology Uncovers Multi-Omic Hallmarks of Lung Cancer in Histopathology Images
Guramare et al., *World Congress on Lung Cancer*

Deep-Learning–Based Prediction of c-MET Status From Digitized H&E-Stained Non-small Cell Lung Cancer Tissue Samples
Rajan et al., *World Congress on Lung Cancer*

AI-powered segmentation and analysis of nuclear morphology predicts genomic and clinical biomarkers in multiple cancer types
Abel et al., *AACR Annual Meeting*

Artificial Intelligence–Powered and Manual Assessment of PD-L1 Are Comparable in Predicting Response to Neoadjuvant Atezolizumab in Patients With Resectable Non-Squamous, Non-Small Cell Lung Cancer
Abel et al., *AACR Annual Meeting*

Quantification of TGFβ protein levels and digital pathology-based immune phenotyping reveal biomarkers for TGF-β blockade therapy patient selection in NSCLC
Pomponio et al., *AACR Annual Meeting*

Posters

Application of an interpretable graph neural network to predict gene expression signatures associated with tertiary lymphoid structures in histopathological images
Shen et al., *AACR Annual Meeting*

Machine Learning Analysis of H&E Lung Adenocarcinoma Tumor Microenvironment Shows Association of Human Interpretable Histopathological Features with KEAP1 Mutations
Egger et al., *AACR Annual Meeting*

AIM PD-L1-NSCLC: Artificial intelligence-powered PD-L1 quantification for accurate prediction of tumor proportion score in diverse, multi-stain clinical tissue samples
Griffin et al., *AACR Annual Meeting*

2021

The utility of AI-powered spatial classification of intratumoral CD8+ immune-cell topology in predicting overall survival in patients with melanoma as part of the CheckMate 067 clinical trial
Lee et al., *SITC Annual Meeting*

Machine Learning Models can Quantify CD8 positivity in Melanoma Clinical Trial Samples
Glass et al., *SITC Annual Meeting*

Machine learning model PD-L1 22C3 scoring of a multi-scanner, real-world reference laboratory NSCLC dataset generates scores comparable with manual pathologist scoring
Brutus et al., *CAP Annual Meeting*

Machine Learning Models to Quantify HER2 for Real-Time Tissue Image Analysis in Prospective Clinical Trials
Glass et al., *ASCO Annual Meeting*

Deep learning identifies pathobiological features within H&E images associated with genomic alterations and progression on anti-PD(L)1 in HUDSON, an AstraZeneca-sponsored Phase II clinical trial
Dillon et al., *AACR Annual Meeting*

Posters

Robust Deployment of ML Models Quantifying the H&E Tumor Microenvironment in NSCLC subjects from an AstraZeneca-sponsored Phase II Clinical Trial
Dillon et al., *AACR: AI, Diagnostics, and Imaging*

2020

Deep-Learning Based Prediction of Homologous Recombination Deficiency (HRD) Status from Histological Features in Breast Cancer, a research study
Taylor-Weiner et al., *San Antonio Breast Cancer Symposium*

Artificial intelligence analysis of advanced breast cancer patients from phase I trial of Trastuzumab Deruxtecan: HER2 and histopathology features as predictors of clinical benefit
Modi et al., *ESMO Annual Meeting*

Association of digital and manual quantification of tumor PD-L1 expression with outcomes in nivolumab-treated patients
Duan et al., *AACR Annual Meeting*

Machine learning based identification of predictive features of the tumor microenvironment and vasculature in NSCLC patients using the IMpower150 study
Taylor-Weiner et al., *ASCO Annual Meeting*

2019

An Empirical Framework for Validating Artificial Intelligence–Derived PD-L1 Positivity Predictions Applied to Urothelial Carcinoma
Beck et al., *SITC Annual Meeting*

Artificial Intelligence powered predictive analysis of atypical ductal hyperplasia from digitized pathology images
Kerner et al., *San Antonio Breast Cancer Symposium*

CD8+ T Cells in Tumor Parenchyma and Stroma by Image Analysis and Gene Expression Profiling: Potential Biomarkers for Immuno-oncology Therapy
Szabo et al., *ASCO Annual Meeting*