What is immune exclusion?
Employee: University Hospital Dresden, University Hospital Heidelberg

Scientific advisory board member, consulting: Owkin (Paris / New York), Panakeia (London), DoMore Diagnostics (Oslo), Histofy (Warwick)

Shareholder: StratifAI GmbH (Germany)

Honoraria for lectures: MSD, Eisai, Fresenius, Roche, Bayer, BMS, Pfizer
What is immune exclusion?

Figure 1  T-cell infiltration patterns in resected human non-small cell lung carcinomas (NSCLCs). (A–C) Representative multicolor immunofluorescence micrographs of NSCLC sections stained with DAPI for all cells/nuclei (blue), CD8 for cytotoxic T-cells (red) and cytokeratin for tumor epithelial cells (CK, green). The tumor infiltrating lymphocyte patterns represent the extremes of a continuum. Figure was contributed by coauthor Dr Kurt Schalper from Yale University. The multiplexed immunofluorescence staining protocols, including tumor and tumor infiltrating lymphocyte markers, was adapted part of a previously studied retrospective cohort. 26 Bar=1 mm.
Can we use computer-based image analysis?
Brightfield microscopy image analysis

A. Diagram showing a tumor and normal tissue.

B. Images labeled CD3 and Hematoxylin, showing positive and negative results.

C. Color-coded diagrams indicating inner, outer, and tumor core margins.
The tool of choice: QuPath

QuPath v0.4.4 is now available!

QuPath
Open Software for Bioimage Analysis

Different immune cells: it is complicated.

Kather et al., eLife 2018
Is immune exclusion a continuum?

Kather et al., eLife 2018
It depends on the tumor type!

Kather et al., eLife 2018
It depends on the tumor type!

Kather et al., eLife 2018
How can computational pathology help?
Strong supervision

original image

strong labels

Class A

Class B

Weak supervision

weak labels

Negative

Positive

Negative

Positive

Deep Learning yields surprisingly good results when trained on weakly labeled data
Genotype determines the phenotype

Deep Learning predicts genotype

now available as a product for clinical use in the EU
Immunotherapy response prediction from pathology (in HCC)

Artificial intelligence predicts immune and inflammatory gene signatures directly from hepatocellular carcinoma histology, Zeng et al., Journal of Hepatology, 2022
AI-Immunoscore with multimodal models

Multistain deep learning for prediction of prognosis and therapy response in colorectal cancer

Sebastian Foersch, Christina Glaeser, Ann-Christin Wörl, Markus Eckstein, Daniel-Christoph Wagner, Stefan Schulz, Franziska Keilers, Aurelie Fernandes, Konstantina Tsereia, Michael Kloth, Arnold Hartmann, Achim Heintz, Wilko Welcher, Wilfried Reth, Carola Geppert, Jakob-Nikolas Kathar, Moritz Jesinghaus, Foersch et al., Nature Medicine, 2023
About us

We are the research group “Clinical Artificial Intelligence”: a young, diverse, and interdisciplinary group of scientists. We use computational methods to extract actionable knowledge from clinical routine data. Our main tools are Artificial Intelligence and Computational Modeling. We combine these tools with a clinical perspective on health and disease. Our main area of expertise is precision.
Be part of a young, interdisciplinary group of scientists.

WE WANT YOU
Researcher
All Levels

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