

Colon cancer - using digital tools to search for old and new biomarkers

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Potential conflicts of interest

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Consulting / Advisory Board / Collaboration

Owkin, France

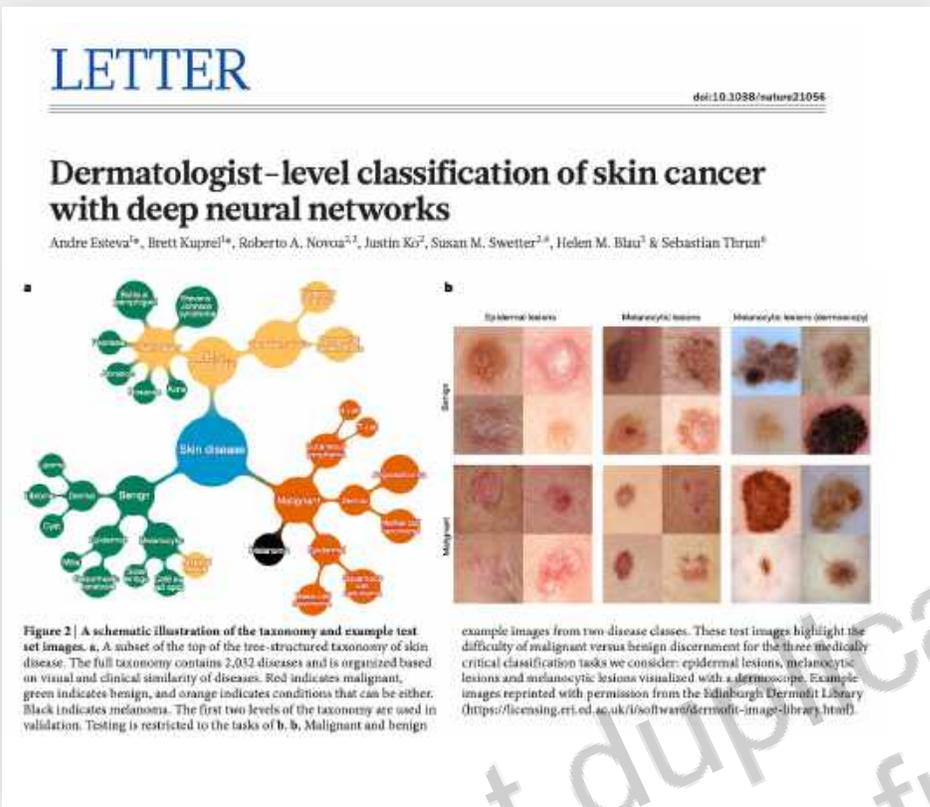
Panakeia, UK

MSD

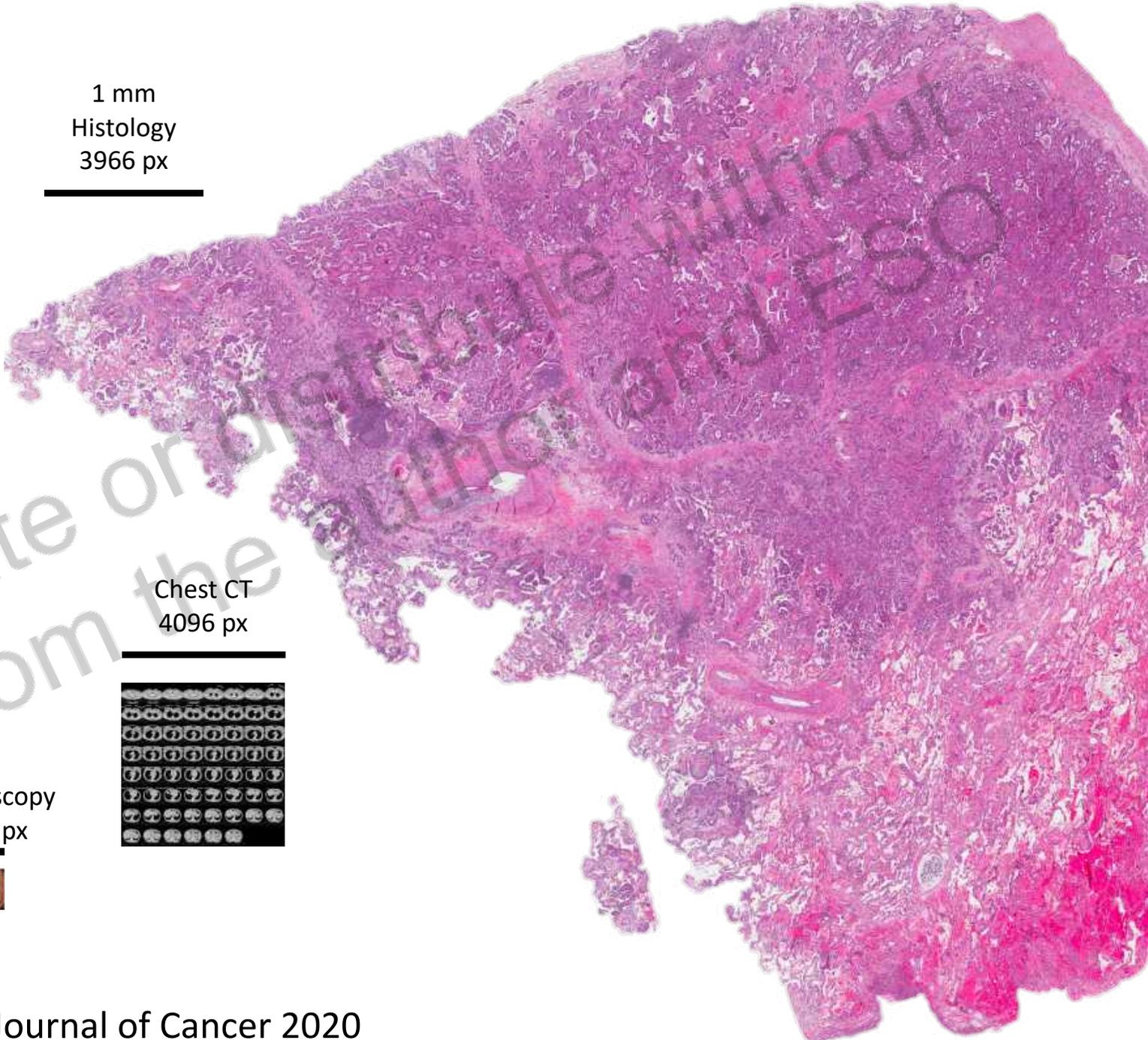
Eisai

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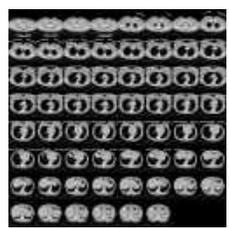
Image classification



1 mm
Histology
3966 px



Chest CT
4096 px



Colonoscopy
1024 px

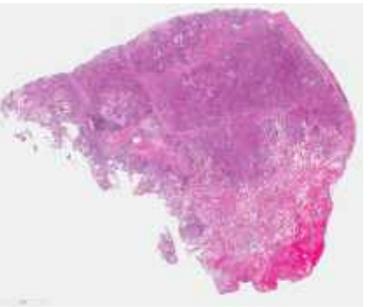


Dermoscopy
299 px

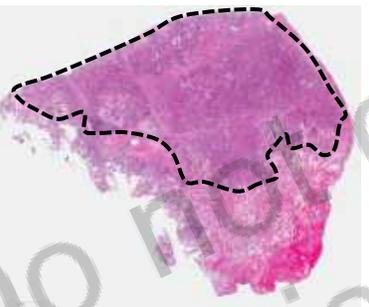


How does it work?

a tumor detection

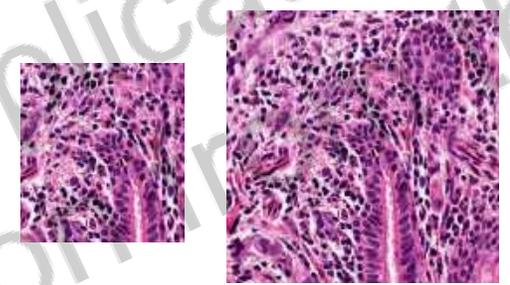
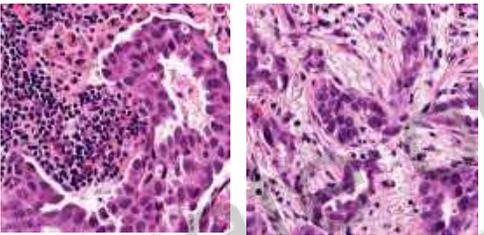
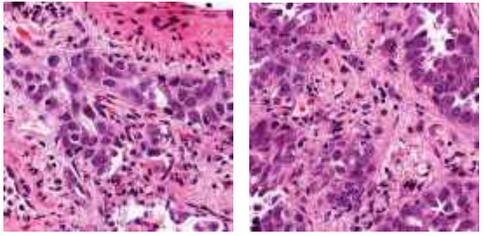


Option 1: weakly supervised learning



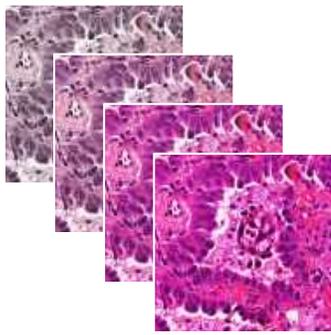
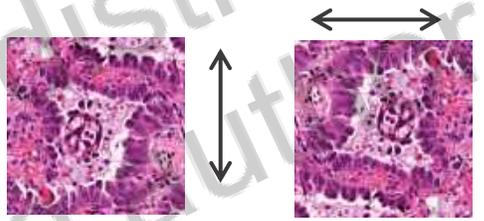
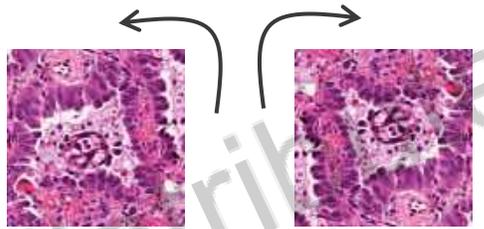
Option 2: restrict to tumor tissue

b library preparation



← size and magnification may vary →

c preprocessing



d training and testing



Option 1: train-test split

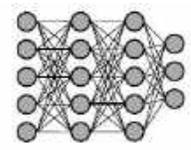


Option 2: cross-validation



Option 3: external testing

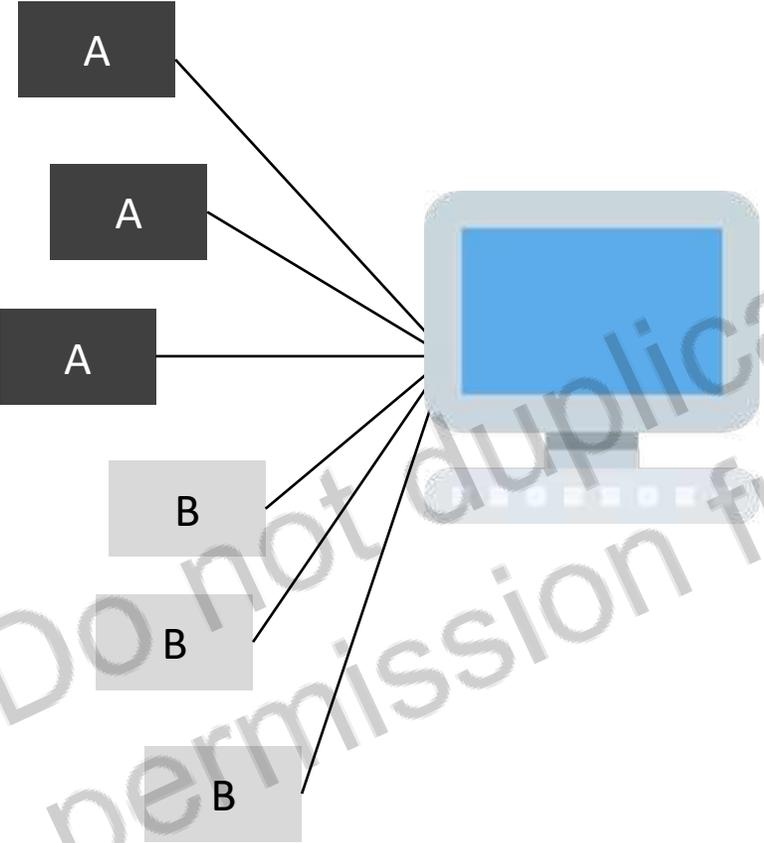
e external validation



The principle of supervised deep learning

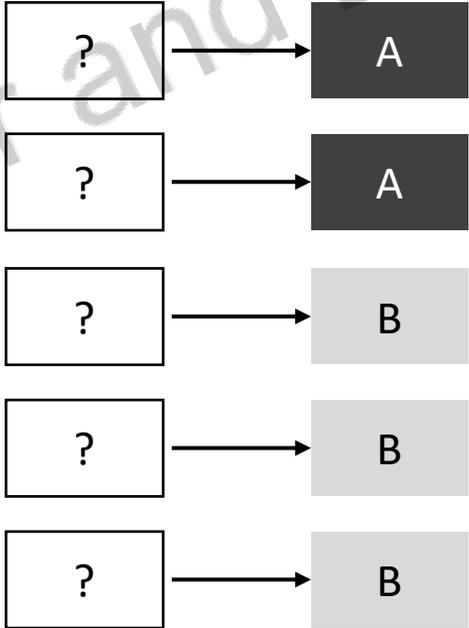
*supervised, unsupervised,
reinforcement learning*

Train



trained
neural
network

Apply



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Image classification is easy



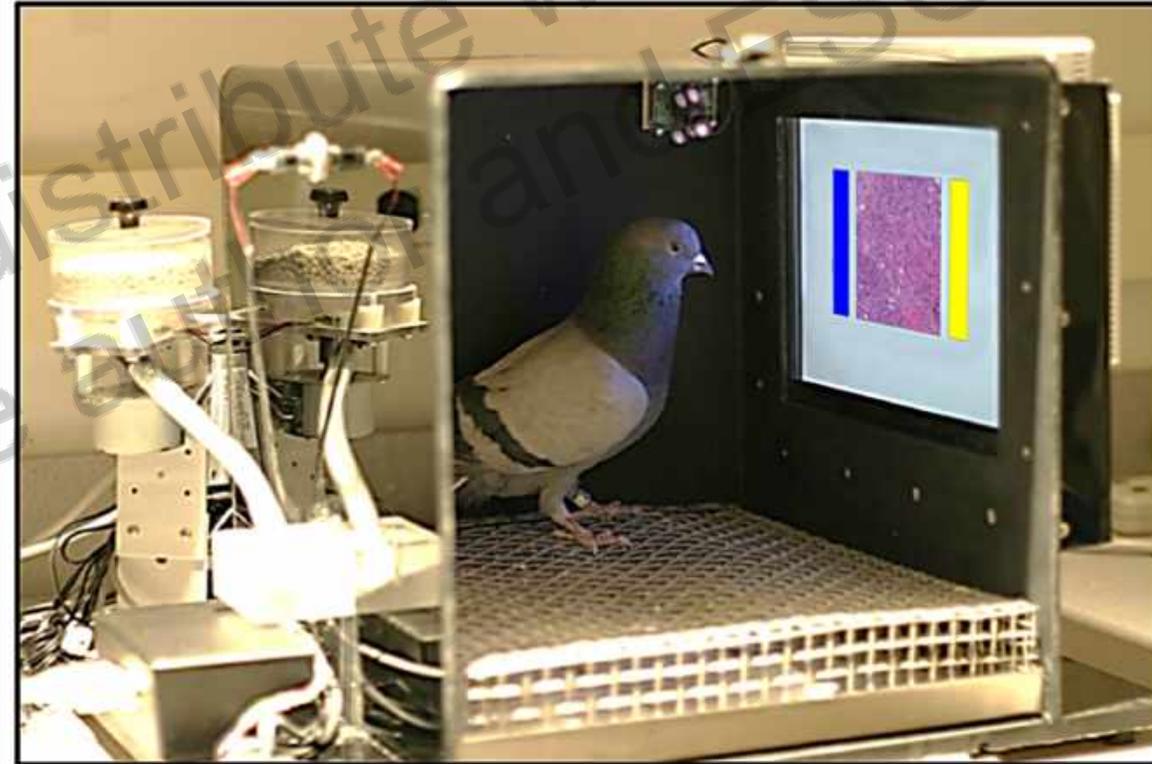
RESEARCH ARTICLE

Pigeons (*Columba livia*) as Trainable Observers of Pathology and Radiology Breast Cancer Images

Richard M. Levenson^{1*}, Elizabeth A. Krupinski³, Victor M. Navarro², Edward A. Wasserman^{2*}

¹ Department of Pathology and Laboratory Medicine, University of California Davis Medical Center, Sacramento, California, United States of America, ² Department of Psychological and Brain Sciences, The University of Iowa, Iowa City, Iowa, United States of America, ³ Department of Radiology & Imaging Sciences, College of Medicine, Emory University, Atlanta, Georgia, United States of America

* levenson@ucdavis.edu (RML); ed-wasserman@uiowa.edu (EAW)



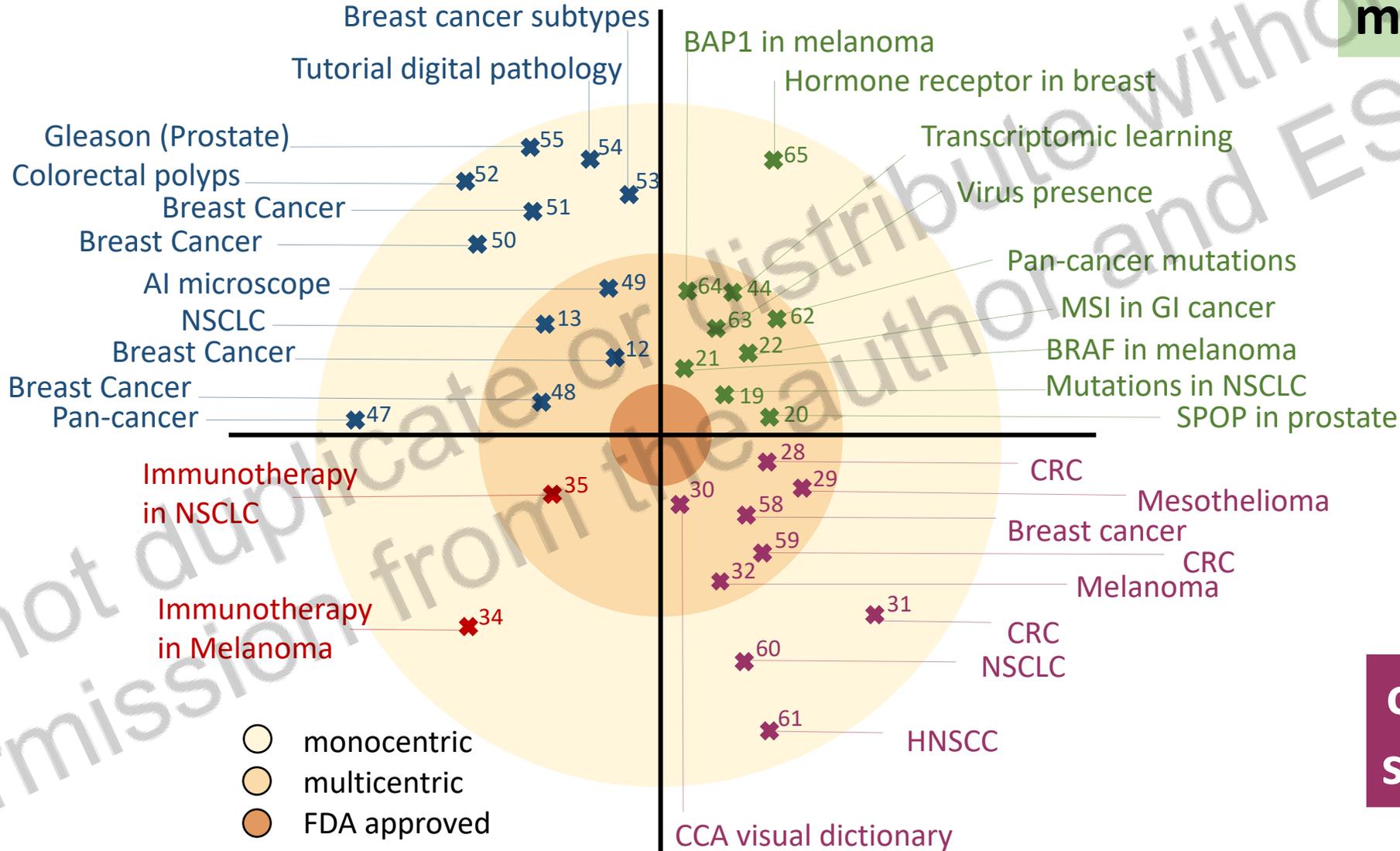
What is the context?

tumor
or not?

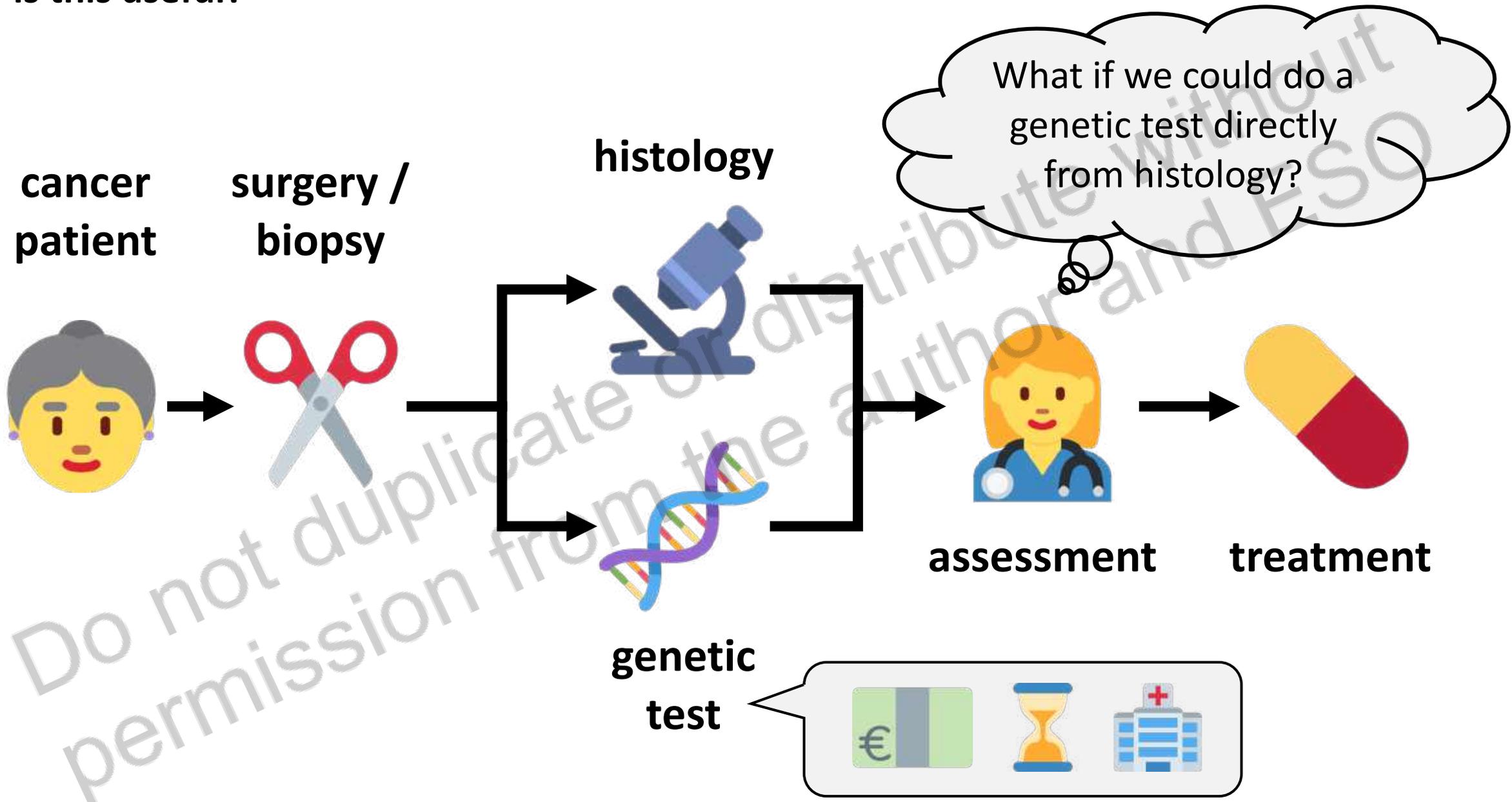
mutations

treatment
response

overall
survival

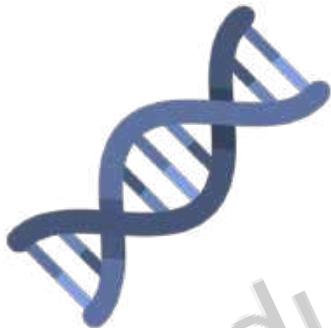


Why is this useful?



Hypothesis

Specific genetic alterations in cancer ...



... elicit changes in the phenotype of ...



- tumor cells (1st order)
- TME (2nd order)

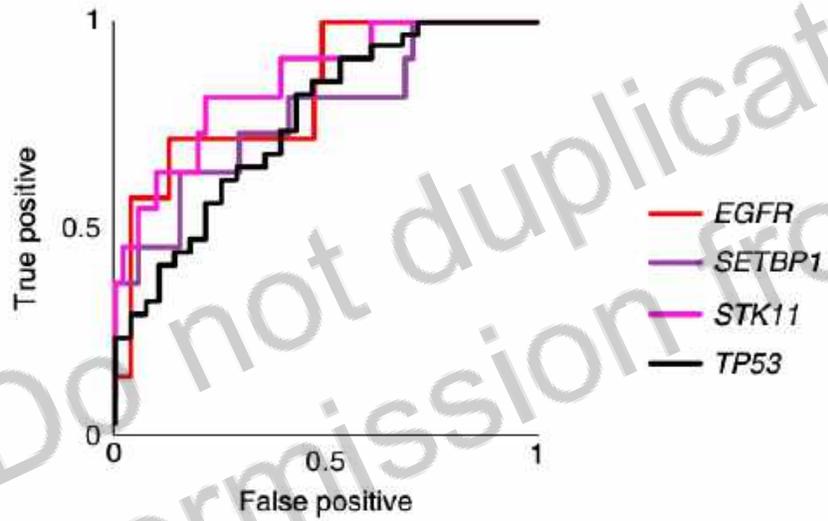


Deep learning can infer genotype from histology images

Histology-based genotyping

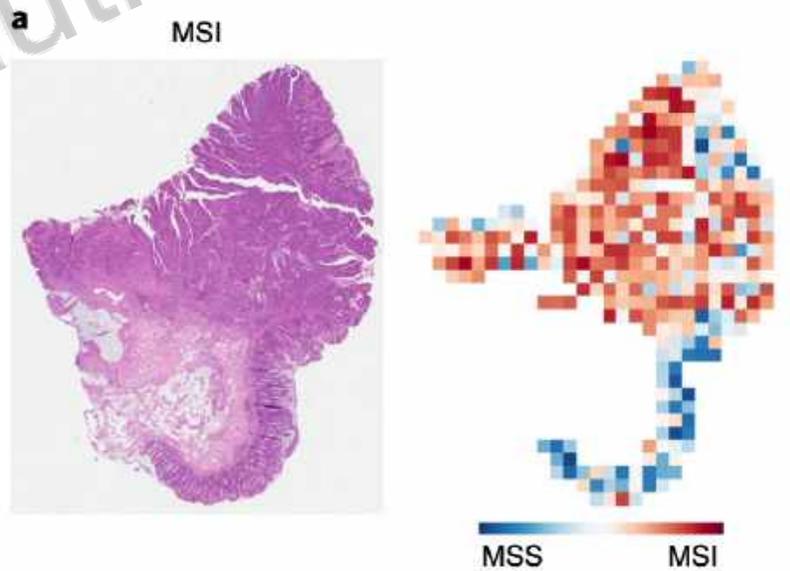
Classification and mutation prediction from non-small cell lung cancer histopathology images using deep learning

Nicolas Coudray^{1,2,9}, Paolo Santiago Ocampo^{3,9}, Theodore Sakellaropoulos⁴, Navneet Narula³, Matija Snuderl³, David Fenyo^{5,6}, Andre L. Moreira^{3,7}, Narges Razavian^{8*} and Aristotelis Tsirigos^{1,3*}



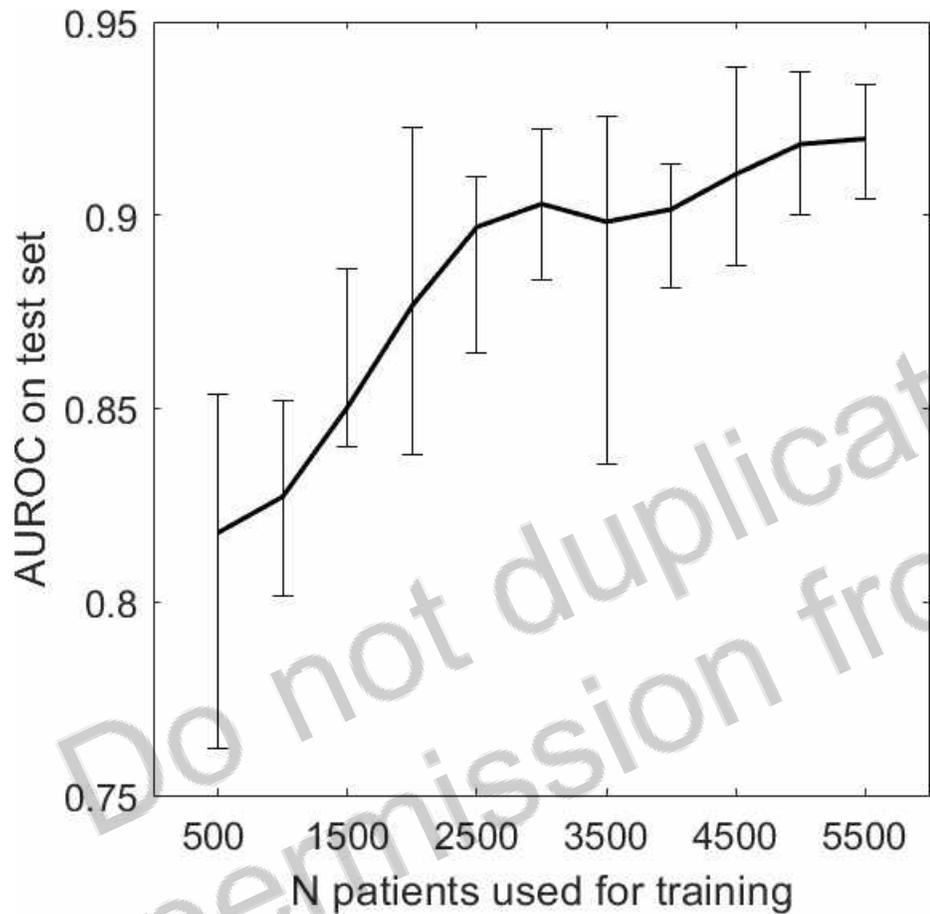
Deep learning can predict microsatellite instability directly from histology in gastrointestinal cancer

Jakob Nikolas Kather^{1,2,3,4,5*}, Alexander T. Pearson⁴, Niels Halama^{2,5,6}, Dirk Jäger^{2,3,5}, Jeremias Krause¹, Sven H. Loosen¹, Alexander Marx⁷, Peter Boor⁸, Frank Tacke⁹, Ulf Peter Neumann¹⁰, Heike I. Grabsch^{11,12}, Takaki Yoshikawa^{13,14}, Hermann Brenner^{2,15,16}, Jenny Chang-Claude^{17,18}, Michael Hoffmeister¹⁵, Christian Trautwein¹ and Tom Luedde^{1*}

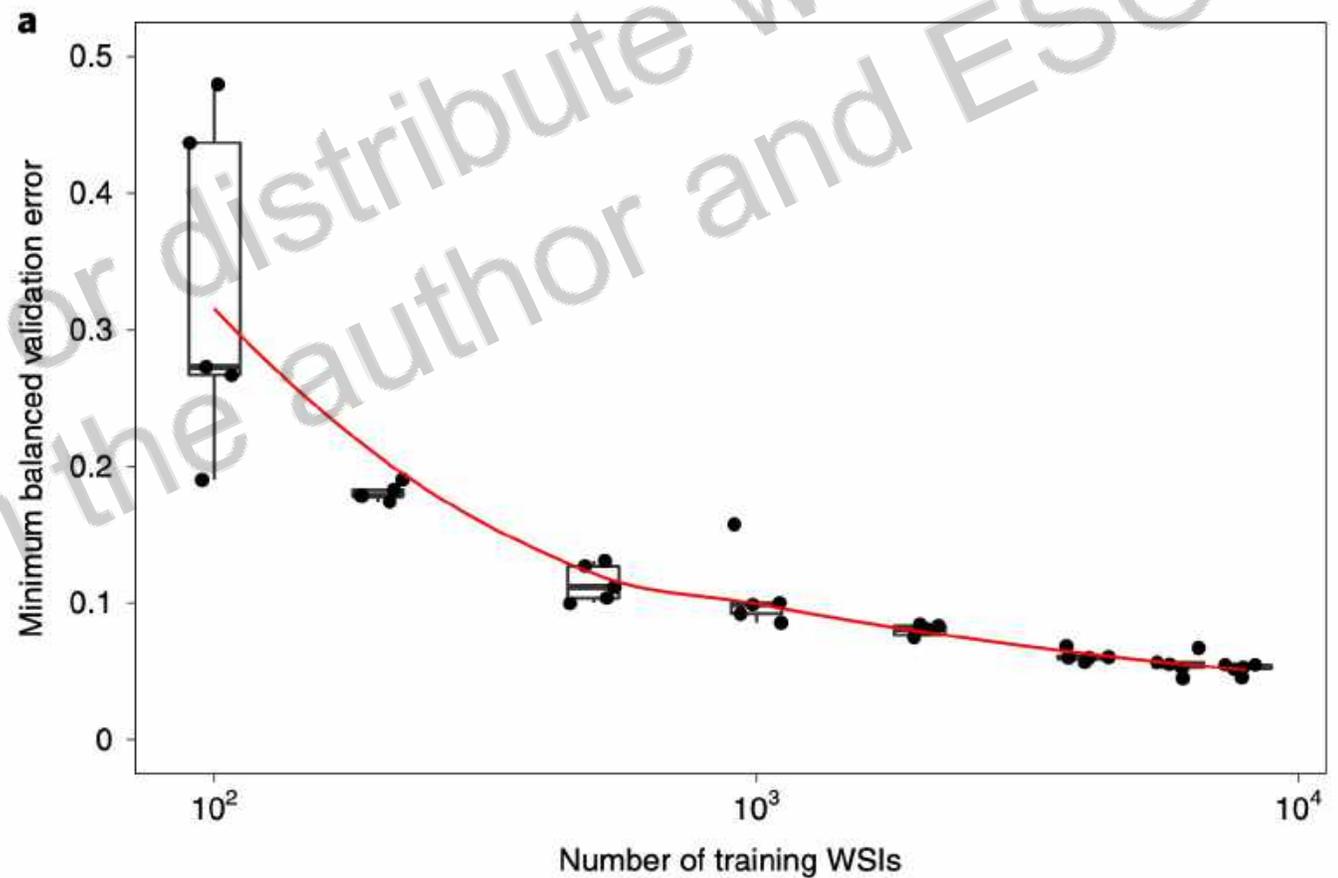


How many patients should we train on?

learning curve for MSI detection
(test on n=906)



learning curve for weakly supervised
prostate cancer detection

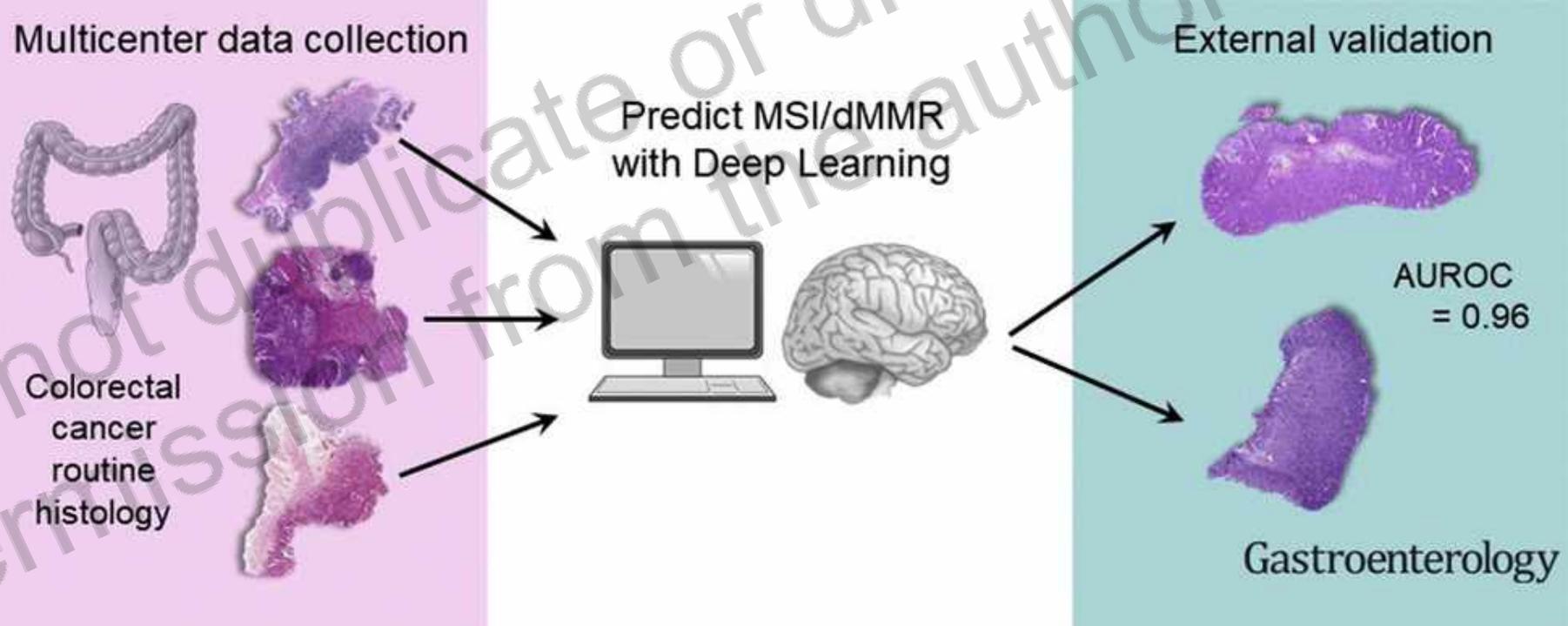


Multicentric, retrospective validation

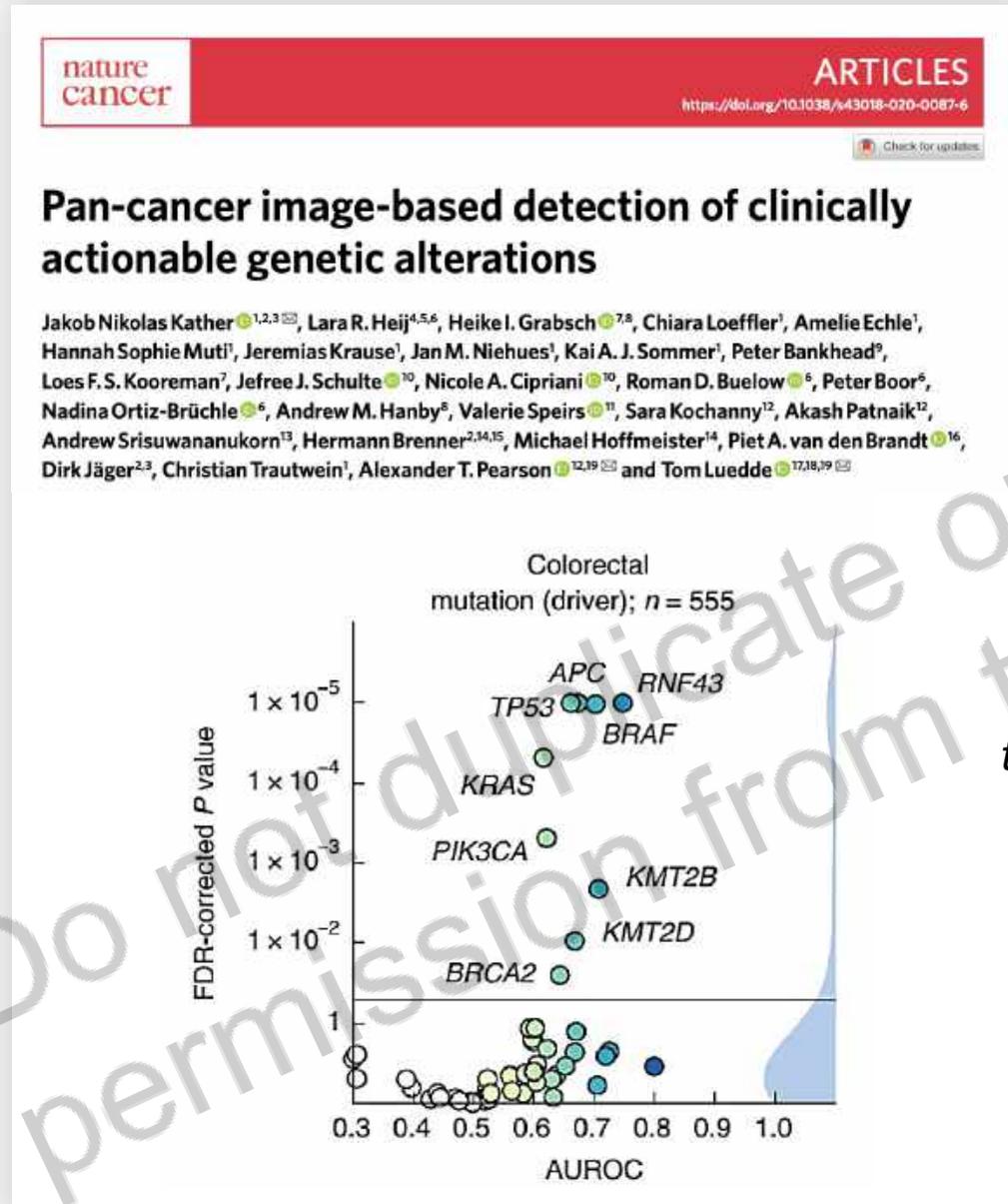
Clinical-Grade Detection of Microsatellite Instability in Colorectal Tumors by Deep Learning



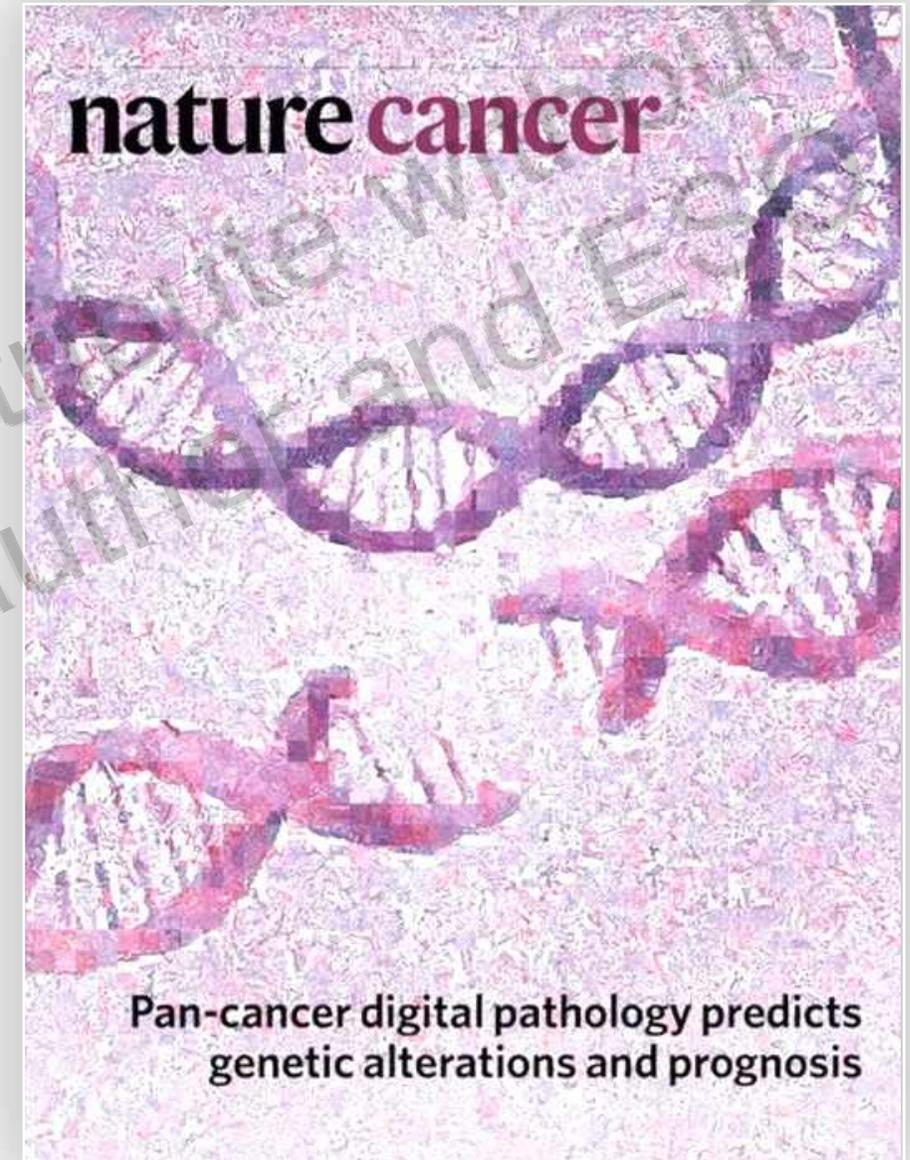
Amelie Echle,¹ Heike Irmgard Grabsch,^{2,3} Philip Quirke,³ Piet A. van den Brandt,⁴ Nicholas P. West,³ Gordon G. A. Hutchins,³ Lara R. Heij,^{5,6,7} Xiuxiang Tan,^{5,6,7} Susan D. Richman,³ Jeremias Krause,¹ Elizabeth Alwers,⁸ Josien Jenniskens,⁴ Kelly Offermans,⁴ Richard Gray,⁹ Hermann Brenner,^{8,10,11} Jenny Chang-Claude,^{12,13} Christian Trautwein,¹ Alexander T. Pearson,¹⁴ Peter Boor,⁷ Tom Luedde,^{1,15} Nadine Therese Gaisa,⁷ Michael Hoffmeister,⁸ and Jakob Nikolas Kather^{1,3,11,16}



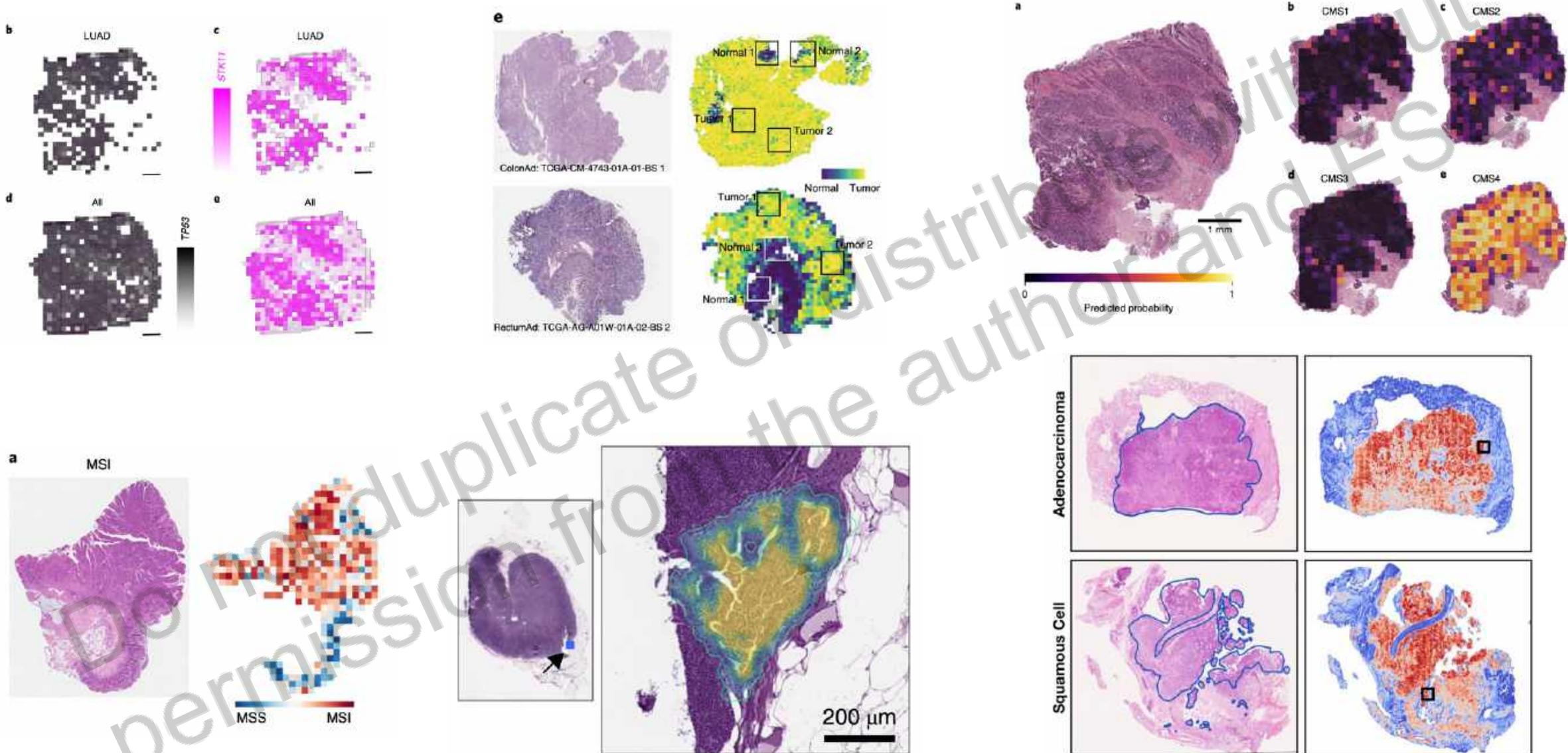
Pan-cancer application



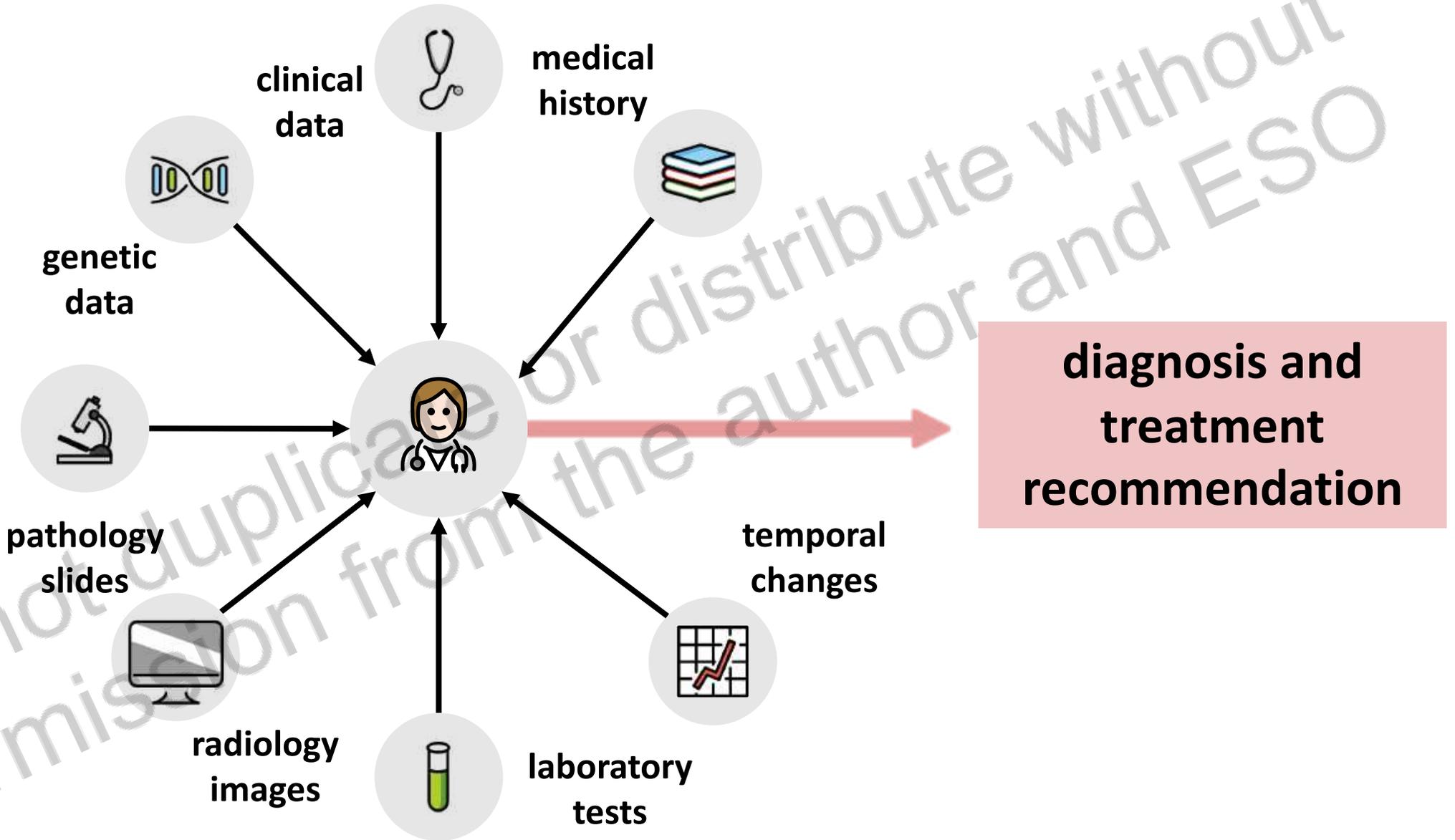
BRAF is directly targetable (2nd line)



Training with only slide labels yields spatially resolved predictions



Real-world decision-making



Human plus AI

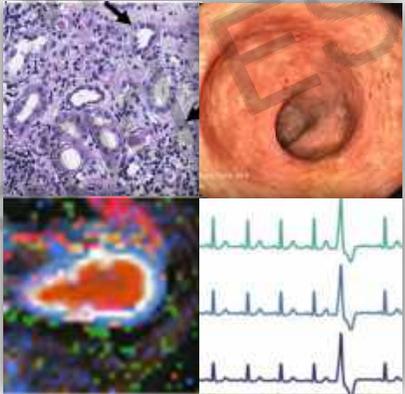
Hardware



Algorithms



Data



Ask the right questions and implement in the real world





Welcome

About us

We are a young, interdisciplinary group of scientists using computational methods to decipher cancer. Our main tools are **Deep Learning** and **Computational Modeling**. We combine these tools with a **clinical perspective** on cancer genomics, targeted treatment and immunotherapy. Our focus is **gastrointestinal cancer**, including cancer of the bowel, stomach, liver and pancreas. To learn more about our research, have a look at our featured [publications](#) or find our most recent preprints and papers below.

Support and awards



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