

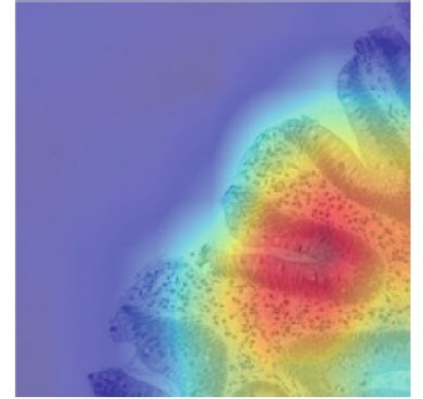
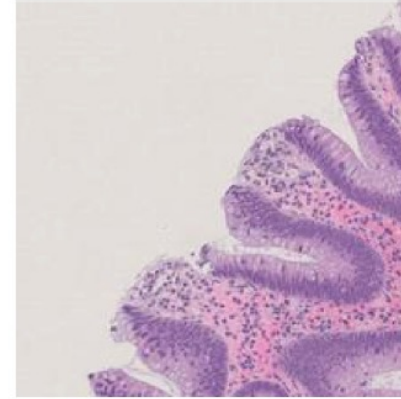


L' intelligenza artificiale nella diagnostica istologica degli adenomi: l'esperienza Torinese

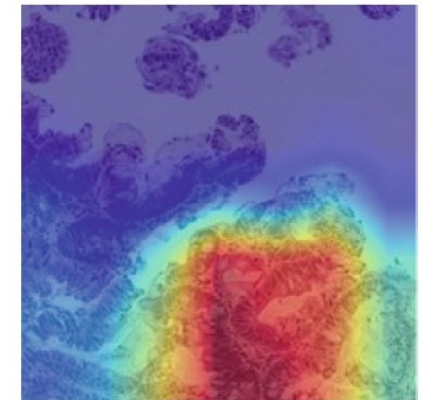
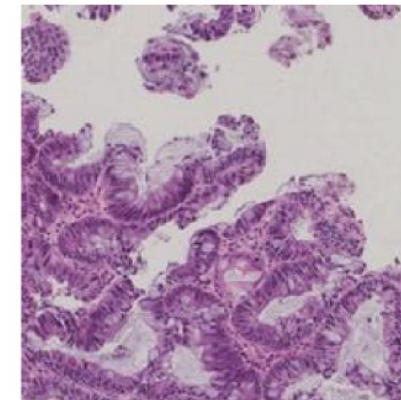
L. BERTERO

Div. of Pathology, Dept. Medical Sciences

University of Turin, Italy



(b) HP



(d) HG



Deep learning in histopathology: the path to the clinic

Jeroen van der Laak^{1,2}✉, Geert Litjens¹ and Francesco Ciompi¹

Computational pathology

Feature engineering



Deep learning

Explicit programming

Automated learning

Box 1 | Definitions

Deep learning

A machine learning approach in which algorithms are trained for a specific task (or set of tasks) by exposing a multilayered artificial neural network to (typically a large amount of) training data, without the need for handcrafted engineering of features to be extracted from the data. The resulting algorithm has learned a hierarchical representation of the data that is subsequently used for tasks such as classification, detection or segmentation. The term deep refers to artificial neural networks built using many layers, in other words a deep neural network.

Digital pathology

The digitization of the traditional diagnostic process of analyzing cells and tissue with a microscope via whole-slide scanners and computer screens.

Computational pathology

The computational analysis of digital images obtained through scanning slides of cells and tissues.

Radiomics/pathomics

Techniques to extract a (usually very large) set of features from radiological or histopathological digital images, respectively, using computational algorithms of data analysis. These features are successively used to feed (usually supervised) prediction models targeting clinically relevant end points, such as prognosis.

End-to-end training

In the context of machine learning models, possibly consisting of a pipeline with multiple steps, end-to-end training refers to the procedure of learning the optimal value of all parameters of a model simultaneously rather than sequentially (that is, one step at a time).

Whole-slide images

Digital images obtained by digitizing complete histopathological glass slides using a high-resolution scanner.

Convolutional neural networks

Deep learning approach consisting of a series of convolutional layers to process data (usually bi-dimensional) from input to output. Each layer implements the convolution operation between the input data and a set of filters (that is, small matrices), whose numerical values are automatically learned in an end-to-end training fashion.

Graphics processing units

Microprocessor specifically designed to process many data samples simultaneously, such as parts of digital images or features extracted from images.

Image segmentation

The operation of decomposing the semantic content of an image into multiple segments, where each segment contains pixels belonging to the same semantic category (for example, the tumor region).

U-Net models

Deep learning models based on two convolutional neural networks, one that encodes the input image into a set of features, and one that decodes those features to produce a segmentation output. The name, introduced in 2015 by Ronneberger et al.¹⁴⁵, indicates the U shape that the two convolutional neural networks form, where the encoder and decoder are connected via skip connections.

Data augmentation

The operation of artificially modifying some properties of input data (for example, image contrast, orientation, color and so on) with the aim of feeding a computational model with multiple variations of the same piece of data.

Model regularization

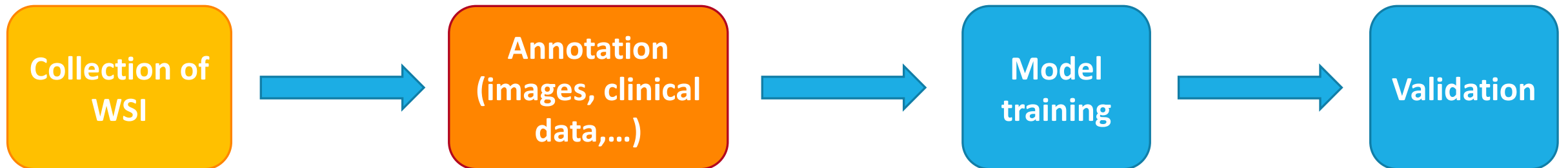
In machine learning, indicates the process of constraining a model's parameters to small values, discouraging complex models, therefore reducing the risk of overfitting the training data.

- Predetermined feature selection
- Multiple interactions pathologists/informaticians needed
- Time consuming



- Automated learning
- Freely available source codes of effective neural network architectures
- Superior results in most cases

Deep learning overall workflow:



ImageNet Large Scale Visual Recognition Competition (ILSVRC)

- Since ~2010
- Efficacy of CNN (convolutional neural networks)

CAMELYON challenge

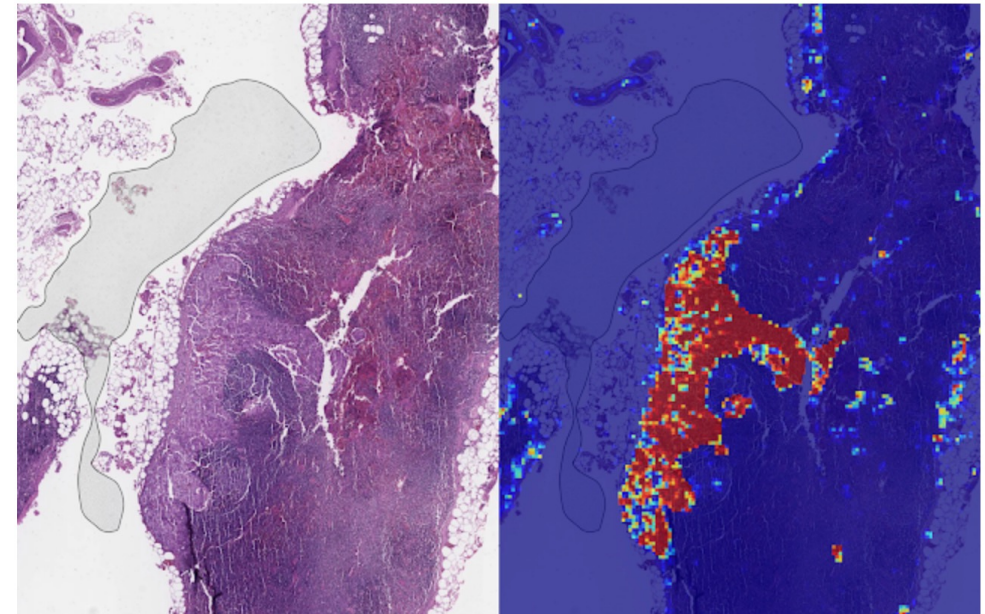
- Breast cancer metastases in sentinel lymph nodes
- Dataset of 1399 manually annotated WSI



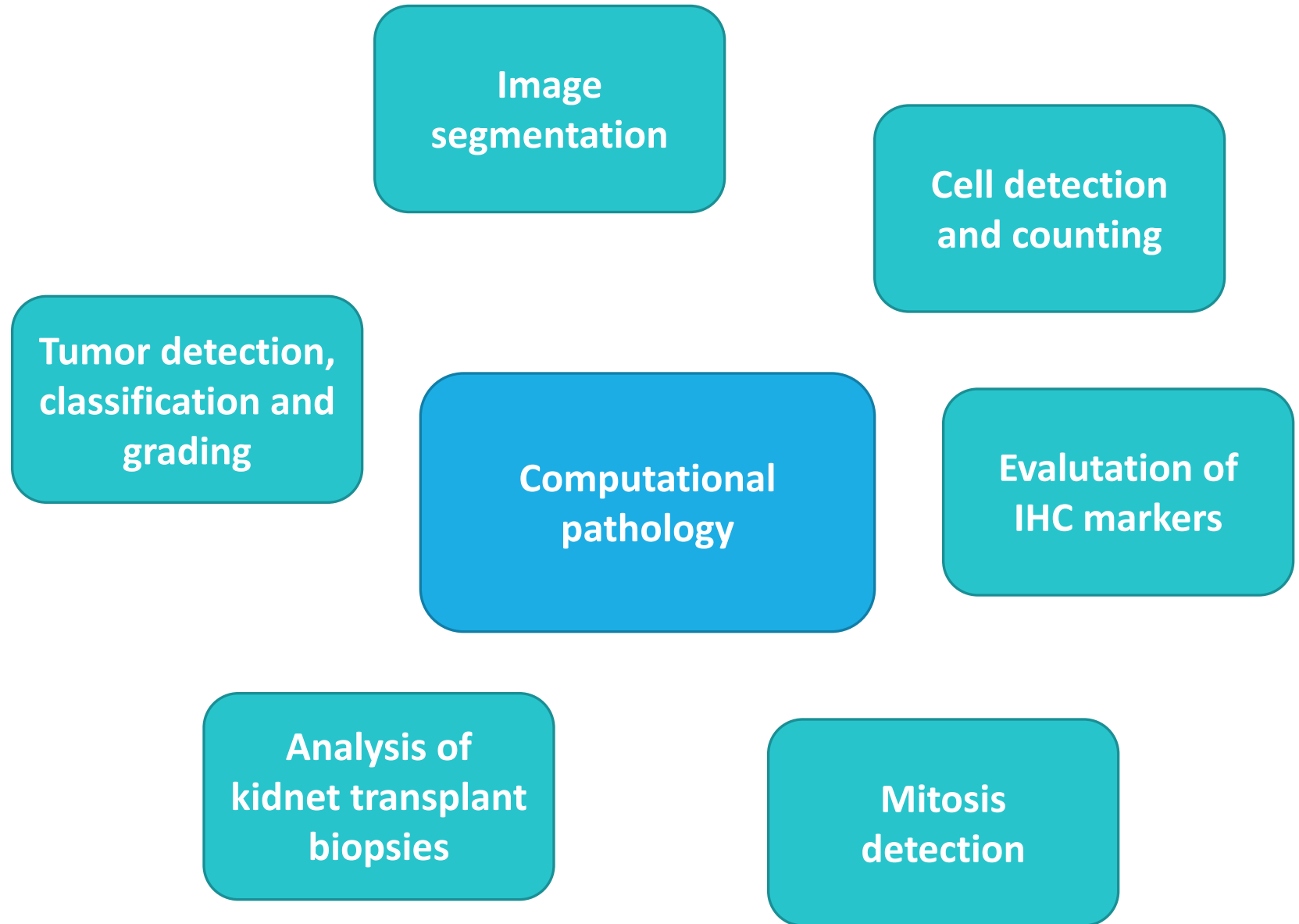
The latest from Google Research

Applying Deep Learning to Metastatic Breast Cancer Detection

Friday, October 12, 2018

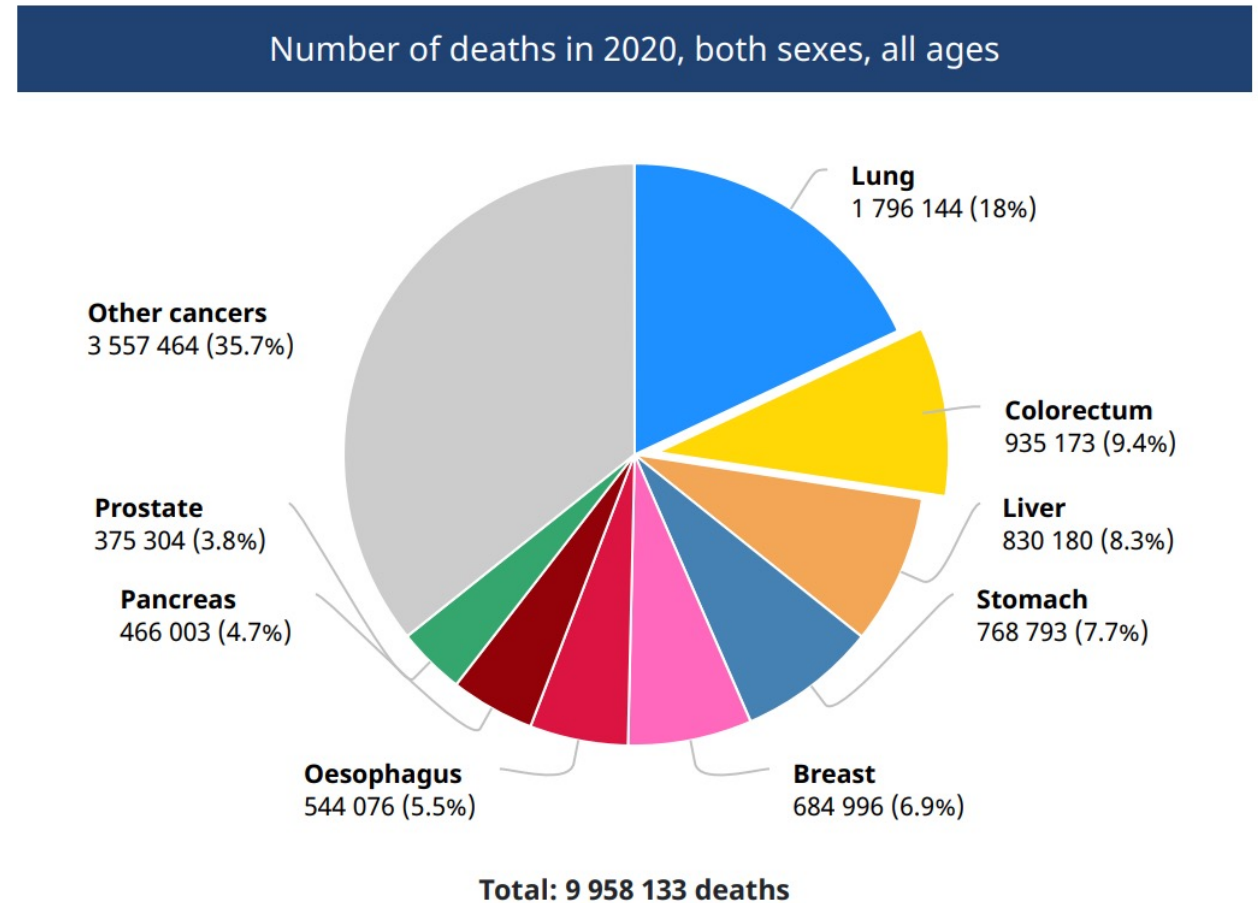


- **Reducing repetitive and time-consuming tasks**
- **Lower interobserver variability**



Colorectal carcinoma

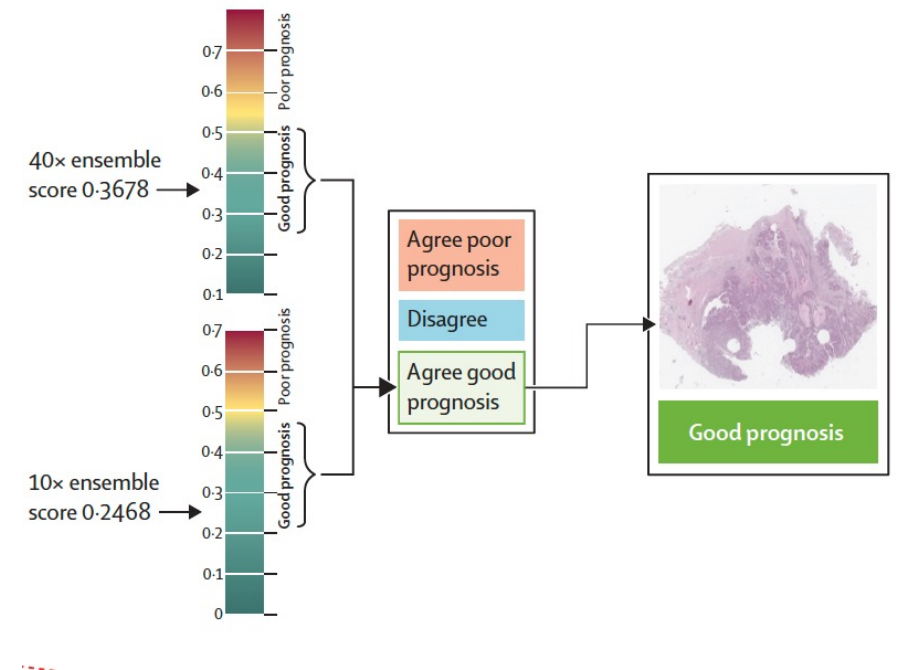
- Colorectal carcinoma (CRC) is the second most deadly and the third most common cancer (Globocan 2020)
- Colorectal cancer screening enables prompt detection of early CRC or preinvasive lesions, but represents a significant workload for both **endoscopy** and **pathology** units



Digital pathology for colorectal carcinoma

- Distinction between tumor tissue and stroma (Kather JN et al. *Sci Rep* 2016)
- Outcome prediction (Bychkov D et al. *Sci Rep* 2018; Kather JN et al. *PLoS Med* 2019; Skrede O et al. *Lancet* 2020)
- Molecular profile prediction (Yamashita R et al., *Lancet Oncol* 2020; Sirinukunwattana K et al. *Gut* 2021; Bilal M et al. *Lancet Digit Health* 2021)

- Adenoma classification...



Adenoma classification

Deep Learning for Classification of Colorectal Polyps on Whole-slide Images

Bruno Korbar^{1,2}, Andrea M. Olofson³, Allen P. Mirafior³, Catherine M. Nicka³, Matthew A. Suriawinata³, Lorenzo Torresani², Arief A. Suriawinata³, Saeed Hassanpour^{1,2,4}

J Pathol Inform 2017, 1:30

Table 1: Our dataset: The distribution of colorectal polyp types in crop images used in this work

Colorectal polyp type	Acronym	Number of image crops
Hyperplastic polyp	HP	405
Sessile serrated polyp	SSP	612
Traditional serrated adenoma	TSA	258
Tubular adenoma	TA	360
Tubulovillous/villous adenoma	TVA/V	202
Normal	-	237
Total	-	2074

Table 4: Whole-slide classification results: Results of our final model for classification of colorectal polyps on 239 whole-slide images in our test set

	HP (<i>n</i> =37) (%)	SSP (<i>n</i> =39) (%)	TSA (<i>n</i> =38) (%)	TA (<i>n</i> =39) (%)	TVA/V (<i>n</i> =38) (%)	Normal (<i>n</i> =48) (%)	Total (<i>n</i> =239) (%)
Accuracy	89.8 (85.3-93.3)	89.5 (85.0-93.1)	94.7 (91.1-97.2)	93.1 (89.2-96.0)	95.8 (92.5-97.9)	95.0 (91.5-97.4)	93.0 (89.0-95.9)
Precision	90.9 (86.6-94.2)	86.11 (81.1-90.2)	100.0 (98.5-100)	83.3 (78.0-87.8)	97.2 (94.3-98.9)	80.7 (75.1-85.5)	89.7 (85.2-93.2)
Recall	81.1 (75.5-85.8)	81.6 (76.1-86.3)	89.5 (84.9-93.0)	89.7 (85.2-93.3)	92.1 (88.0-95.2)	95.8 (92.5-98.0)	88.3 (83.6-92.1)
F1 score	85.7 (80.6-89.9)	83.8 (78.5-88.2)	94.4 (90.8-97.0)	86.4 (81.4-90.5)	94.6 (90.9-97.1)	87.6 (82.8-91.5)	88.8 (84.1-92.5)

HP: Hyperplastic polyp, SSP: Sessile serrated polyp, TSA: Traditional serrated adenoma, TA: Tubular adenoma, TVA/V: Tubulovillous/villous adenoma

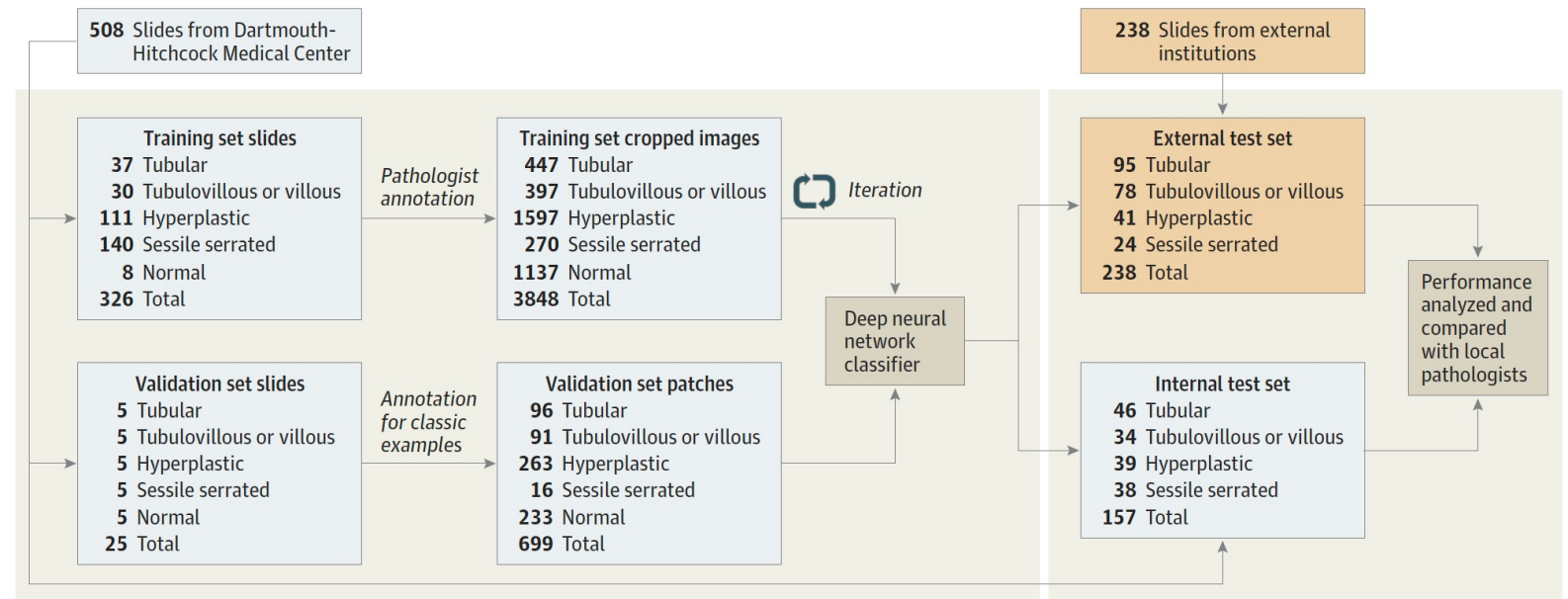
Adenoma classification

Evaluation of a Deep Neural Network for Automated Classification of Colorectal Polyps on Histopathologic Slides

Jason W. Wei, BA; Arief A. Suriawinata, MD; Louis J. Vaickus, MD, PhD; Bing Ren, MD, PhD; Xiaoying Liu, MD; Mikhail Lisovsky, MD, PhD; Naofumi Tomita, MS; Behnaz Abdollahi, PhD; Adam S. Kim, MD; Dale C. Snover, MD; John A. Baron, MD; Elizabeth L. Barry, PhD; Saeed Hassanpour, PhD

JAMA Network Open. 2020;3(4):e203398. doi:10.1001/jamanetworkopen.2020.3398

Figure 1. Data Flow Diagram for the Study



Adenoma classification

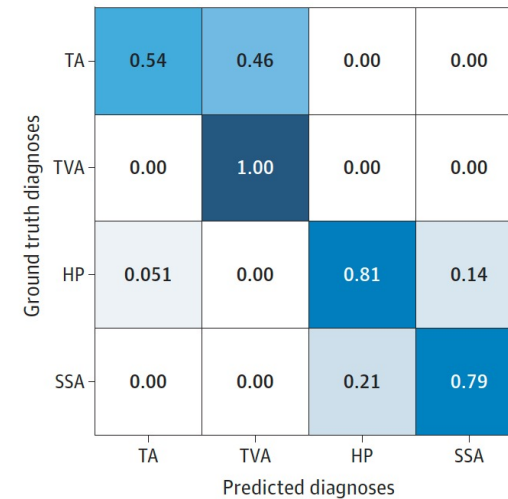
Table. Per-Class Comparison Between Local Pathologists and the Deep Neural Network Model in Classifying Colorectal Polyps on Internal and External Test Sets

Polyp type	Internal test set (n = 157)						External test set (n = 238)					
	Local pathologists			Deep neural network			Local pathologists			Deep neural network		
	Accuracy, %	Sensitivity, %	Specificity, %	Accuracy, %	Sensitivity, %	Specificity, %	Accuracy, %	Sensitivity, %	Specificity, %	Accuracy, %	Sensitivity, %	Specificity, %
TA	89.8	76.1	95.5	93.0	89.1	94.6	79.8	53.7	97.2	84.5	73.7	91.6
TVA	94.3	88.2	95.8	95.5	97.1	95.1	81.5	100	77.7	89.5	97.6	87.8
HP	89.8	76.9	94.1	92.4	82.1	95.8	91.6	80.8	96.8	85.3	60.3	97.5
SSA	91.7	81.6	95.0	93.0	78.9	97.5	93.3	79.2	94.8	88.7	79.2	89.7
Mean	91.4	80.7	95.1	93.5	86.8	95.7	86.6	78.4	91.6	87.0	77.7	91.6

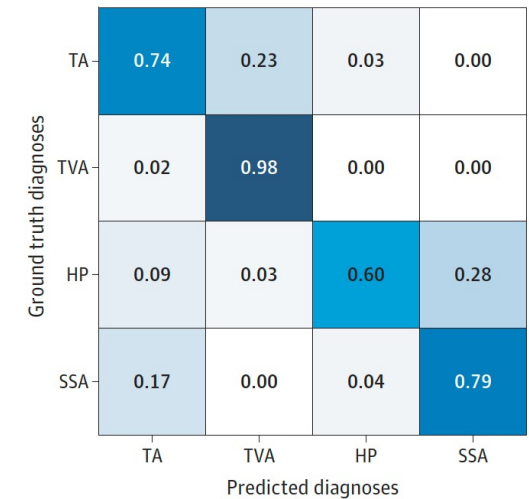
Limitations:

- Lack of dysplasia grading
- Lack of normal tissue
- Lower performance during external testing

A Local pathologists



B Model



High Performance Computing boosting Biomedical Applications



DEEPHEALTH

PARTNERS

22 partners from 9 European Countries

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OTTO VON GUERICKE UNIVERSITÄT MAGDEBURG



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Fundación para el Fomento de la Investigación Sanitaria y Biomédica de la Comunitat Valenciana



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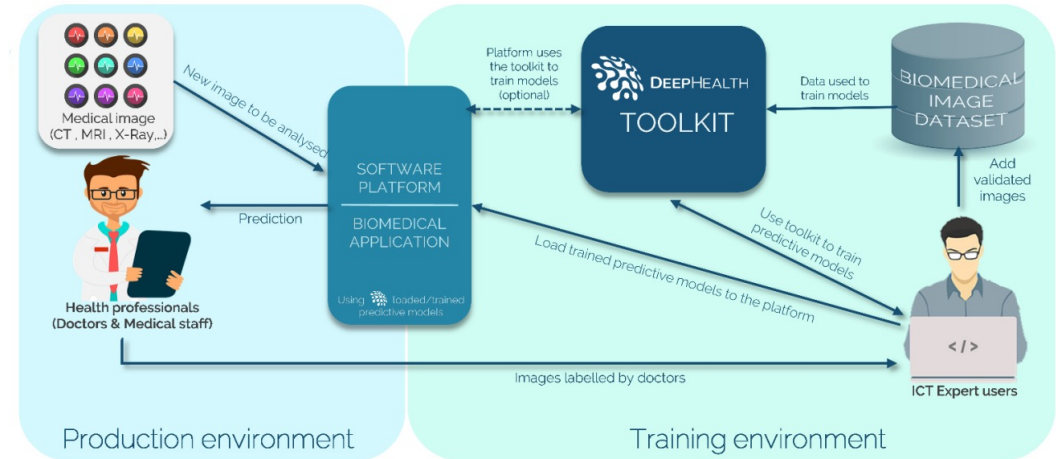


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Aim

Provide **High Performance Computing (HPC)** power at the service of biomedical applications; and apply **Deep Learning (DL)** and **Computer Vision (CV)** techniques on large and complex biomedical datasets to support new and more efficient ways of diagnosis, monitoring and treatment of diseases



This project has received funding from the European Union's Horizon 2020 research innovation programme under grant agreement No. 825111



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Use Cases

14 pilot test-beds in 3 areas:

Neurological diseases

- Migraine and Seizures prediction
- Major Depression
- Dementia
- Study of structural changes in lumbar spine pathology
- Population model for Alzheimer's Disease
- Epileptic seizures detection
- Objective fatigue assessment for multiple sclerosis patients

Tumor detection and early cancer prediction

- Chest cancer detection
- Prostate tumor diagnosis
- Skin cancer melanoma detection

Digital pathology and automated image annotation

- Classification of whole-slide histological images of colorectal biopsy samples
- CT brain perfusion maps synthesis
- Deep Image annotation
- Image Analysis and prediction for Urology

Colon cancer diagnosis

Colon cancer is one of the most frequent causes of death. Screening programs can enable prompt diagnosis and treatment of this aggressive disease, but they also lead to higher caseloads and costs for the already strained European healthcare services. DeepHealth can help streamline pathological diagnosis of colon biopsies.

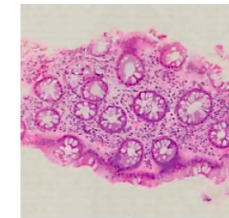
DeepHealth



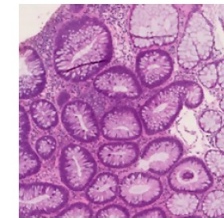
Dataset (WSI images)

	HP	NORM	TA.HG	TA.LG	TVA.HG	TVA.LG	Total
Slides	62	30	34	232	44	55	457
R_t	158	112	145	777	264	245	1701
A_t [cm ²]	9.91	18.38	7.94	71.74	60.45	41.86	210.29

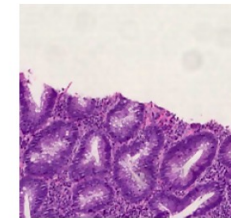
- H&E slide acquired on the Hamamatsu Nanozoomer S210 scanner (200X)
- Manual annotation according to 6 classes:
 - NORM: normal tissue
 - HP: hyperplastic polyp
 - TA.LG: tubular adenoma, low-grade dysplasia
 - TA.HG: tubular adenoma, high-grade dysplasia
 - TVA.LG: tubulo-villous adenoma, low-grade dysplasia
 - TVA.HG: tubulo-villous adenoma, high-grade dysplasia



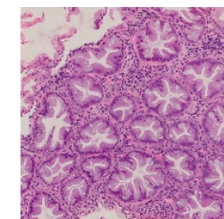
(a) NORM



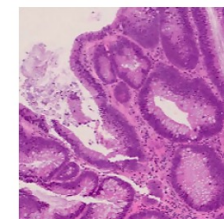
(b) TA.LG



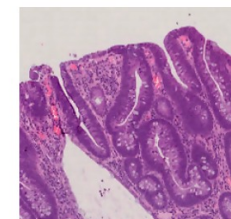
(c) TA.HG



(d) HP



(e) TVA.LG



(f) TVA.HG

- CNN: ResNet-18
- Pre-training on the ImageNet classification task
- Data augmentation: one random operation between rotation, equalization, solarization, inversion and contrast enhancing

Patches normalization: relevant features are not embed in color, but in image texture and signal strenght

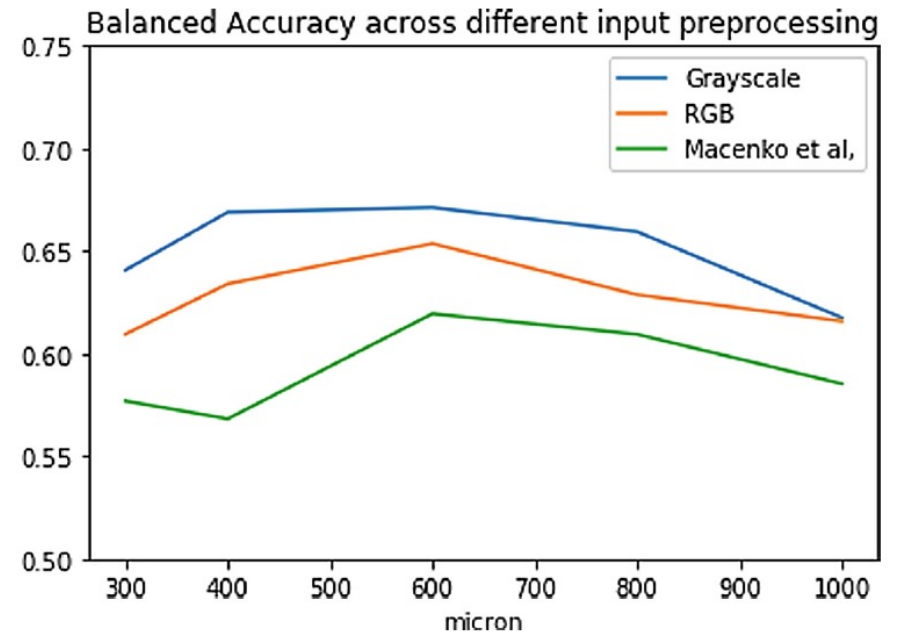
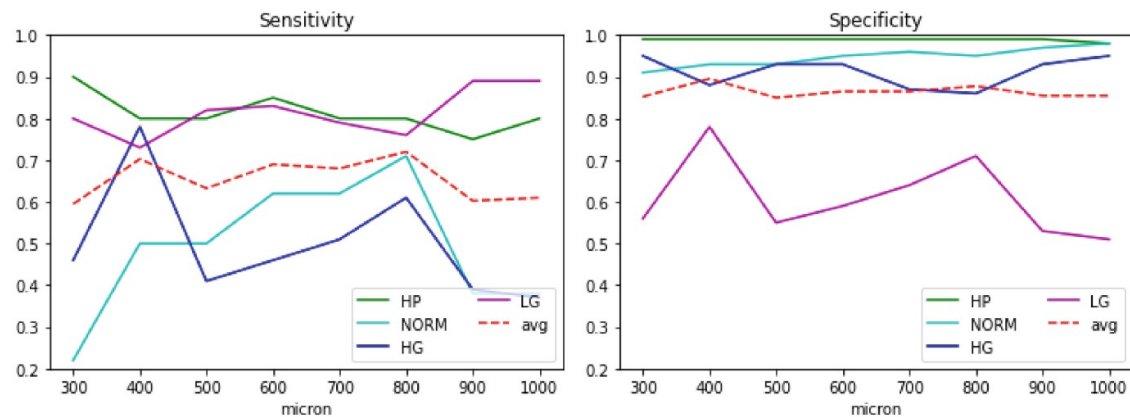


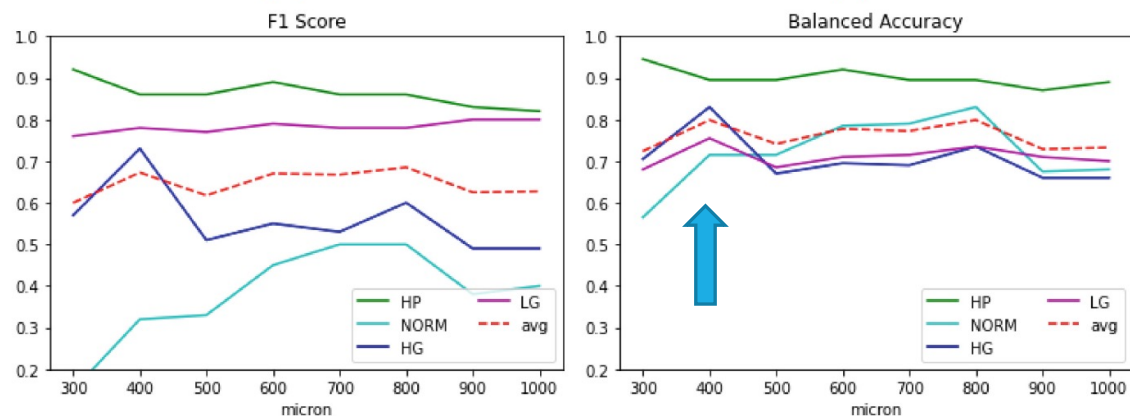
Fig. 2. Patches classification performance.

Patches resolution:



(a)

(b)



(c)

(d)

Table 3. Human dysplasia diagnostic performance comparison

		Accuracy	Sensitivity	Specificity
Hyperplastic	Our (400 μm)	0.90	0.80	0.99
	Our (600 μm)	0.92	0.85	0.99
	Pathologist [8]	0.79	0.30	0.97
Low grade	Our (400 μm)	0.76	0.73	0.78
	Our (600 μm)	0.71	0.83	0.59
	Pathologist [8]	0.66	0.57	0.69
High grade	Our (400 μm)	0.83	0.78	0.88
	Our (600 μm)	0.70	0.46	0.93
	Pathologist [8]	0.83	0.81	0.84

- Achieved results are similar to those reported by Denis B et al. (*Eur J of Gastroenterol Hepatol* 2009)

Dysplasia grading

Table 4. WSI inferences: confusion matrices.

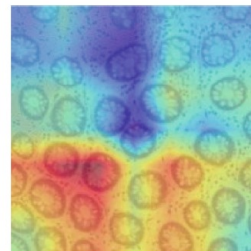
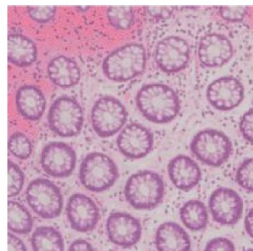
(a) $\varphi = 600 \mu\text{m}$, gray-scale

		Predicted			
		HP	NORM	HG	LG
Gr. truth	HP	0.85	0	0.05	0.1
	NORM	0.12	0.75	0	0.12
	HG	0.02	0	0.63	0.35
	LG	0.03	0.09	0.18	0.7

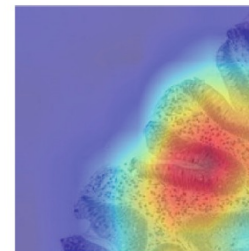
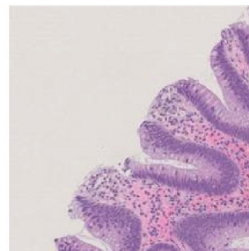
(b) $\varphi = 600 \mu\text{m}$, RGB

		Predicted			
		HP	NORM	HG	LG
Gr. truth	HP	0.75	0.05	0	0.2
	NORM	0	0.62	0	0.38
	HG	0	0.02	0.61	0.37
	LG	0.03	0.06	0.15	0.76

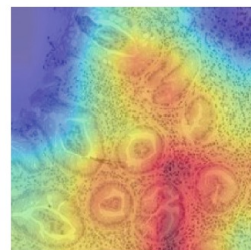
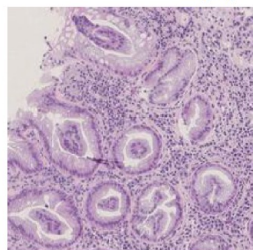
- Poor results in distinguishing TA versus TVA/VA



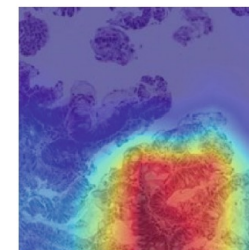
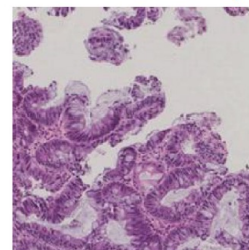
(a) NORM



(b) HP



(c) LG



(d) HG

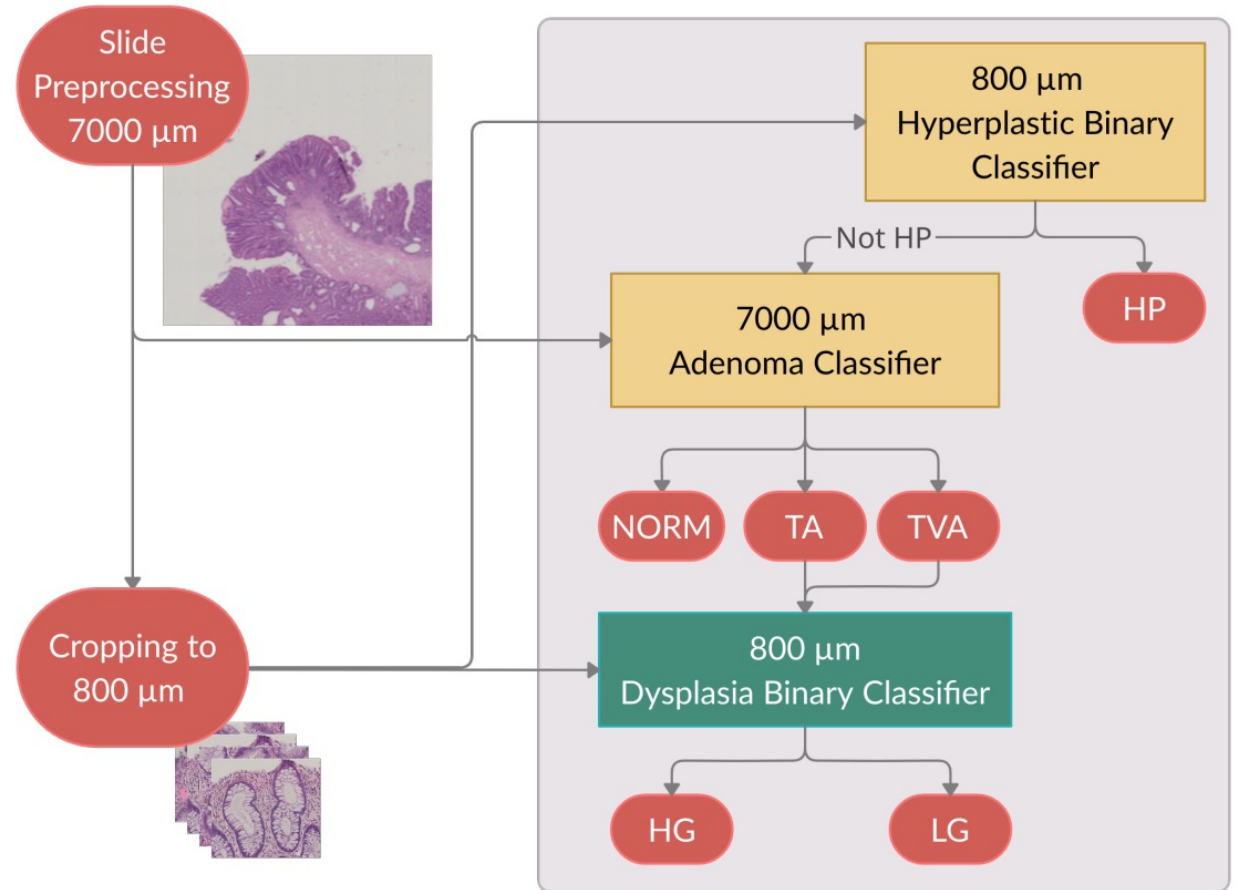


Multi-resolution analysis

Type	Patch scale σ [μm]					
	100	800	1500	4000	7000	8000
BA (6-class)	0.40	0.45	0.46	0.41	0.37	0.38
NORM	0.70	0.66	0.72	0.76	0.78	0.71
HP	0.81	0.92	0.85	0.70	0.60	0.69
TA (HG+LG)	0.65	0.66	0.65	0.71	0.76	0.70
TVA (HG+LG)	0.64	0.67	0.68	0.74	0.84	0.76

Table 2: Preliminary experiments: overall BA for all of the six classes (first row) and BA for each polyp type, plus normal tissue.

- Adenoma type and dysplasia grade are best classified at different scales



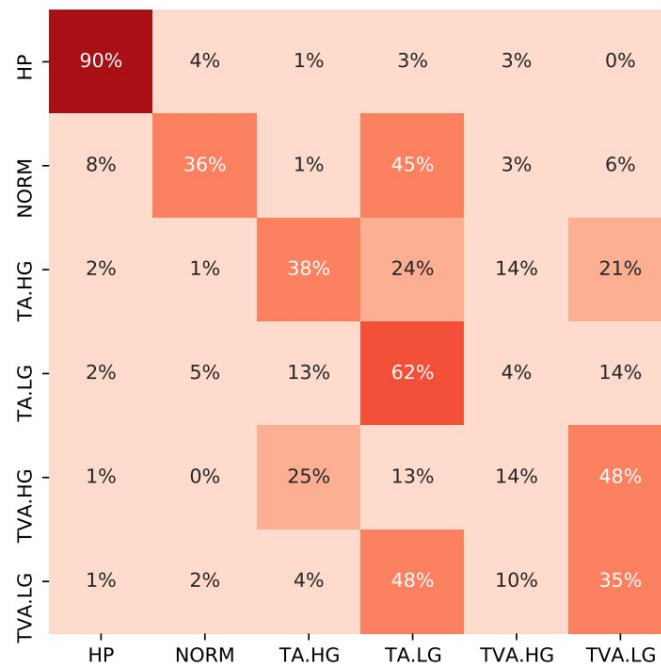
Multi-resolution analysis

	HP	NORM	TA		TVA	
			HG	LG	HG	LG
Sensitivity	0.86	0.79	0.60	0.50	0.78	0.52
Specificity	0.93	0.87	0.92	0.94	0.96	0.92
BA	0.89	0.83	0.76	0.72	0.87	0.72

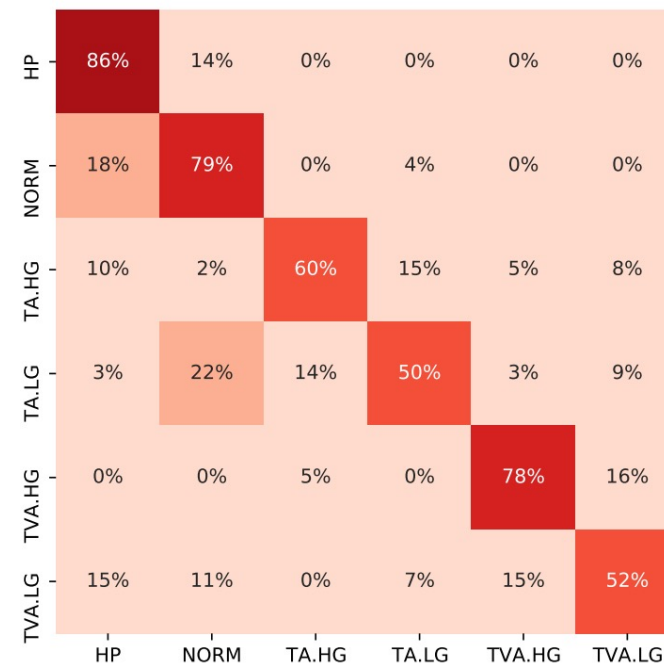
Table 3: Sensitivity, Specificity and BA per class.

	σ	HP	NORM	TA	TVA
Baseline	800	0.92	0.66	0.66	0.67
Baseline	1500	0.85	0.72	0.65	0.68
Baseline	7000	0.60	0.78	0.76	0.84
Multi-resolution	-	0.89	0.83	0.81	0.87

Table 4: Comparison of the class BA between the baseline and the proposed multi-resolution approach.



(a) Baseline



(b) Multi-resolution Ensemble

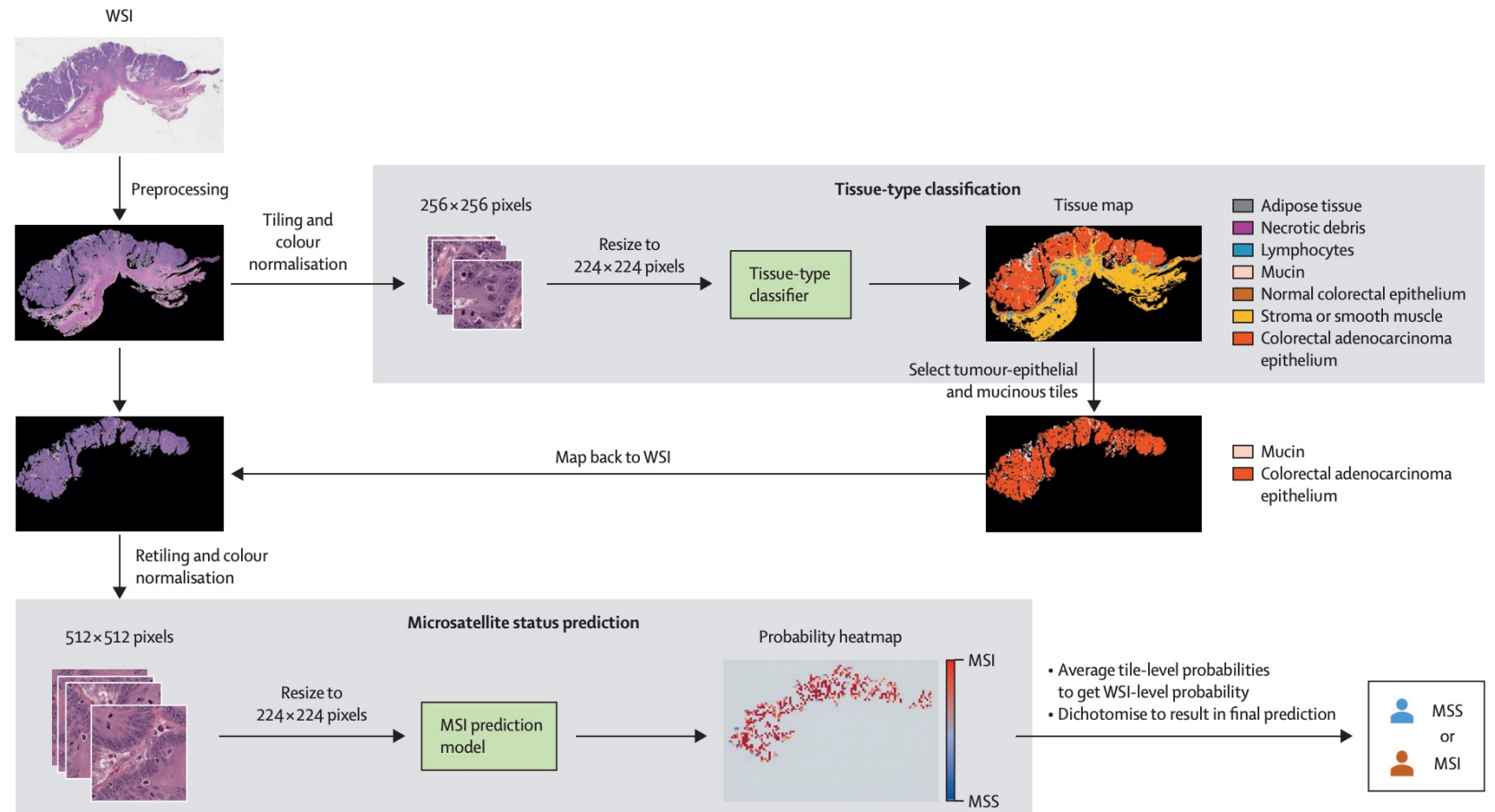
Limitations:

- Some entities missing (serrated adenomas, invasive adenocarcinomas,...)
- Larger dataset is warranted
- Lack of external validation

Deep learning model for the prediction of microsatellite instability in colorectal cancer: a diagnostic study

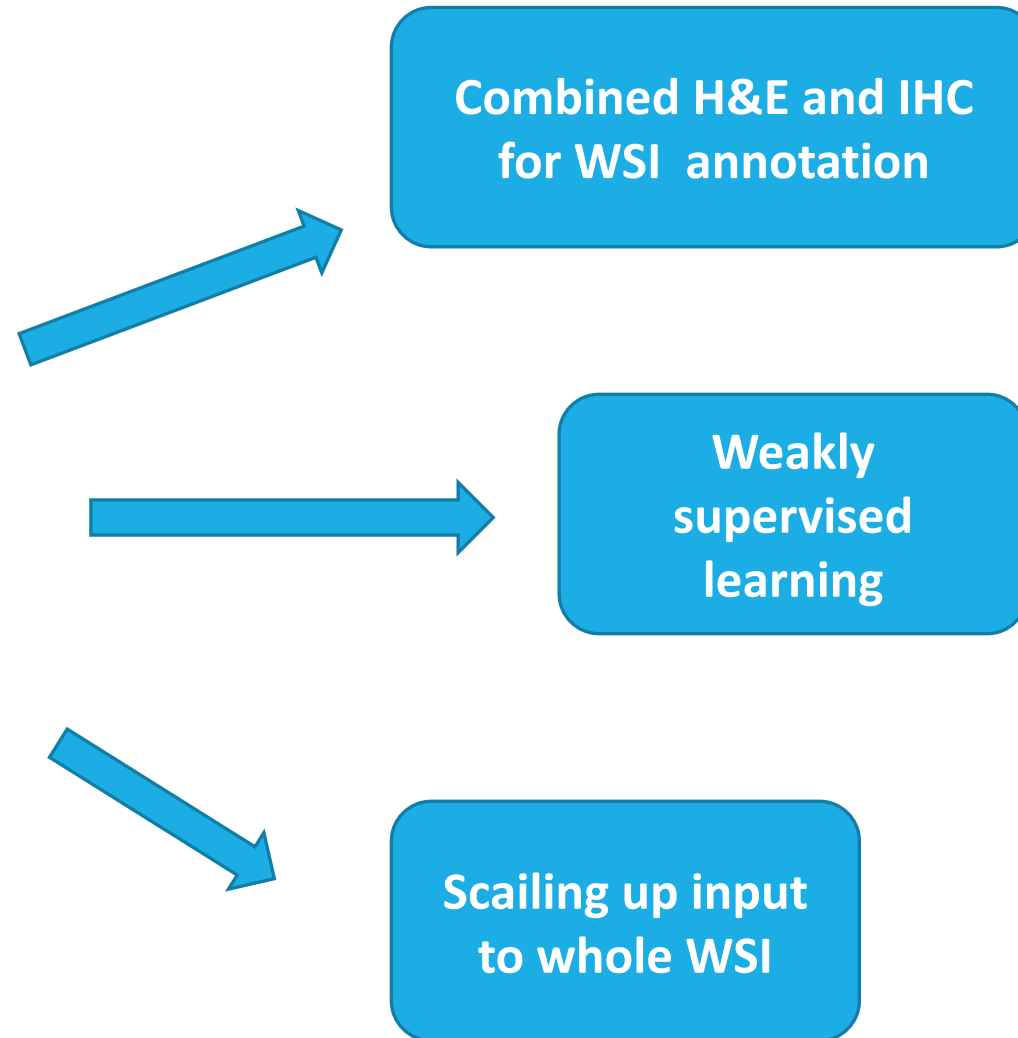
Rikiya Yamashita, Jin Long, Teri Longacre, Lan Peng, Gerald Berry, Brock Martin, John Higgins, Daniel L Rubin*, Jeanne Shen*

Lancet Oncol 2020; 22: 132-41

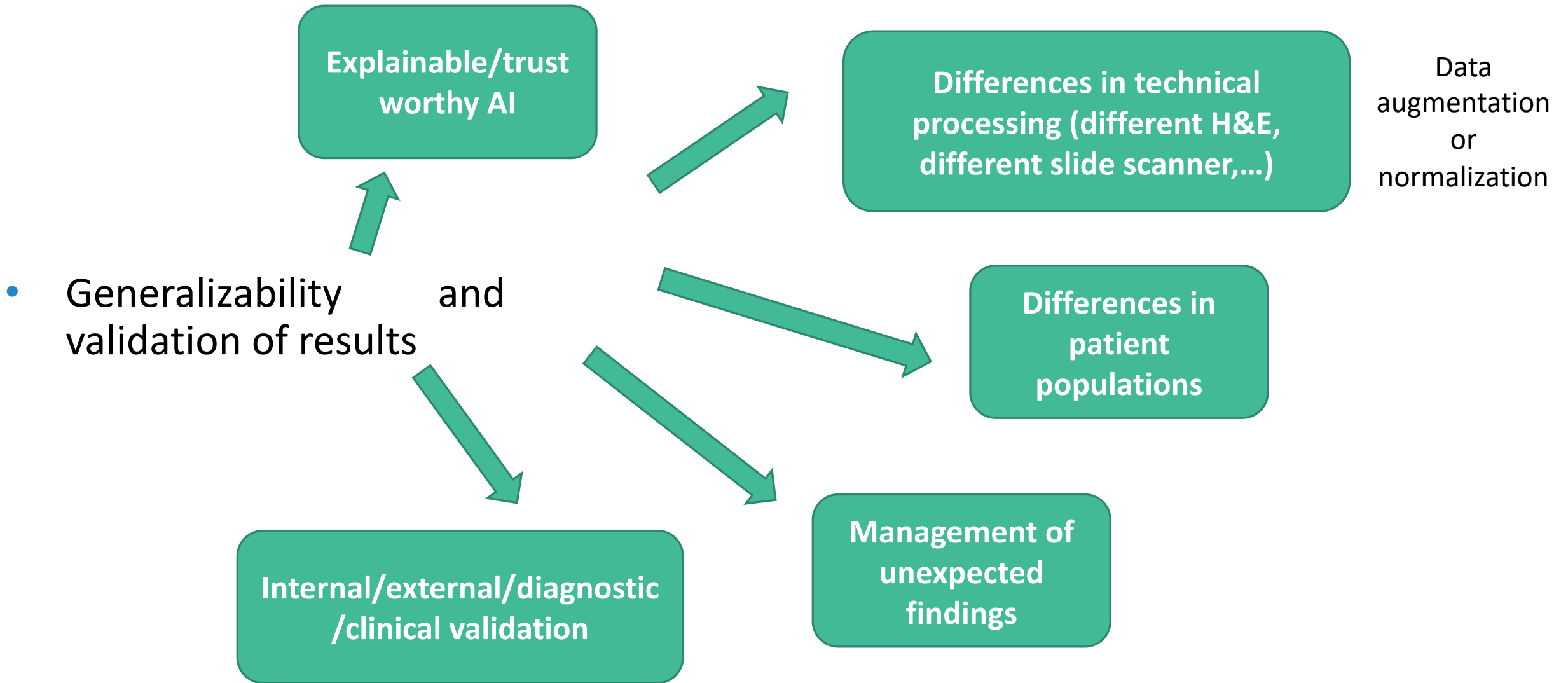


Challenges

- Collect large-scale annotated datasets (images and clinical annotations)



Challenges



Thank you!



- Prof.ssa P. Cassoni
- Dr. L. Bertero
- Dr. A. Gambella
- Dr. E. Bottasso



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- Barcelona Supercomputing Center
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