Project POCHI

Companion test, translational projects and data challenges
When AI meets Computational Pathology

Université de Paris

LIPADE
Laboratoire d'Informatique PAris DEscartes

Nicolas Loménie, Camille Kurtz
Zografoula Vagena

data intelligence institute of Paris

This work is supported by the Data Intelligence Institute of Paris (diiP), IdEx Université de Paris, ANR-18-IDEX-0001

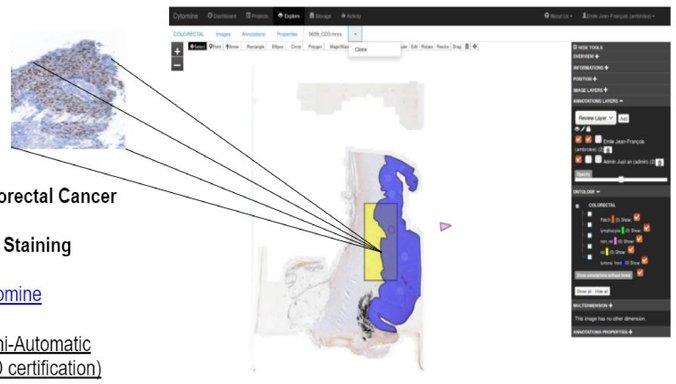


Figure 1. This image is a WSI. At a low magnification (X1.5).
At the highest resolution for instance 40x it weights between 5 and 10 GB of data just for one single patient examination.

Figure 1. (follow.) By automatic analysis of thousands of them we can build up efficient models for immuno-oncology treatments for instance. Deep learning is a core mechanism to achieve this goal.

A Companion Test

POCHI Project - Collaboration with PUPH JF. Emile – Hôpital Ambroise Paré.

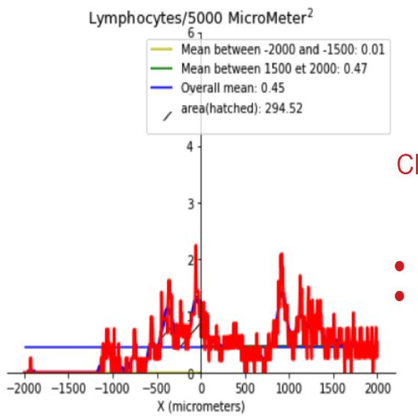


Colorectal Cancer

IHC Staining

Cytomine

Semi-Automatic
(IVD certification)



Classify infiltration curve into 4 types:

- using rules provided pathologist
- automatically through ML/AI

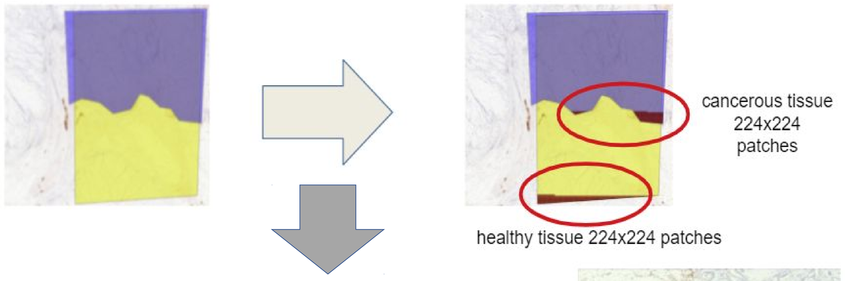
Djiro, Kurtz, and Loménie, "Assessment of Anti-Tumor Immune Response in Colorectal Carcinomas from Whole Slide Images.", 2018

Automatic Semantic Segmentation with AI

Predict pixel class using patch classification

WSI image preparation for training

- image annotation
- pixel sampling and patch extraction
- class balancing
- data augmentation, normalization



DL to classify patches (tumor vs healthy)

- popular CNN-based model (MobileNet)
- transfer learning from ImageNet
- fine tune with classification over IHC stained patches

	precision	recall	f1-score	support
heatlhy_tissue	0.65	0.97	0.78	1601
tumoral_tissue	0.97	0.69	0.81	2731
accuracy			0.79	4332
macro avg	0.81	0.83	0.79	4332
weighted avg	0.85	0.79	0.80	4332



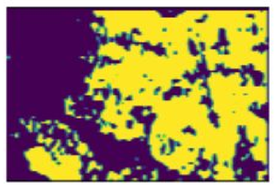
potential annotation error



healthy vs cancerous tissue heatmap

Post-processing to produce semantic segmentation heatmap

- interpolation to predict missing pixel labels
- smoothing through fully-connected CRFs



After interpolation

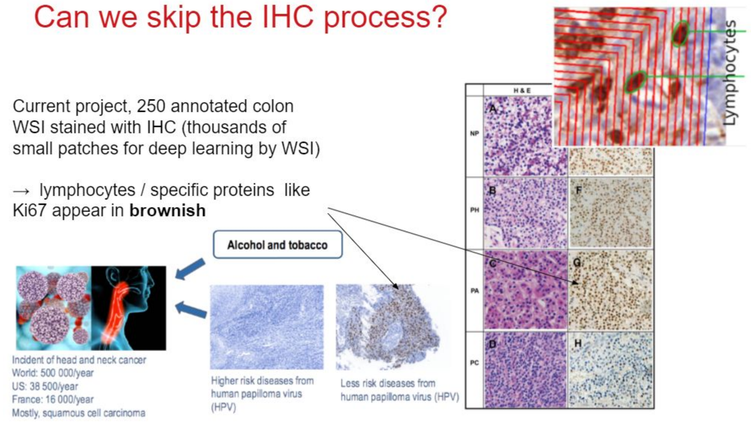


After smoothing

Can we skip the IHC process?

Current project, 250 annotated colon WSI stained with IHC (thousands of small patches for deep learning by WSI)

→ lymphocytes / specific proteins like Ki67 appear in **brownish**



A funded Translational Project

(funded by INCa-DGOS : National foundation and agency for cancer research and care
https://www.e-cancer.fr/Professionnels-de-la-recherche/Recherche-translationnelle/Le-PRT-K)

Title : **Artificial intelligence to estimate the prognostic of colorectal cancer in adjuvant setting using hematoxylin eosin safran histological slides**

Goal : do everything with only the routine H&E (plus Safran) staining
Major partner : AP-HP, Centre Georges Francois Leclerc (CGFL) (Dijon)
with the support of FFCD (https://www.ffcd.fr/)

GHIRINGHELLI Francois, PUPH Oncologist, CGFL



AI traction

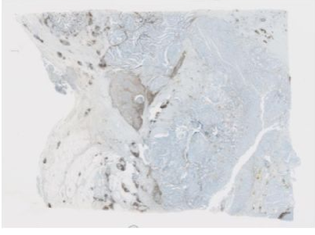
Jean-Francois Emile, PUPH Antomo-Pathologist, APHP



Data AI of !

Can we learn the tumoral front independently of tissue / staining etc. ?

POCHI Project
With JF Emile (APHP Ambroise Paré)
Colorectal Cancer (IHC Staining)



Immunohistochemistry Stain

69632pixels x 48384pixels, 9.41 GB
uncompressed

MONDOR Project
With Julien Caldarero
Hepato Carcinoma (H&E Staining)



Stained with Hematoxylin and Eosin Stain (HES)

59520pixels x 41216pixels, 6.85 GB
uncompressed