### When AI meets Histopathology

X1.

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. Computer Sciences Lab (LIPADE) Intelligent Systems of Perception team (SIP)

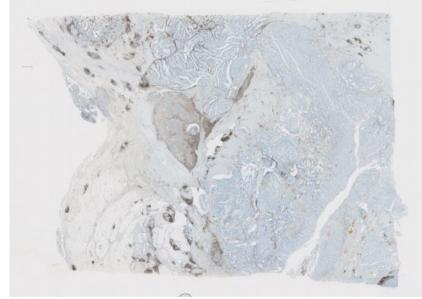
#### Université Paris Cité with the DIIP

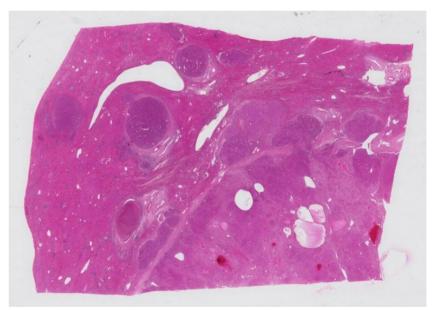
Prof. Nicolas Loménie, PhD. Qinghe Zeng PhD. Zhuxian Guo Research Engineer Amine Marzouki Prof. Camille Kurtz

#### **Clinical Context**

#### What is a Whole Slide Image (WSI)?

A digital representation of a microscopic slide, at multi-scale level of magnification such as 20x or 40x <u>https://cloud.cytomine.com/#/project/8596634/image/8612979/slice/16107736?viewer=q2lafymrl</u>

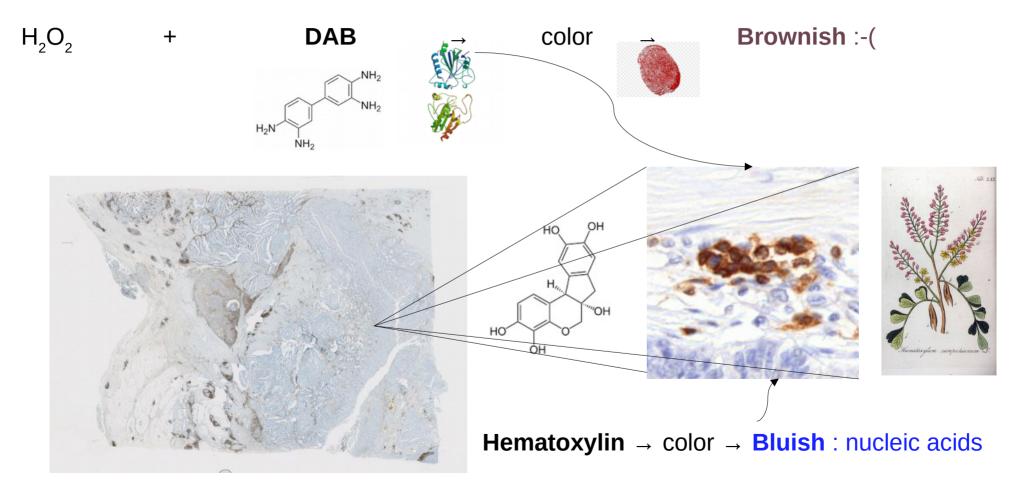




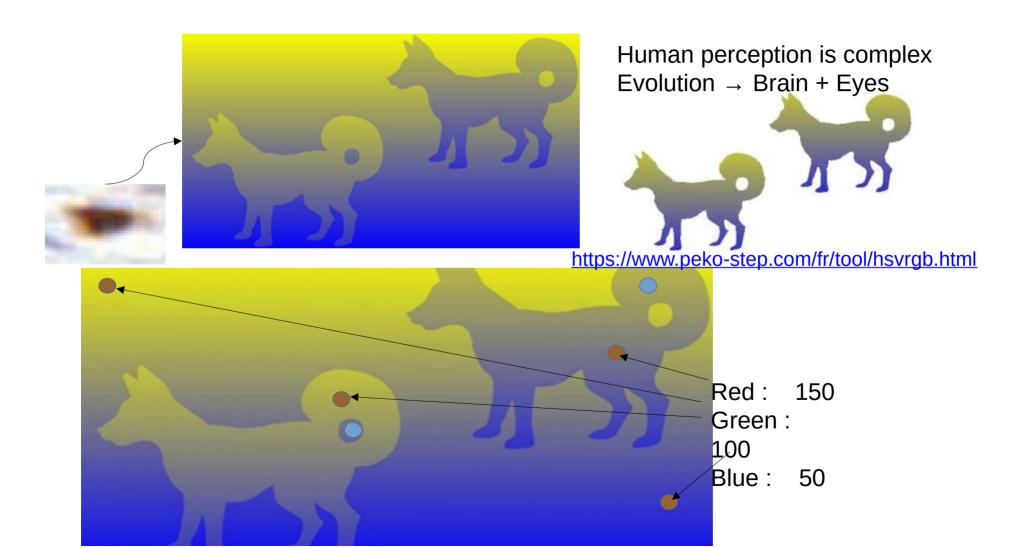
Immunohistochemistry stainingStained with hematoxylin and eosin (H&E)69632pixels x 48384pixels, 9.41 GB uncompressed59520pixels x 41216pixels, 6.85 GB uncompressed

#### Chemistry Context → ImmunoHistoChemistry

How to spot proteins like ki67, CD3 in bright-field microscopy ?



#### WHAT IS BROWNISH → Human perception / interpretation vs. Machine perception



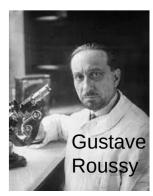
#### Chemistry Context → clinical routine H&E H&E Coloration (+Safran sometimes)

 $= \underbrace{\bigcirc}_{O_2N} \underbrace{\bigcirc}_{O_2N} \underbrace{\bigcirc}_{O_2} \underbrace{O_2} \underbrace{\bigcirc}_{O_2} \underbrace{\bigcirc}_{O_2} \underbrace{\bigcirc}_{O_2$ 

Eosin (basophile) stains the cytoplasm (acidophile) → redish or pinkish

Bright Field Microscopy (vs. Fluorescence) :

- Basophile nuclei (H) : purple
  - Nuclei : blue/violet
- Acidophile cytoplasm (E) : red
- (Muscle : dark pink, Erythrocytes : cherry-red, Collagen : light pink)

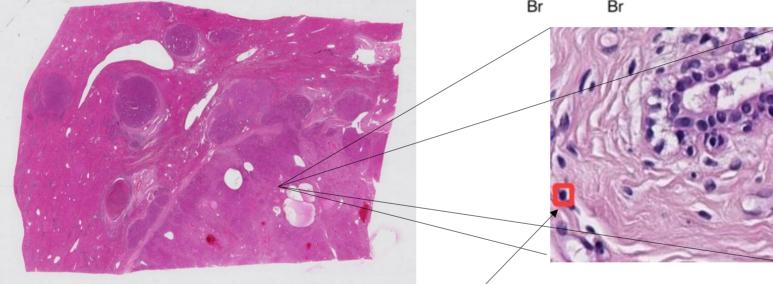


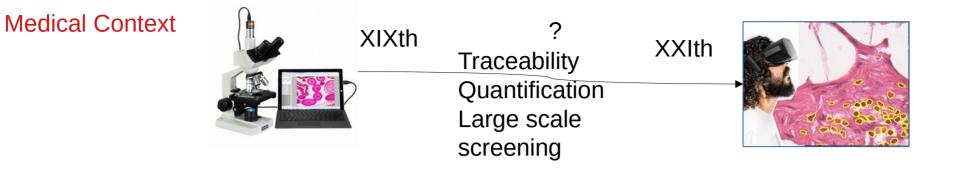


**How to detect lymphocyte ?** "Specific color" + shape + texture

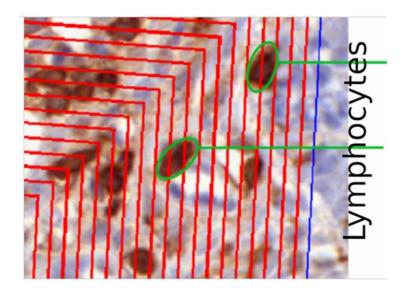
Color analysis (Computer Vision) or Machine Learning ?

 $\rightarrow$  Deep Learning <u>https://tiger.grand-challenge.org/</u>





IHC : Immuno Histo-Chemistry → the lymphocytes appear in brownish

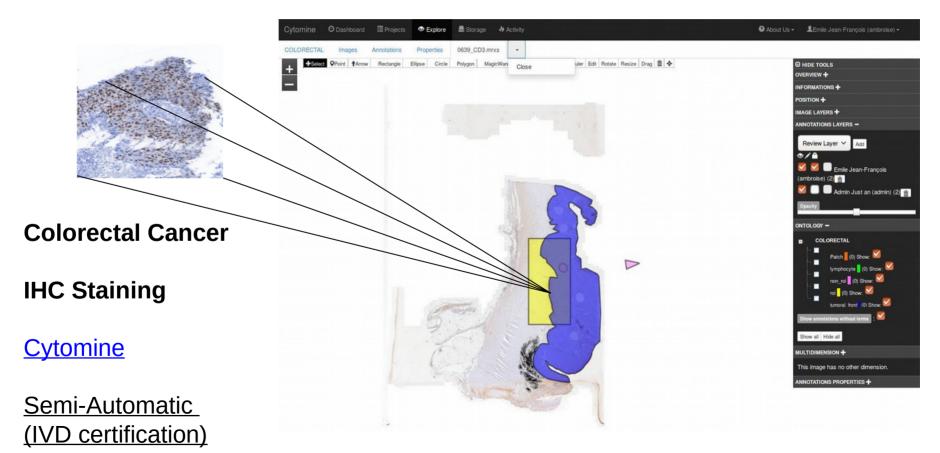


Computer Vision to Ease quantify and scale up assessment + IVD for immunotherapy (In Vitro Diagnosis, Companion test)

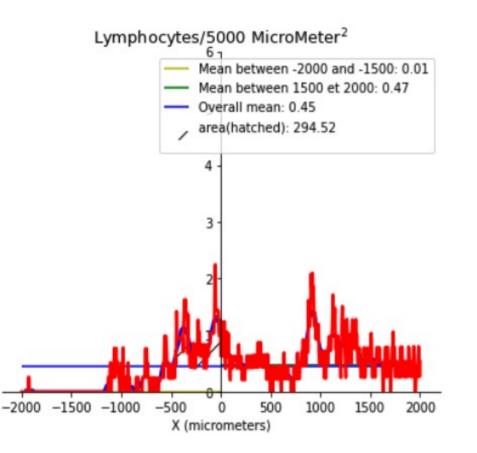
#### **Medical Context**

### A Companion Test

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



#### **Medical Context**



Classify infiltration curve to detect patients benefiting from immunotherapy

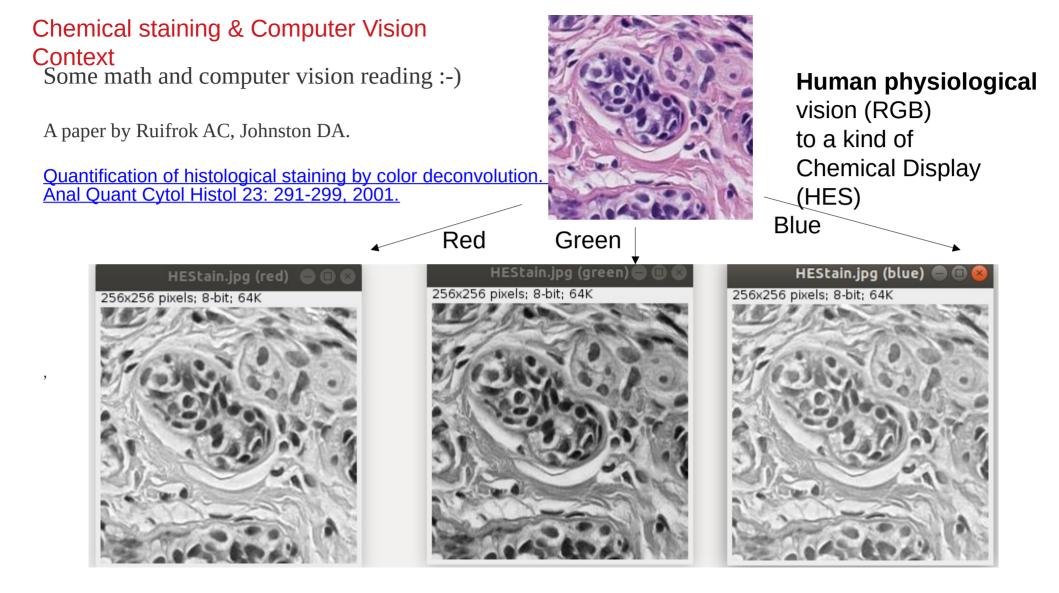
- using rules provided pathologist
- automatically through ML/AI

#### Currently, Phase 2 clinical trial IVD

Pembrolizumab with Capox Bevacizumab in patients with microsatellite stable metastatic colorectal cancer and a high immune infiltrate: The FFCD 1703-POCHI trial

Claire Gallois <sup>1</sup>, Jean-François Emile <sup>2</sup>, Stefano Kim <sup>3</sup>, Carole Monterymard <sup>4</sup>, Marine Gilabert <sup>5</sup>, Jérémie Bez <sup>4</sup>, Astrid Lièvre <sup>6</sup>, Laetitia Dahan <sup>7</sup>, Pierre Laurent-Puig <sup>8</sup>, Laurent Mineur <sup>9</sup>, Romain Coriat <sup>10</sup>, Jean-Louis Legoux <sup>11</sup>, Vincent Hautefeuille <sup>12</sup>, Jean-Marc Phelip <sup>13</sup>, Thierry Lecomte <sup>14</sup>, Harry Sokol <sup>15</sup>, Claude Capron <sup>16</sup>, Violaine Randrian <sup>17</sup>, Come Lepage <sup>18</sup>, Nicolas Lomenie <sup>19</sup>, Camille Kurtz <sup>19</sup>, Julien Taieb <sup>1</sup>, David Tougeron <sup>20</sup>

Affiliations + expand PMID: 34215534 DOI: 10.1016/j.dld.2021.06.009 Free article



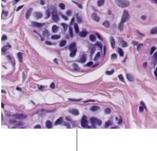
#### Staining

Beer-Lambert Law of absorbance

 $A = \epsilon lc$ 



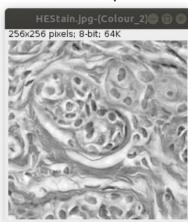
The trick : The E stain in the displayed



The H stain Green channel

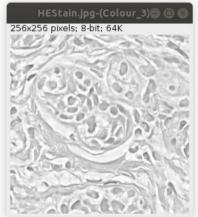
in the displayed Red channel

HEStain.jpg-(Colour\_1) 256x256 pixels: 8-bit: 64K



Human physiological vision (RGB) to a kind of **Chemical Display (HES) Colour Deconvolution** 350x65 pixels; RGB; 89K Colour deconvolution: H&E Colour\_1 R: 0.6443186, G: 0.7166757, B: 0.26688856 Colour\_2 R: 0.09283128, G: 0.9545457, B: 0.28324 Colour 3 R: 0. 63595444. G: 0. 001. B: 0. 7717266

> Safran or orthogonal channel



An explanation of this article and the *colour\_deconvolution* plugin in ImageJ/Fiji (Menu Image/Color) can be read up here : https://biii.eu/colour-deconvolution

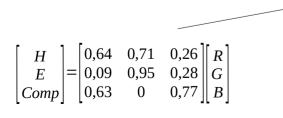
Python Material inhere : https://helios2.mi.parisdescartes.fr/~lomn/Cours/CV/BME/HistoPatho/Color/PythonColorDecony/

#### **Computer Vision & Machine learning**





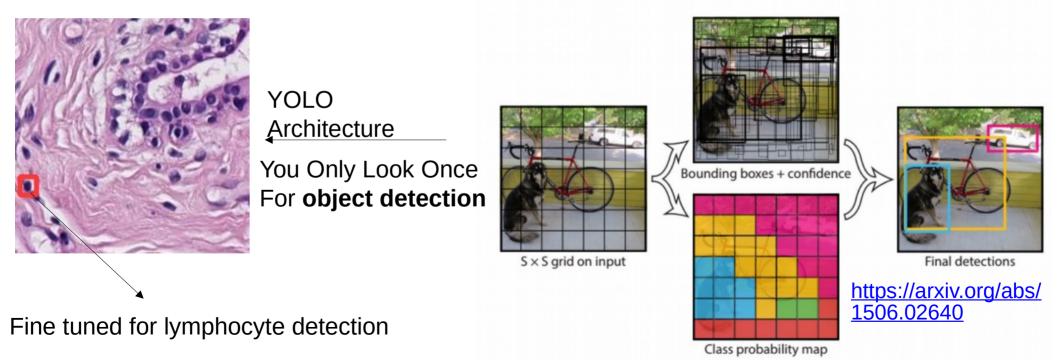
Threshold 📀
And the first state of the first
50.95 %
255
Default 💷 B&W 💷
▼Dark background □Stack histogram
⊒Don't reset range
Auto Apply Reset Set



Learning the matrix coef ? But more to come.... : texture, shape, organization etc.

# What's the promise of deep learning or AI ?

Open question but a new way to explore micro-tumoral environment



https://towardsdatascience.com/volo-vou-only-look-once-real-time-object-detection-explained-492dc9230006

## What Deep Learning revolution can bring ?

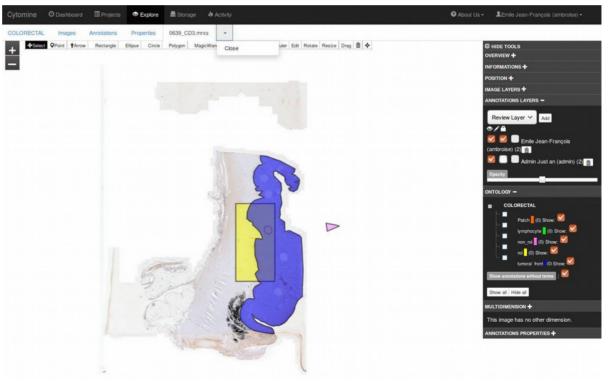
Open question but a new way to explore micro-tumoral environment

Automatic recognition of tumoral tissue ?

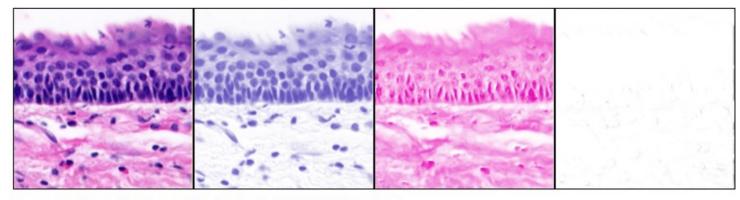
Classification for diagnostic ?

Improved care ?

A new ecosystem : <u>https://tissuepathology.com/</u> (like <u>https://owkin.com/</u>)

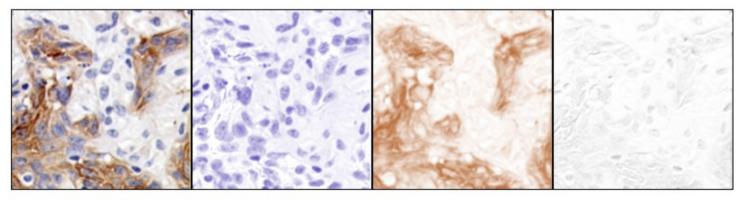


#### Examples



Haematoxylin and Eosin unmixing (using the built-in H&E vectors).

From left to right: original, Haematoxylin, Eosin, virtually empty 3rd (complementary) component (showing that the vectors match the image quite well, except a column of corrupted pixels at the right border of the image).



Haematoxylin and DAB unmixing (using the H DAB built-in vectors).

From left to right: original, Haematoxylin, DAB, 3rd component (the vectors did not perfectly matched the stains in this image, so they should be determined again from single-stained samples).

#### Annex 1

#### Annex 2

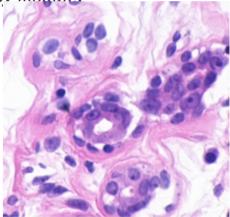
## **Staining Deconvolution**

Demo

Material here : <u>https://helios2.mi.parisdescartes.fr/~lomn/Cours/CV/BME/HistoPatho/Color/PythonColorDeconv/</u>

A corresponding python code to the FiJi plugin is given in **color.py** (using **color\_decon.pv** module)

First, with a python command line, reproduce the code step by step using the instructions in *color.py*.



Then, you can run the color.py over another image like RNA1.tif *\$python color.py RNA1.tif* 

This image takes much more time to be processed in python and is IHC staining then the deconvolution matrix will not work.

#### Annex 3

- <u>https://tissuepathology.com/2022/06/30/visiopharm-supports-umc-utre</u> <u>cht-to-improve-patient-care-with-the-launch-of-an-automated-and-ivdr</u> <u>-certified-ai-driven-digital-pathology-workflow/</u>
- <u>https://bci.grand-challenge.org/</u>
- <u>https://tiger.grand-challenge.org/</u>
- Watch the video on TILs
   <u>https://rumc-gcorg-p-public.s3.amazonaws.com/i/2021/10/20/TILs+Education+What+They+Are+and+What+They+Do.mp4</u>