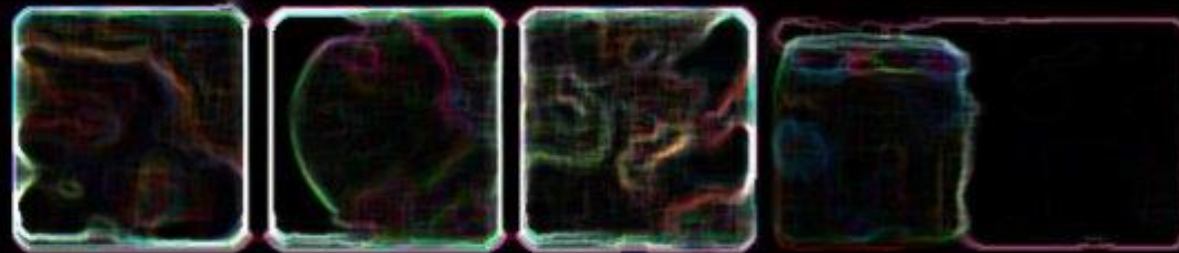


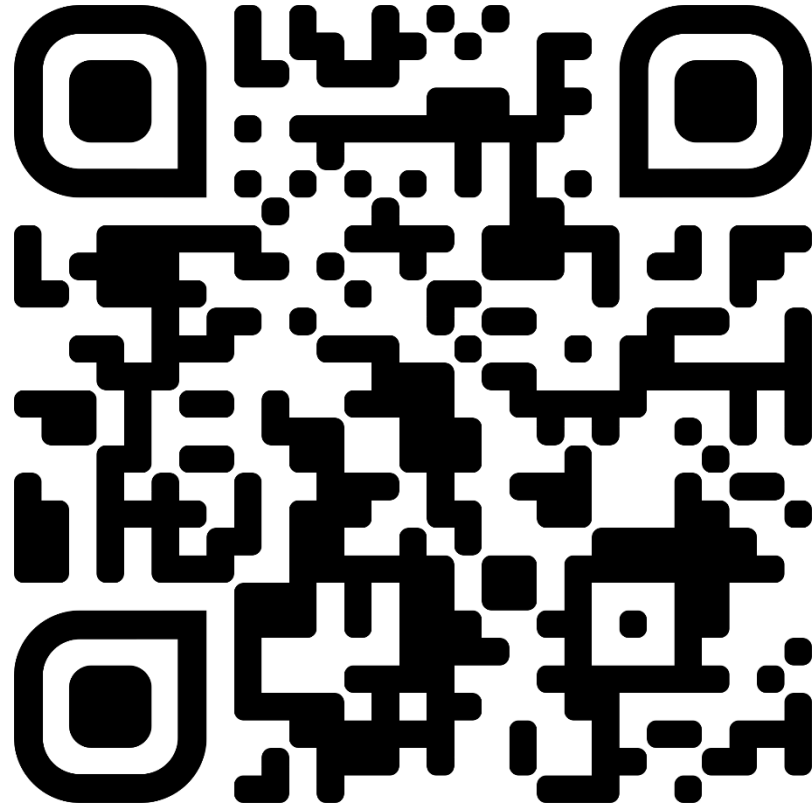
Empowering Healthcare with Automated Analysis:
***Building a Platform for Integrative
Discovery and Diagnostics in Cancer***



Dr Ferran Cardoso Rodriguez

Accessibility

Open Link for Slides and Transcript



Background



BSc in Biotechnology

- *Universitat de Barcelona, 2014-2018*



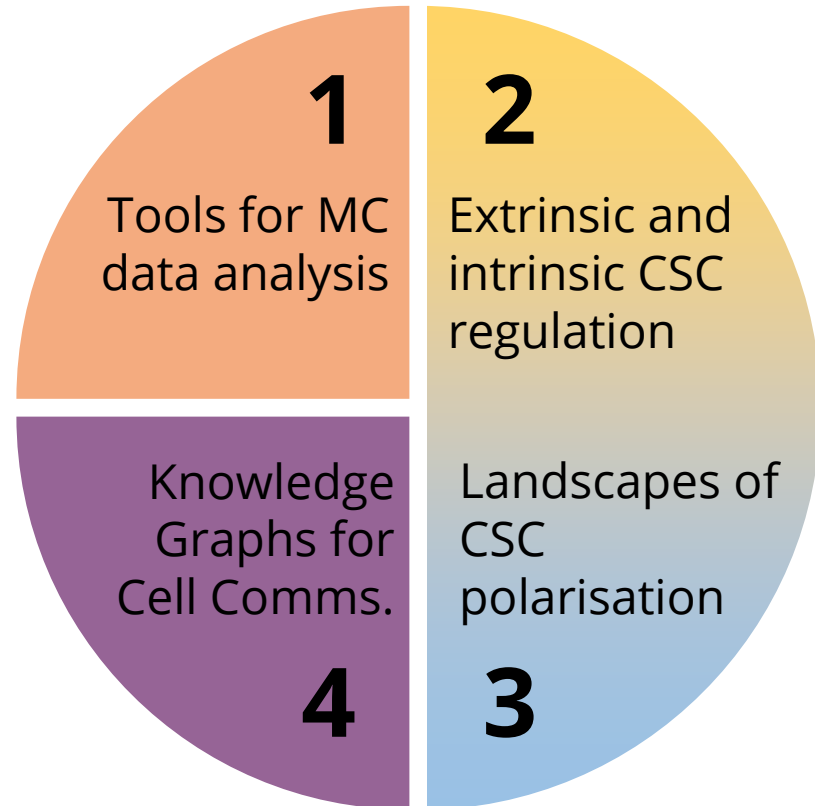
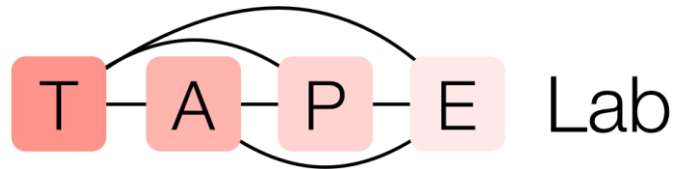
MSc in Bioinformatics and Theoretical Systems Biology

- *Imperial College London, 2018-2019*



PhD in Computational Biology

- *University College London, 2019-2023*



The Integrated Pathology Unit

ICR

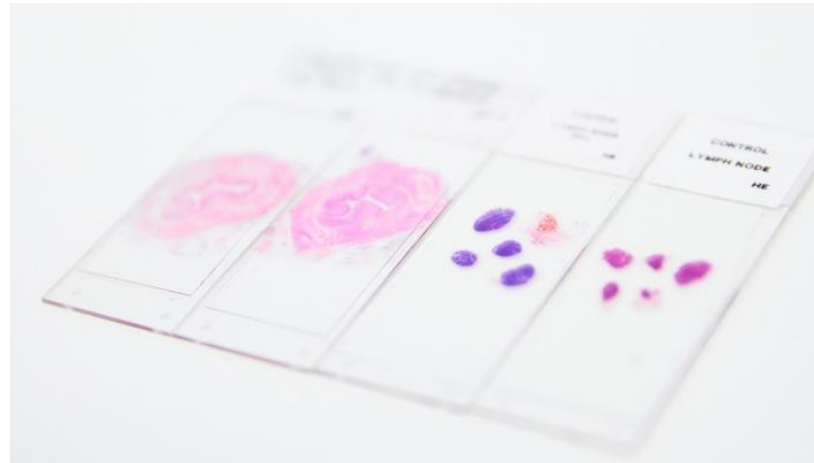
Senior Scientific Officer

- Institute of Cancer Research

ICR The Institute of
Cancer Research



Integrated Pathology Unit



The ROYAL MARSDEN
NHS Foundation Trust

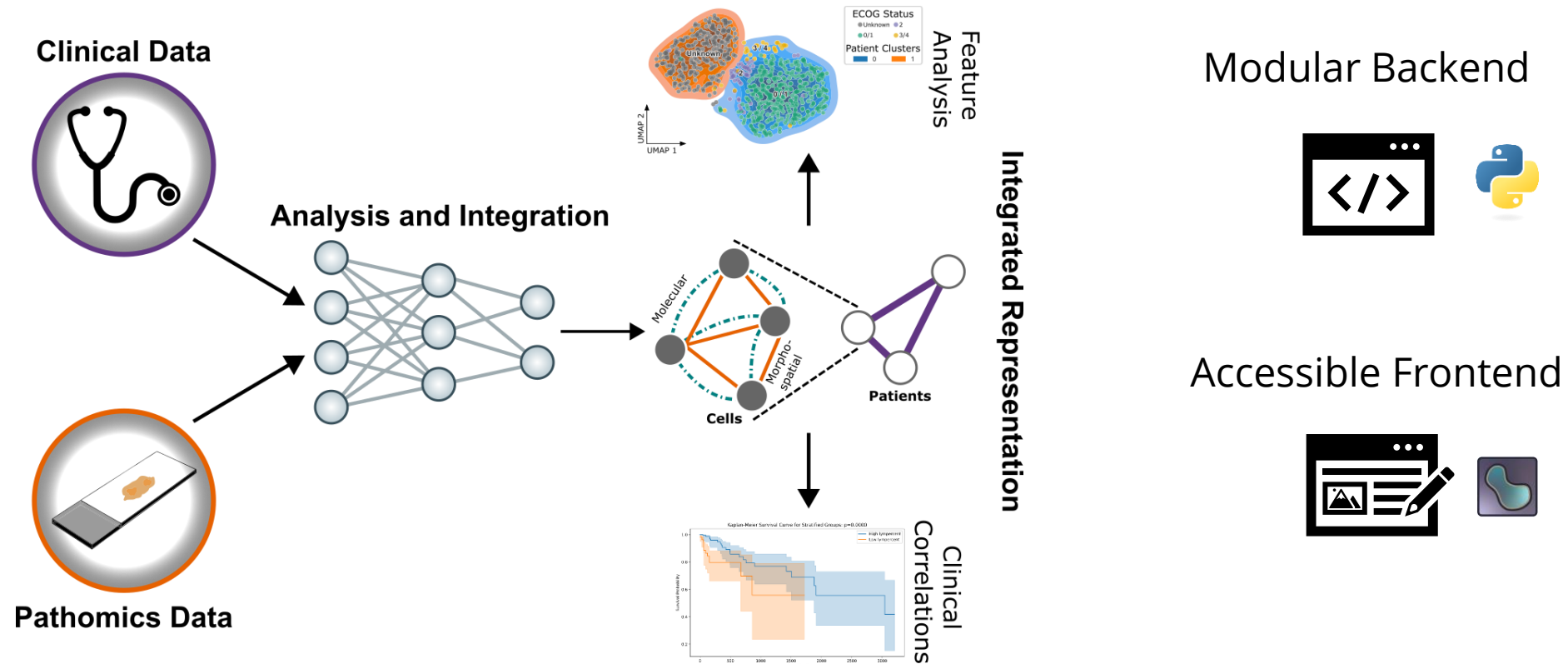


Our Challenge

We Need an Analysis Platform!

The Solution: POPIDD

Platform for Integrative Discovery and Diagnostics



Main Pipeline

- napari_tma
- popidd
- TDintegration
- TDpatientcodedir
- gui
 - backend
 - _init_.py
 - main.py
 - widgets.py
 - ipupathml
 - _init_.py
 - analysecells.py
 - classextensions.py
 - processtma.py
 - utils.py
 - utils
 - _init_.py
 - data_integrity.py
 - tiff_convert.py
 - _init_.py
 - res
 - .gitignore
 - README.html
 - README.md
 - popidd.yml
 - popidd_arm.yml
 - popidd_twin.yml
 - readme.pdf
 - setup.py

POPIDD

IMPORTANT: Do not make any changes or add any files to the copy of this repository on the RDS. That copy is meant to be used ONLY for internal distribution, not direct usage.

Setup

Instructions for Windows Users

Before running anything ensure the following is installed

- JDK from https://download.oracle.com/java/21/latest/jdk-21_windows-x64_bin.msi or the RDS
- VisualStudioSetup: C++ compilation build tools need to be installed, and the VisualStudioSetup executable is an automated way to do so. Get it from [here](#) or the RDS.

- Install Conda by running the installer [from the following link](#).
- Download (or copy) this repository to a local folder of your choosing.
 - It is recommended to put the local copy somewhere accessible and easy to remember, like your *Documents* folder
- Open a Conda terminal (*Miniforge prompt* if installed using the link above) and navigate to the POPIDD folder using the `cd` command.
 - For example, if you had copied the POPIDD folder into your Documents folder you will have to run the following commands in a newly opened terminal:
 - `cd Documents`
 - `cd POPIDD`
- Create a new Conda environment by running the following command:
 - `conda env create -f .\popidd.yml`
 - Notes:
 - Conda environments automate the installation of software and dependencies. You will only need to create the environment once, however you will need to ensure the environment has been "activated" whenever you want to use the tool.
 - If the command above takes too long, use mamba instead of conda (`mamba env create -f .\popidd.yml`).

Napari Plugins

- main
- .github
- .napari-hub
- src
 - .gitignore
 - pre-commit-config.yaml
 - LICENSE
 - MANIFEST.in
 - README.md
 - developing.py
 - pyproject.toml
 - tox.ini

popidd-io

license GPLV3 | pypi v0.0.2 | python 3.10 | 3.11 | 3.12 | tests passing | codecov 52% | napari hub popidd-io | DOI 10.5281/zenodo.14185576

A simple plugin to read digital pathology images and annotations. Made by Ferran Cardoso at the Integrated Pathology Unit (ICR/RMH).

This is still an experimental and in-development project, so expect considerable additions and changes to existing methods. Documentation and tests will be added in the coming weeks.

Standalone Packages

- main
- .github
- nbs
- pyhscore
 - _init_.py
 - _modidx.py
 - score.py
 - .gitignore
 - LICENSE
 - MANIFEST.in
 - README.md
 - settings.ini
 - setup.py

pyhscore

CI passing | pypi package 0.0.2 | DOI 10.5281/zenodo.12531732

Install

First set up a new conda environment with some basic dependencies:

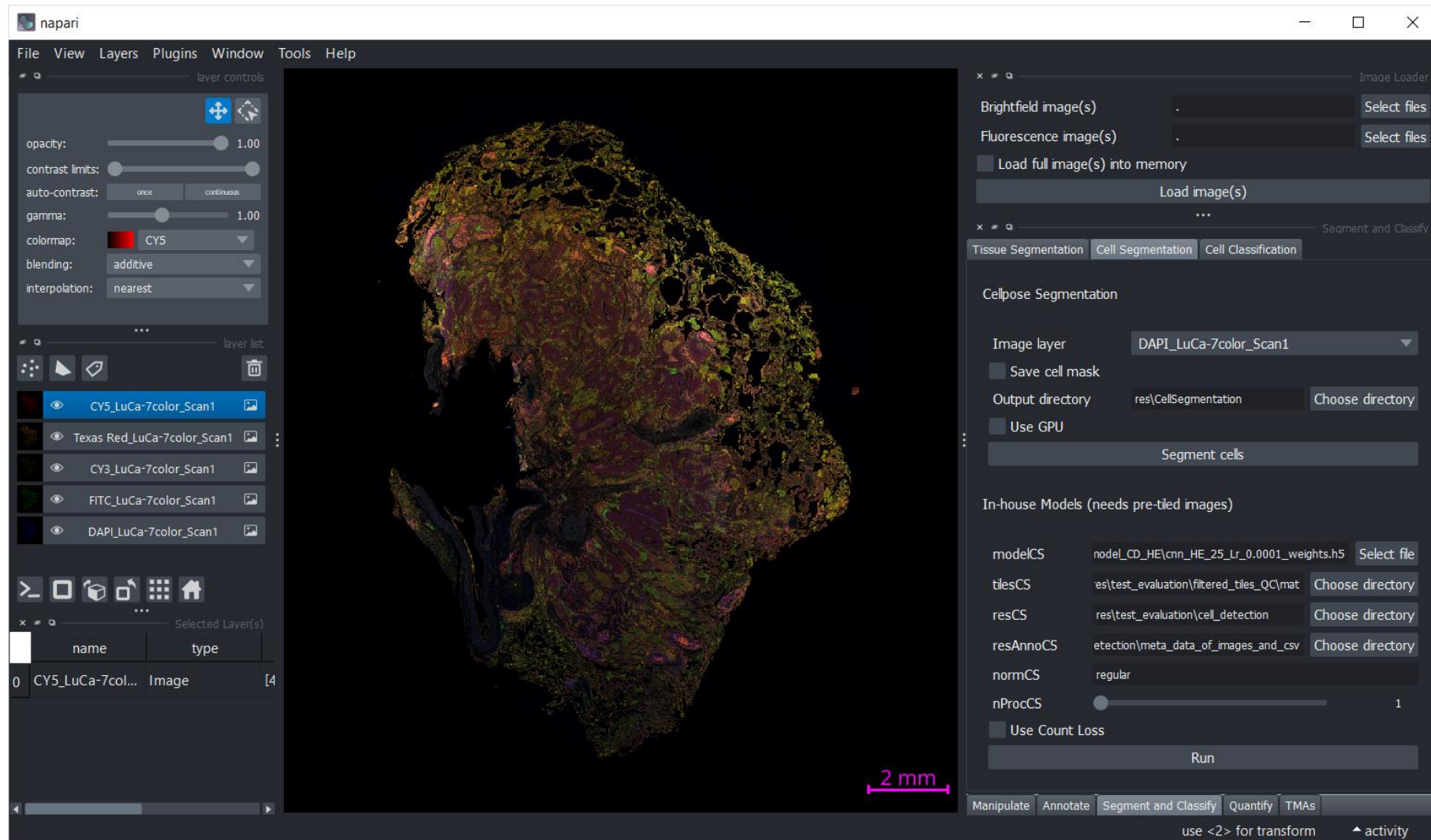
```
conda create -n pyhscore python pip ipykernel
```

Then activate the environment and install the package:

```
conda activate pyhscore
```

```
pip install pyhscore
```

Frontend: Tissue and Cell Segmentation



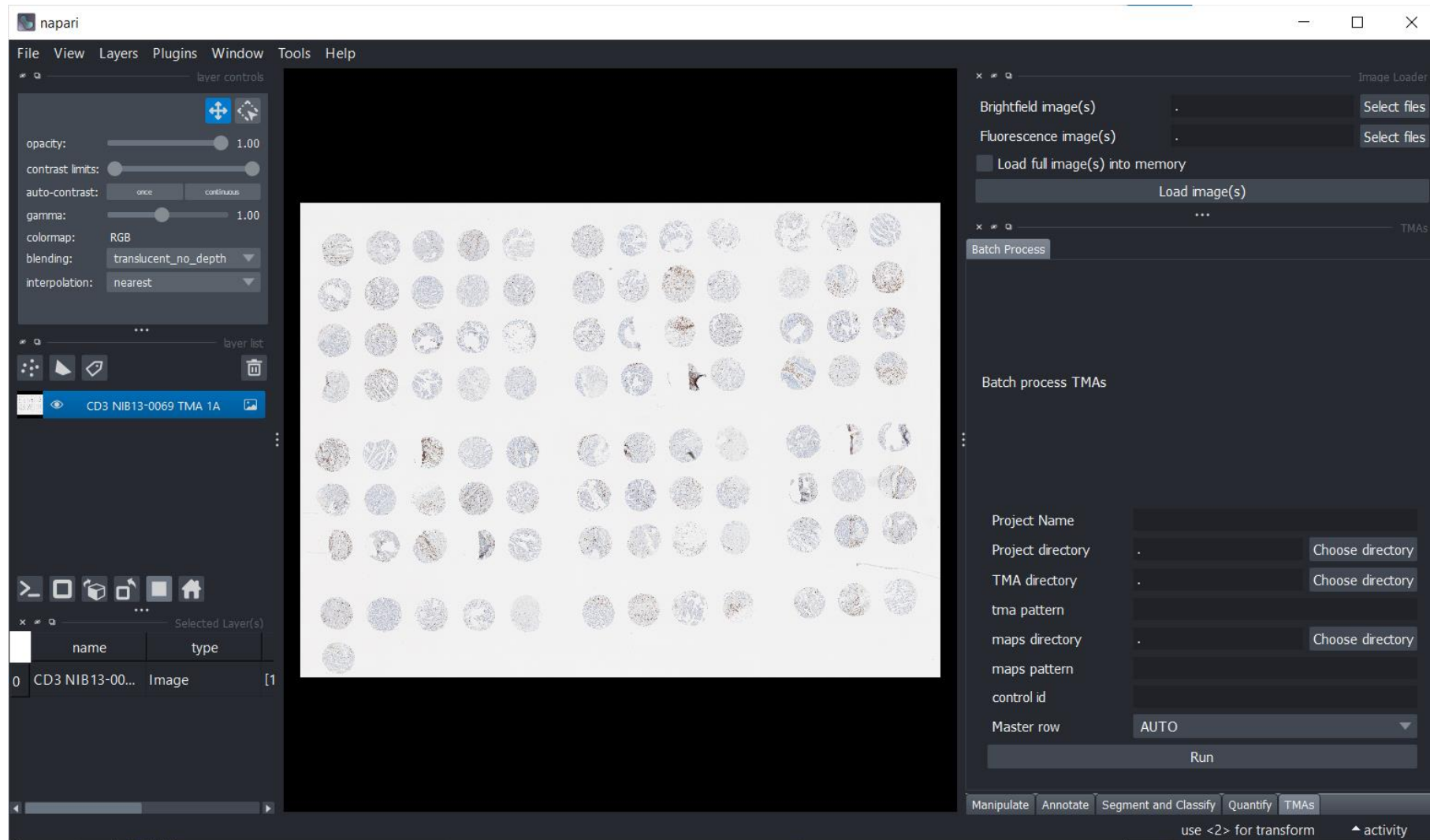
Frontend: IHC Quantification

The screenshot displays the napari software interface for IHC quantification. The central window shows a histology image of a tissue section with brown-stained cells. A pink scale bar in the bottom right corner of the image indicates a length of 2 mm.

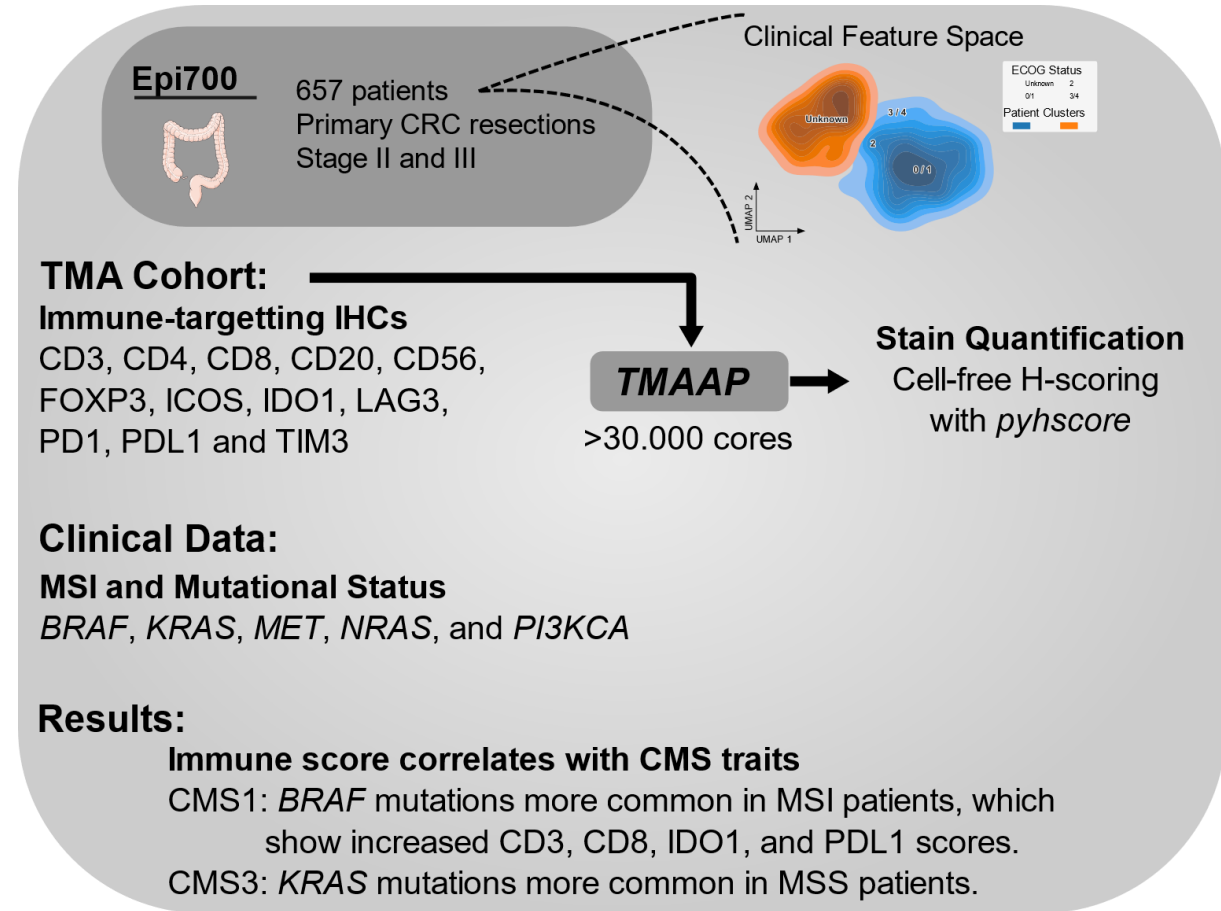
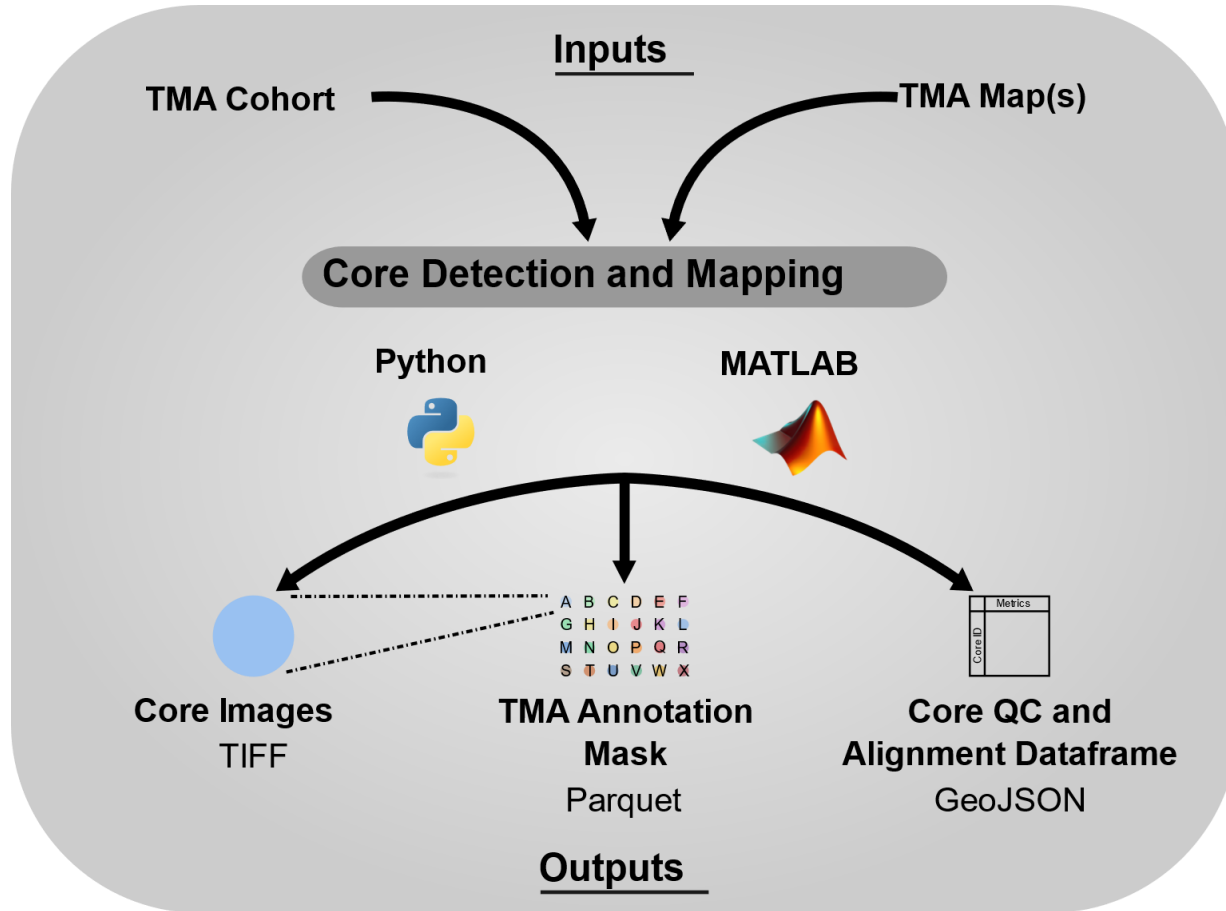
The interface includes several panels:

- Layer Controls:** Contains sliders for opacity (set to 1.00), contrast limits, auto-contrast (set to 'once'), gamma (set to 1.00), colormap (set to 'RGB'), blending (set to 'translucent_no_depth'), and interpolation (set to 'nearest').
- Layer List:** Shows a single layer named 'Cntrl TONSIL KI67 1-300 AST...' of type 'Image'.
- Image Loader:** Includes fields for 'Brightfield image(s)' and 'Fluorescence image(s)', each with a 'Select files' button, and a 'Load image(s)' button.
- Quantify Panel:** Features a 'Pixel-wise H-score (WIP)' section with dropdowns for 'Image layer' (set to 'Cntrl TONSIL KI67 1-300 ASTER...') and 'Image level to analyse' (set to 'Small'). It also has a 'Label layer (optional)' dropdown, a 'Hematoxylin' slider (set to 0.05), and a 'DAB' slider (set to 0.00). The 'Output directory' field has a 'Choose directory' button. A 'Compute pxHscores' button is located below these settings.
- Bottom Panel:** Shows 'H-score' and a row of buttons: 'Manipulate', 'Annotate', 'Segment and Classify', 'Quantify', and 'TMAs'. A note at the bottom right says 'use <2> for transform' and an 'activity' button is visible.

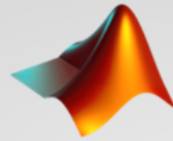
Frontend: TMA Alignment



Applied to IHC TMA Cohort



The Integrated Pathology Unit



TMAAP MATLAB (@ CCRA)



pyhscore (@ FCR), ***c-pmat*** (@ PLN),
TMAAP Python (@ FCR)



popidd-io napari plugin (@ FCR)

Acknowledgements

The Integrated Pathology Unit St George's, University of London

Prof. Manuel Salto-Tellez
Dr Tom Lund

Dr Priya I
Dr Elena

Constantino C. Reyes-Aldasoro

.....

ICR The Institute of
Cancer Research

The ROYAL
NHS

NIHR



biobank
Northern Ireland Biobank

Research Centre at
Marsden and the ICR