PathONE : from one thousand patients to one cell

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Introduction

Digital Pathology is an image-based information environment, where tissue glasses are digitized by high-speed scanners. Whole-slide-images (WSIs) are generated and pathologists are empowered to analyzed and diagnose them directly on a computer monitor.

In coming years, the technology uptake will harmonize the flow of images, information from Electronic Health Records (EHRs) and image analysis results. However, integration of this heterogeneous data into a single application is still one of the challenges in the evolution of pathology to a digital practice.

Aim

- Provide a tool to facilitate simple queries in an EHRs database
- Directly link patients' data to Whole-Slide-Images
- Introduce WSIs-filtering by slides content and image analysis results
- Empower researchers tasks in one-single-screen solution
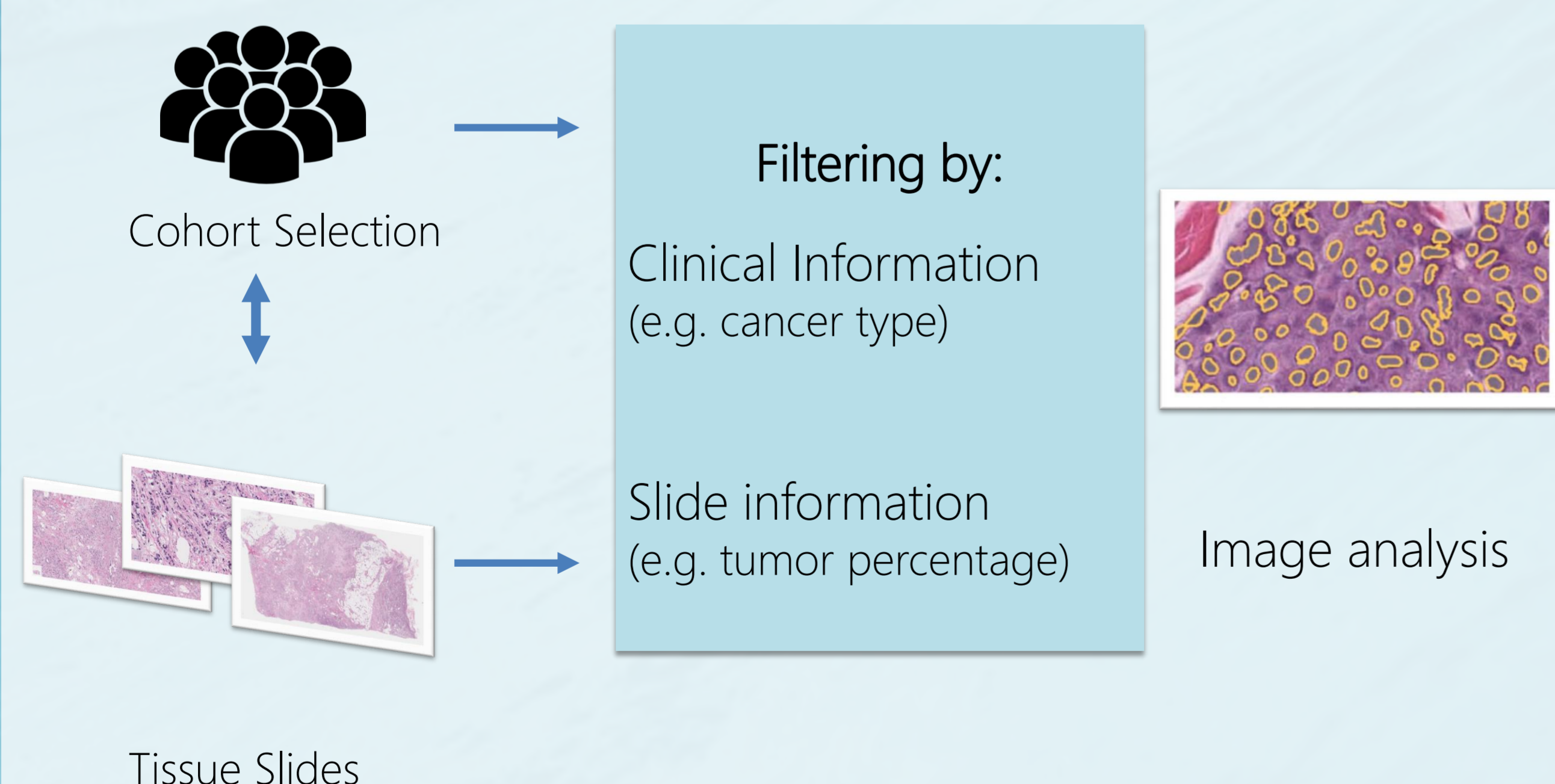
TASKS

Standard researchers' tasks enabled by PATHONE, currently achieved by accessing separate services.

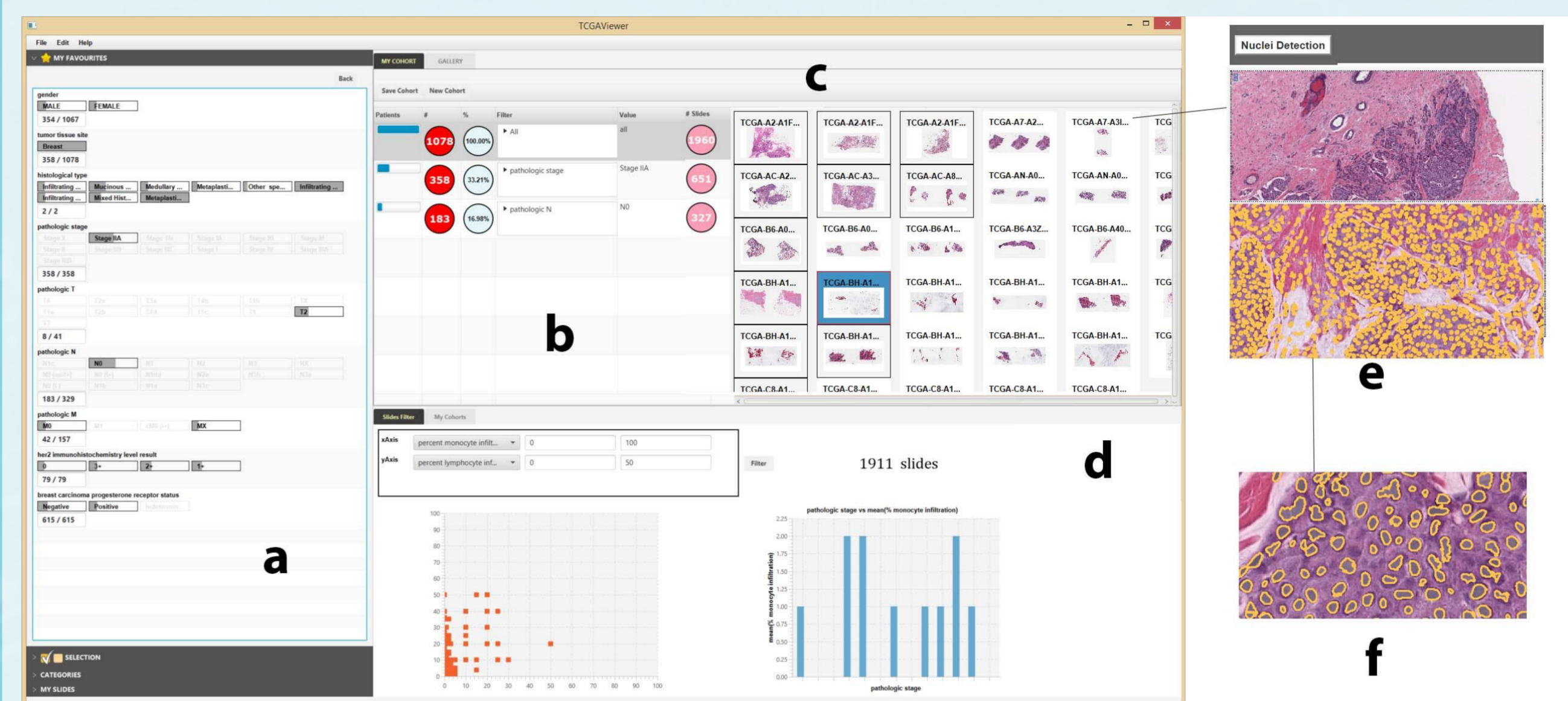Task 1. Search a cohort that fits the research question in the clinical information system.

Task 2. Look for respective tissue slides in the archive

Task 3. Make a list of suitable images for image analysis or clinical studies.

Task 4. Pre-process images and run detection algorithms on digital slides

Cohort Selection

Filtering by:

Clinical Information
(e.g. cancer type)

Slide information
(e.g. tumor percentage)

Image analysis

Tissue Slides

Application

a. Cohort Selection (Task 1): Patients can be filtered by a click on each box, representing a a different value for each attribute. Current number of patients still available is represented as a gray bar
b. Current query information: Insight on current cohort selection
c. Slides Gallery (Task 2): respective patients' images are immaediately displayed
d. Slides filtering (Task 3): Images can be filtered by biological information
e. Example of nuclei detection (Task 4): User can run an algorithm on the same screen on a desired slide.
f. Analysis of results: User can inspect the computed features on by a standard virtual microscopy viewer.

Future work

We implemented a visualization tool to enable researchers to perform the standard steps which they are used to go through before starting image analysis studies.

We collected informal feedback to assess the satisfaction of potential users.

We aim to extend the tool with machine learning techniques to enhance the explorative experience and to integrate more image analysis computations to enhance the slide filtering on more biological information.

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