

Pathology Image Informatics Platform (PathIIP)

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Year 2 Update



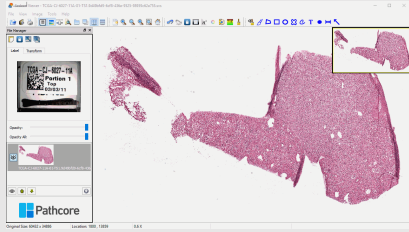
Develop a digital pathology platform to facilitate wider adoption of whole slide imaging and the use of digital pathology analysis by the cancer research community.

Platform will support:

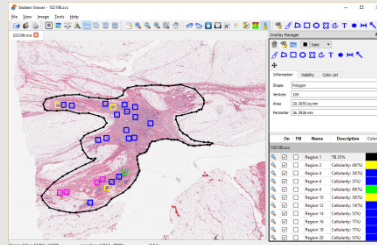
- Visualization of WSIs from multiple vendors
- Annotation tools for pathologists
- Plug in architecture to allow integration of algorithms
- Multimodality support

- Creation of an archive of richly annotated datasets
- Evaluation and validation of algorithms on benchmarked datasets

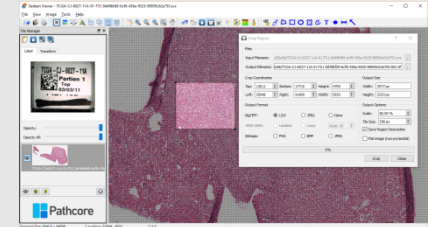
WSI viewer



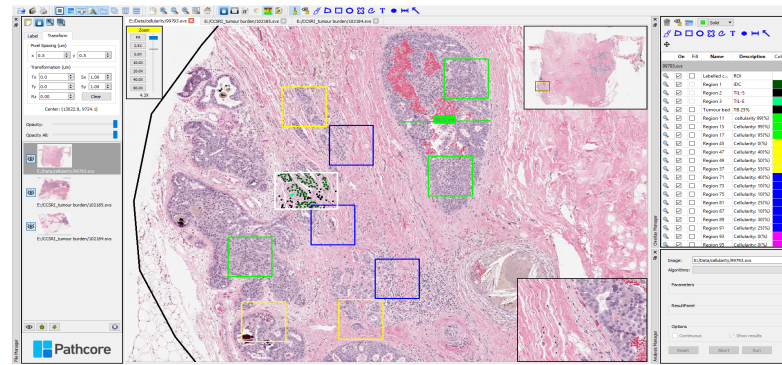
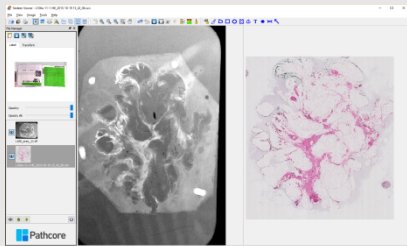
Annotation Tools



Conversion and crop tools



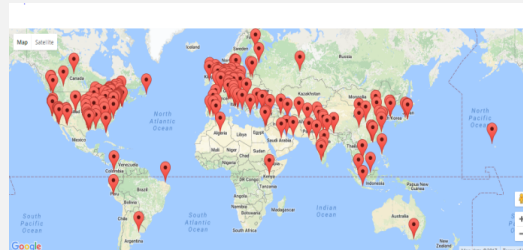
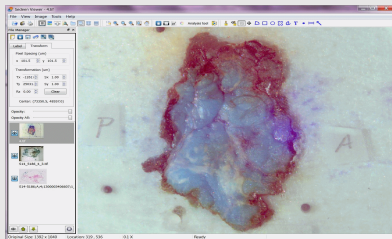
Multimodality imaging



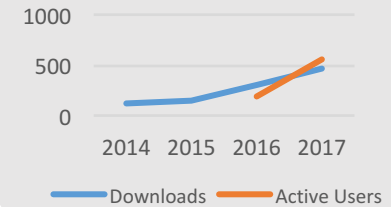
File formats supported:

- Aperio (.svs)
- Hamamatsu (.vms, .vmu, .ndpi)
- Leica (.scn)
- MIRAX (.mrxs)
- Sakura (.svslide v2.6)
- Generic tiled TIFF (.tif)
- Generic BigTIFF (.tiff)
- Generic JPEG 2000 (.jp2, .jpc)
- DICOM (.dcm)

Manual registration



Historical and Projected Usage Trends



Annotation Tools

Sedeen Viewer - 102198.svs

File View Image Tools Help

102198.svs

Overlay Manager

Information Visibility Color List

Shape: Polygon

Vertices: 105

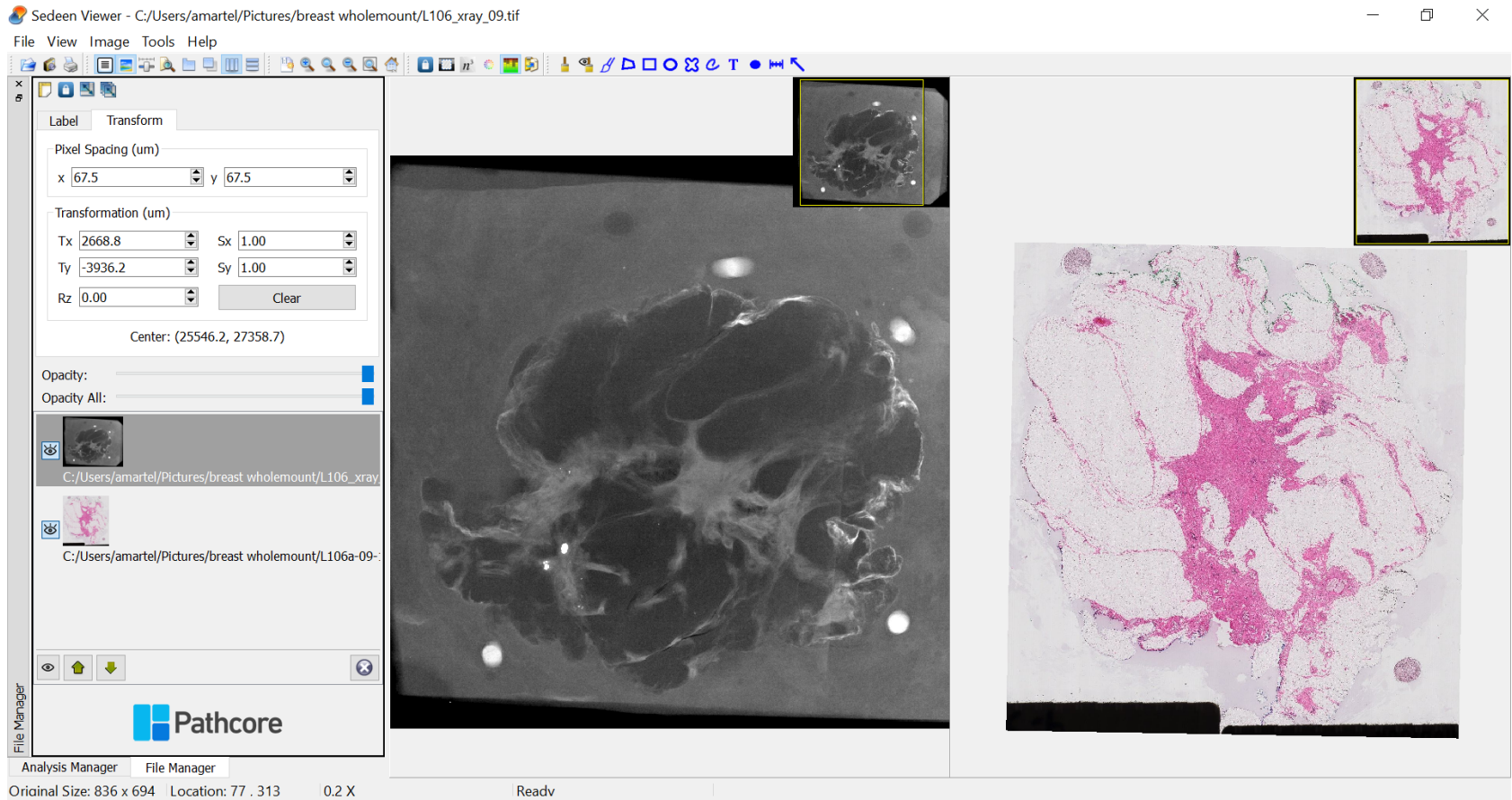
Area: 29.3055 sq mm

Perimeter: 36.3926 mm

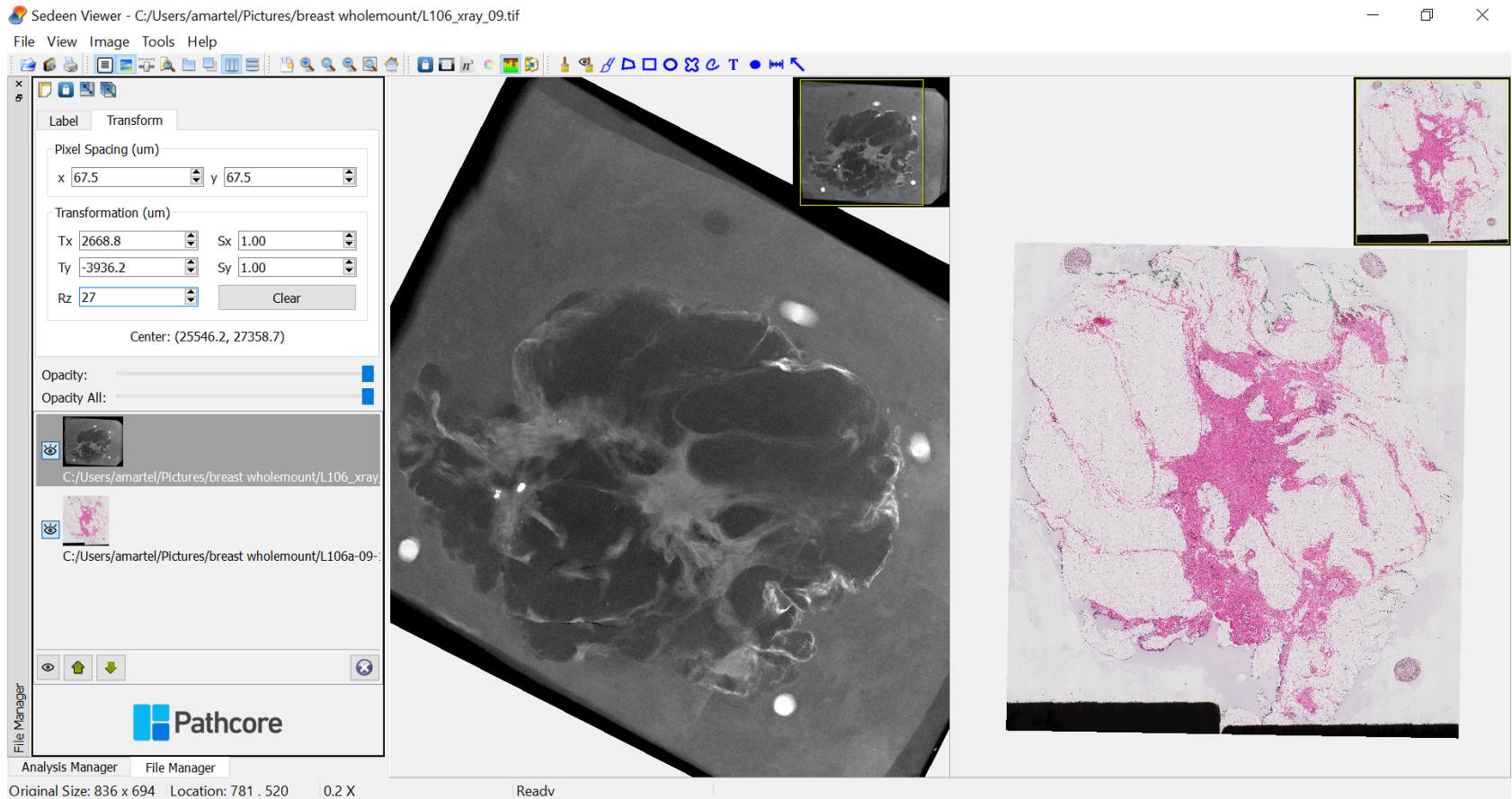
On	Fill	Name	Description	Color
<input checked="" type="checkbox"/>	<input type="checkbox"/>	Region 1	TB 25%	Black
<input checked="" type="checkbox"/>	<input type="checkbox"/>	Region 2	Cellularity: 40(%)	Yellow
<input checked="" type="checkbox"/>	<input type="checkbox"/>	Region 4	Cellularity: 30(%)	Blue
<input checked="" type="checkbox"/>	<input type="checkbox"/>	Region 6	Cellularity: 3(%)	Blue
<input checked="" type="checkbox"/>	<input type="checkbox"/>	Region 8	Cellularity: 80(%)	Green
<input checked="" type="checkbox"/>	<input type="checkbox"/>	Region 10	Cellularity: 50(%)	Yellow
<input checked="" type="checkbox"/>	<input type="checkbox"/>	Region 12	Cellularity: 10(%)	Blue
<input checked="" type="checkbox"/>	<input type="checkbox"/>	Region 14	Cellularity: 5(%)	Blue
<input checked="" type="checkbox"/>	<input type="checkbox"/>	Region 16	Cellularity: 7(%)	Blue
<input checked="" type="checkbox"/>	<input type="checkbox"/>	Region 18	Cellularity: 7(%)	Blue
<input checked="" type="checkbox"/>	<input type="checkbox"/>	Region 20	Cellularity: 5(%)	Blue

Original Size: 54264 x 34105 Location: 14312 , 28384 0.5 X

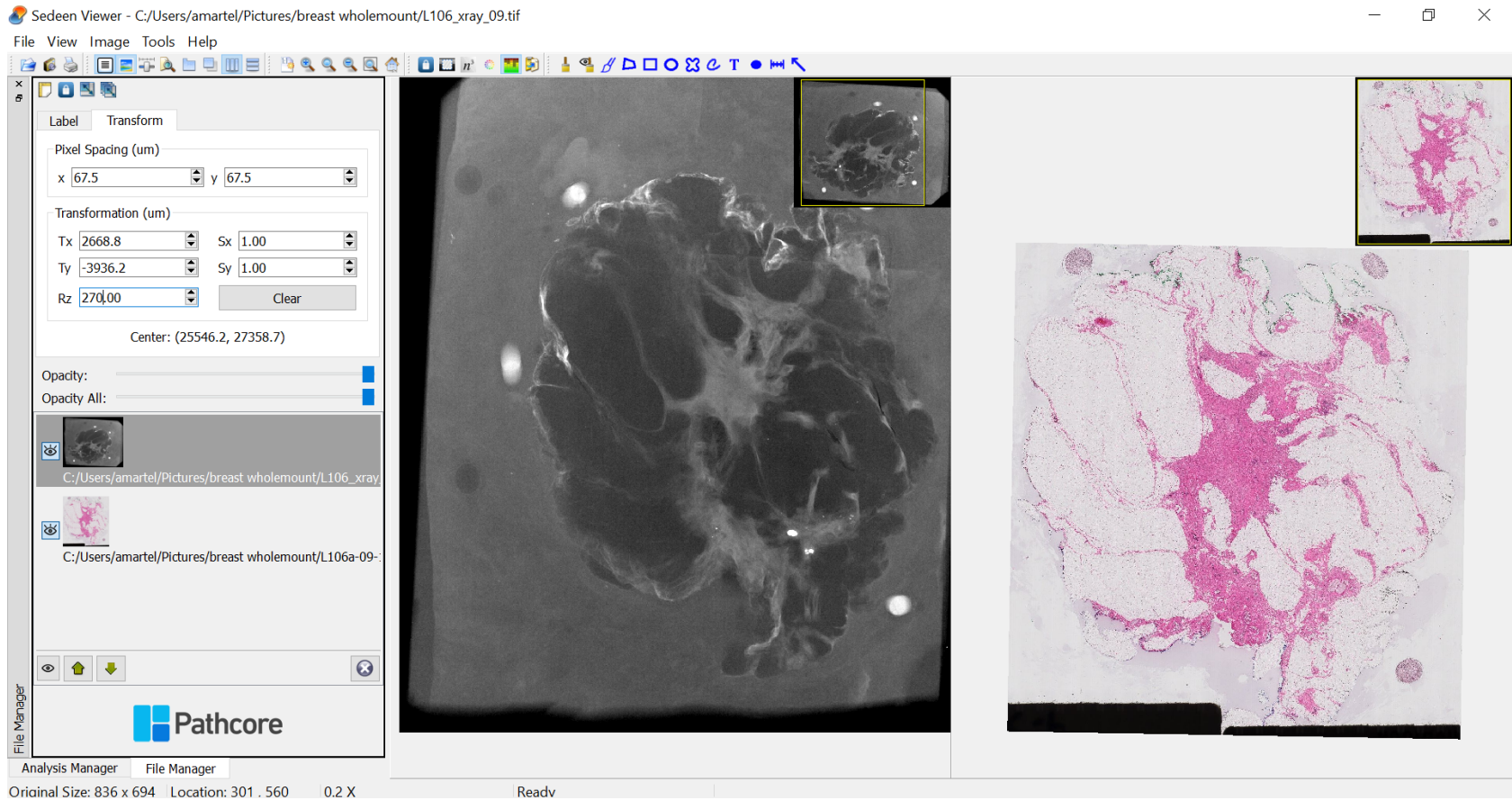
Multi-modal imaging



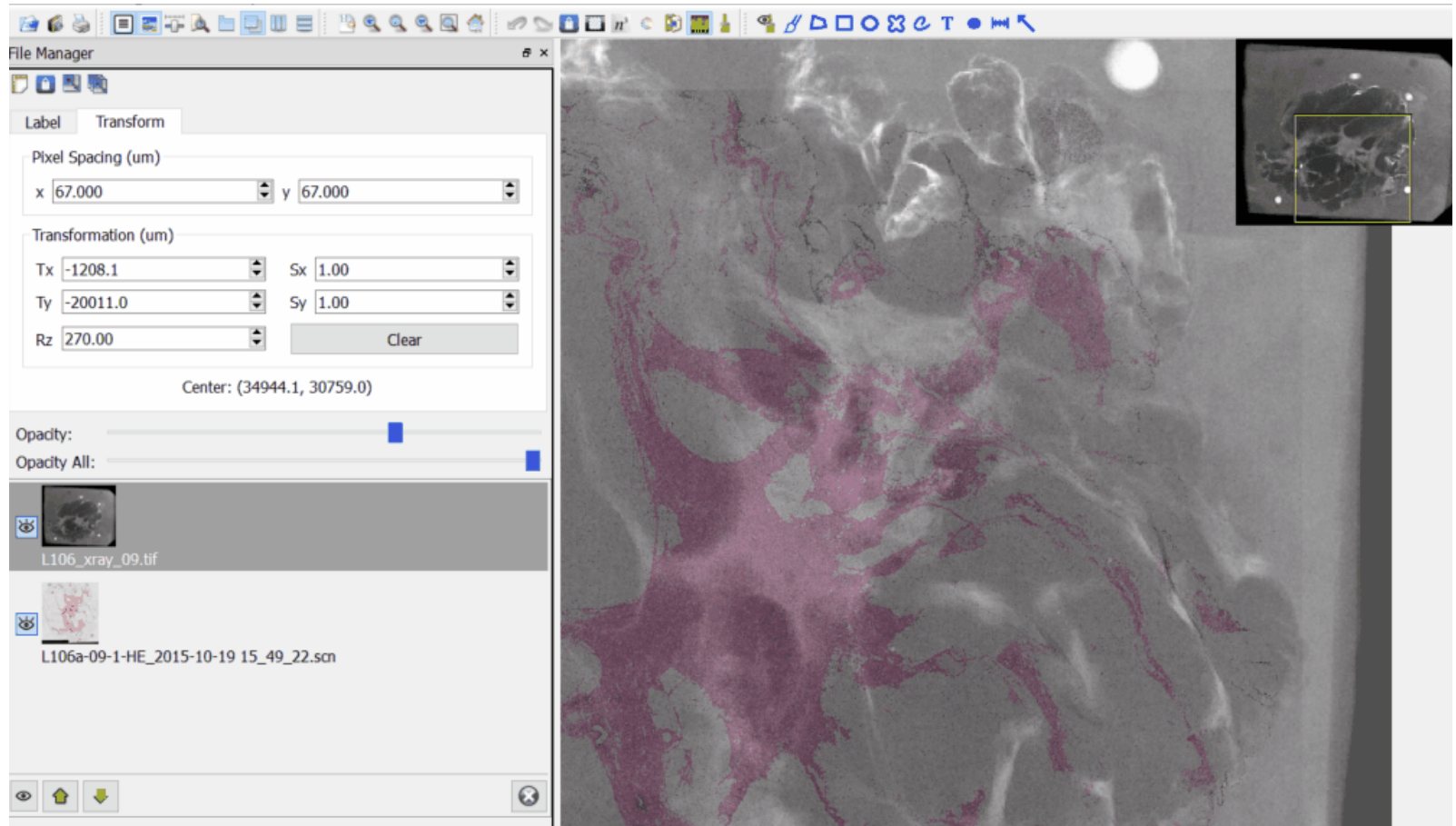
Multi-modal imaging



Multi-modal imaging



Multi-modal imaging



Multi-modal imaging

Sedeen Viewer - W:/histology/Rushin/LumpectomywithCT/L106/L106_x-ray_Blks_2-12/ContrastAdjustedXray/Block_09/L106_xray_09.tif

File View Image Tools Help

Label Transform

Pixel Spacing (um)

x 68.0 y 68.0

Transformation (um)

Tx -3187.5 Sx 1.00

Ty -18375.0 Sy 1.00

Rz 270.00 Clear

Center: (35693.8, 31650.0)

Opacity: [Slider]

Opacity All: [Slider]

W:/histology/Rushin/LumpectomywithCT/L

W:/histology/Rushin/LumpectomywithCT/L

Pathcore

Original Size: 836 x 694 Location: 84, 316 0.2 X

Information Visibility Color List

Shape Polygon

Vertices 225

Area 86.4596 sq mm

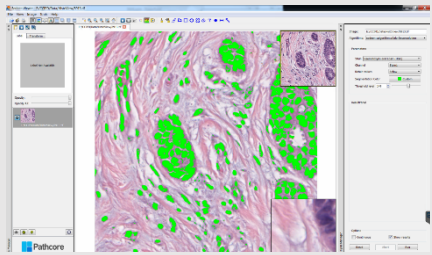
Perimeter 85.3879 mm

On	Fill	Name	Description	Color
<input checked="" type="checkbox"/>	<input type="checkbox"/>	Region 1		Green
<input checked="" type="checkbox"/>	<input type="checkbox"/>	Region 1		Green

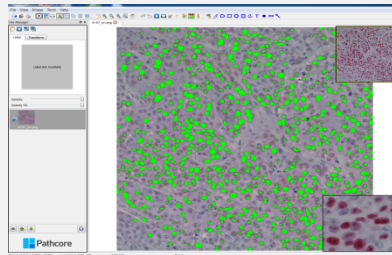
File Manager

Overlay Manager

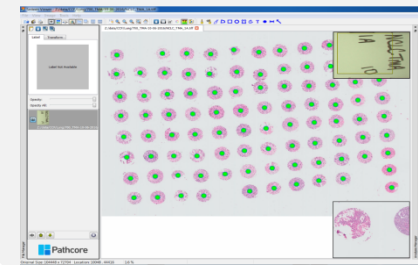
Color Normalization



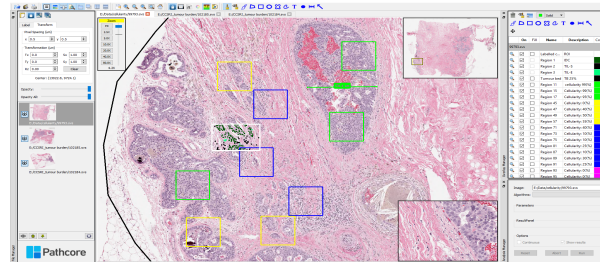
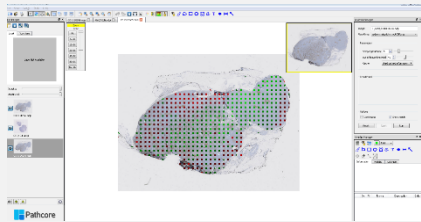
Biomarker Quantification



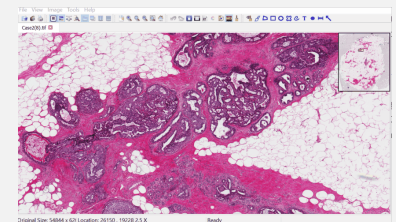
Auto TMA spot extraction



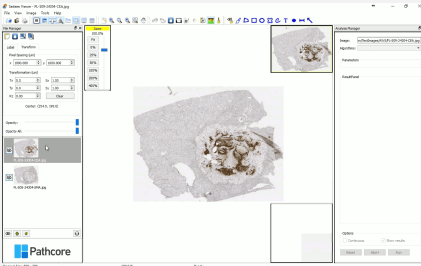
Out of Focus Detection



Stain Analysis

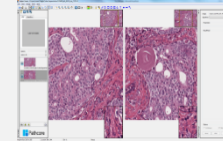
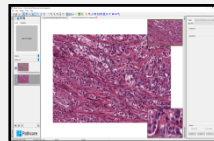


Automatic registration

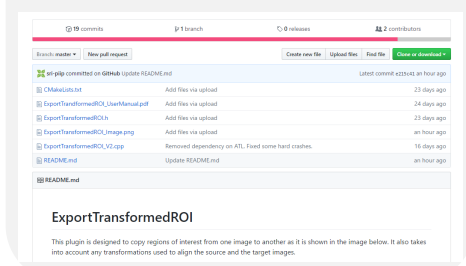


Human Factors Engineering

- Understanding cognitive challenges informs use cases
- Identifying useful leverage points and 'design seeds'
- Improving usability by modifying interface

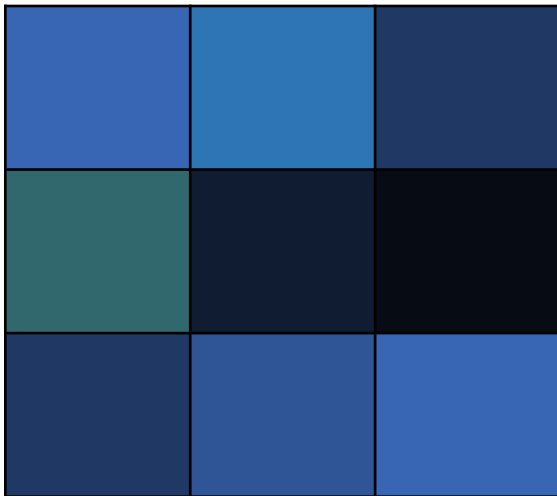


Opensource - Github

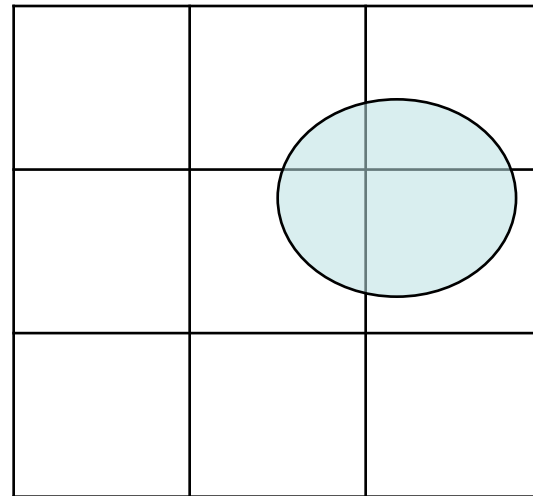


Plugins and the SDK

- Written in C++
- Support for ITK and openCV
- CMake is used for compilation, doxygen documentation
- Algorithm developer is shielded from details of file structure
- SDK provides utilities to efficiently access pixel data



Tile access – colour manipulation



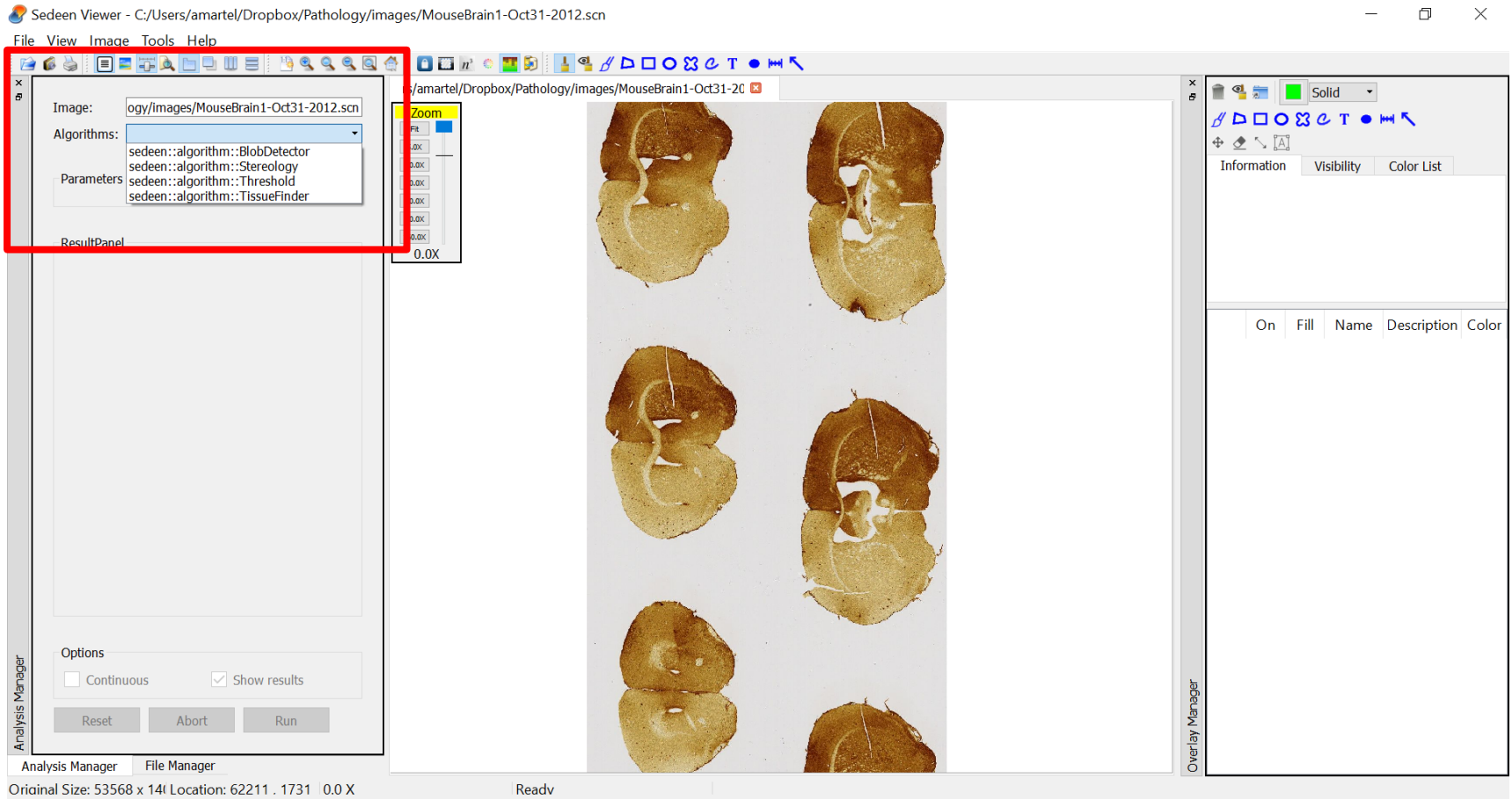
Pixel access – morphology

Plugins and the SDK

- Pipeline consists of a chain of kernels
- Kernel objects carry out specific tasks
- Each kernel may have parameters which can be set using controls exposed in the user interface
- Kernels can also access image metadata

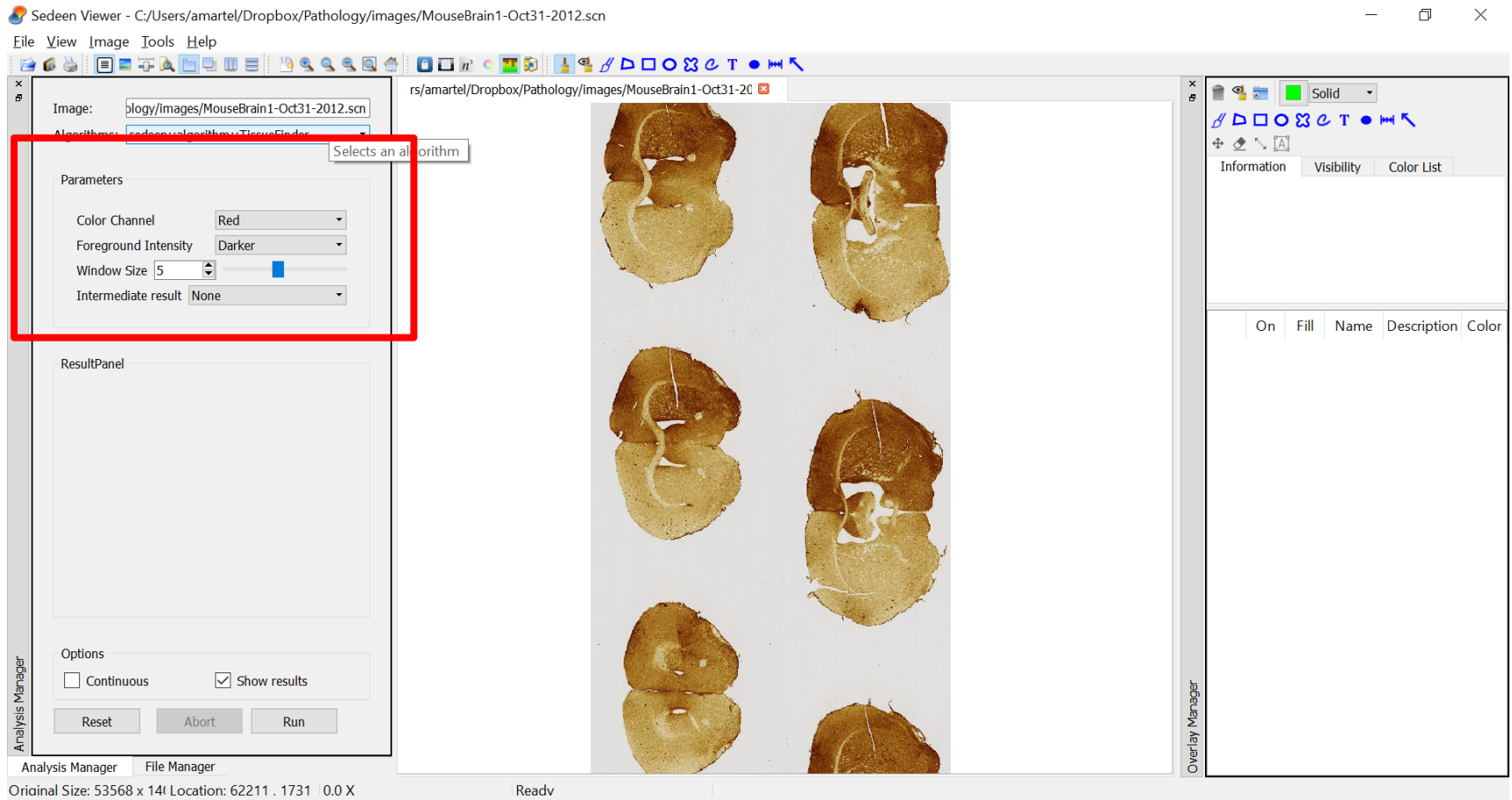


Example plugin: tissue finder



Plugins loaded from a drop down menu

Example plugin: tissue finder



Widgets available for user input

Example plugin: tissue finder

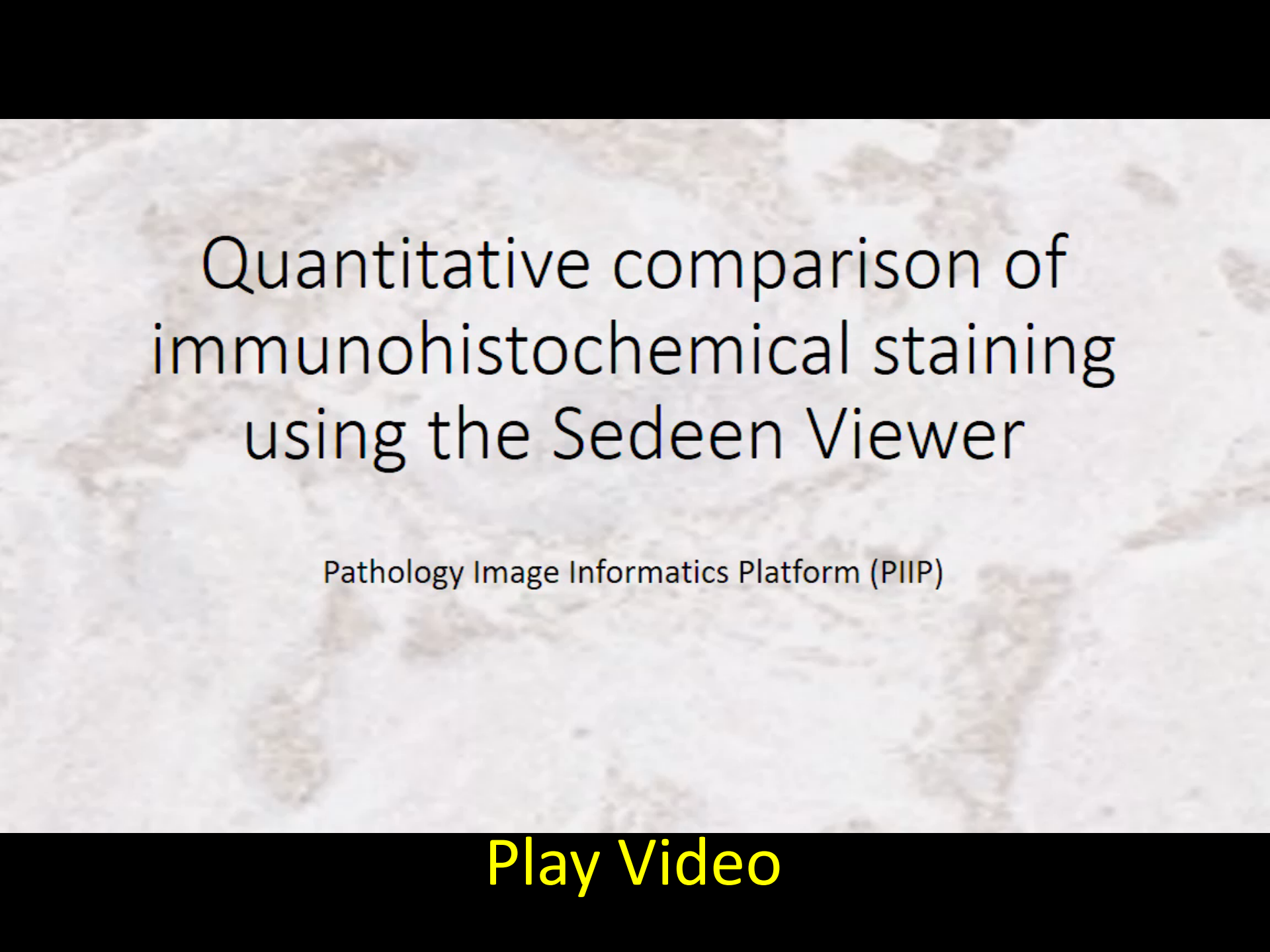
The screenshot displays the Seden Viewer application window. The main window shows a grid of six processed images of mouse brain tissue, each outlined with a green border. The left sidebar contains the 'Analysis Manager' with the 'TissueFinder' plugin selected. The 'Parameters' section is highlighted with a red box and includes:

- Image: `ology/images/MouseBrain1-Oct31-2012.scn`
- Algorithms: `seden::algorithm::TissueFinder`
- Color Channel: Red
- Foreground Intensity: Darker
- Window Size: 5
- Intermediate result: Otsu Threshold

The 'Options' section at the bottom left has 'Continuous' unchecked and 'Show results' checked. The right sidebar shows the 'Overlay Manager' with a table of processing results. The table is highlighted with a red box and contains the following data:

	On	Fill	Name	Description	Color
MouseBrain1-Oct31-2012.scn					
	<input checked="" type="checkbox"/>	<input type="checkbox"/>			Green
	<input checked="" type="checkbox"/>	<input type="checkbox"/>			Green
	<input checked="" type="checkbox"/>	<input type="checkbox"/>			Green
	<input checked="" type="checkbox"/>	<input type="checkbox"/>			Green
	<input checked="" type="checkbox"/>	<input type="checkbox"/>			Green
	<input checked="" type="checkbox"/>	<input type="checkbox"/>			Green

Several options for output of processing results



Quantitative comparison of immunohistochemical staining using the Sedeen Viewer

Pathology Image Informatics Platform (PIIP)

[Play Video](#)

github.com/sedeen-piip-plugins/

sedeen-piip-plugins / Info

Watch 0 Star 0 Fork 0

Code Issues 0 Pull requests 0 Projects 0 Wiki Pulse Graphs

Not sure where to start? Look in here!

7 commits 1 branch

Branch: master New pull request

deyuw Readme

README.md

Sedeen PIIP Plugins

This organization contains repositories for PIIP plugins d

How to Contribute

If you haven't already, please email Deyu (deyu.wang@p organization).

The structure in this organization looks like this, where e

```
Sedeen-PIIP-Plugins
|--AwesomePlugin
|--CoolPlugin
|--NeatPlugin
```

19 commits 1 branch 0 releases 2 contributors

Branch: master New pull request

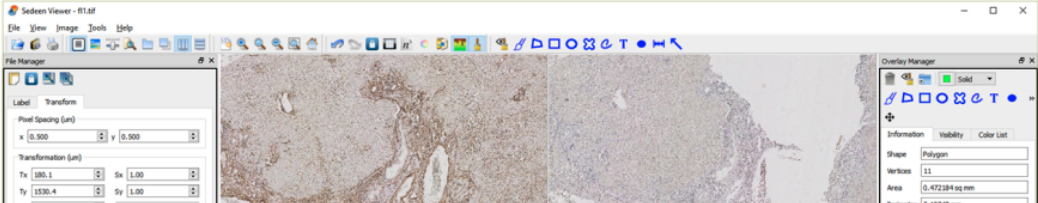
Create new file Upload files Find file Clone or download

sri-piip committed on GitHub Update README.md Latest commit e215c41 an hour ago

CMakeLists.txt	Add files via upload	23 days ago
ExportTransformedROI_UserManual.pdf	Add files via upload	24 days ago
ExportTransformedROI.h	Add files via upload	23 days ago
ExportTransformedROI_Image.png	Add files via upload	an hour ago
ExportTransformedROI_V2.cpp	Removed dependency on ATL. Fixed some hard crashes.	16 days ago
README.md	Update README.md	an hour ago

ExportTransformedROI

This plugin is designed to copy regions of interest from one image to another as it is shown in the image below. It also takes into account any transformations used to align the source and the target images.

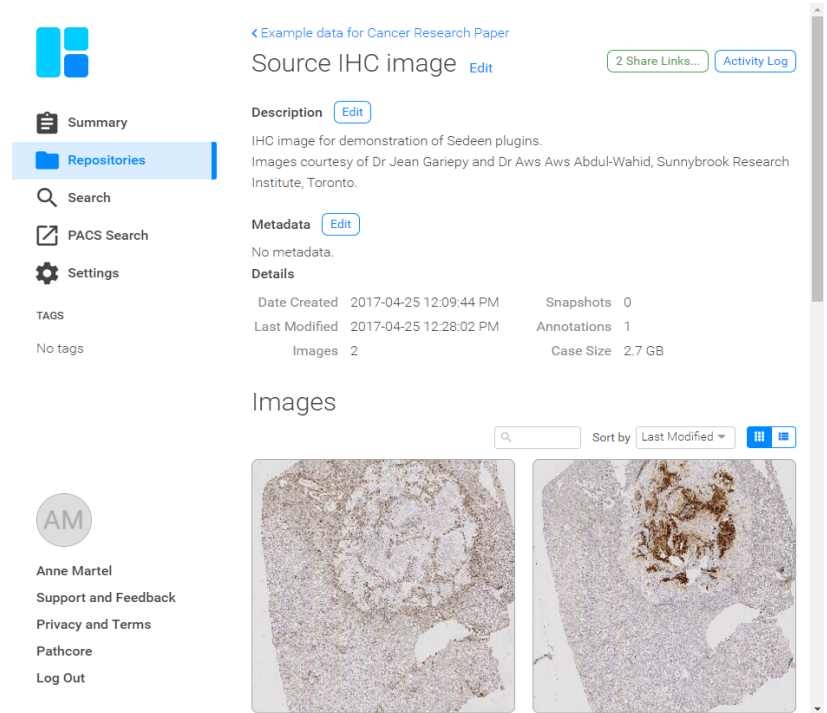


In the pipeline....

- Improved support for Matlab routines
- Mechanism to call Python procedures from plugin
- Distributing SDK to a wider research community
- MacOS and linux versions
- Support for web based image tile servers
- Collection of datasets for validation

Curated Datasets

- Collect image databases
- Richly annotated by pathologists
- Develop ontologies
- Benchmark datasets



Images and annotations made available through Pathcore Web



Ulysses Balis, MD



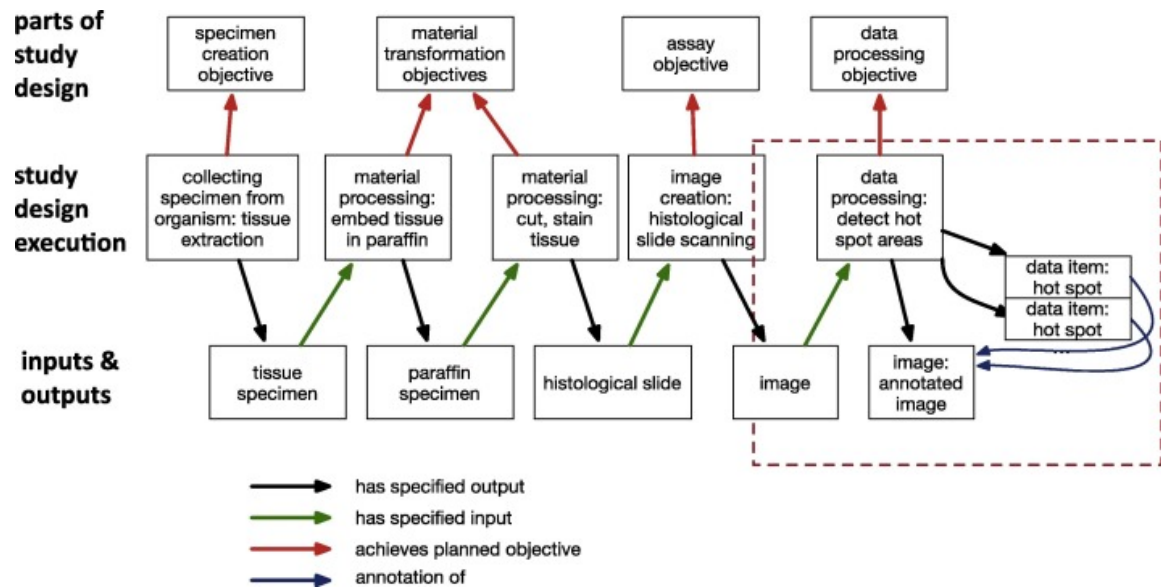
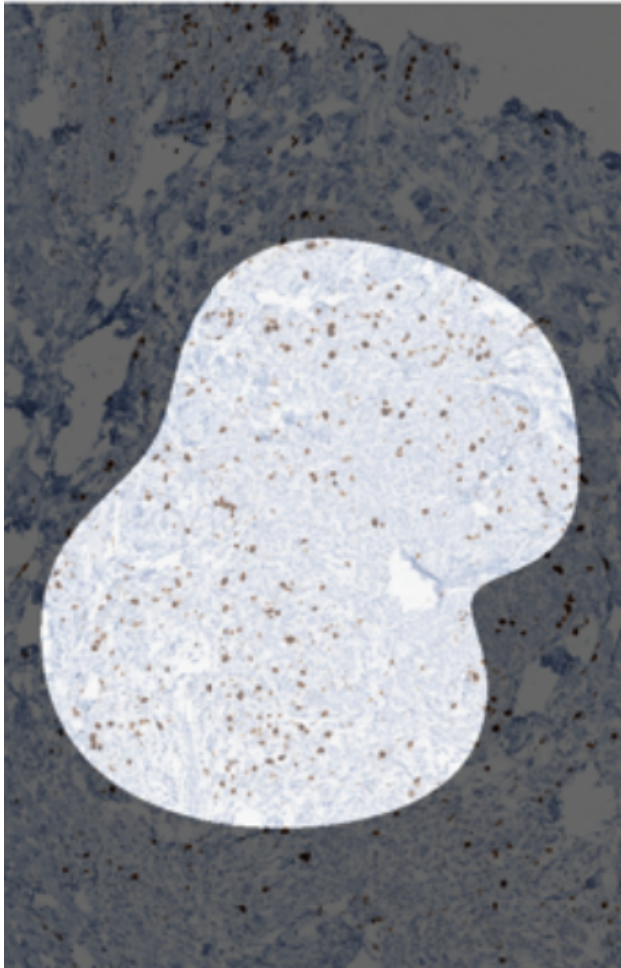
Michael Feldman, MD, PhD



John Tomaszewski, MD, MASCP



Test case: Ki67



Task	Deliverables	Y1	Y2	Y3	Y4	Y5
Improve Plugin Framework	New version released Dec 2016, 4 updates in 2017, distribution mechanism established	Green	Green	Light Green	Light Blue	Light Blue
Documentation and Training	SDK documented, 2 training sessions for developers	Green	Green	Light Green	Light Green	Light Green
Add existing algorithms	Cell segmentation, stain normalization, out of focus detection, biomarker quantification	Green	Green	Light Green	Light Green	Light Green
Rad-pathology co-reg	Manual pipeline established	Green	Green	Light Green	Light Green	Light Green
Algorithm Evaluation		Light Blue	Light Blue	Light Green	Light Green	Light Green
Create image repository	Pathcore Web made available	Green	Green	Green	Light Blue	Light Blue
Accrual of annotated WSIs	Collection of Ki67 WSIs in progress	Green	Green	Light Green	Light Green	Light Green
Otology creation	J Biomed Inform publication on QHIO	Green	Green	Light Green	Light Green	Light Blue
Conference Demos	MICCAI 2016 workshop on pathomics	Light Blue	Light Blue	Light Green	Light Green	Light Green
HCI feedback	Report on GUI from HCI expert	Light Blue	Green	Light Green	Light Green	Light Green
Organize Grand Challenge		Light Blue	Light Blue	Light Blue	Light Green	Light Green



Visit us at: www.pathiip.org

