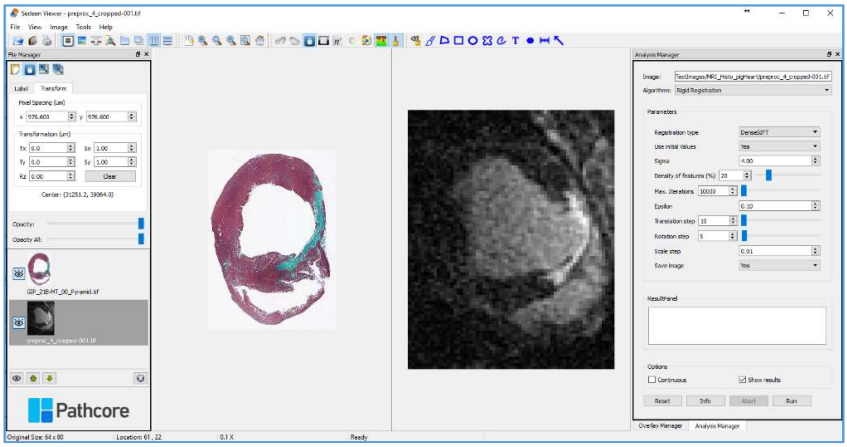
Demonstrating MRI/histopathology co-registration with the Sedeen viewer

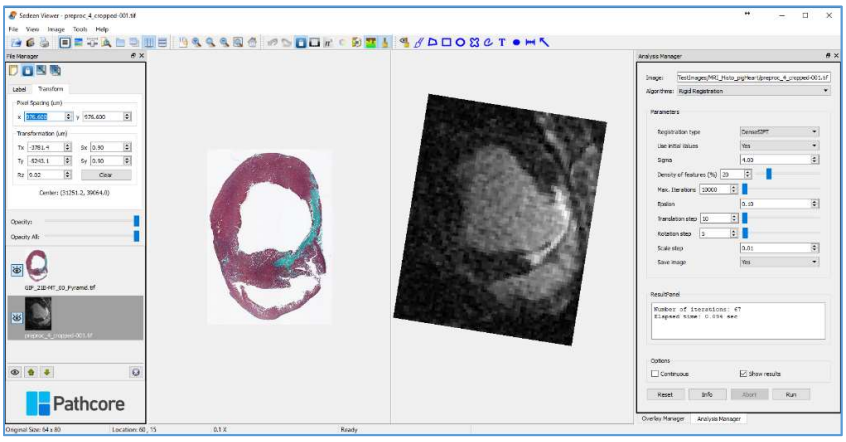
R. Shojaii, M. Pop, A.Yazdanpanah, A. Martel
Sunnybrook Research Institute, Toronto, Canada

The aim of Pathology Image Informatics Platform (PIIP) project, sponsored by NCI/NIH, is to expand the image analysis resources in Sedeen Viewer, which is a freely available pathology image viewer software, https://pathcore.com/sedeen/ . This document demonstrates the use of Sedeen viewer to validate the quantitative analysis of infarct tissue heterogeneity assessed with contrast enhanced MRI.In this case study a pair of in vivo contrast enhanced MRI and the Whole Slide Image (WSI) of the corresponding histology slide of a swine heart with infarction is used. The histology slide is stained with Masson's Trichrome (MT) to identify the extent of fibrosis. The Sedeen viewer is able to open a variety of images including DICOM. For the purpose of this demonstration the heart region is cropped from the MR image and saved as TIFF file. Two fibrotic regions are delineated manually on the MR image based on the T1* maps obtained from multi-contrast late enhancement (MCLE) MRI. The MR image with a resolution of 1 x 1 mm is automatically aligned with the histology image with a resolution of 5 x 5 µm. No down-sampling of the histology is necessary. Two regions of interests outlining the fibrotic regions in MRI are transferred to the histology image. Quantitative analysis are then performed on histology image on these regions of interests.

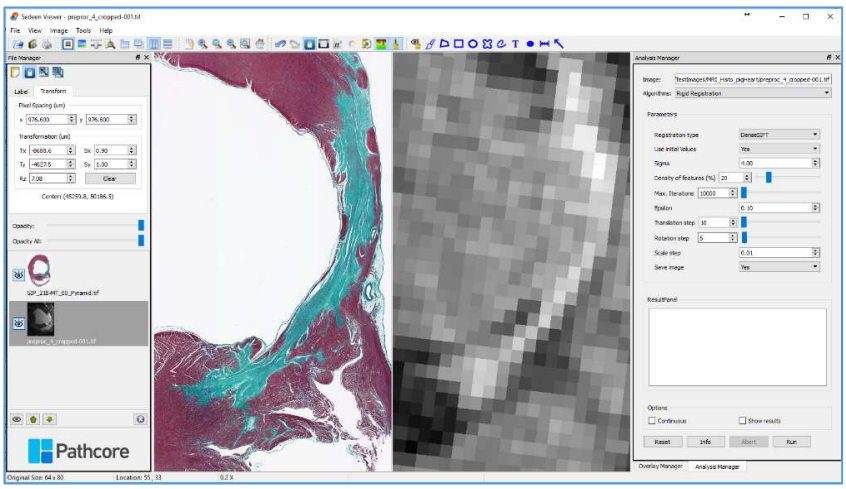
1. Load the histology and the MR images in Sedeen. The histology image is the target image and should be the first in the list of loaded images.
2. From the list of images select the MR image, which is the source image.
3. In the Analysis Manager panel choose the RigidRegistration algorithm, which uses dense SIFT features to automatically register the images (1).



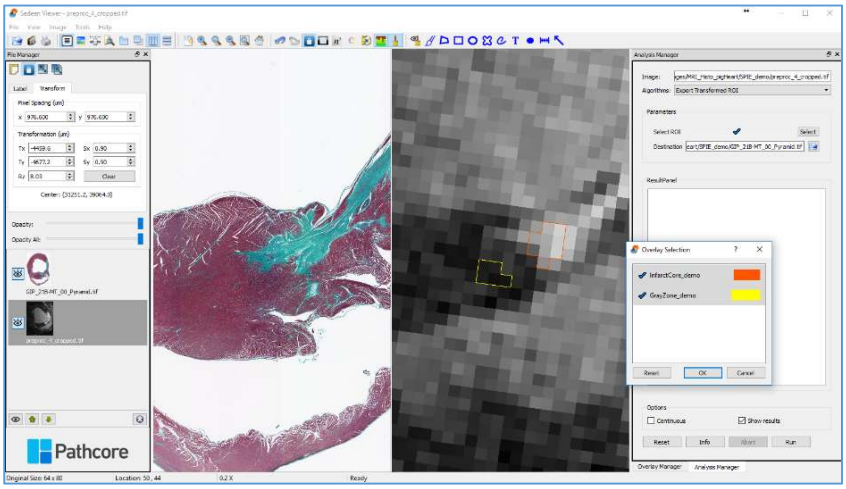
4. In the Transform tab page of the File Manger panel provide initial values for the registration.
5. In the Analysis Manager panel change the registration parameters if required.
6. The sparsity of the SIFT features used for registration can be changed by the parameter Density of features (%).
7. Click on the Run button at the bottom of the Analysis Manager panel.



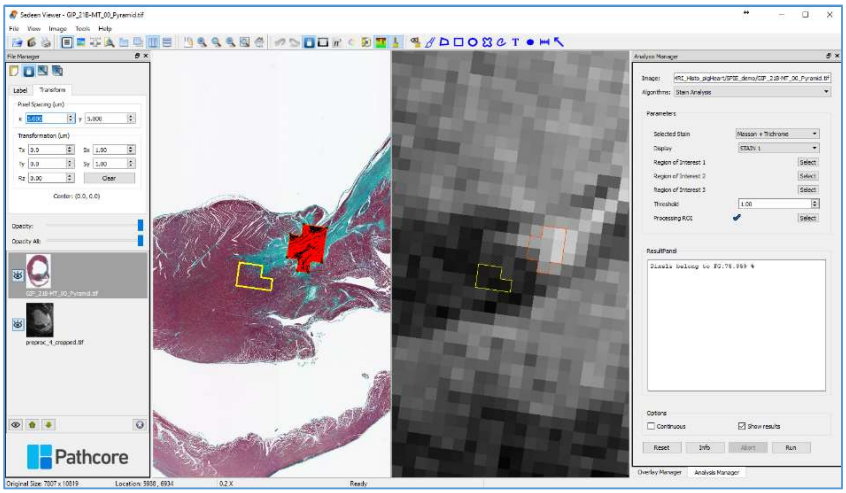
8. The resulting transformation parameters show up in the Transform tab of File Manager.
9. The images can be zoomed in to check the registration.
10. Run the registration again if required.
11. Refine the registration manually if required.



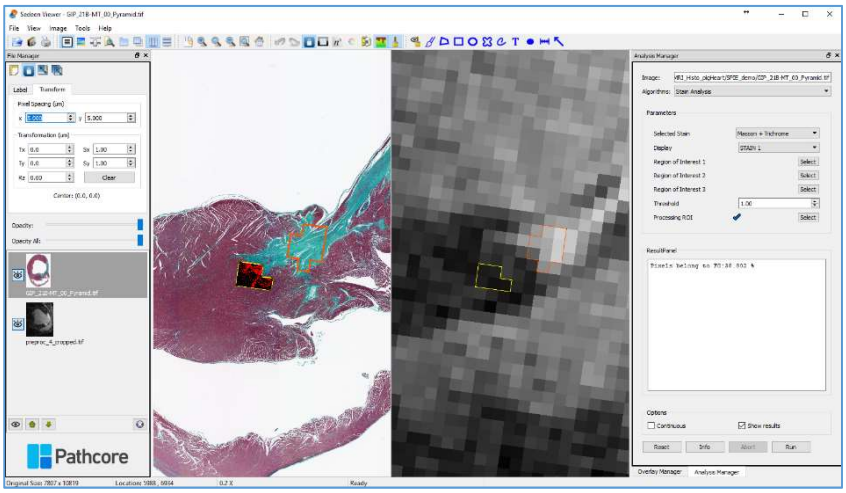
12. Draw regions of interest using the Overlay Manager to outline the different regions of fibrosis, i.e. Infarct Core and Gray Zone.
13. In the Analysis Manager panel choose the ExportTransformedROI algorithm.
14. Click on the Select button and select the ROIs to be transferred and then click OK.
15. Click on Browse button to select the file of the histology image as the destination.
16. Click on the Run button at the bottom of the Analysis Manager panel to transfer the regions from MRI to histology.
17. Reload the histology image with the fibrosis regions.
18. The instructions for this algorithm can be found here: https://github.com/sedeen-piip-plugins/ExportTransformedROI/blob/master/ExportTrandformedROI_UserManual.pdf



19. In the Analysis Manager panel choose the StainAnalysis algorithm.
20. From the Selected Stain dropdown list select Masson's Trichrome stain.
21. From the Processing ROI click on Select to choose a fibrotic region.
22. Click on the Run button at the bottom of the Analysis Manager panel
23. The percentage of the stain positivity shows up in the result panel.
24. If it is required, change the Threshold and run the algorithm again.
25. The Infarct Core region selected here has ~74% stain positivity, which complies with literature (2).
    Normal Myocardium: < 20%
    Gray Zone: 20 - 70%
    Infarct Core: > 70%



26. Select another region in the gray zone of the myocardium with infarct.
27. Run the StainAnalysis algorithm.
28. The result shows ~39% stain positivity for the selected gray zone, and this percentage also complies with literature (2).
29. The instructions for StainAnalysis algorithm can be found here: https://github.com/sedeen-piip-plugins/StainAnalysis-plugin/blob/master/StainAnalysis_Plugin.pdf



1. Shojaii R, Martel AL. Optimized SIFTFlow for registration of whole-mount histology to reference optical images. J Med Imaging. 2016;3(4).
2. Pop M, Ramanan V, Yang F, Zhang L, Newbigging S, Ghugre NR, et al. High-resolution 3-D T1 mapping and quantitative image analysis of gray zone in chronic fibrosis. IEEE Trans Biomed Eng. 2014;61(12):2930–8.