

HistoStitcher Installation and Usage Manual

HistoStitcher is a tool for the reconstruction of stitched whole mount histology sections (WMHS) by selecting common fiducials on the edges of adjacent histology quadrants. HistoStitcher offers real-time rendering of histology images by using a multi-resolution pyramid for each histology quadrant. This software is intended for research purposes only, not for diagnostic or clinical use.

Software Version: 1.02

Prerequisites:

Please make sure that your computer meets the following requirements:

- Windows 7 64-bit operating system or later

Installation:

The following components are included in the install package. Leave the checkboxes filled unless you previously installed those packages.

- 1) The HistoStitcher Software
- 2) The Data Conversions tool
- 3) The Matlab runtime compiler 7.14
- 4) The AMD-APP-SDK v2.7

The user must agree with the License agreement provided with the installer in order to install the application. After accepting this agreement, follow the instructions and specify the destination folder where you would like HistoStitcher installed. To complete the installation, restart the computer.

We would like to acknowledge the use of some external libraries in this project:

- Qt 4.8.4
- Python 2.7.3
- Matlab Runtime compiler 7.14
- Glew 1.7.0
- freeGlut 2.8.0
- Openjpeg 1.5.0
- OpenSlide 3.2.6

- JPeg-turbo 1.2.0
- FreeImage 3.15.3
- Zeromq 2.2.0
- Lua 5.1
- Db & db_stl 5.3 (Berkeley database library)
- Boost 1.49
- MPL

Data conversion

HistoStitcher can only load images that have been converted into db format. These images are tile-based multi-resolution JPEG-encoded images. The **svsConverter** is a tool that transforms standard multi-resolution TIFF-encoded svcs files into a db image format.

In order to convert a svcs file to a db file, you must create a configuration file. A sample config file is shown below:

```
sourceNames=13118.svs
targetNames=13118.db
#use berkeleyDB format or standard ldv format?
useDB=1
# 0 for no compression, 1 for jpeg
compressionType = 1

# quality of compression, 1-100 (100 best)
jpegQuality=80

# if true pad to sector/page size for unbuffered reading. Will lead to
larger files.
pageFilePadded=1

# \R for resource path, \A for application path and leave empty for
absolute paths
sourceDir=c:\data\imgConvRelease
targetDir=c:\data\imgConvRelease\output

padding = 2
hostName = pccs000538ws
```

The *source name* corresponds to the .svcs file you want to convert. Do not include the path in this value. Currently this file **MUST** exist in the same folder as the svcsConverter.exe file

The *target name* corresponds to the DB file you want to create. Do not include the path in this value

The *sourceDir* points to the folder that contains the source SVS file you set in step 1.

The *targetDir* specifies the folder you would like the output DB file saved to. Make sure this path already exists in the file system. Currently this folder **MUST** exist as a subfolder of the folder containing svcsConverter.exe

Change to the DataConverter sub-directory located under the directory where HistoStitcher was installed. Run the **svcsConverter.exe** from the command line and specify the config file as the first parameter:

```
C:\HistoStitcher\DataConverter> svcsConverter.exe converter.cfg
```

Stitching- Generating Whole Mount Histological sections (WMHS)

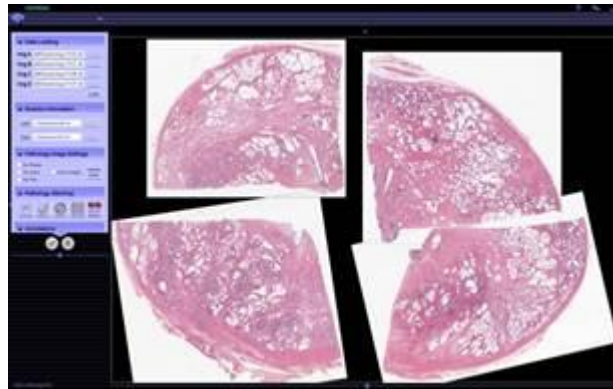
After installing the HistoStitcher, you will see a shortcut on the Desktop named "HistoStitcher". Running this icon would launch the application.

There are two alternative methods of stitching, (1) using fiducial points and (2) by manual image manipulation.

(1) Stitching by selecting fiducial points:

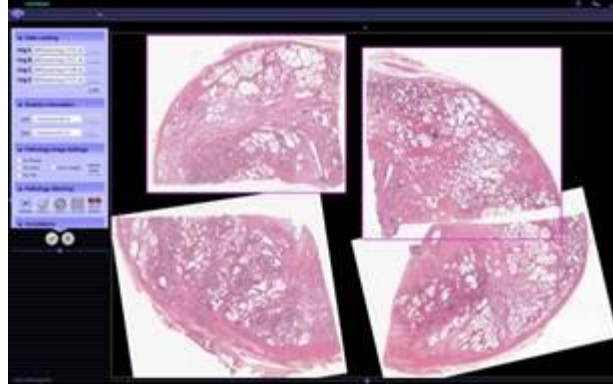
- a. Under the **Data loading Menu**, enter the complete path of the four image filenames corresponding to the four histology quadrants. The images must be in db format (see Data conversion above)

- b. Press the **Load** button. After few moments you should see the four quadrants rendered in the main window.

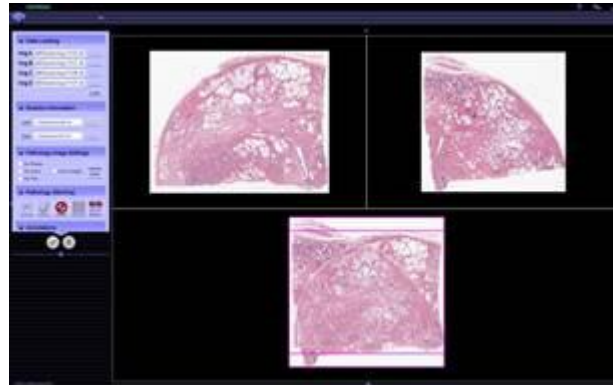


Each individual quadrant can be selected by clicking on it with the left mouse. A **green** bounding box would appear to indicate the selected image. The selection can be scaled (Middle mouse), translated (left mouse) or rotated (right mouse). If there are xml files describing annotations, with the same name as the images, they are also loaded at this time.

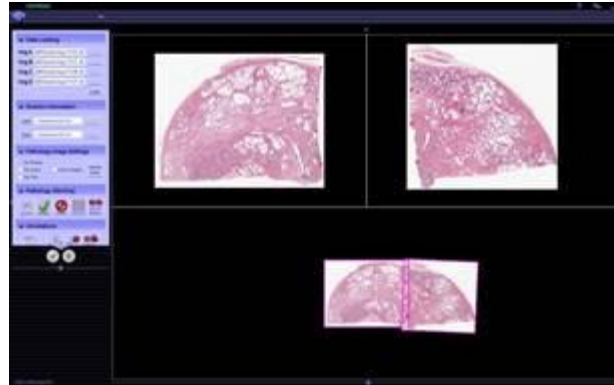
- c. Select the two quadrants you would like to stitch together by pressing CTRL-Left mouse click on top of the images. A **pink** bounding box appears around each of the two selected images



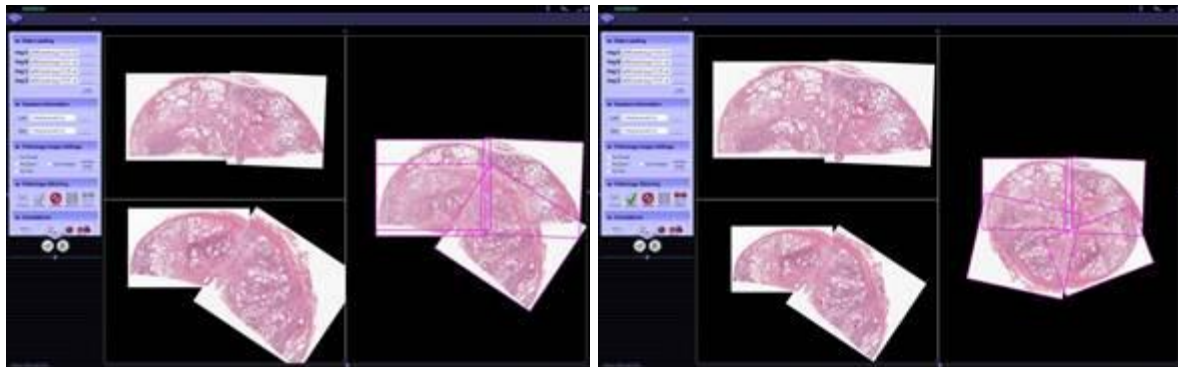
- d. Select **Stitching** under the **Pathology Stitching** menu. A split window appears with the two images side by side (or top/bottom) and an output window where the stitched image will be rendered.



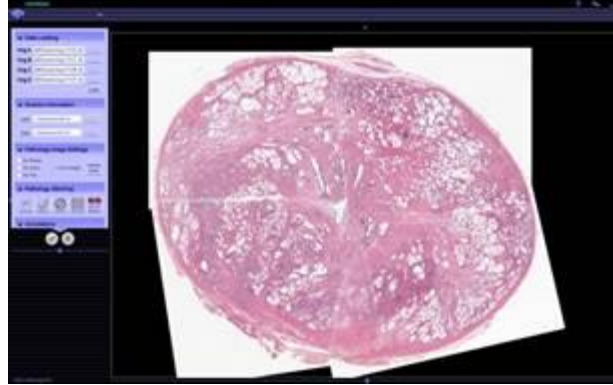
- e. You can scale each of the images with the middle mouse, rotating them with the right mouse and move them with left mouse.
- f. By holding down the CTRL key and clicking with the right mouse, add four pairs of fiducials alternating between the two images. When the last marker is added, the stitching occurs and the result is shown in the output window



- g. If satisfied with the stitching result, select **Accept** under the **Pathology Stitching** menu, otherwise select **Reject** and repeat the process. Once the two quadrants are stitched together, they move as a single image.
- h. Repeat steps 3-7 to stitch the images corresponding to the other two quadrants.
- i. Finally, complete the stitching process by stitching the two images generated during the previous steps



- j. Select Accept (or Reject) to go back to the main window



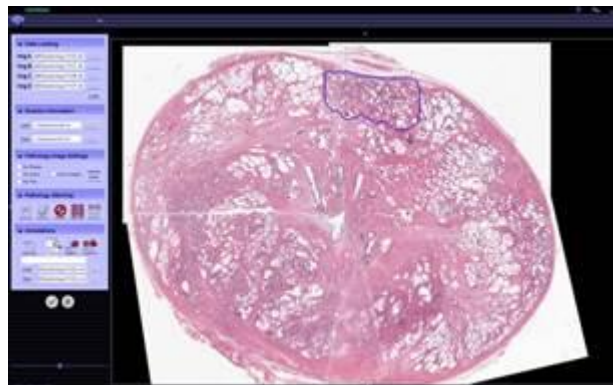
k. At any time, the current session can be saved as a text file to be later retrieved.

(2) Stitching by manual image manipulation:

As an alternative approach to the stitching, each quadrant can be manipulated independently by a sequence of rotations, translations and scaling. When you are satisfied with the location of every quadrant, select **Lock Images** under the Pathology Image Setting menu. The images will be locked and moved together as a single image. Press and hold middle mouse to move and/or scale the image as a whole. The image will translate when the middle mouse is pressed near the viewport center and moved in any direction, whereas zooming occurs when the middle mouse cursor is pressed near the viewport borders and drag up or down.

Annotations

Annotations can be drawn by selecting **Place Polygon** under the **Annotations** tab and using the left mouse to draw it. Annotations can be exported/imported as .xml files. If no individual image is selected, the annotations are saved with respect to the quadrant in which the annotation is drawn and the quadrant information is also saved. On the other hand, if a specific quadrant is selected the annotation is imported/saved with respect to that quadrant



Saving the results

Once the stitching is complete, the resulting image can be saved by pressing CTRL+P and a dialog box will appear for selecting the name of the file you want to create or save.

References

[1] Toth R, Shih N, Tomaszewski J, Feldman M, Kutter O, Yu D, Paulus J, Paladini G, Madabhushi A, others. HistostitcherTM: An informatics software platform for reconstructing whole-mount prostate histology using the extensible imaging platform framework. *Journal of Pathology Informatics* 2014;5(1):8.