

# eeDAP

**Evaluation Environment for Digital & Analog Pathology**

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## User Manual

2015

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## I. Introduction

This is a tool to design and execute correlated optical and digital pathology reader studies. This application supports two modes of reading, Digital and MicroRT. Digital mode uses a set of regions of interest (ROIs) identified and extracted from digital whole slide images (WSIs). MicroRT mode offers the reader a real-time view of the identical set of ROIs from a glass slide, through the optics of a microscope. In other words, the two modes are registered to one another. Furthermore this tool allows for the administrator of the study to have a high level of control over the format of the tasks presented to the readers through specifications in an input file. Several simple default tasks are available to the administrator: multiple choice, continuous sliders, or binary responses. These simple tasks can be modified through a graphical user interface in conjunction with moderate MATLAB programming skills. Furthermore, the administrator can also specify whether the reader is allowed to pan or zoom while confirming in real time the registration of MicroRT ROIs and Digital ROIs.

The ability to either present the readers with an analog image (MicroRT) or a digital image of the same specimen ROI allows for the reduction or elimination of a large source of variability in comparing these modalities: the cells being viewed. The registration of areas strengthens the evaluation of digital pathology and its comparison to the microscope.

## Abbreviations

<b>WSI, WSIs</b>	Whole Slide Image(s)
<b>ROI, ROIs</b>	Region(s) of Interest
<b>MicroRT</b>	Microscope Real-Time Viewing
<b>RT</b>	Real Time
<b>FOV</b>	Field of View
<b>Administrator</b>	The (task) administrator is responsible for task set up and monitoring
<b>Reader</b>	Person evaluation the ROI's
<b>Scan Scale</b>	WSI scanning
<b>IOP</b>	Intermediate Ocular Plane
<b>FN</b>	Field Number

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## Credits

- Brandon Gallas: 6/2012 - present
  - Project lead and software development
- Adam Ivansky: 6/2012 - 8/2012
  - Original Creator
- Tyler Keay: 7/2012 - 4/2013
  - Create user manual, improve eeDAP workflow and registration precision, consolidate distribution and create self-contained software package, modify hardware for simultaneous viewing of specimen (camera and eyepiece), manage first pilot study
- Neil O'Flaherty: 7/2012 - 4/2013
  - Evaluate registration precision, investigate WSI file formats and resolution (physical relationship between WSI resolution, the camera, and stage steps), organize hardware specifications and manuals
- Qi Gong: 10/2014 - Present
  - Extend eeDAP software to USB camera, Ludl 6000 and Prior stages
  - Create Linux version eeDAP
  - Create new features, debug and improve performance for eeDAP.
  - Create "Stage and Camera Control" software to test and control the camera and microscope stage outside of eeDAP files.
  - Create user manual by Dr. Explain.
  - Public code and release version to GITHUB
- A. Jessica Handoko: 10/2015- Present
  - Updating user manual, making it more simple and user friendly
  - Using GitHub to keep track of changes and updates made to the manual
  - Testing eeDAP

Other contributors:

- Wei-Chung Cheng
- Stephen Hewitt
- Catherine Conway
- Marios Gavrielides
- Adam Wunderlich.

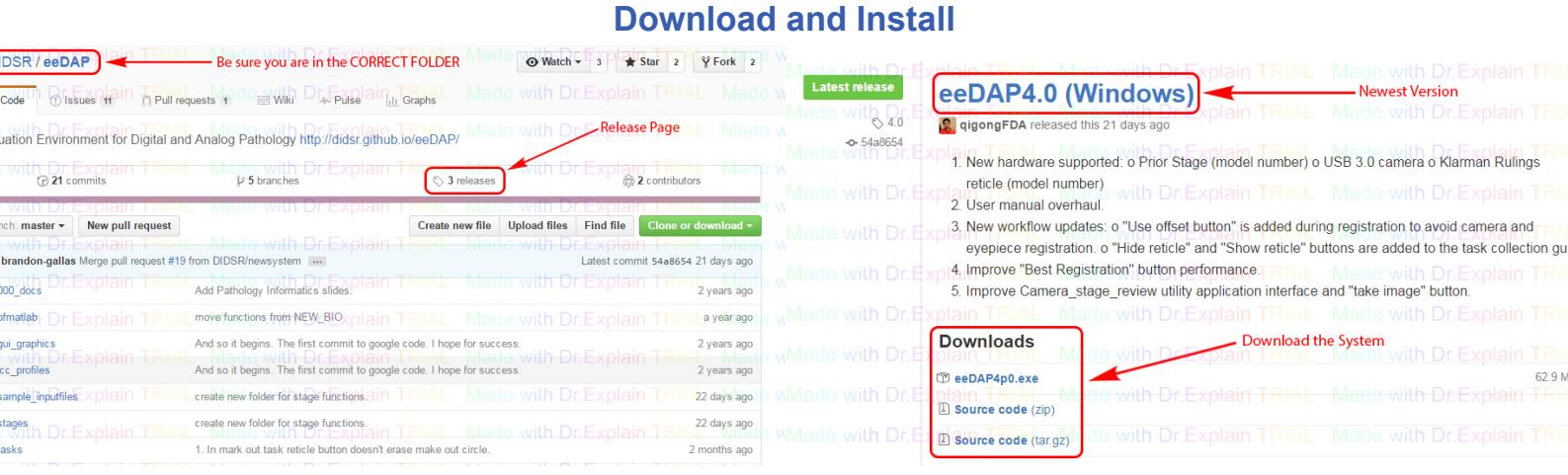
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## II. Getting Started with eeDAP

Information on how to download, install, and run eeDAP. eeDAP is available for download for Windows and Linux users.

eeDAP is used to design and complete an associated optical and digital pathology reader study. Users will have two options either Micro RT or Digital.

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Go to <https://github.com/DIDSR/eeDAP>. Download the latest version from the [GitHub eeDAP Release Page](#). There are two versions inside. One is for windows system the other is for linux system.

Jump to [Run Software](#).

### Install eeDAP according to what system you have:

#### Windows:

1. Click the eeDAP\_windows.exe file. It will install the eeDAP in current directory.
2. Click eeDAP.exe file to launch eeDAP

#### Linux:

1. Extract the eeDAP\_linux.zip file
2. Open a terminal and visit the extracted folder
3. In terminal input "./run\_eeDAP.sh" + " " + "matlab runtime libraries directory"

Download a sample WSI image from: [openslide-testdata](#)

\*Be aware of where eeDAP is saved after downloading!!\*

#### Office Computer (Restricted Laptop) Notes:

- Users won't be able to edit sample .dapsi input files (Users have to use sample input files as is)
- Create a **000\_whole\_slides** folders or the sample input file will not run
- Don't save into "**Program Files**" because you will not be able to edit the input files

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## Run Software

**\*If this is your first time using eeDAP, we recommend you use the links in this page to go to the Workflow page for more information on how to run eeDAP.**

How to run a sample eeDAP input file:

Download Sample WSI Image

1. Download the WSI from CMU openslide page <http://openslide.cs.cmu.edu/download/openslide-testdata/Aperio/CMU-1.svs>
2. Save it to your computer (directory should be same as wsi\_slot\_x in input file )

- Setting up Hardware

1. Install the camera on the microscope and connect it to the computer
2. Following the "[Camera Setup and Test](#)" page, download and install the camera driver
3. [Test](#) and [align](#) the camera
4. Connect the stage controller with microscope and the stage to the computer
5. Following the "[Stage Setup & Test](#)" page, download and install the stage driver
6. Check and [test the connecting status](#) between the computer and joystick

**\*When opening eeDAP, the application does not open immediately, may take a few seconds to open.**

- Load input file

1. From the [eeDAP Administrator Input Screen](#) page, click the button "Click to browse for .dapsi input file."
2. Navigate into the folder "**sample\_inputfiles**"
  - Select one of the input files according to the given WSI image, camera, stage, and microscope
3. Extract the chosen sample file by clicking "**Extract ROIs**".
4. Select viewing mode, **Digital or MicroRT**
5. Click **Start** button to begin (If MircoRT is chosen, continue to [Serial Port configuration](#) or MicroRT Registration. If Digital is chosen, continue to eeDAP study)

- MicroRT Registration (Both the **WSI image** and corresponding **glass slide** is needed)

- [Low Resolution Registration](#) (More info on Low Resolution Page)

1. Place selected tissue glass (label\_pos) onto the stage and change lens (mag\_lres) according to the [input file](#)
2. Move stage using the joystick and center and focus a unique location (that stands out on the thumb WSI) on the tissue and click **Take Stage Position**
3. Click the same unique location on the thumb WSI and click **Take WSI Position**
4. Check results, Click on "**Registration is Good!**" if the registration is accurate
5. If results are accurate, repeat steps 2,3, and 4 with 2 other unique points
6. Select **Load last calibration** (Zoomed in image will appear)  
\* To skip High Resolution Registration and use only Low Resolution Registration, click on **Finish Registration** (Not recommended)

- [High Resolution Registration](#) (More info on High Resolution Page)

1. Change lens (mag\_hres) according to input file, the WSI will show the zoomed up area on the screen
2. Click on **GoTo Position**, the stage will move automatically to previously taken Stage Position (Low Resolution)
3. Adjust and center the stage using the joystick to a unique location in the same ROI of the low resolution registration (that stands out on the thumb WSI) and click **Take Stage Position**
4. Click the same unique location on the thumb WSI and click on **Take WSI Position**
5. Check results, Click on "**Registration is Good!**" if the registration is accurate
6. Repeat steps 2,3,4, and 5 with the 2 other unique points

- [Camera and Eyepiece Registration](#)

\*It this is the 1st time, do not skip. If done before, press **Skip Offset**

1. In the camera image, move the center of reticle to one small cell

2. Click **Feature Centered in Camera**
3. Look through the eyepiece, move the center of reticle to the same small cell
4. Click **Feature Centered in Eyepiece**

- eeDAP Study

1. Input user ID and click Next (*Micro RT Model continue to 2, Digital Model bypass to 6*)
2. Microscope stage will automatically move to last known tissue location and do "Fast Registration"
3. Focus microscope and check registration result, registration may fail due to unfocused tissue (*Passed registration bypass to 6*)
4. If registration is **not** valid, click on "**Reset**". If the registration is valid, skip to **6**
5. Then select either "**Fast Registration**" or "**Best Registration**" in the [control panel](#)
6. Follow the [task instructions](#) to complete each given tasks and press next
7. Use the [control panel](#) to manage the studies
8. When you reached the end "Thank You" will appear, click **Next** to save your data and exit

- eeDAP Results

1. From "**sample\_inputfiles**" folder click on "**Output\_Files**"
2. Output file name is formatted by, "Study Model, User ID, Time, & Input File Name .dapso"
3. Output tissue images folder name is formatted same as the output file
4. Output task results are formatted by, "Task Name, Task ID, Task Order, Slot (Where the glass was placed)"

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## Tasks Instructions

In real study the order of task can be random.

### "select\_region" (Select Region)

1. Click on image in the region of the cell that is specified in the description
2. Test will automatically give you the correct X-Y coordinates on the ROI and WSI (*Figure 1*)

### "count"

1. Enter the number of cells that appear to accommodate the description (*Figure 2*)
2. Click outside of the box

### "radio1of4"

1. Select the one of the options that accommodates the description (*Figure 3*)

### "slider"

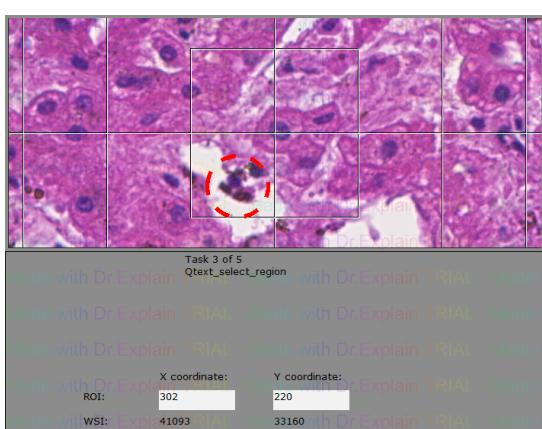
1. On a scale 0-100, rate the tissue using the slider or typing in the number (*Figure 4*)

### "mitotic\_train"

1. Check all the boxes that apply to the image
2. Using the slider or by typing the number, give the tissue a score
3. Click on "**expert results**" (Boxes highlighted are incorrect, Highlighted number is correct)

### "mitotic\_expert"

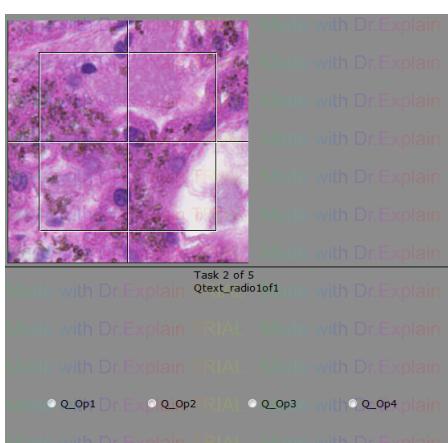
1. Write a discription of what you observe in the image above
2. Click "**Next Part**"
3. Check all the boxes that apply to the image above
4. Using the slider or by typing the number, give the tissue a score



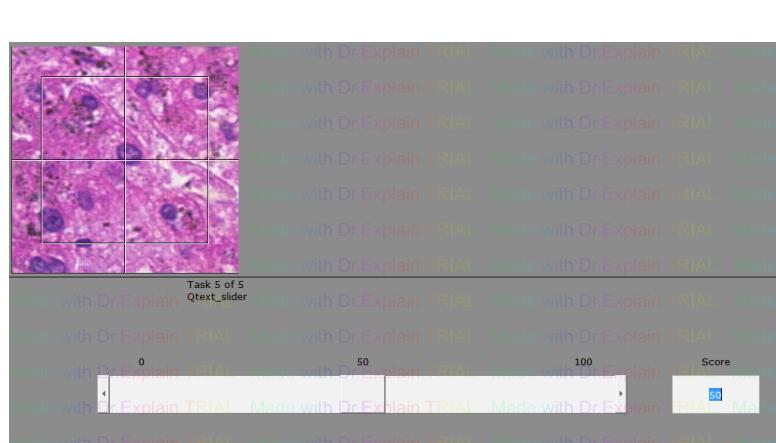
*Figure 1*

--	--

*Figure 2*



*Figure 3*



*Figure 4*



### III. Hardware and Software Requirement

Directions on how to set up the hardware and all the equipment to complete the experiment

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## Camera

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## Requirements

The code is written to work with DCAM and USB compatible cameras.  
 eeDAP requires camera images to be RGB24 (8 bit for each channel).  
 eeDAP requires camera images to have width > 640 and height > 480.  
 FDA has used 3 Point Grey cameras for this eeDAP software

Name and model	Description
<b>Point Grey Grasshopper Color (GRAS-03K2C-C)</b>  <b>Interface:</b> Firewire 1394 <b>Specifications:</b> <a href="https://www.ptgrey.com/support/downloads/10147/">(https://www.ptgrey.com/support/downloads/10147/)</a> <b>Technical Manual</b> <a href="https://www.ptgrey.com/support/downloads/10172/">(https://www.ptgrey.com/support/downloads/10172/)</a>	<p><b>Default Format:</b>      The default Matlab format code is RGB24_640x480, which has an aspect ratio of 1.333. The pixel size and format of the default format equals that of the native sensor specs.</p> <ul style="list-style-type: none"> <li>• sensor size = 1/3"</li> <li>• sensor size = 640x480 pixels (0.3MP)</li> <li>• pixel size = 7.4um</li> </ul> <p>When attached to the microscope, the scale factors are equal to the pixel size divided by the camera adapter magnification (if any) and the objective magnification. When there is no camera magnification:</p> <ul style="list-style-type: none"> <li>• 0.185um/pixel at 40x</li> <li>• 0.370um/pixel at 20x</li> <li>• 0.740um/pixel at 10x</li> <li>• 1.480um/pixel at 5x</li> <li>• 1.850um/pixel at 4x</li> <li>• 2.960um/pixel at 2.5x</li> </ul>
<b>Point Grey Flea2 Color (FL2G-50S5C-C)</b>  <b>Interface:</b> Firewire 1394 <b>Specifications:</b> <a href="https://www.ptgrey.com/support/downloads/10143/">(https://www.ptgrey.com/support/downloads/10143/)</a> <b>Technical Manual</b> <a href="https://www.ptgrey.com/support/downloads/10117/">(https://www.ptgrey.com/support/downloads/10117/)</a>	<p><b>Native Pixel Format:</b>      The Matlab format code that uses all of the native pixels is F7_RGB24_2448x2048. It is a non-standard format (Format_7) with aspect ratio 1.953 and the following specs:</p> <ul style="list-style-type: none"> <li>• sensor size = 2/3"</li> <li>• sensor size = 2448x2048 pixels (5.0MP)</li> <li>• pixel size = 3.45um</li> </ul> <p><b>Default Format:</b>      The default Matlab format code is RGB24_1024x768, which has a standard aspect ratio of 1.333. The default pixels are 2x2 bins of the native pixels. Consequently, the pixel size is 6.9um.</p> <p>When attached to the microscope, the scale factors are equal to the pixel size divided by the camera adapter magnification (if any) and the objective magnification. When there is no camera magnification, the pixel size of the default Matlab format (6.9um) is divided by the objective magnification.</p> <ul style="list-style-type: none"> <li>• 0.1725um/pixel at 40x</li> <li>• 0.3450um/pixel at 20x</li> <li>• 0.6900um/pixel at 10x</li> <li>• 1.3800um/pixel at 5x</li> <li>• 1.7250um/pixel at 5x</li> <li>• 2.7600um/pixel at 2.5x</li> <li>• 3.4500um/pixel at 2x</li> </ul> <p><b>Alternative Format:</b></p>

	The Matlab format code F7_RGB24_1600x1200 uses the native pixels but a smaller standard format.
<b>Point Grey Grasshopper3 Color (GS3-U3-50S5C-C)</b>  <b>Interface:</b> USB <b>Specifications:</b> ( <a href="https://www.ptgrey.com/support/downloads/10146/">https://www.ptgrey.com/support/downloads/10146/</a> ) <b>Technical Manual</b> ( <a href="https://www.ptgrey.com/support/downloads/10125/">https://www.ptgrey.com/support/downloads/10125/</a> )	<b>Default Format:</b> <ul style="list-style-type: none"><li>• sensor size = 2/3"</li><li>• sensor size = 1384 x 1036</li><li>• pixel = 6.45 um</li></ul>

User could get more Point Grey Camera document from <https://www.ptgrey.com/support/downloads>

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## Camera Setup and Test

For Point Grey camera, users need install special diver to run it under eeDAP software.

### Windows:

After plugging in the camera (USB), you should disable the default Windows driver and update the driver for the attached device to the industry standard driver.

#### Download, Install, and Test DCAM Driver:

1. Go to [Carnegie Melon \(CMU\) Download Driver Page](#)
2. In the **Download** tab, click "I agree to the Terms of the LGPL".
3. Download **1394camera646.exe**
4. Click **Installation** tab and install the driver following the instruction
5. Select "**1394CameraDemo32.exe**" and run it

#### Download, Install, and Test Fly Capture Driver:

1. eeDAP only support the 2.5 version of FlyCap2
2. Windows bit64 version is available on: [http://ftp.ptgrey.com/Installers/FlyCapture2.5.3.4\\_x64.msi](http://ftp.ptgrey.com/Installers/FlyCapture2.5.3.4_x64.msi)
3. Install the 2.5 FlyCap2 and test camera through it
4. Restart computer

### Linux:

In Linux, users should install two packages libdc1394-22 and libraw1394-11, as mentioned in the documentation link below, <http://www.mathworks.com/help/imaq/linux-dcam-ieee-1394-hardware.html>

If the users don't run the eeDAP under a root account, users need provide permission to the account they want to use. They could log in to root account and use following command to provide permissions.

- a. Command "nano /etc/group"
- b. Add linux account name to video group
- c. logout and relogin linux account.

### Camera Test:

If "MircoRT" mode is selected:

1. Click the button "**imaqtool**".

\*This launches a Matlab utility which is an interactive GUI that allows you to explore, configure, and acquire data from your installed and supported image acquisition devices. If this doesn't work, Matlab can't find your camera. (Whenever you plug-and-play a camera, Windows enables the default Windows driver, which may actually be the camera manufacturer's driver. If the default Windows driver isn't *DCAM* compatible, Matlab can't find your camera.)

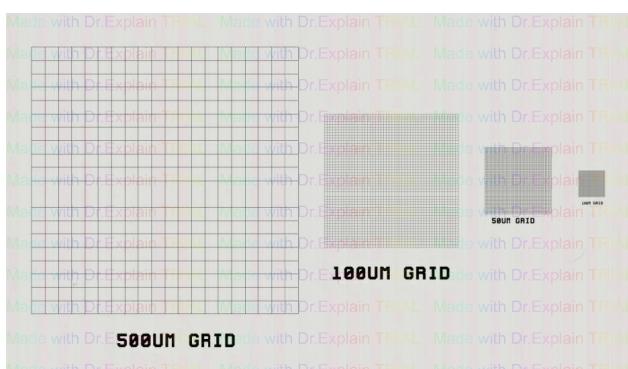
Go back to [Run Software](#)

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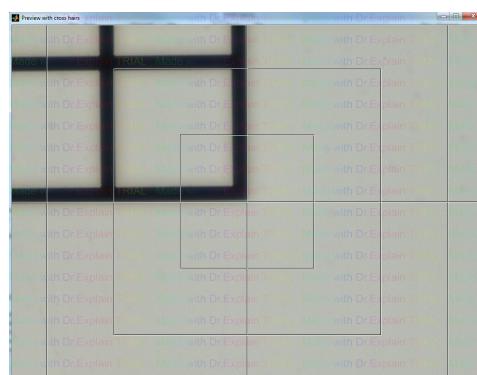
## Alignment

Depending on hardware, you may have the ability to completely align the camera with the eyepiece by rotating and shifting the camera. This process is made possible by loosening and tightening **one - three screws on the camera mount**. This can only be done while setting up the equipment and before beginning the experiment. The alignment should persist over time and need to none little adjustments unless the screws are ineffective or the system is bumped. A **calibration slide, reticle, and virtual reticle** are very useful for this alignment. A good camera mount also has a focus screw that can be adjusted so that the camera and the eyepiece are nearly in focus at the same time.

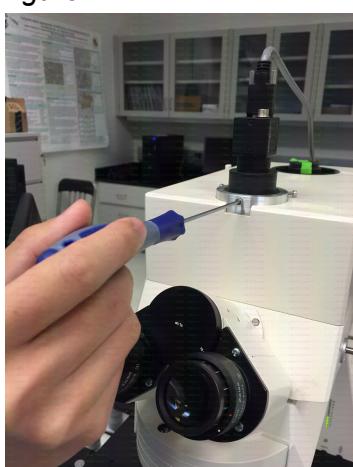
1. Place the grid slide on the stage and change to the highest magnification optics (Figure 1)
  2. Look through the eyepiece and focus the microscope.
  3. Still looking through the eyepiece move stage to let the reticle just touch the boundary of the grid corner.
  4. Depending on your camera:
    - a. If you are **able** focus your camera, **don't focus** camera image using your microscope
    - b. If you are **unable** to focus your camera, **focus** camera image using your microscope
  5. Loosen the screws around camera. (*Figure 3*)
  6. Use your hand to adjust the camera to make the reticle in camera image just touch the same boundary of the grid corner. (*Figure 2*)
  7. Hold the camera and while looking at the camera image, start tightening the screws until it is aligned.
- \*Note: 1. Small shift could be solved by eyepiece and camera register processing.  
       2. Large shift might influence the fast registration during task. Because our fast registration use a small center area of camera image, larger shift between eyepiece and camera will lead outstanding feature goes out of the camera registration area. Best registration is another method to solve the large shift problem.



*Figure 1*



*Figure 2*



*Figure 3*

Go back to [Run Software](#)

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## Stage

We have used following 3 stage controllers.

Name and model	Interface	Document
Ludi (MAC5000)	RS232	Specifications and Manaul ( <a href="http://ludl.com/downloads/?wpdmc=mac5000">http://ludl.com/downloads/?wpdmc=mac5000</a> )
Ludi (MAC6000)	RS232	Specifications and Manual ( <a href="http://ludl.com/downloads/?wpdmc=mac6000">http://ludl.com/downloads/?wpdmc=mac6000</a> ) Note: MAC6000 uses same command as MAC 5000
Prior ProScan III (H31XYZE-US/A)	USB	Specifications and Manual ( <a href="http://www.well.ox.ac.uk/_asset/file/prior-proscan-iii-motorised-stage-controller-manual.pdf">http://www.well.ox.ac.uk/_asset/file/prior-proscan-iii-motorised-stage-controller-manual.pdf</a> )

We use following 3 stages in development.

Name and model	Document	Description
Marzhauser (SCAN 8Praparate Axioplan2)	Specifications ( <a href="http://www.marzhauser.com/en/pim/produktdetail-popup.html?view=details&amp;pimid=a210&amp;no_cache=1&amp;m=null&amp;p=null">http://www.marzhauser.com/en/pim/produktdetail-popup.html?view=details&amp;pimid=a210&amp;no_cache=1&amp;m=null&amp;p=null</a> )	8 slots (Works with Ludi controllers)
Ludi (96S109-LE2)	Specifications ( <a href="http://www.bioimagingolutions.com/Ludi/ludl_bioprecision_upright_96S100.html">http://www.bioimagingolutions.com/Ludi/ludl_bioprecision_upright_96S100.html</a> )	5 slots (Works with Ludi controllers)
Prior (H101A/B)	Specifications ( <a href="http://www.prior-us.com/files/H101A%20ProScan%20Stage%20Datasheet.pdf">http://www.prior-us.com/files/H101A%20ProScan%20Stage%20Datasheet.pdf</a> )	4 slots (Works with Prior controllers)

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## Stage Setup and Test

### **Windows system:**

1. Users can find the stage by Start -> Control Panel -> Device Manager -> Ports(COM & LPT). The name of the Port should be something like Prolific USB-to-Serial Comm Port (COM\*).
2. Choose COM\* in eeDAP to connect with stage.
3. Download and install the proper driver

### **Prior Stage:**

#### **Downloading Stage Driver:**

1. Go to Prior offical Download Center Website: <http://www.prior-us.com/Customer-Support/Download-Centre/>
2. Download the "ProScan III USB Driver" and software depend on operating system.

#### **Installing Stage Driver:**

1. Make sure the stage is connected before installing
  2. Install driver from device manager.
- Option: Try to use Prior software control the stage.

### **Ludl Stage:**

Normally User can use default driver. User can also download driver and software from Ludl official download page: <http://lndl.com/downloads/>.

### **Linux:** use the stage by command: "ls -l /dev/tty\*".

The port of stage name could be "ttyUSB0". As the default setting of matlab only automatically recognizes serial port names of the form /dev/ttyS[0-255]. User should create a symbolic by command "ln -s /dev/ttyPS0 /dev/ttyS101" under root account. The S101 could be any integer port between S101 to S109. And please choose the same prot in eeDAP software. The following link provide detail information about build link: [Building link](#)

If the users don't run the eeDAP under root account, users need provide permission to the account they want to use. They could log in to root account and use following command to provide permissions.

1. Serial prot permission:  
"chmod 777 /dev/ttyXXX", where ttyXXX is the port name like ttyUSB0
2. Lock group permission:
  - a. Command "nano /etc/group"
  - b. Add linux account name to lock group
  - c. logout and relogin linux account.

### **Stage Test:**

When the user selects the mode to be "MicroRT", Microscope Real Time, the program will force the user to set the communication port for the stage. The stage must be plugged into one of the communication ports, and the correct communications port must be selected.

Go back to [Run Software](#)

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## Microscopes

Here are a couple notes on understanding the size of the field of view and the size of the intermediate image (the apparent size of the image viewed by the pathologist).

The page that opened was Field of View Diameter at [microscopy](#). The first sentence is, "The diameter of the field in an optical microscope is termed the field number and represents the diameter of the field measured in millimeters at the intermediate image plane."

Microscopy from the very beginning - Carl Zeiss, Inc.:<http://www.microscopy-news.com/news/carl-zeiss-microscopy-from-the-very-beginning.html>

"Eyepieces (or oculars) are the magnifiers with which you view the intermediate image in the microscope, produced by the objective and the tube lens. In the Axiolab microscope, the intermediate image has a useful diameter of 20 mm. Eyepieces are not just simple lenses, but are corrected optical systems consisting of several lenses. It would be a pity if the intermediate image produced with such sophisticated optics were to be impaired just before it reaches the eye.

Normally, the additional magnification provided by the eyepiece is 10x. The intermediate image in this example then has a diameter of 20 cm at a reading distance of 25 cm to the eye. A comparison: this diameter is about as large as the width of this page."

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## Types of Microscopes

There are currently only two microscopes that we have used with the software. The basic microscope requirements are the following:

- 1) It has a trinocular tube: a camera can be mounted and the camera view is the same as the eyepiece view.
- 2) It is compatible with one of the computer controlled stages.

Name and model	Description
<b>Axioplan 2 Imaging microscope with an Axiophot 2 head</b>  Specifications and Manual <a href="http://otolic.stanford.edu/documents/Axioplan2-Axiophot-99-2000.pdf">(http://otolic.stanford.edu/documents/Axioplan2-Axiophot-99-2000.pdf)</a>	<ul style="list-style-type: none"> <li>• Field Number (FN) of the oculars (eyepieces) = 23mm</li> <li>• Magnification of eyepiece (mag_e) = 10x</li> <li>• Magnification of objective (mag_o) = 2.5x, 5x, 10x, 20x, 40x</li> <li>• FOV at Mag_o = FNmm/mag_o</li> <li>• FOV at 2.5x = 23mm/2.25 = 9.200mm</li> <li>• FOV at 5x = 23mm/5 = 4.600mm</li> <li>• FOV at 10x = 23mm/10 = 2.300mm</li> <li>• FOV at 20x = 23mm/20 = 1.150mm</li> <li>• FOV at 40x = 23mm/40 = 0.575mm</li> <li>• Apparent diameter of microscope image "at 25cm" = FN*mag_e = 23cm</li> </ul> <p>Diameter for ocular micrometer (reticle) = 26mm</p>
<b>Olympus BX43</b>  Specifications and Manual <a href="http://www.olympus-lifescience.com/en/downloads/detail/?0[downloads][id]=847249461">(http://www.olympus-lifescience.com/en/downloads/detail/?0[downloads][id]=847249461)</a>	<ul style="list-style-type: none"> <li>• Field Number (FN) of the oculars (eyepieces) = 22mm</li> <li>• Magnification of eyepiece (mag_e) = 10x</li> <li>• Magnification of objective (mag_o) = 2x, 4x, 10x, 20x, 40x</li> <li>• FOV at Mag_o = FNmm/mag_o</li> <li>• FOV at 2x = 22mm/2 = 11.00mm</li> <li>• FOV at 4x = 22mm/4 = 5.50mm</li> <li>• FOV at 10x = 22mm/10 = 2.20mm</li> <li>• FOV at 20x = 22mm/20 = 1.10mm</li> <li>• FOV at 40x = 22mm/40 = 0.55mm</li> <li>• Apparent diameter of microscope image "at 25cm" = FN*mag_e = 22cm</li> </ul> <p>Diameter for ocular micrometer (reticle) = 24mm</p>

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## Reticles

Reticle is placed in eyepiece at Intermediate Ocular Plane (IOP). It is used to define the position of the tissue under microscopes.

Name of Reticle	Display View	Description
Klarmann Rulling: KR-871		This reticle contains 5 squares with actual lengths of 2, 4, 6, 8, and 10mm.
Klarmann Rulings KR-32536		This is a custom reticle with cross-hair-like fiducials pointing to gaps: 2 are 1mm x 1mm and 3 are 0.5mm x 0.5mm.
Klarmann Rulings KR-429		This reticle has a width and length of 10x10 grid at IOP = 12.5mm, an apparent width and length of 10x10 grid "at 25cm" = 12.5cm, a grid spacing at IOP = 1.25mm, a grid spacing at stage at mag_o ( $5x = 1.25mm/5 = 0.2500mm$ , $10x = 1.25mm/10 = 0.12500mm$ , $20x = 1.25mm/20 = 0.06250mm$ , $40x = 1.25mm/40 = 0.03125mm$ ), and apparent grid spacing "at 25cm" = 12.5mm.

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## Scanners

These are currently 4 different scanners we have tested with the eeDAP software.

The scale factors can also be found embedded in the image files.

Scanner Name	Description
<b>Hamamatsu Nanoozomer 2.0HT (at NIH AT)</b>	<ul style="list-style-type: none"><li>• scan_scale at 20x = .4558um/pixel</li><li>• scan_scale at 40x = .2279um/pixel</li></ul>
<b>Aperio CS (at NIH ATC and FDA White Oak)</b>	<ul style="list-style-type: none"><li>• scan_scale at 20x = 0.50um/pixel</li><li>• scan_scale at 40x = 0.25um/pixel</li></ul>
<b>Aperio T2 (at NIH AT)</b>	<ul style="list-style-type: none"><li>• Specs are the same as Aperio CS.</li></ul>
<b>Aperio Scanscope XT</b>	<ul style="list-style-type: none"><li>• Specs are the same as Aperio CS.</li></ul>

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## Software Requirements

As you use the software there are some requirements that should be followed for the software to run smoothly. Here are some instructions on how you will be able to fix problems you may come across when using eeDAP.

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## Read and Extract WSI image

There are two methods to extract ROI from WSI image "BIO formats" and "Image Scope". The individual pages for the methods will go into more depth with the details of each of them.

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## BIO Formats

Bio-Formats is currently being used in eeDAP. It is a stand-alone Java library for reading and writing life sciences image file formats. It is capable of parsing both pixels and metadata for a large number of formats, as well as writing to several formats. It was developed by the Open Microscopy Environment consortium, including development teams at LOCI at the University of Wisconsin-Madison, University of Dundee and Glencoe Software. Licensing and citing information is on the [OME licensing page](#).

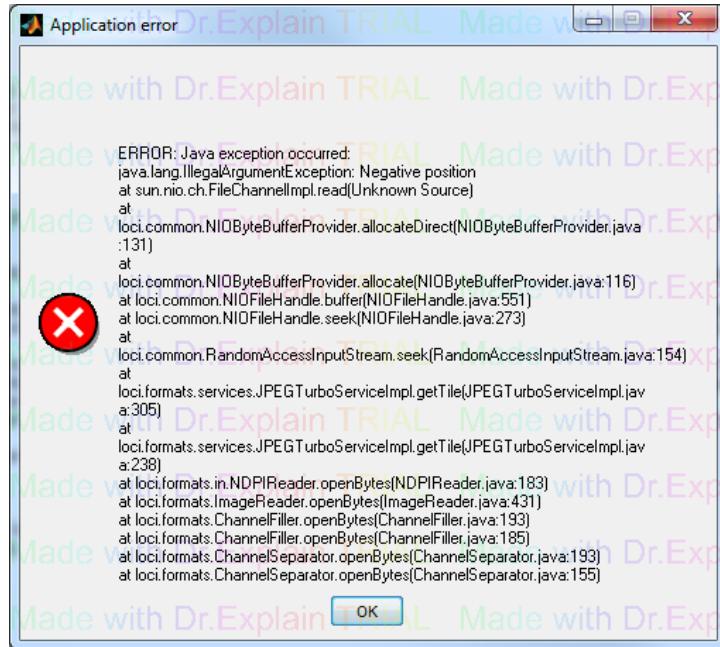
The primary goal of Bio Formats is to facilitate the exchange of microscopy data between different software packages and organizations. It achieves this by converting proprietary microscopy data into an open standard called the OME data model, particularly into the OME-TIFF file format.

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# BIO Formats: Possible Errors

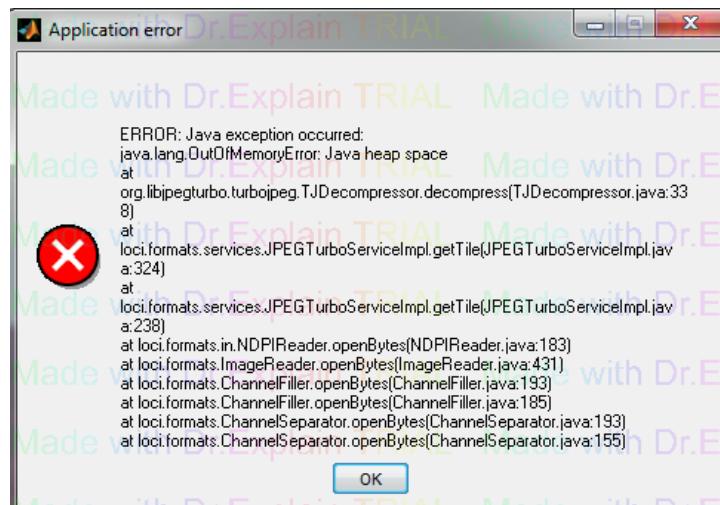
The BIO formats might have some problems when extracting the WSI. In this section we show two normally errors and the solving methods

## **1. Image File is too Large**



This error is because the input WSI image file is too large. Now we are using 5.1.2 version Bio formats. It works for file smaller than 4 GB. If you want to use a larger image, you might face this problem.

## 2. Out of Memory/Storage



When we process a large image, there might be an error message about being out of memory. For large image a minimum of 512 MB is suggested.

Users can download the java.opts and paste it in the matlab root directory, or follow this website : [Mathwork Answers](#)

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## Image Scope by Aperio

Image Scanscope is our previous used method, which is a product of Aperio: <http://www.aperio.com/healthcare/eslide/view>. This software contains an Active X controller name TIFFcomp which allows for manipulating of WSI images (panning, zooming, etc.). eeDAP uses TIFF comp to extract the ROI's from the WSI images. The reason we chose a new method is Image Scanscope could only work in 32 bit Matlab.

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## Matlab Compiler Runtime Libraries

The precompiled stand-alone eeDAP application requires that the Matlab compiler runtime (MCR) library be installed. Which works on Windows and Linux, but it does not require any Matlab license or libraries.

The MCR library must be the same version as was used to create the stand-alone application. The current versions of the MCR library that eeDAP is using are Windows 64-bit R2016a (9.1.1) and Linux 64-bit R2015a(8.5)

**Installer can be found at:**

- possible local folder: C:\Program Files (x86)\MATLAB\R2013a\toolbox\compiler\deploy\win
- internet: <http://www.mathworks.com/products/compiler/mcr/>
- internet: <http://medviso.com/download/mcrinstaller>

**Installer will create a folder like:** C:\Program Files (x86)\MATLAB\MATLAB Compiler Runtime\v91

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## IV. Input File

All Input files for this program have the extension .dapsi. Two sample files have been provided for instructional purposes. They can be located under the “**eeDAP→Sample\_Input\_Files**”. In the following, we use *Phantom\_Test.dapsi* to illustrate our discussion.

An input file has three sections: Header, Study Settings, and Body. The Header includes free text that describes the experiment and formatted text that specifies global variables. The Study Settings are just the setting for the following experiment. The Body is a list of ROIs and corresponding tasks.

```
tissue40x-8B-olympus - USB.dapsi - Notepad
```

**Header**

```
File Edit Format View Help
Author : Made with Dr.Explain TRIAL Made with Dr.Explain TRIAL Made with Dr.Explain TRIAL M
Date : Made with Dr.Explain TRIAL Made with Dr.Explain TRIAL Made with Dr.Explain TRIAL M
Time : Made with Dr.Explain TRIAL Made with Dr.Explain TRIAL Made with Dr.Explain TRIAL M

For the Hamamatsu scanning at 20x scan_scale = .4558
For the Hamamatsu scanning at 40x scan_scale = .2279
Point Grey Grashopper Color (GRAS-03K2C-C)
cam_format = RGB24_640x480
cam_pixel_size = 7.4um
Point Grey Flea2 Color (FL2G-50S5C-C): Full resolution, full format
cam_format = F7_RGB24_2448x2048
cam_pixel_size = 3.45
Point Grey Flea2 Color (FL2G-50S5C-C): standard format, aspect ratio = 1.33
cam_format = RGB24_1024x768
cam_pixel_size = 6.9
Reminder:
taskorder=2 user specified order
taskorder=1 listed order
taskorder=0 random order
saveimages = 1 save WSI and camera images
saveimages = 2 only save WSI image
saveimages = 3 only save camera image
saveimages = 4 don't save WSI and camera images

Input File Task Formats
Task,TaskID,Taskorder ,slot,ROI_X,ROI_Y,ROI_W,ROI_H,IMG_W,IMG_H,Qtext ,MoveFlag ,ZoomFlag ,Q_Op1 ,Q_Op2 ,Q_Op3 ,Q_Op4
```

**Study Settings**

```
SETTINGS
NUMBER_OF_WSI      = 1
wsi_slot_1          = C:\000_whole_slides\tissue40x-8B.ndpi
rgb_lut_slot_1      = icc_profiles\rgb_lut_gamma_inv1p8.txt
label_pos           = 12
reticleID           = KR-871
cam_kind             = USB
cam_format           = F7_RGB_1224x1024_Model1
cam_pixel_size       = 6.9
mag_cam              = 0.5
mag_tres             = 10
mag_hres             = 40
scan_scale           = 0.2279
stage_label          = H101-Prior
BG_Color_RGB         = 0.55 = 0.55 = 0.55
FG_Color_RGB         = 0.00 = 0.00 = 0.00
AxesBG_color_RGB     = 0.10 = 0.20 = 0.10
Fontsize              = 13
saveimages            = 1
taskorder             = 0
```

**Body**

```
radio1of4,1st0001,-1,1,038459,16192,300,300,300,300,Qtext_radio1of1,1,1,Q_Op1,Q_Op2,Q_Op3,Q_Op4
count,2nd0001,-1,1,027728,11381,300,300,300,300,Qtext_count,1,1,description
slider,3rd0001,-1,1,19220,49879,300,300,300,300,Qtext_slider,1,1,Q_Op1,Q_Op2,Q_Op3,Q_Op4
mark1,4th0001,-1,1,041163,33208,300,700,300,700,Qtext_select_region,1,1,Q_Op1,Q_Op2,Q_Op3,Q_Op4
mark1_out,5th0001,-1,1,041163,33208,700,700,700,700,Qtext_select_region,1,1,Q_Op1,Q_Op2,Q_Op3,Q_Op4
```

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## Input File Header

The Header is all the text before the line containing “**SETTINGS**”.

Refer to the figure on the previous page which shows the input file being edited in a plain text editor.

**Header** outlines the author, experimental setup, date, time, description of the experiment, dareware (camera, scanner, & microscope)

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## Input File Study Settings

The input file Study Settings begins with “**SETTINGS**”.

**Study Settings** include:

**NUMBER\_OF\_WSI**: Number of WSI image in the study.

**wsi\_slot\_1**: WSI image saving directory and name.

**rgb\_lut\_slot\_1** : International Color Consortium file directory and name.

**label\_pos**: Direction of the glass slide in microscope stage.

Sit in front of microscope eyepiece, the glass slide label clock position

label_pos	3	6	9	12
example				

**reticleID**: Reticle used in study

**cam\_kind**: Kind of camera

**cam\_format**: Camera image format.

**cam\_pixel\_size**: Camera pixel size

**mag\_cam**: Magnification between camera and eyepiece

**mag\_lres**: Low magnification registration lens

**mag\_hres**: Low magnification registration lens

**scan\_scale**: WSI image scan scale

**stage\_label**: Stage name

**BG\_Color\_RGB**: GUI back ground color (3 color channels)

**FG\_Color\_RGB**: GUI front ground color (3 color channels)

**AxesBG\_Color\_RGB**: Axes color (3 color channels)

**FontSize**: GUI font size

**saveimages**: Study image saving options

**taskorder**: Controls the order of the tasks

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The input file Body begins with the line containing “**Body**” and follows with a line of column labels. Each line below the line of column labels represents a task, identifying an ROI and the task. There are 19 columns identifying the ROI and task.

## Default Task Input Format:

### A. Task Instructions

**Task Name:** Describe name for each task

**Task ID:** Identification number of the task independent from the order that they are presented

**Task Order:** The order the slide is to be presented to the reader if the value of “taskorder” defined in the Header is set to “1”.

**Slot:** Specifies the stage slot for the task. This, consequently, specifies the glass slide for the task based on the header information.

### B. Input Variables

**ROI\_X:** Defines center of the ROI; point of reference for the extraction process

**ROI\_Y:** Defines center of the ROI; point of reference for the extraction process

**ROI\_W:** Width of the area in pixels to be extracted for the ROI

**ROI\_H:** Height of the area in pixels to be extracted for the ROI

**IMG\_W:** This parameter defines the size of the image that will be presented to the reader.

**IMG\_H:** This parameter defines the size of the image that will be presented to the reader.

**Q\_Text:** This field contains the question (free text) displayed to the reader.

\*Do not use commas here or the input file format will be corrupt.\*

**MoveFlag:** A value of 1 allows for the Reader to pan, value of 0 prohibits

**ZoomFLag:** A value of 1 allows for the Reader to zoom, value of 0 prohibits

**Q\_Op1:** Displays text for this answer

**Q\_Op2:** Displays text for this answer

**Q\_Op3:** Displays text for this answer

**Q\_Op4:** Displays text for this answer

## Customized Input File Body:

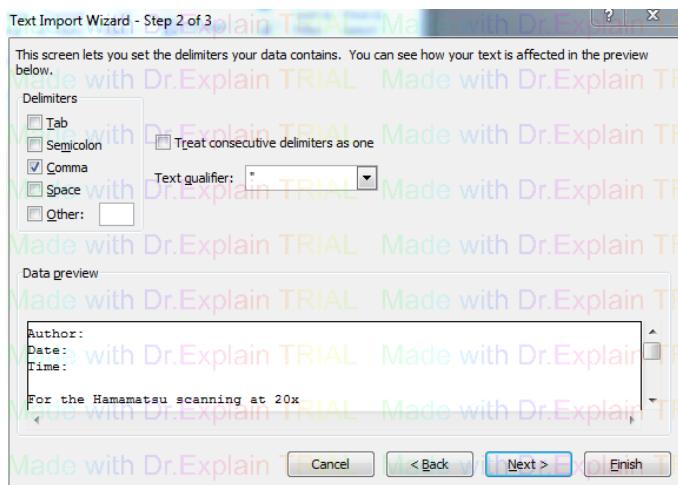
Customized Input File format should follow "Task Name, Task ID, Task Order and Slot". The other sections could be different depending on the design for that specific task.

## Editing Input File Body

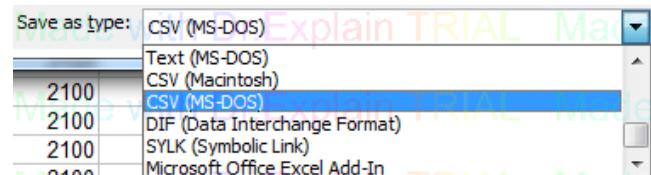
The Body of an input file is editable by a spreadsheet editor such as Excel.

### Editing and Opening an Input File in Excel:

1. Open Excel, double check Excel's open dialogue "all files is selected"
2. Navigate to eeDAP→Sample\_Input\_Files→Phantom\_Test
3. Open "Phantom\_Test.dapsi"
4. "Text Import Wizard" will open automatically
5. Select the "Delimited" option and click "Next".
6. Find "Delimiters", and select "Comma" in this case (*Figure 1*)
7. Select "Finish" not "Next"
8. The file will open in Excel automatically
9. Edit what is necessary for this case
10. Once Complete, click "Save As" a ".CSV" file which is plain text with comma separated variables (*Figure 2*)



*Figure 1*



*Figure 2*

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## WSI Formats

The current version of BIO Formats can load these types of images:

- .svs
- .ndip
- .tiff

\*New soon to be released version will be able to load .czi images.

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## V. Output File

An “Output\_Files” folder will be created in the folder where the input file is located. eeDAP writes to this folder the experiment output files (file extension .dapso). The naming convention is “**Mode.ReaderName.Date .InputFileRootName.dapso**”. eeDAP also writes to a subfolder (name similar to output file) images captured by the microscope’s camera and WSI depending on the setting of “saveimages” in input file. The images captured are taken when the task is completed, and the Administrator selects the “**Next**” button, advancing to the next task. The captured images provide further opportunities for verification of registration and other considerations.

eeDAP Output files are very similar in appearance to input files. They are comma delimited and have a Header (mostly free-text) and Body (comma-separated variables). Refer to the [Input File](#) section for basics on the content of the Output file and instructions for opening and editing the Output file. Once this file is open the header will be displayed. Much of this information should be repetitive from the input file’s header.

The main differences between the Input file and the Output file are as follows:

- The **Header** begins with the Output file filename, which specifies the *reading mode, reader name, date, time* and the *input file name*
- The **Body** includes an additional column for the *task duration* (amount of time the reader spent on each task in recorded in seconds) and some other columns related to the reader’s answers.

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## VI. WorkFlow

Guidelines of eeDAP in more detail.

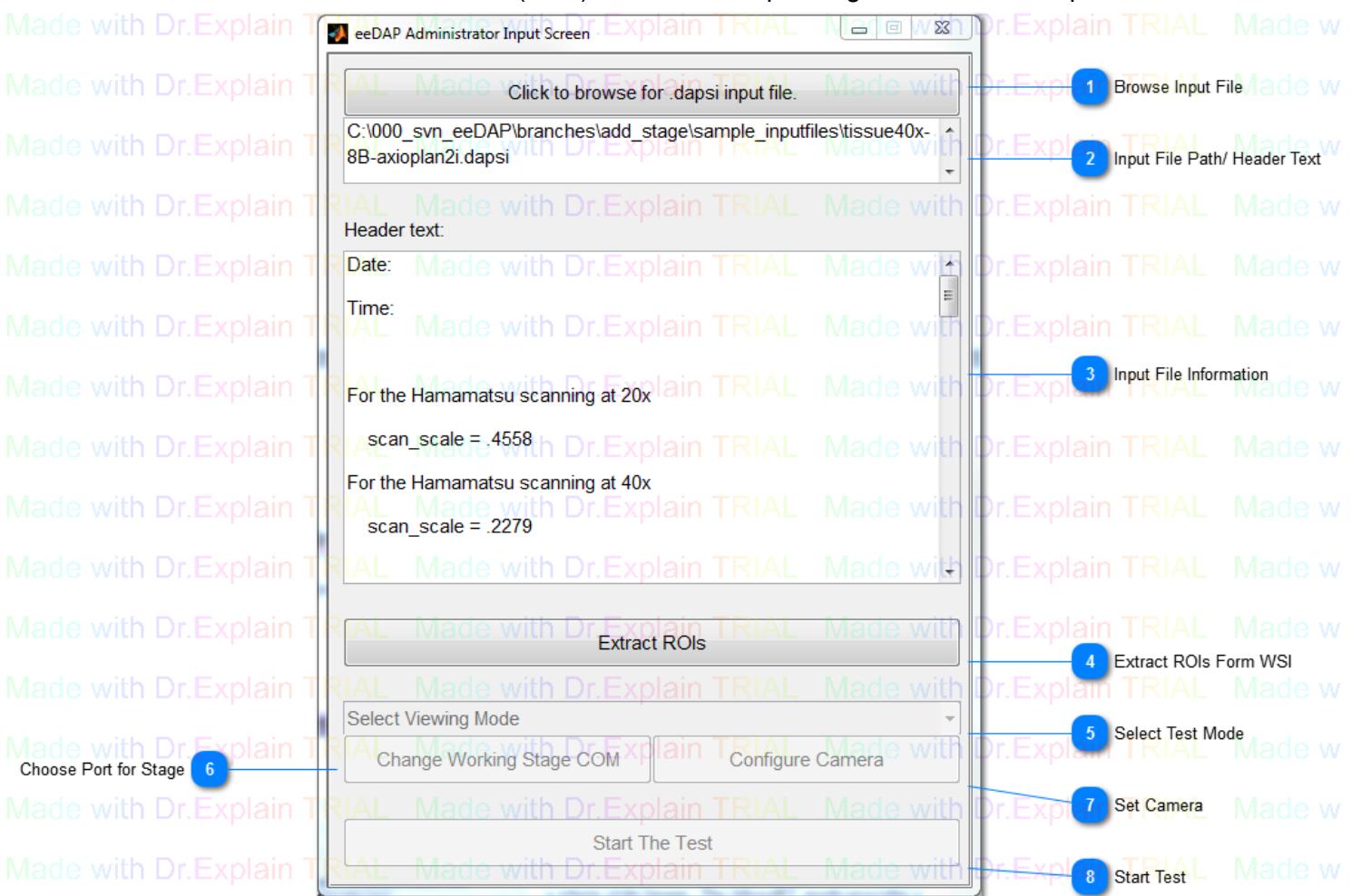
\*To return to [Run Software](#)

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### eeDAP Administrator Input Screen Window(c)

In the first box the admin selects the input file containing the tasks; see the “[Input File](#)” section for formatting of this file. It is selected using the “Browse” button. Once chosen the header of the file is displayed in “Header text” box. Selecting “Extract ROIs” button will extract the experiment ROI’s from the WSI images. Extracting ROI’s may take a few minutes depending on the size of the experiment and the computer capabilities.

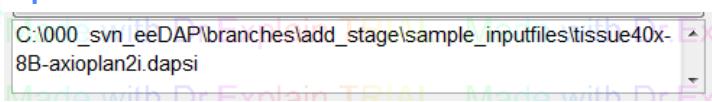
The drop down menu (Testing Mode) allows for the administrator to choose either the *Digital* or *MicroRT* reading mode. The Digital mode allows for the evaluation of ROI’s identified and extracted from a whole slide Image. The MicroRT mode provides a real-time (RT) view of the same ROI’s through the optics of an adjoining microscope. Furthermore, the administrator is able to track a reader’s progress during MicroRT mode; a camera provides the administrator with the reader’s field of view (FOV) and the corresponding WSI ROI for comparison.



#### 1 Browse Input File



#### 2 Input File Path/ Header Text



#### 3 Input File Information

Date: Made with Dr.Explain TRIAL Made with Dr.Explain TRIAL  
 Time: Made with Dr.Explain TRIAL Made with Dr.Explain TRIAL  
 Made with Dr.Explain TRIAL Made with Dr.Explain TRIAL  
 For the Hamamatsu scanning at 20x  
 $\text{scan\_scale} = .4558$   
 Made with Dr.Explain TRIAL Made with Dr.Explain TRIAL  
 For the Hamamatsu scanning at 40x  
 Made with Dr.Explain TRIAL Made with Dr.Explain TRIAL  
 $\text{scan\_scale} = .2279$   
 Made with Dr.Explain TRIAL Made with Dr.Explain TRIAL

After browse input file, shows the detail information of the file

#### 4 Extract ROIs Form WSI

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WSI

Following the input file, extract Region of interest from

- This will create folders in the "**sample\_inputfiles**" directory "**Output\_Files**", "**Temporary\_Registration\_Images**", and "**Temporary\_Task\_Images**"
- This will also create .tif files in the "**Temporary\_Task\_Images**" directory (One for each task listed in the .dapsi input file)

#### 5 Select Test Mode

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- Choose Digital mode for just use WSI digital image in experiment
- Choose microRT mode use both WSI digital and microscope live image in experiemnt

#### 6 Choose Port for Stage

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In microRT mode, set the stage controller connect port

#### 7 Set Camera

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In microRT mode, set camera

#### 8 Start Test

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Start test

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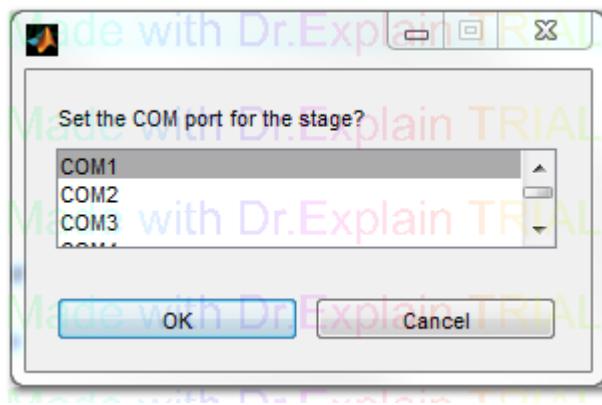
## MicroRT Registration

Before data collection in MicroRT mode, the glass slides must be registered to the corresponding WSIs. After registration, the ROIs viewed through the microscope eyepiece in MicroRT mode will be the same as those extracted from the WSI in Digital mode.

### Serial Port Configuration:

Set the *COM port* connection for the microscope stage controller.

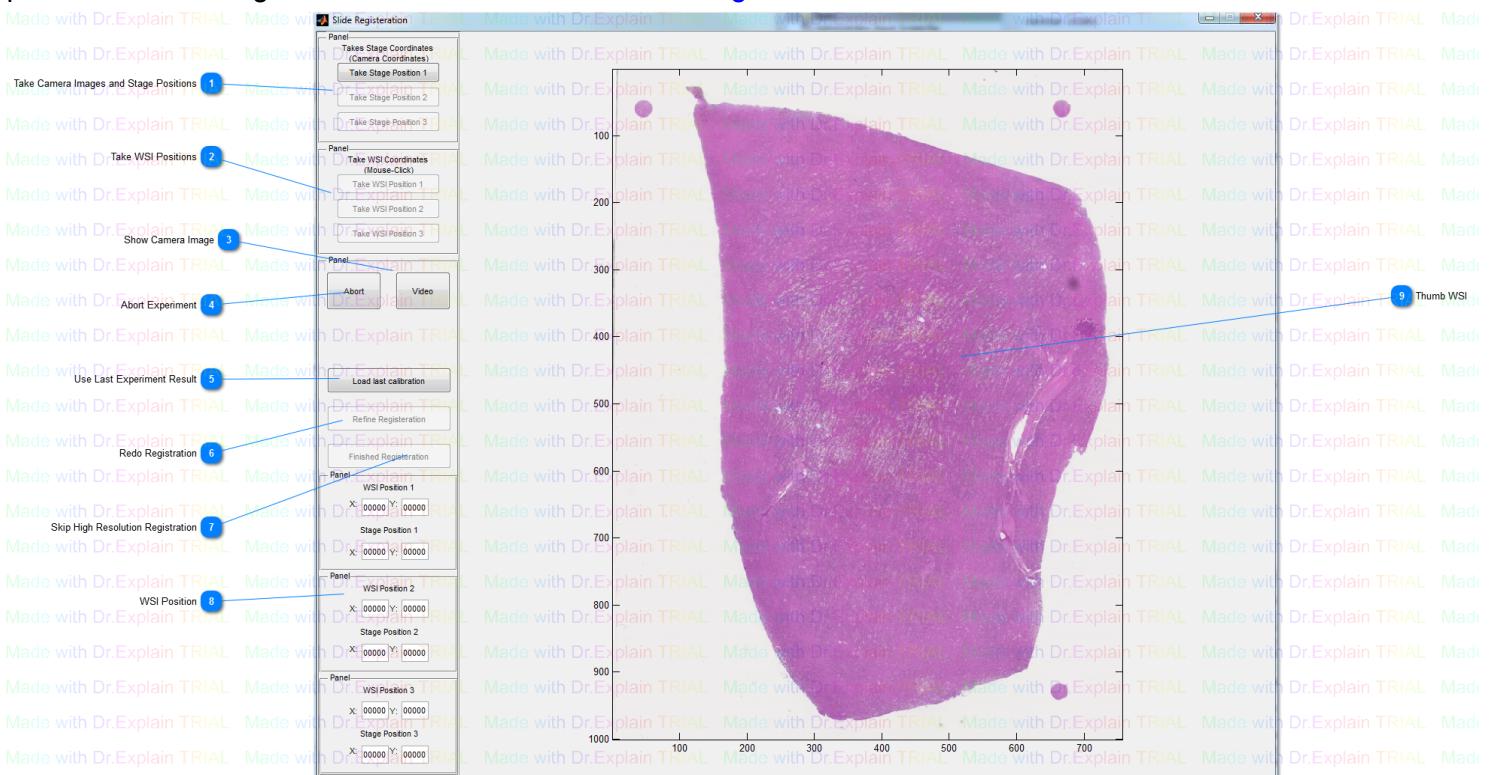
\*To specify the correct COM port, open the PC's control panel then open Device Manager and expanded the Ports.



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## Slide Registration Window

When the MicroRT mode is selected the Slide Registration window will open. The microscope camera will also engage, and a video preview window will appear. In this step the Administrator verifies and registers the glass slides to the corresponding WSIs. This ensures that the reader's FOV in MicroRT will be the same as the ROI presented in the Digital mode. Refer to the "[MicroRT Registration](#)" section for details.



### 1 Take Camera Images and Stage Positions



Take the microscope live image and stage position for 3 areas

### 2 Take WSI Positions



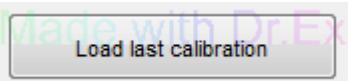
Take the related WSI position for 3 areas

### 3 Show Camera Image

Show the real time image

### 4 Abort Experiment

Exit and discard the experiment

**5 Use Last Experiment Result** Load last calibration

Load the past 3 areas WSI and stage positions from the most recent experiment

**6 Redo Registration** Refine Registration

Redo registration

**7 Skip High Resolution Registration** Finished Registration

Skip high-resolution registration, directly uses low-resolution or the last experiment postions

**8 WSI Position**

Shows the exact position of what was chosen on the WSI image and Camera image

**9 Thumb WSI**

Digital image of the WSI image

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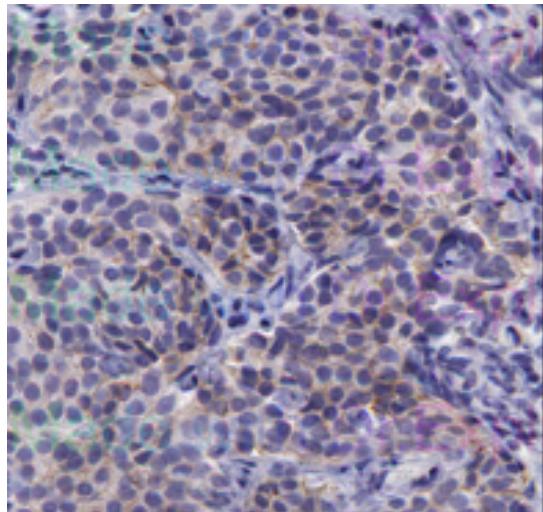
**Unregistered version**

## Semi-Automated Registration

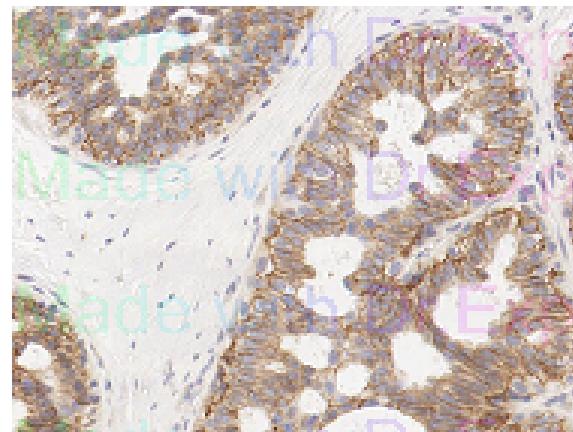
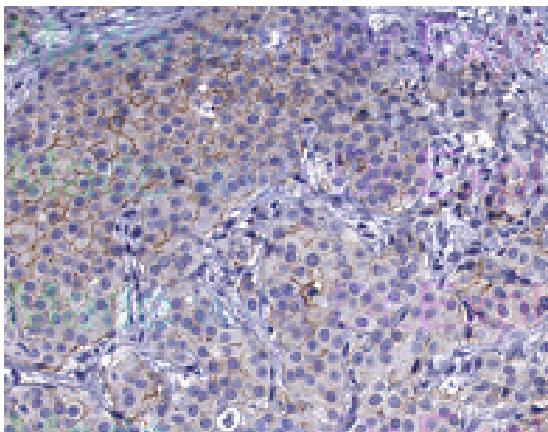
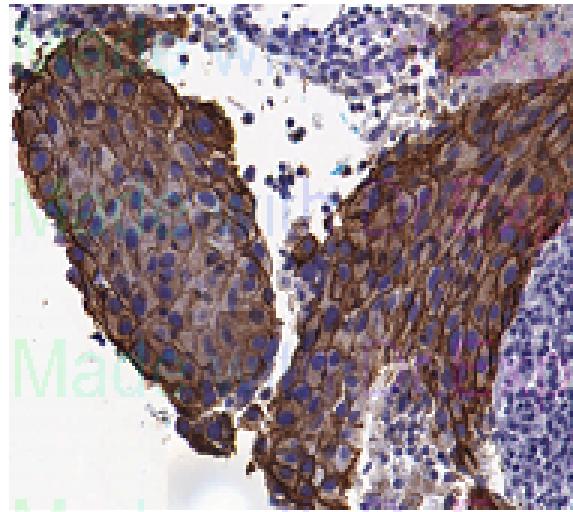
Verify the *glass slide's label* corresponds to the WSI presented in that slot of the motorized stage, also verify that the video preview window and lens has been launched.

Use the joystick to control the microscope stage. Navigate to a non-homogenous area of the slide, such as the end of the tissue, or a unique feature in the tissue. Good and Bad features are displayed below

Bad



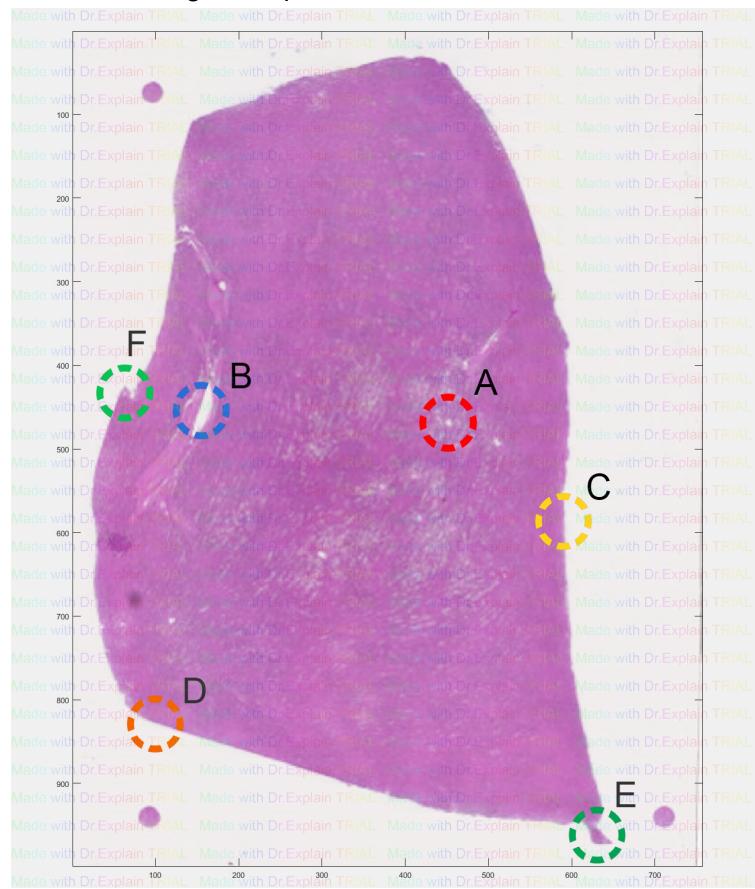
Good

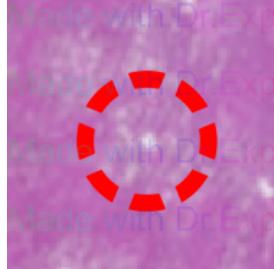
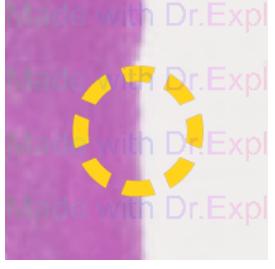
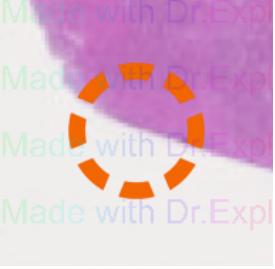
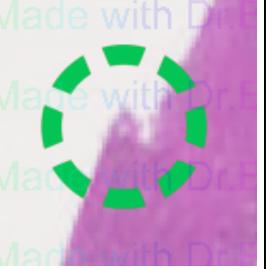


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## Unique Locations

Here are a few examples of what selecting a unique location means:



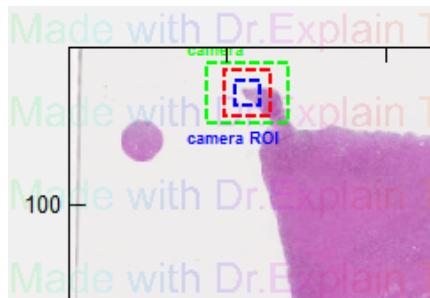
	Not Unique	Not Unique Enough or Centered	Unique and Centered
Example 1	 A	 C	 E
Example 2	 B	 D	 F

## Low Resolution Registration

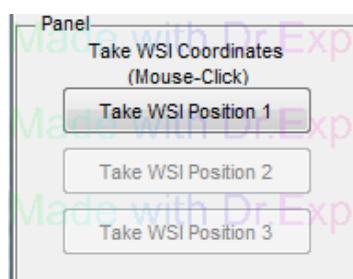
1. After finding the unique desired area, press "Take Stage Position 1"



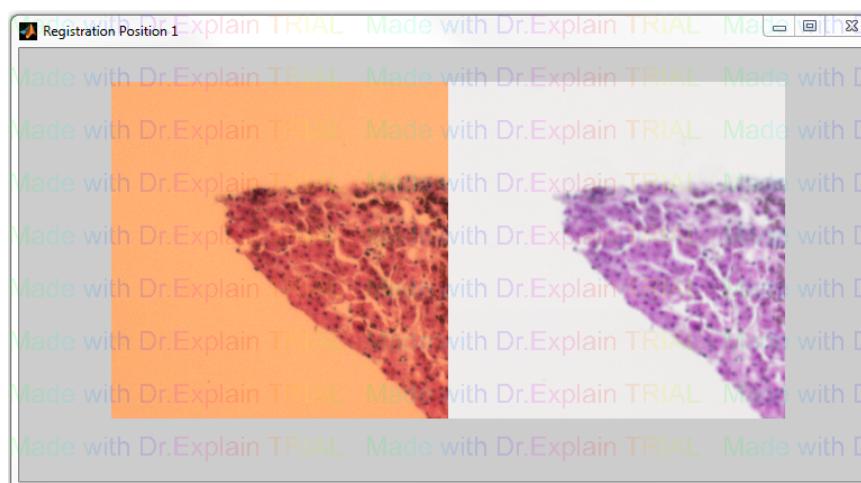
2. Click the same position in the WSI thumb image



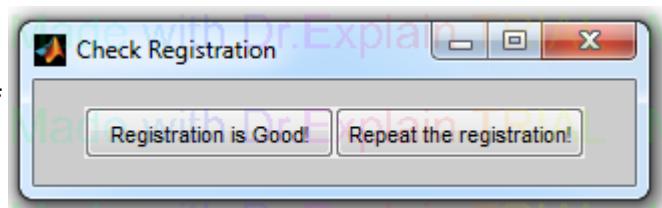
3. Press "Take WSI Position" to start registration



4. Check the registration result in Reigstration Position 1 window



5. Decide whether satisfied the registration. If yes press "Registration is Good!" to continue. If not, press "Repeat the registration!" to redo registration for this position



6. Repeat process twice for 2 other positions

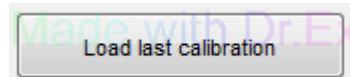
\* "Load last calibration" button can be used to skip low resolution registration

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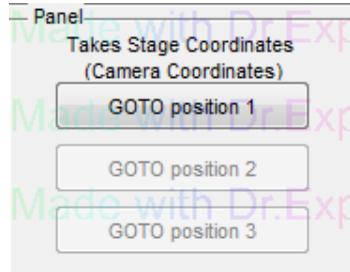
## High Resolution Registration

1. Change lens to high resolution registration's setting (Digital image is a zoomed up interface of the low resolution registration and WSI image may not be focused well)

2. After completing the low resolution registration, press "**Load last calibration**" to get into high resolution registration. If users decide to use "**Load last calibration**" the stage will move the glass slide to the previous experiment's position.



3. Press "**GOTO position 1**" to move stage to first low resolution registration position



4. Similar as [low resolution registration](#) part, click WSI image for related area for high resolution registration.

5. Repeat steps 3, 4 twice for two other positions

\*Note: User could use "**Finished Registration**" button to skip High Resolution Registration (Not Recommended)



## Manual Registration

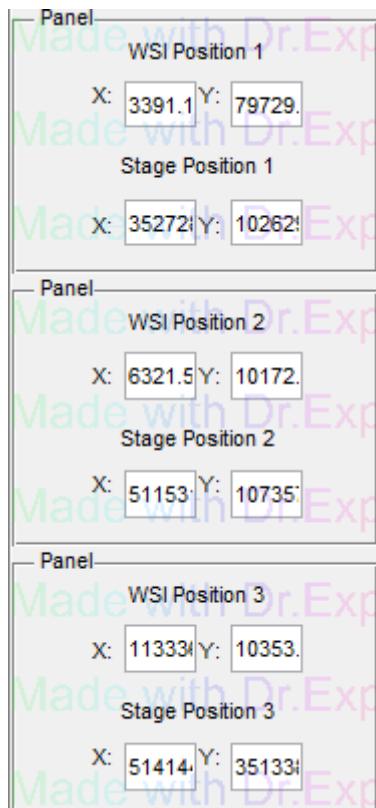
When automated registration fails for a slide, manual registration process may be necessary. This method requires the Administrator to identify three registration points and find them in the WSI and the glass slide.

### Selecting WSI points:

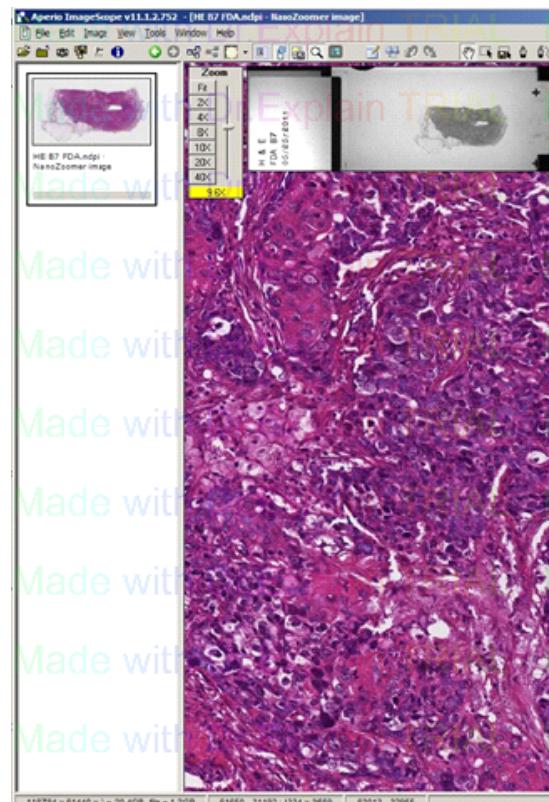
1. Select points that have unique features in non-homogenous areas of the WSI (Remember to maximize the distance between the registration points) (*Figure 1*)
2. Administrator will input the corresponding pairs of x,y coordinates in the Registration window: the x,y coordinates in the WSI and the x,y coordinates on the glass slide.

### Determining an x,y coordinate in the WSI:

1. Open the WSI file in Aperio's ImageScope
2. Select the “Extract Region”  tool in ImageScope
3. Pan over the image and note that the current x,y coordinates of the cursor are displayed at the bottom of the window (*Figure 2*)
4. Identify a registration point and record the x,y coordinate in the Registration window to determine the corresponding x,y coordinate on the glass slide.
5. Using the joystick to control the microscope’s motorized stage, locate the same point selected in the WSI. It is useful to have a reticle with cross hairs at the center.
6. If you do not have a reticle with cross hairs, you can use the Video Preview image to center the registration point.
7. Press “Take position 1”, this fills in the glass slide coordinates.
8. Once the x,y coordinates have been recorded for a registration points, press “Register ROI” (This may take a few minutes to execute)
9. Repeat this process twice more locating and registering Points 2 and 3
10. Repeat this procedure for all slides loaded into slots 1-8 and hit “done” button.



*Figure 1*

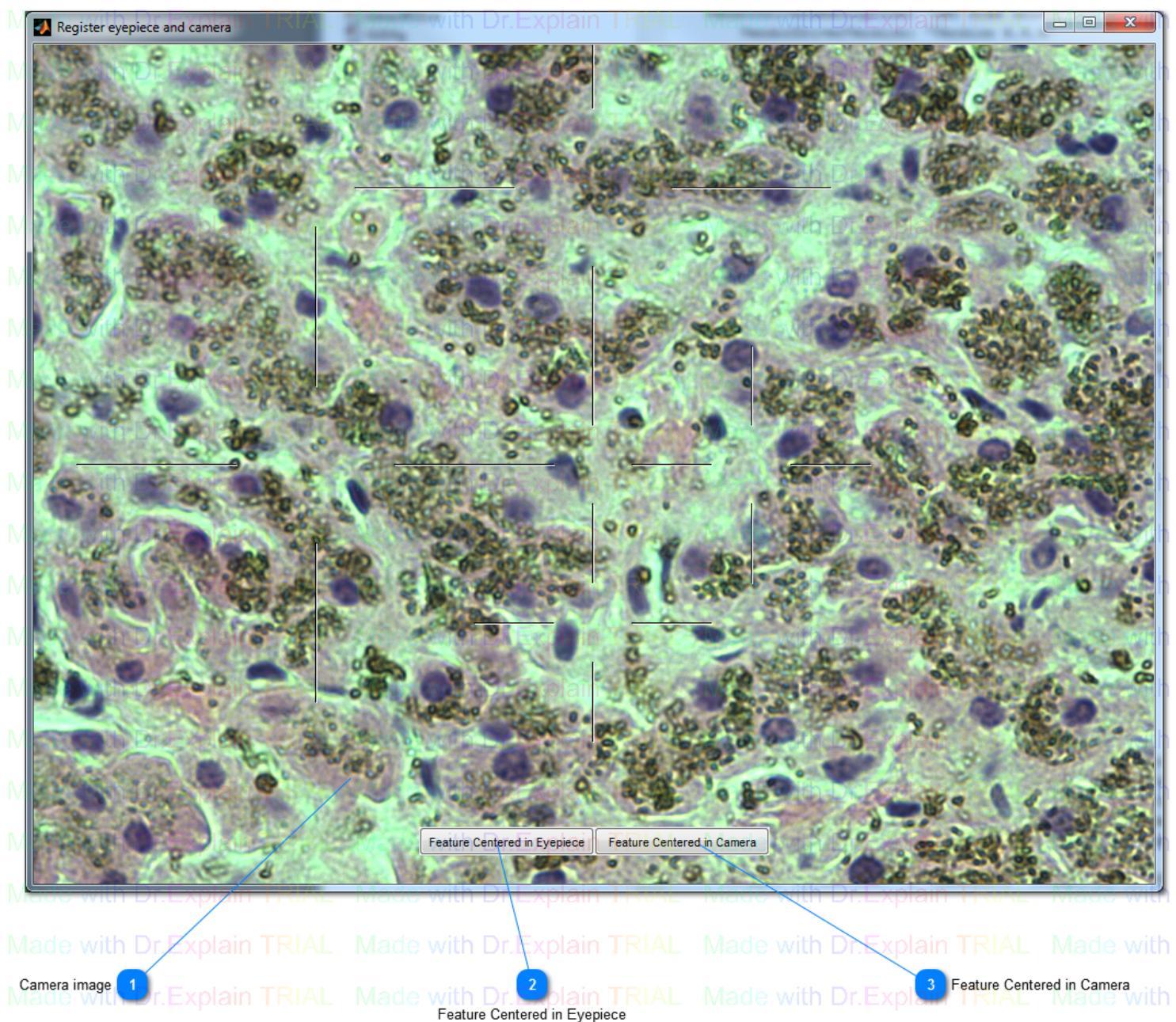


*Figure 2*

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## Register Eyepiece and Camera Window

In most the, there is offset between camera image and microscope eyepiece. User can do registration of the camera image with eyepiece image in this section.



### 1 Camera image

Real time image of the WSI image

### 2 Feature Centered in Eyepiece

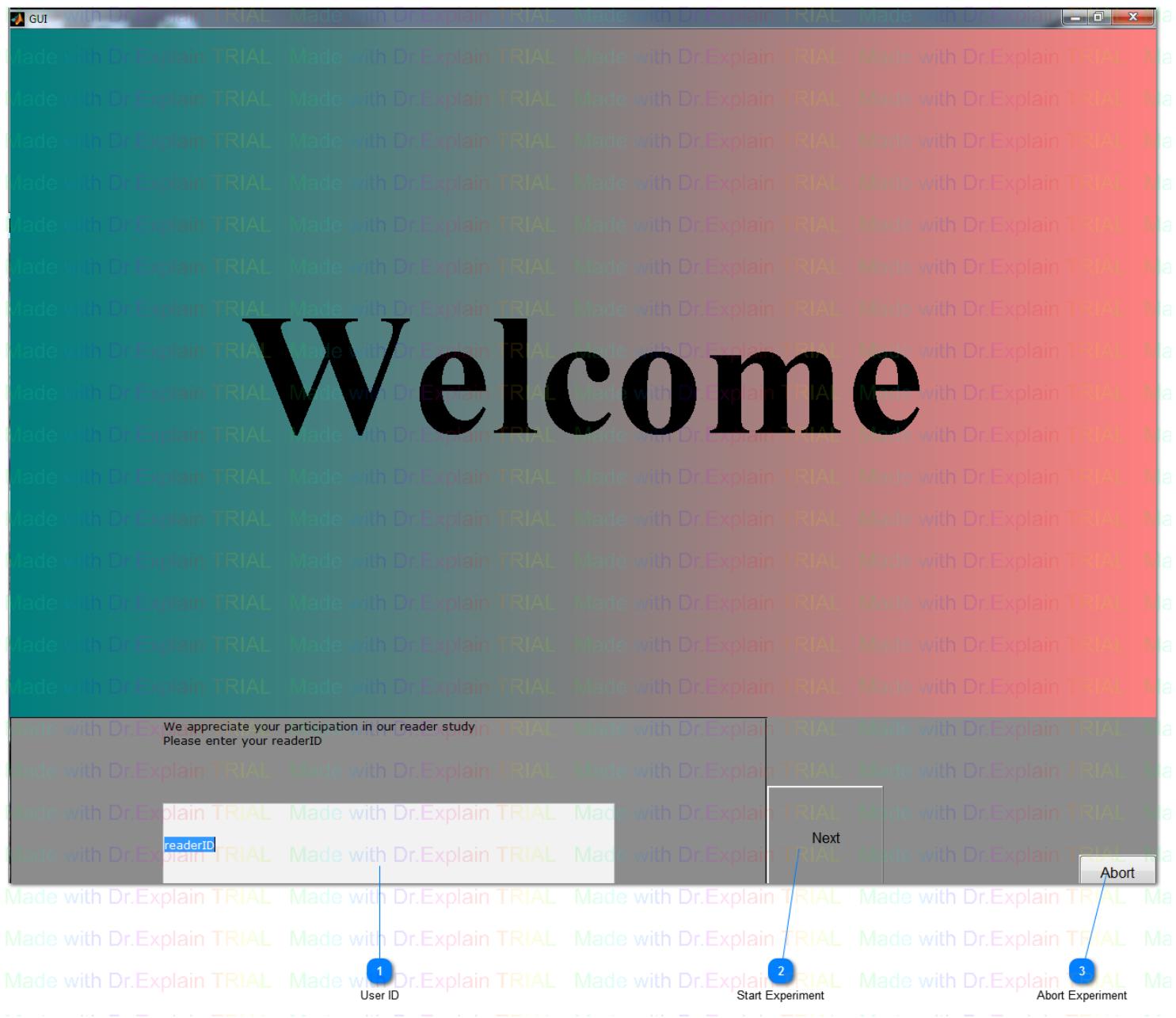
Take the stage position for eyepiece

### 3 Feature Centered in Camera

Take the stage position for camera image

## GUI Welcome Page Window

The Administrator will enter the reader's name or unique identifier and then proceed by clicking on the “**Next**” button.



### 1 User ID

Input user name

### 2 Start Experiment

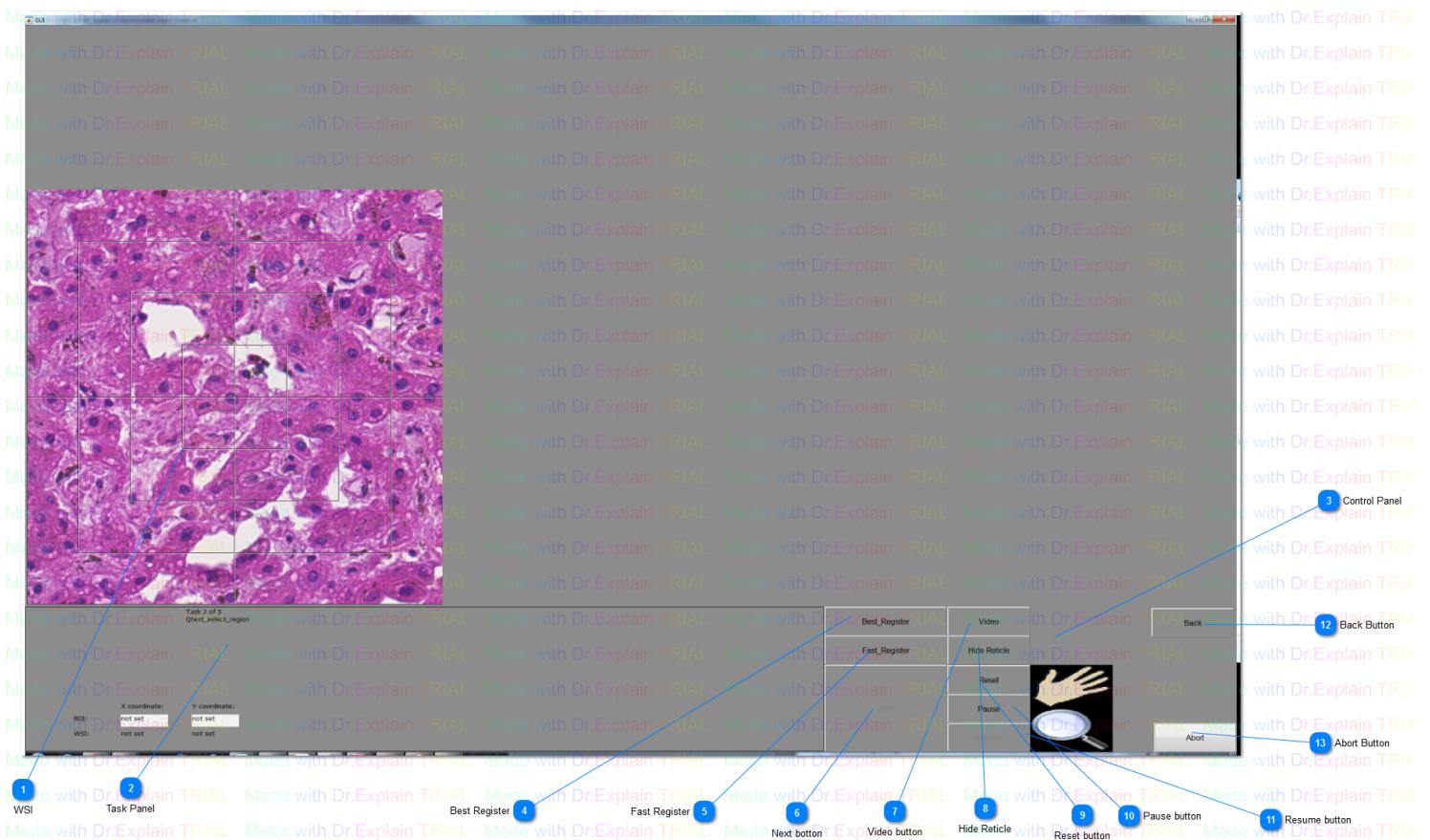
After input user name start experiment

### 3 Abort Experiment

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## Experiment Interface

Once you input the reader's ID, the evaluation tasks will begin when the ROI Image Presentation Screen opens. It is presented in a fashion identical to the Digital mode experiment. The Administrator is expected to read the tasks to the reader and record the responses of the Reader so that the Reader may stay engaged with the microscope. Please refer to the section on "[Tasks Instructions](#)".



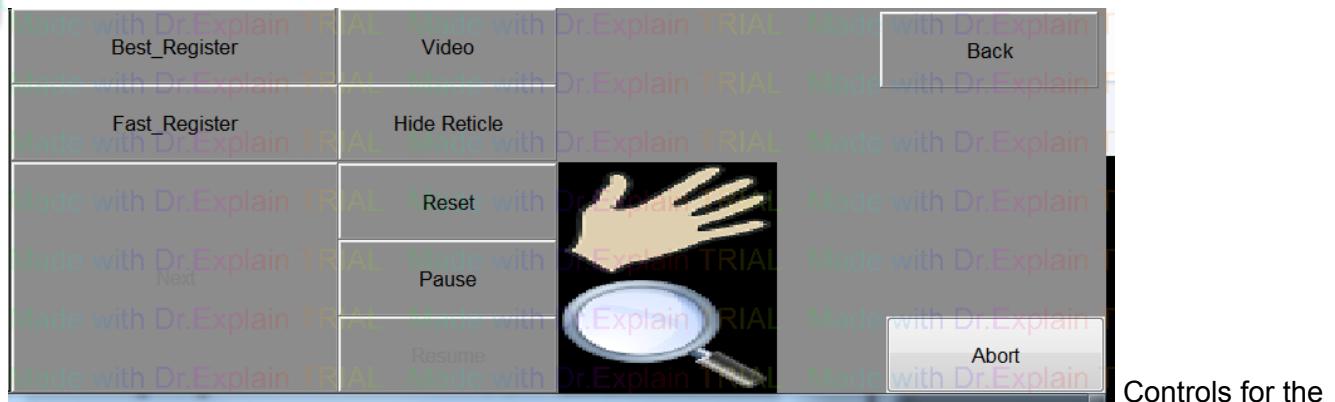
### 1 WSI

ROI of WSI

### 2 Task Panel

Shows the information and question for each task

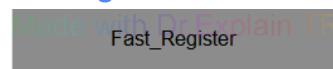
### 3 Control Panel



Digital experiment

**4 Best Register**

Do high quality registration WSI and camare image and adjust the stage position, only available in MicroRT mode

**5 Fast Register**

Do fast registration WSI and camare image and adjust the stage position, only available in MicroRT mode

**6 Next button**

Go to next task

**7 Video button**

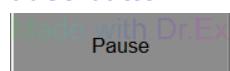
Display camera image

**8 Hide Reticle**

Hides the reticle shown on the current digital WSI image  
(Show Reticle: Reveals the hidden reticle on the current WSI image shown)

**9 Reset button**

Reset all the result in this task and move stage to original position

**10 Pause button**

Pause current task

**11 Resume button**

Resume task from pause status

**12 Back Button**

Go back to previous task

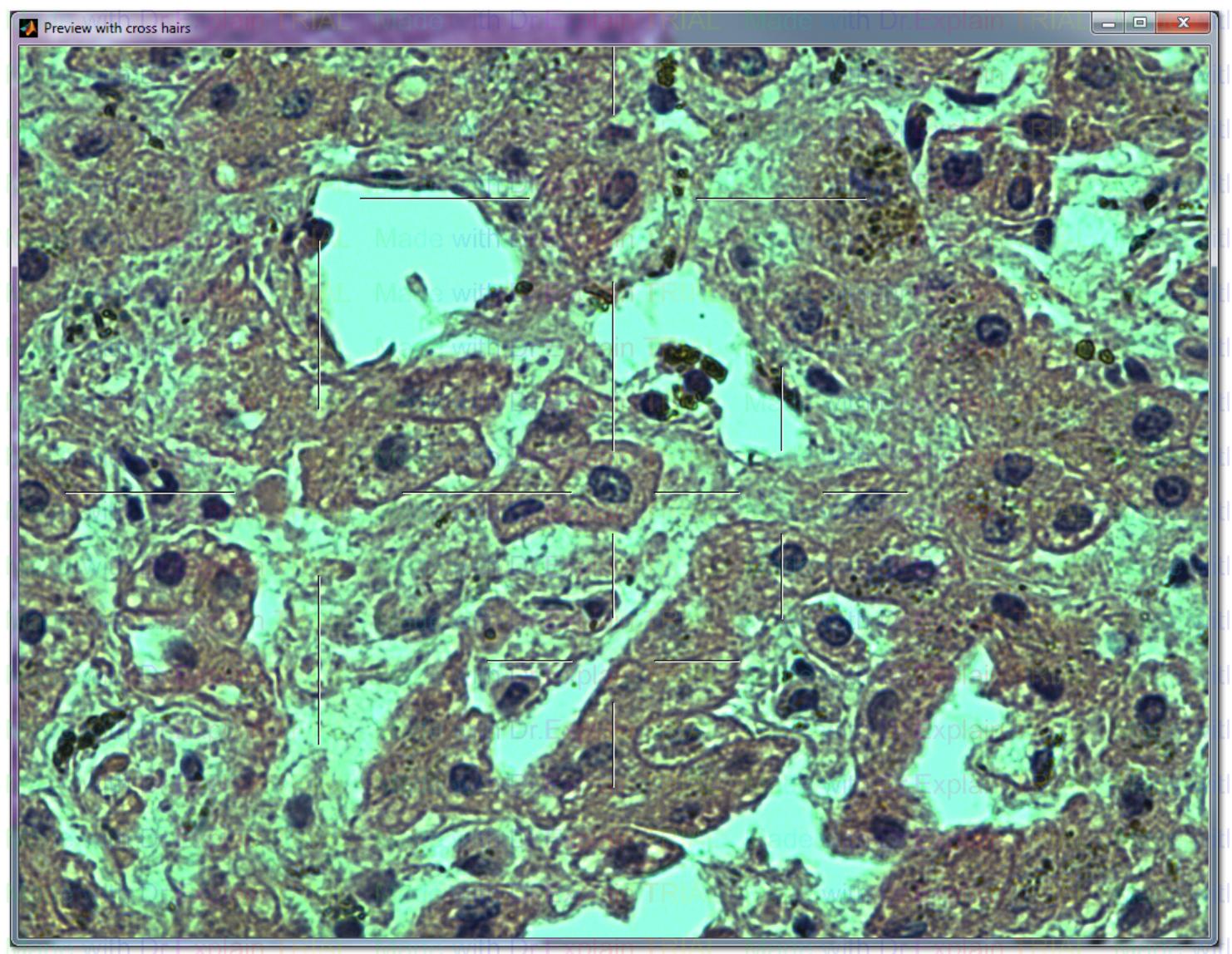
**13 Abort Button**

Abort/ Exit the current experiment



### Preview with Cross-Hairs Window

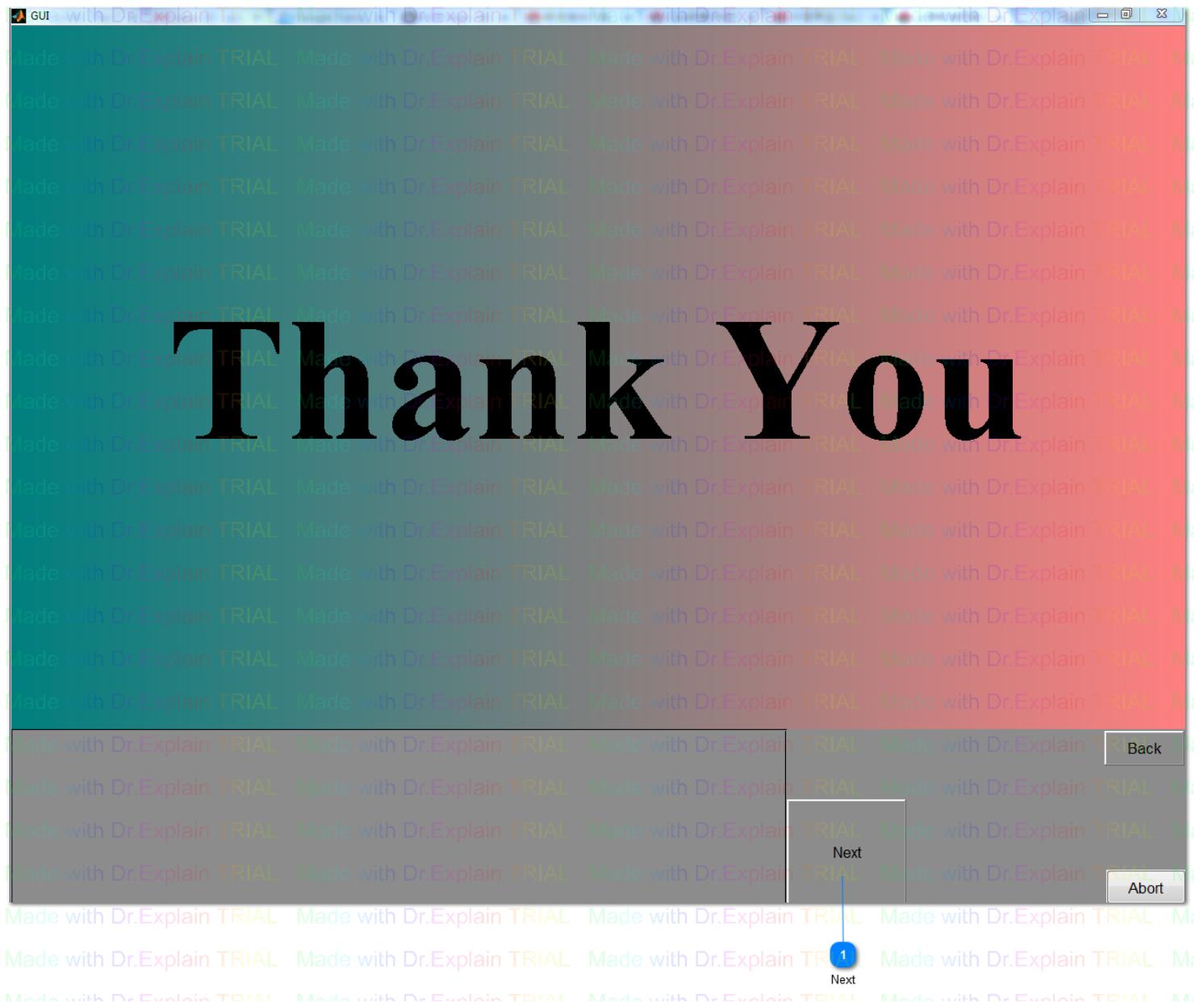
In MicroRT mode, users can preview with Cross-Hairs window and show the camera's live microscope image for the administrator view and registration between WSI and camera image.



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## Thank You Window

In conclusion of the last task, responses are saved in the output file. Please refer to the "[Output File](#)" section



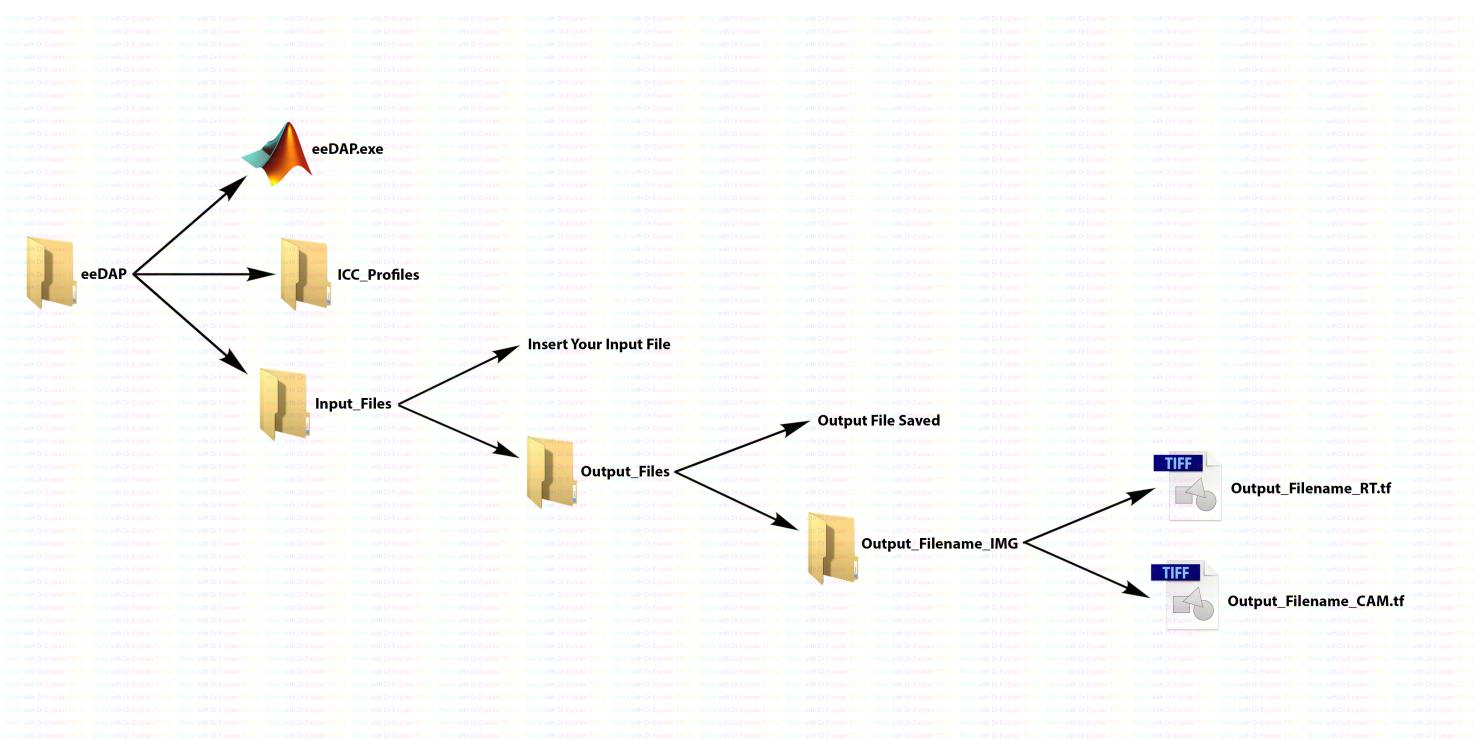
**1** **Next**

Finish experiment and save result

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## Directory Structure

A typical eeDAP installation will have the following structure. This is a sample structure of where your results/data will be stored.



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## VII. Stage and Camera Control Utility Functions

There is another stand-alone application (individual software) "Camera\_stage\_review.exe", which could run the test and control the camera, microscope, and stage outside of the eeDAP file.

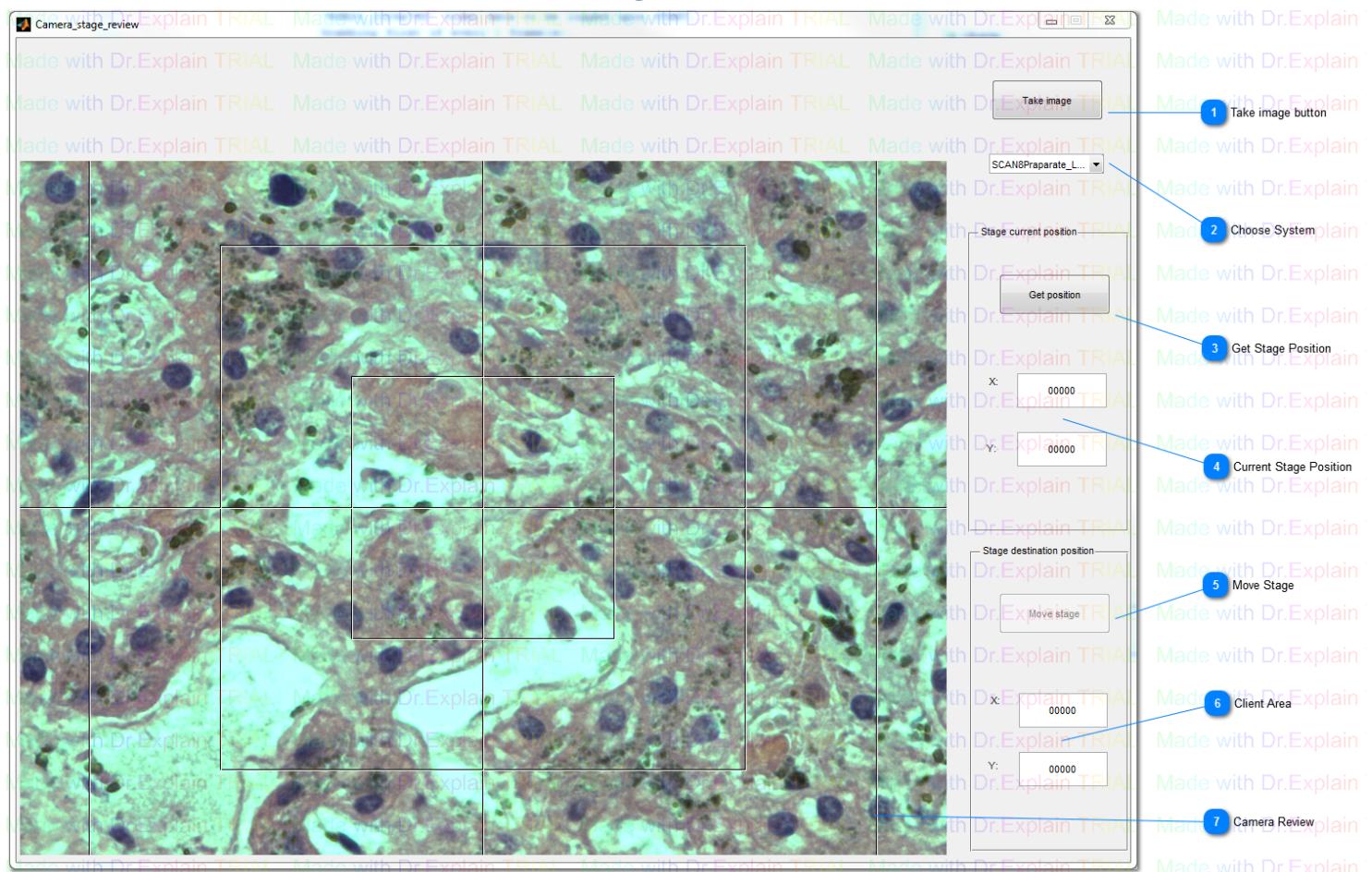
It has the following features:

1. Take a picture and save it to a file.
2. Get stage position coordinates.
3. Move to stage position coordinates.

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## Camera Stage Review Window



### 1 Take image button

User could use this button to take image of the current camera review. If the user has chosen stage control system, the default image name has stage position information. Otherwise, the default name is in format "cam\_+number". User could also edit the image name and saving directory.

### 2 Choose System

User could choose the working system here. Without choosing a system "Stage current position" and "Stage destination position" will be disabled. But the user could still use "**Take image**" button to get camera image

### 3 Get Stage Position

Get current stage positions and display them in part 4

### 4 Current Stage Position

When user clicks "Get position", "Move stage" or "Take image" buttons, current stage position will update to here

### 5 Move Stage

Move the stage to the position that user input in part 6. This button only enables when user inputs both X and Y position in part 6

6 Client Area

Input the destination positions for stage

7 Camera Review

Exact view of the WSI image

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## VIII. FDA Hardware Specifications

FDA specifications that are suitable for the eeDAP software.

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## Cameras and Displays

Current **Cameras** that are compatible with the eeDAP software.

- Point Grey Grasshopper Color (GRAS-03K2C-C)
- Point Grey Flea2 Color (FL2G-50S5C-C)
- Point Grey Grasshopper3 Color (GS3-U3-50S5C-C)

Different **Displays** and a few of their descriptions.

<b>Name of Display</b>	HP L2335	Dell 1908 FPt	Lenovo Thinkvision L220XWC
<b>Size</b>	49.6cm x 31.1cm	37.6cm x 30.1cm	47.4cm x 29.6cm
<b>Pixel Size</b>	1920 x 1200	1280 x 1024	1920x1200
<b>Pixel Pitch</b>	258um	294 um	247 um
<b>Contrast</b>	500:1	800:1	1200:1
<b>Brightness</b>	250 cd/m^2	300 cd/m2	325 cd/m2

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## IX. For eeDAP Developers

Extra information for eeDAP Developers

The [GitHub Master Page](#)

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## Creating the Stand-Alone Application

### Build the Stand-Alone Application

Move the main file into the build (Administrator\_Input\_Screen.m). Also add the "tasks" folder to the build. Click on the "Build" button. The build takes as much as 5 minutes! The build creates the "src" folder underneath the project folder.

File required to run (complied):

- btmatlab
- stages
- tasks folder

File installed (package):

- sample\_inputfiles
- gui\_graphics
- icc-profiles

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