

Fuji: From Fumbling to Functional

A brief introductory survival/how-to guide for understanding and operating the FUJI Picture Archiving and Communication System (PACS)

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Introduction

As a Radiologist, understanding how to use the PACS of your practice is of the utmost importance. A smooth experience can drastically improve efficiency by limiting distractions from spending time discerning how to work the software you are using. We spend a *lot* of time interacting with our PACS, and this can lead to increasing frustration when it feels like we must stop multiple times a day to troubleshoot a problem or remember how to adjust a setting. Especially when getting started with a new PACS, learning to become efficient can be a cumbersome task, and it is only natural to want to learn just enough to get by. That's where this guide comes in. I hope to produce a functional, user-friendly reference material that will help reduce frustration and improve efficiency with FUJI PACS. This guide is not in any way intended to be an all-encompassing masterclass on how to be the greatest FUJI techno-wizard of all time. However, if you want to learn how to create a user-friendly experience with FUJI, improve your efficiency, and have a basic settings/troubleshooting reference guide, then you are in the right place.

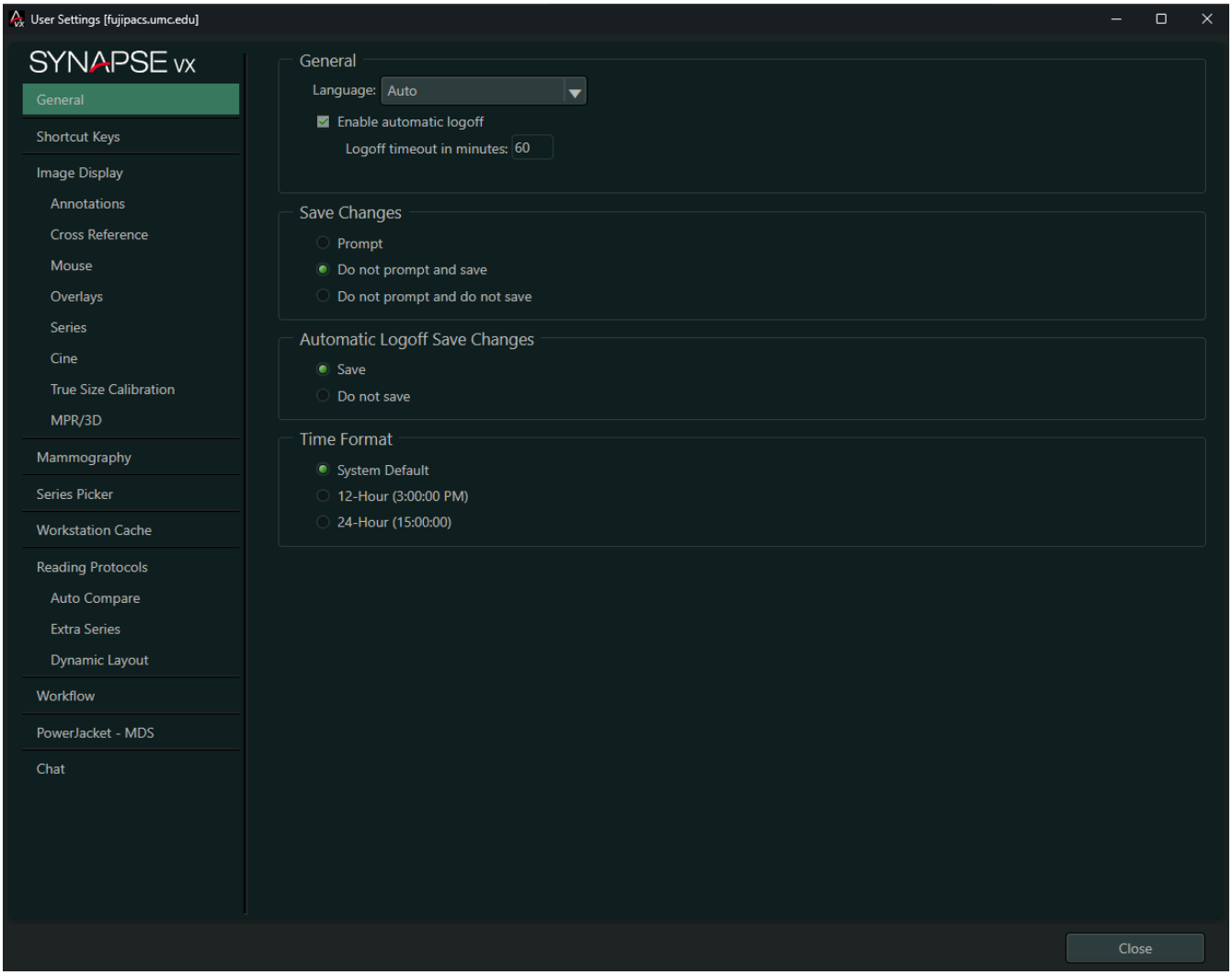
My advice for how to use this guide: it depends on who you are and where you are in your experience. If you are just getting started with FUJI, I would recommend reading through the "getting started" and "using the viewer" sections to get your setup and workflow ready for use. For those of you who have been using FUJI for some time now, I would use this as a reference guide when you are having issues or forget how to adjust settings, utilizing the detailed table of contents to quickly find the answers you need to minimize the interruption to your workflow.

Getting Started

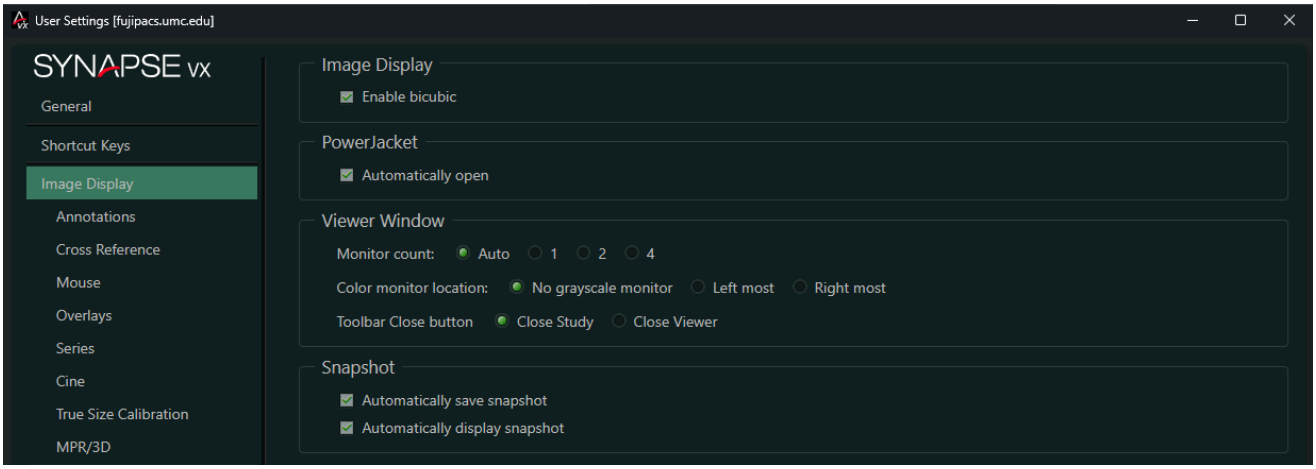
Initial Settings Recommendations

In this section, we will give an overview of the many settings of FUJI and how to set them for an optimal starting experience. This is merely meant to be a launch point for new trainees with FUJI, and more in-depth discussion of the different options and what they do will be left for later sections.

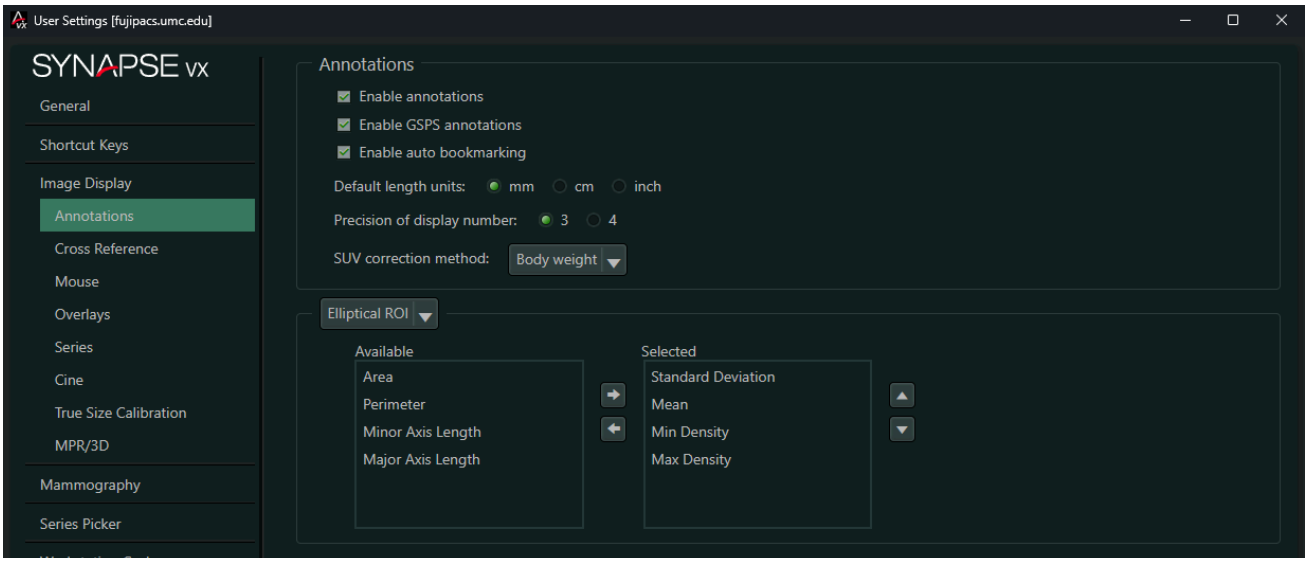
The layout of the settings window is shown below. We will start from the top of the options on the left and work our way down. Under the “General” tab, see the recommended settings as selected below. These settings will allow you to step away without getting immediately booted, and when studies are closed, you will not have an extra click to save your state.



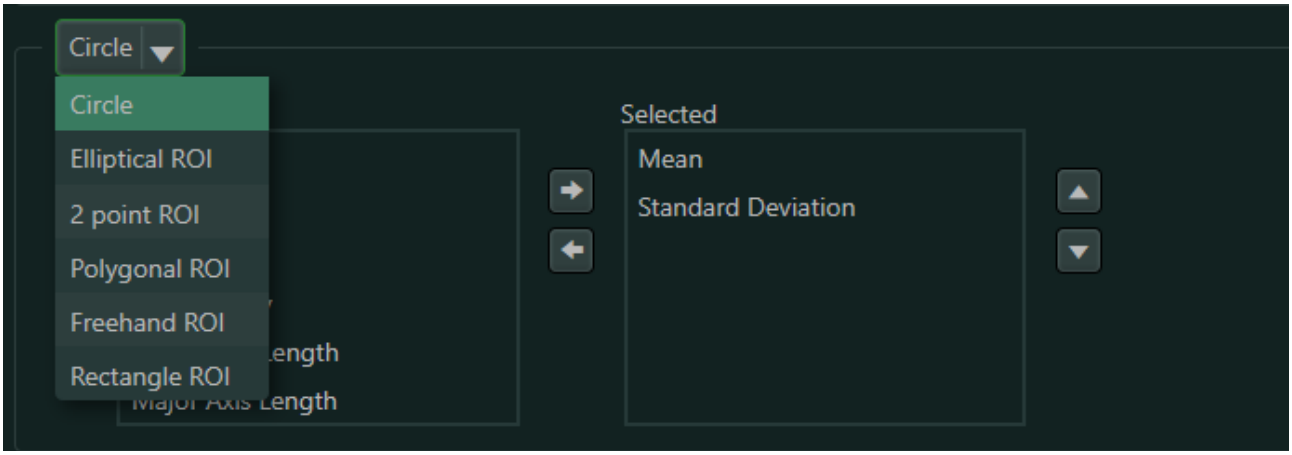
We're going to skip the shortcut keys section for now since there are so many options here it will be more efficient to discuss the relevant defaults as they come up in "using the viewer." For "Image Display," feel free to copy the recommended settings below. The "snapshot" settings here will allow a study to be reopened immediately to the saved state it was in when you closed it. This is user login dependent and will not affect how the study opens for others. I have not personally had issues with the auto detect for monitor count for normal use, but it is worth noting that if you want to use a 2 or 4-monitor station to prepare a case for a conference presentation on a single TV monitor, you can simply set this to "1" and refresh the viewer (default F5) before you save the snapshot and it will open in the same way it is saved.

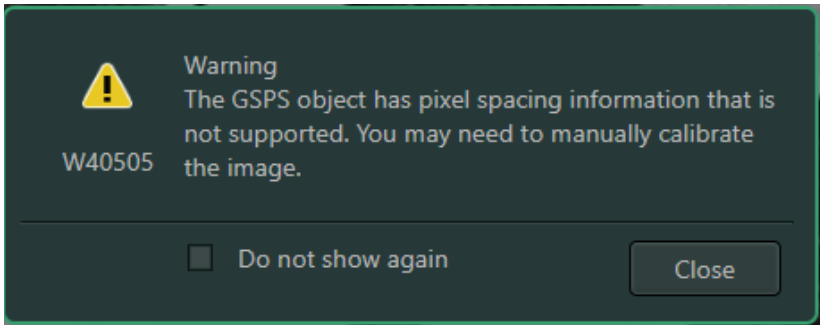


Under the "annotations" section, we can begin adjusting how our annotations will appear and what they will do within the viewer. In addition to the recommended base annotations settings, the box below will allow you to select what information you would like to have appear within certain annotations.

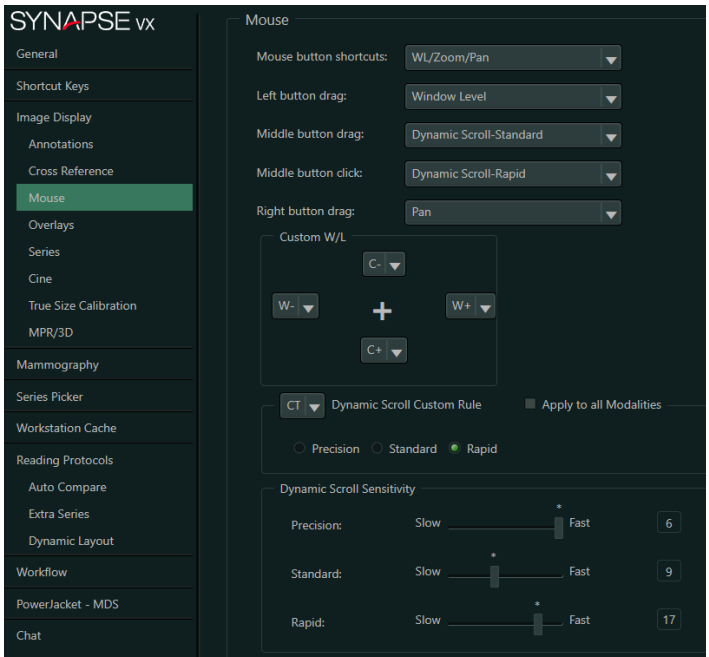

User Settings [fujipacs.umc.edu]
SYNAPSE VX
General
Shortcut Keys
Image Display
Annotations
Cross Reference
Mouse
Overlays
Series
Cine
True Size Calibration
MPR/3D
Mammography
Series Picker
Annotations
Enable annotations
Enable GSPS annotations
Enable auto bookmarking
Default length units: mm cm inch
Precision of display number: 3 4
SUV correction method: Body weight
Elliptical ROI
Available
Area
Perimeter
Minor Axis Length
Major Axis Length
Selected
Standard Deviation
Mean
Min Density
Max Density

For example, the elliptical ROI has LOTS of information set to display by default. Here you can remove or add optional data points to display using the arrows between the boxes. You can also select a different shape, such as a circle, and add ROI data to display with your circle annotations as shown below.



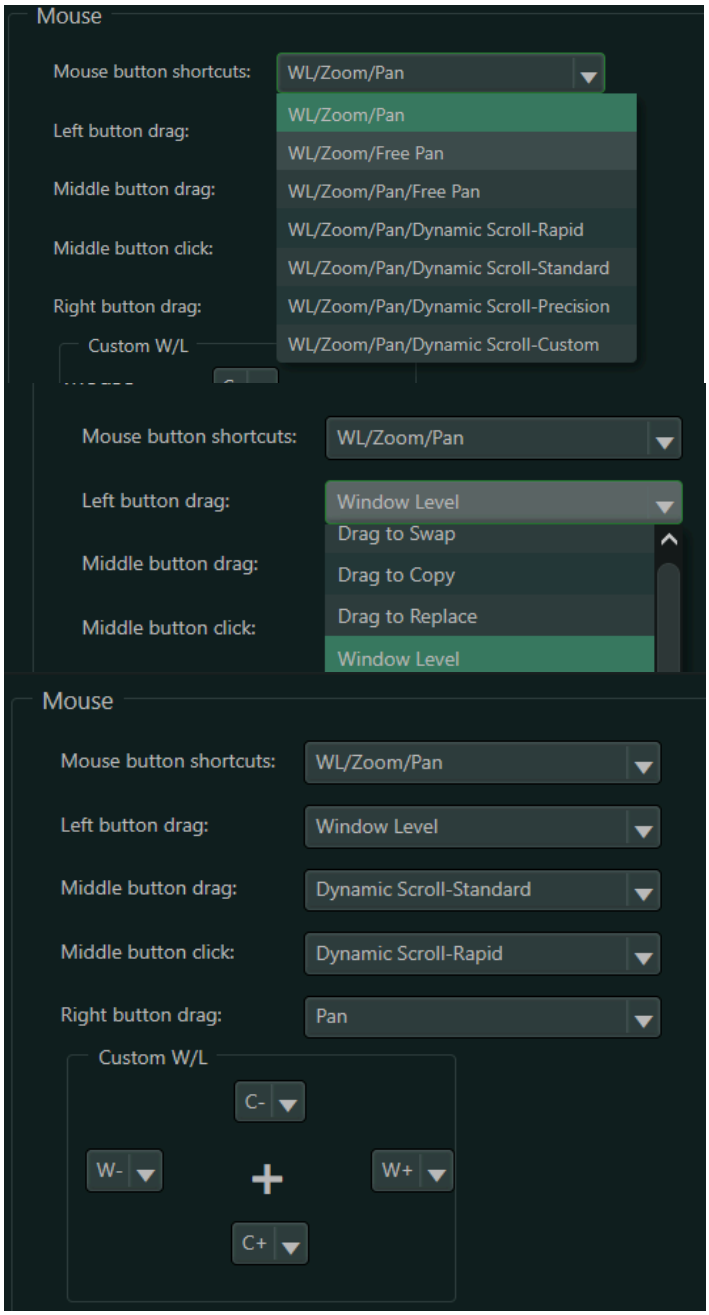


You may note a not-infrequent error message about GSPS annotations that pops up upon opening certain old studies. We were informed by FUJI representatives that this is due to our old PACS not implementing this data into the data sets, so FUJI encounters an error when it queries this data. Unfortunately, they informed us there is no way to stop that box from coming up (even if you check the box it will still open on studies other than that one you are viewing), but it should appear less with time as our priors are more likely to be coming from newer image sets obtained while using FUJI.



There are many different settings for the mouse. As you get more experienced with FUJI, this is one section you may revisit to tweak and find what is most comfortable for you. One setting many agree upon is the rapid dynamic scroll. When scrolling through long CT CAPs, the rapid setting allows you to move through quickly using the mouse movement rather than scrolling.

Using this in combination with the normal scroll wheel for slower scrolling will allow you to move through large image sets with speed and precision. Although the mouse wheel scroll sensitivity is set to fast here, it does not feel fast in the viewer, you will want this on the fastest setting possible. By checking the 'apply to all modalities' box, you only need to do these settings once, rather than going through each modality to set it.



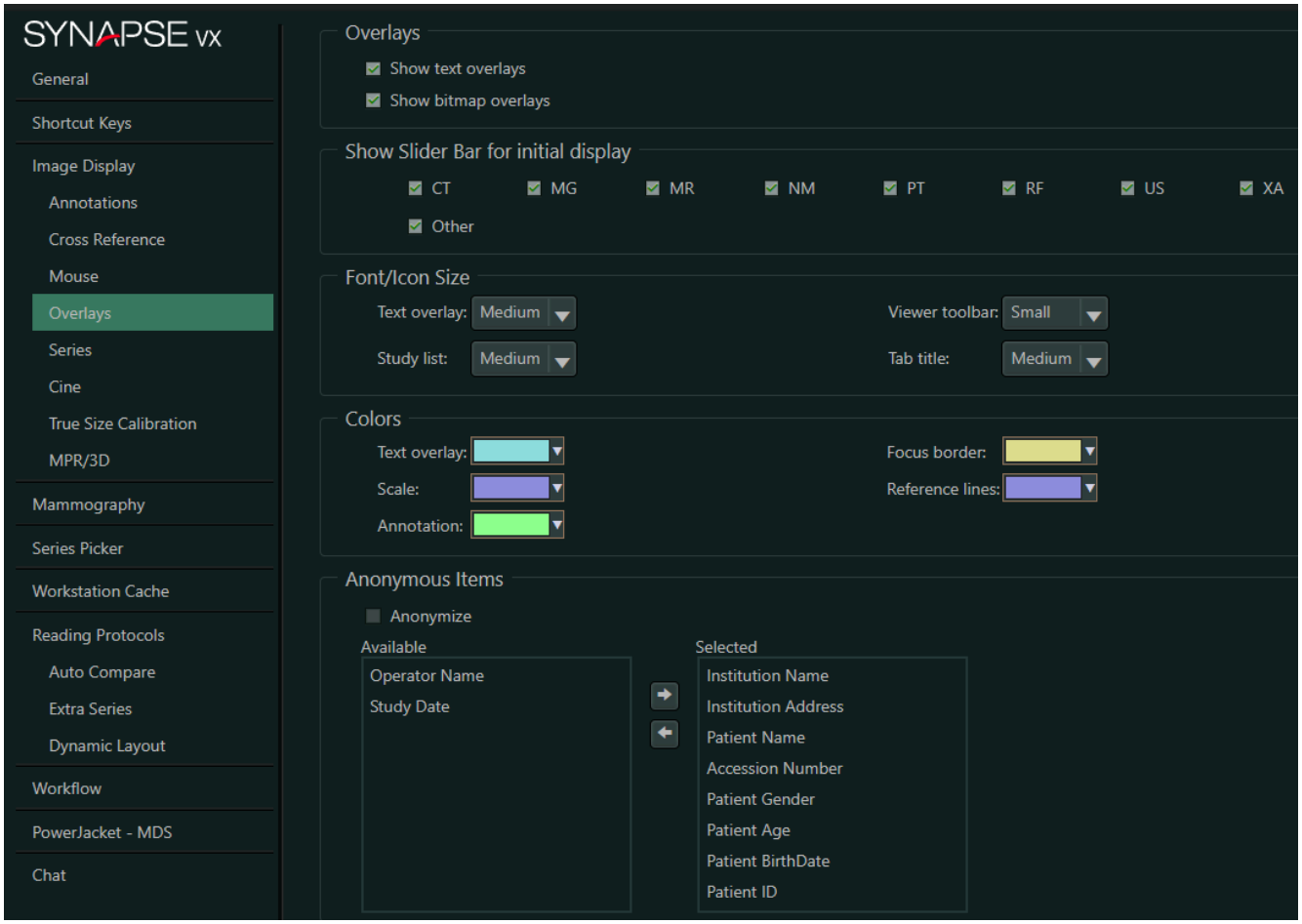
As for what to set your regular mouse clicks to, this is left up to you. I personally find windowing and panning to be the most useful to me on my left and right mouse buttons respectively. I use a macro to zoom, eliminating the need to use one of my mouse clicks for this (discussed in the "helpful macros" section).

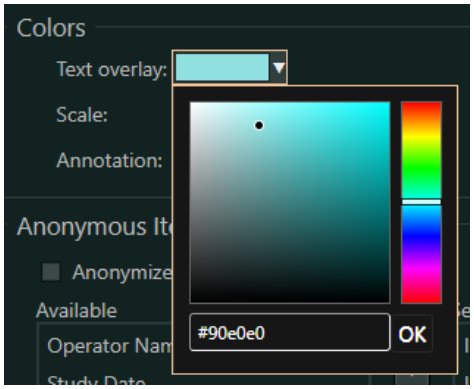
Others find the 'drag to swap' useful, as it allows you to move an image series from one pane to another simply by clicking and dragging. The window level setting will allow you to customize what happens when you drag in each direction.

For our institution at the University of Mississippi Medical Center, most attendings are familiar with dragging up increasing brightness (C-), down to darken (C+), left to narrow the window (W-), and right to open the window (W+); though some have the narrow/widen window options reversed. Instead of only using the scroll wheel to scan through slices, there are additional options for the middle mouse button that will allow you to scroll through slices by moving the mouse up and down. To change the speed that mouse movement will scroll, there are different settings (i.e. standard, rapid) that you can select. You can also use a mouse setting either in windows or your custom mouse software (Logitech G Hub on our computers) to change your mouse speed, which will subsequently affect how fast you scroll through images with mouse movement. If you use G Hub to do this, there are several different DPI settings you can select and cycle through, giving you near infinite customizability for scroll speed with mouse movement using these settings.



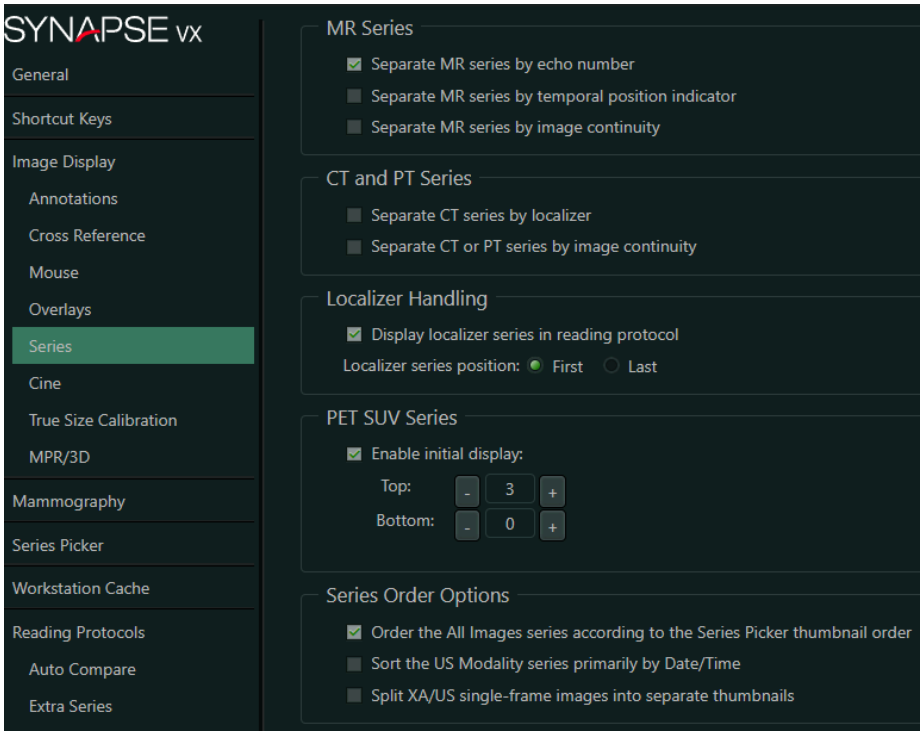
On the overlays page, you will be able to adjust several settings that change the appearance of your viewer 'HUD.' It is recommended to leave text and bitmap overlays on. The slider bar (page left) can be used to scroll through images by dragging the slider bar up and down. Beware, the 'H' and 'F' labels will sometimes be reversed, even between different series in the same image set. This means that instead of scrolling down moving caudal (with slider bar OR mouse) it will move rostral. We have been informed by FUJI representatives that this issue has to do with how the images are obtained and loaded into PACS and is not something that can be adjusted post-acquisition to flip everything to be the same orientation within an image set.





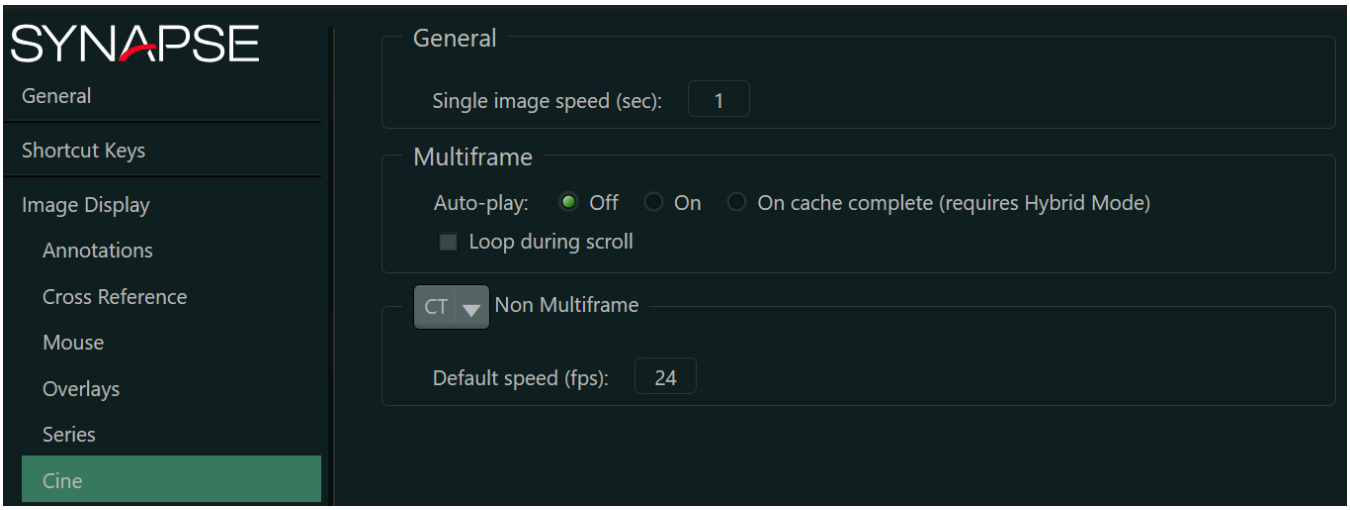
You can adjust the colors of your overlays here to any color you like. Note that this will only change the colors to YOU as a user for all of that type placed by yourself or anyone else. Others will see the colors selected in their own settings. In 'shortcut keys,' there is a setting to hide

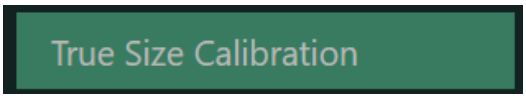
anonymous information. Here you can also select the items that will be hidden upon using this shortcut.



For the series settings, there is not much to say here. These are the recommended settings that seem to work best with our systems. If you do decide to experiment and find something that works, we can update recommendations as needed with further details.

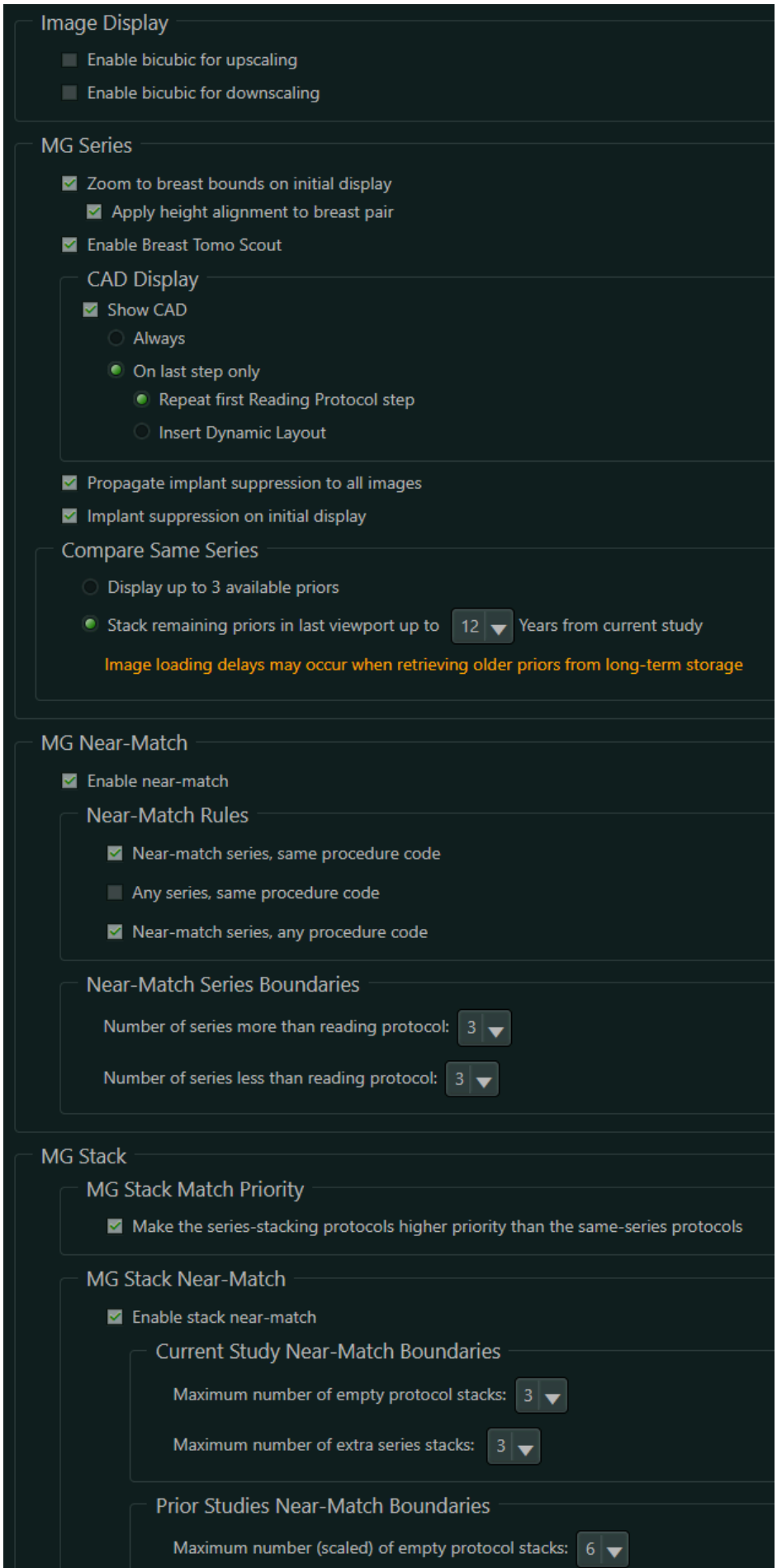
For the Cine settings, I would highly recommend leaving auto play and loop during scroll OFF. The default speeds are adjustable here per-modality, but aren't particularly useful for most basic use cases.





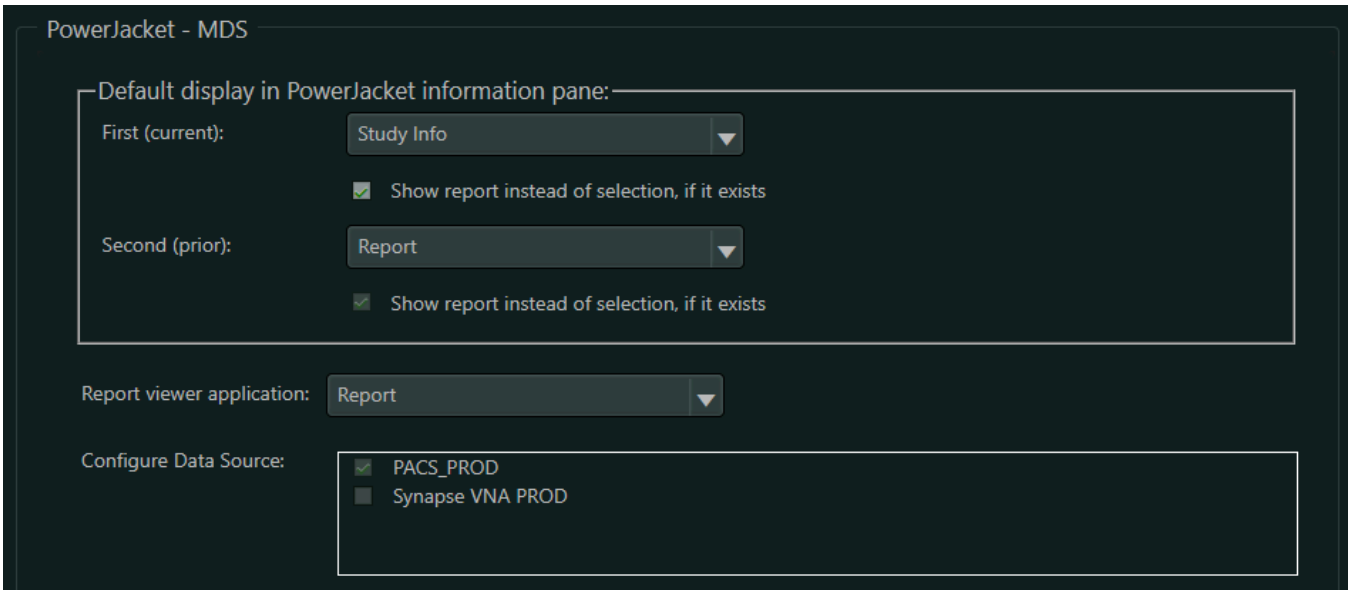


You don’t need to touch these tabs for now. If you’re looking for how to calibrate the on-screen ruler, that can be found here. Creating custom MIPS and 3D recons is discussed under Advanced use.


Image Display
Enable bicubic for upscaling
Enable bicubic for downscaling
MG Series
Zoom to breast bounds on initial display
Apply height alignment to breast pair
Enable Breast Tomo Scout
CAD Display
Show CAD
Always
On last step only
Repeat first Reading Protocol step
Insert Dynamic Layout
Propagate implant suppression to all images
Implant suppression on initial display
Compare Same Series
Display up to 3 available priors
Stack remaining priors in last viewport up to 12 Years from current study
Image loading delays may occur when retrieving older priors from long-term storage
MG Near-Match
Enable near-match
Near-Match Rules
Near-match series, same procedure code
Any series, same procedure code
Near-match series, any procedure code
Near-Match Series Boundaries
Number of series more than reading protocol: 3
Number of series less than reading protocol: 3
MG Stack
MG Stack Match Priority
Make the series-stacking protocols higher priority than the same-series protocols
MG Stack Near-Match
Enable stack near-match
Current Study Near-Match Boundaries
Maximum number of empty protocol stacks: 3
Maximum number of extra series stacks: 3
Prior Studies Near-Match Boundaries
Maximum number (scaled) of empty protocol stacks: 6

you should use. Not much to say about these.

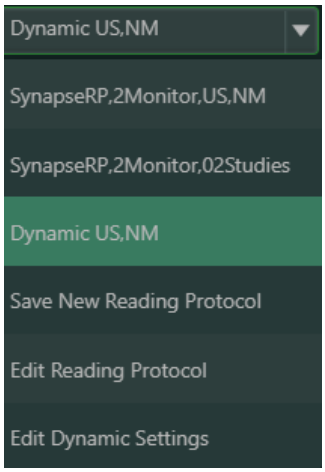
For the PowerJacket settings, there isn't much to decide other than the default display under your patient's list of available images. For your 'current' exam, there should not be a report available, so setting the 'current' study option to display other information by default may be of some use.



At this point, your basic settings are complete. Chat options will be discussed under the FUJI chat section of this guide, and the 'series picker' and 'workstation cache' options should not need adjustment since we are not using the FUJI worklist.

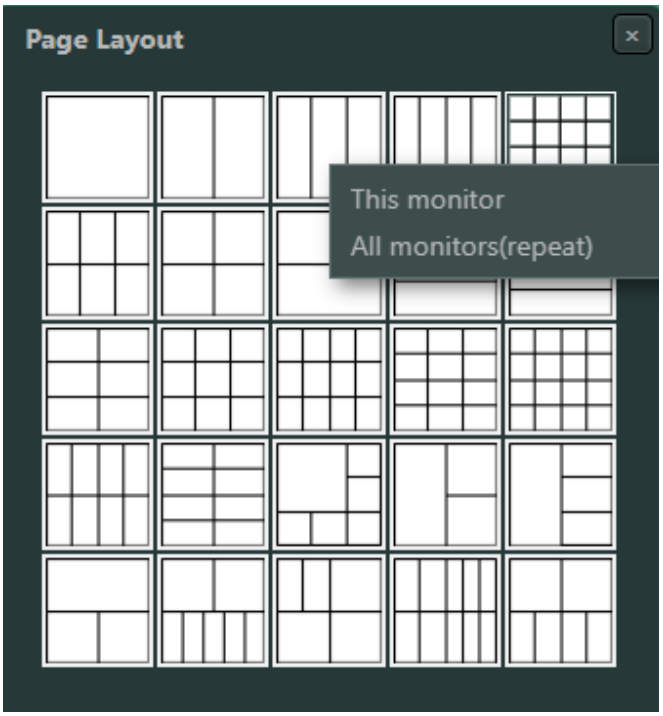
Hanging Protocols

This will be a VERY basic introduction to the complex custom possibilities available in FUJI. My intention here is to get you started with the basic 'building block' protocols that you can use in almost any situation and further customize as you get more comfortable using FUJI.

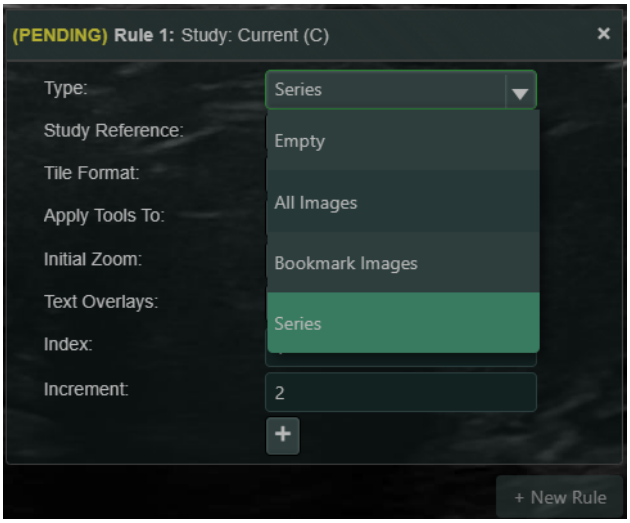


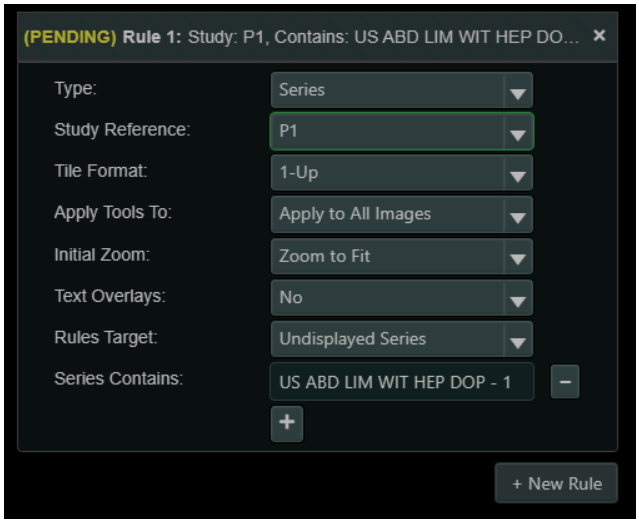
When you select the dropdown of hanging protocol options along your toolbar, you are presented with several options. I will walk you through an example of how I build a basic 'building block' hanging protocol during my workflow that doesn't take more than a minute once you learn how to get the setup you want. From this dropdown menu, I first select the Dynamic protocol. For some studies on two monitor setups, this may be all you need to do, but I would still recommend then re-opening the dropdown menu and selecting 'edit reading protocol' so that you can further customize the setup. A bit of foreshadowing: with the method of setting things up I will show you here, while it is very simple and quick to do once you get the hang of it, you will have to do it again for every unique combination of studies you open with the viewer. For example, if you set up a reading protocol for a CT but then open a CT with a prior comparison CT, you will have to make a new CT+CT protocol. Yes, it does seem a bit tedious, but after a day or so of doing this consistently, it will become increasingly rare to come across a new combination of studies that you haven't had open before.

Once you open the reading protocol editor, the first thing to do is select your page layout for each monitor. For example, on x-rays I typically use the full single layout, but for CT's I like the 2x2. Feel free to select from the many different options and see what kind of screen real estate you are given for viewing the images. This can be adjusted manually within the viewer by using 'CTRL + scroll,' but it is nice to have a comfortable starting point, and keep in mind that these are going to be our general building blocks for all studies of a specific modality, so best to keep it flexible.

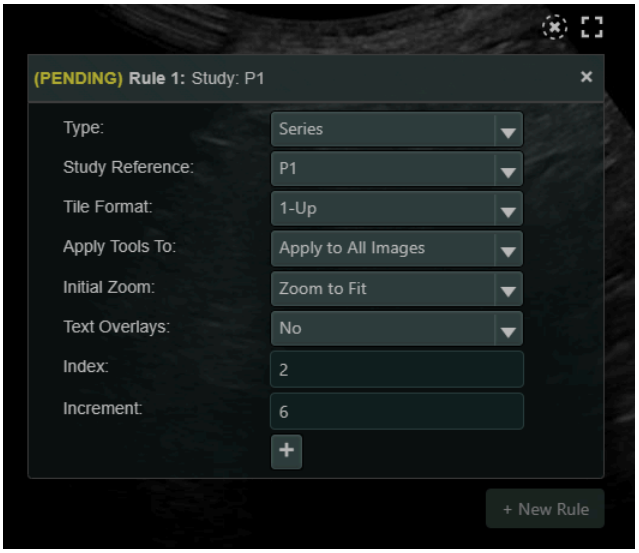


Once you have your window layout selected, each window will have a rule box allowing you to select specific settings for each window. I like to keep things simple, usually running the same settings for each window of my setup; and this is what I would recommend starting out with. First up, at the bottom of the box there may be a line following 'series contains,' click the minus sign next to these to remove them on all your windows; they will not be needed for our basic building block protocols. Under 'type,' for all modalities that involve series of scrollable images, select 'series.' For image sets of plain films, I find the 'all images' preferable as this will allow you to simply scroll through the different views if there are any.





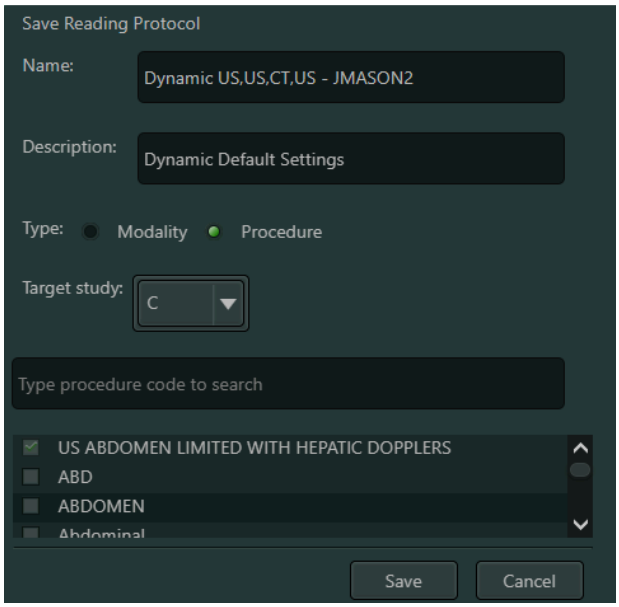
The second box labeled 'study reference' will be used to determine which study will be queried to select the series. C is for your currently open study, P1 for the most recent prior study open, and so on. Once you have your layout set up, if you wish to have blank boxes that do not populate with anything, simply click the 'x' in the top right corner of the rule box on that window and it will be left blank until you manually place an image series there.

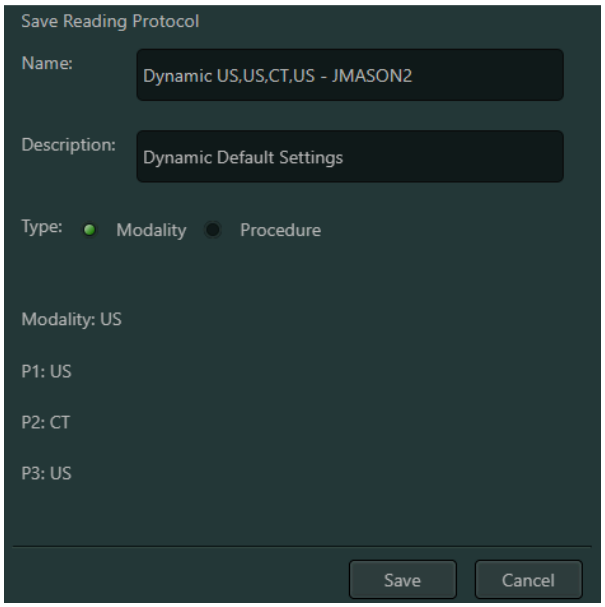


Now let's save our changes so they go into effect on the currently open study. In the top of the viewer, click the save icon next to the X to bring up the save options menu.



Feel free to name and describe your protocols as you wish. I find it most efficient to just leave my username at the end so that I know what the protocol is for if I want to go back and do any editing later not from within the viewer – not what we are focusing on right now. The only important thing to change here is to make sure you switch the default selection of 'procedure' to 'modality' under type. Once you have done that, you can click save and your new protocol will populate in the viewer. If it doesn't seem to have changed anything, check along the top bar to make sure that it is using the named protocol you created and not one of the defaults. If anything is not to your liking, you can re-enter edit mode using the previously described method, though ensure that the protocol you want to edit is the one that is currently selected.

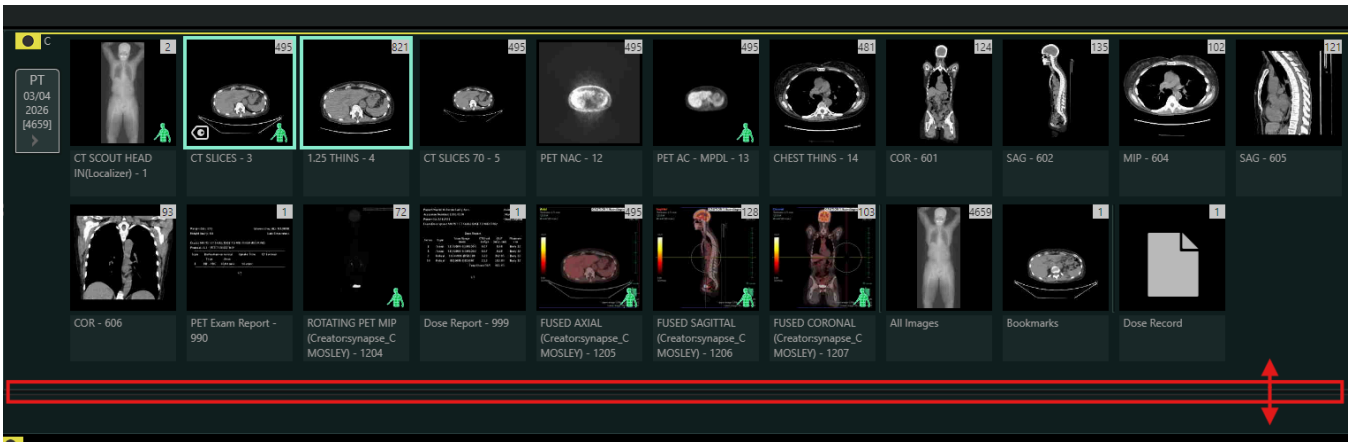




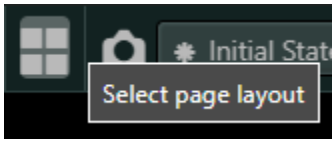
In the 'reading protocols' section of the user settings window, you can view and edit hanging protocols of your own or anyone else in our system. If you edit and save them, it should only save them to your own profile, so you will not be messing up anyone else's hanging protocol by doing this if you would rather start with someone else's protocol as a template.

Using the viewer

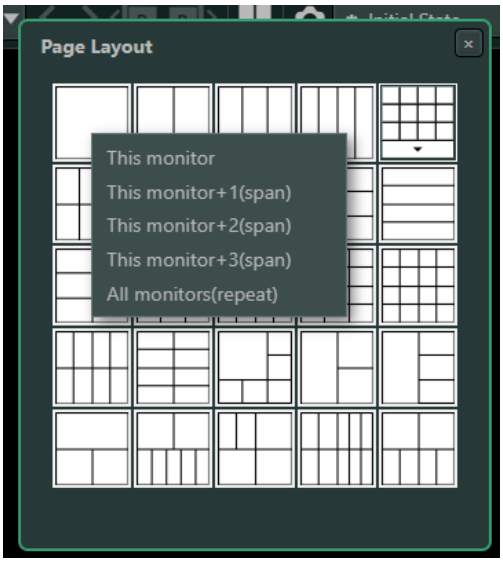
Adjusting your monitor windows & HUD

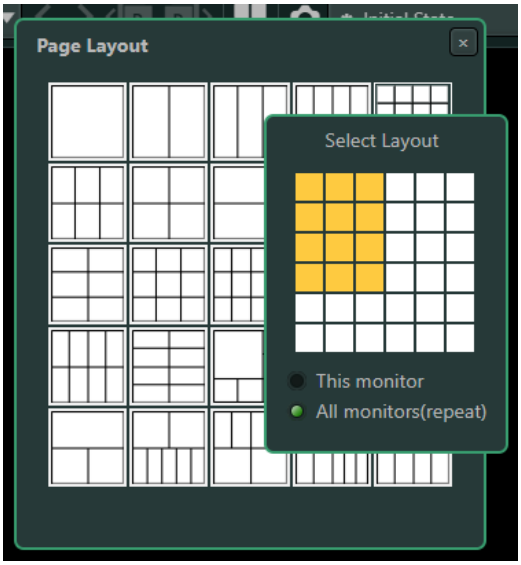


One of the first things to note about the viewer is the bar across the top (be default) which contains thumbnails of all current and prior series that have been opened for comparison. The outlined line at the bottom can be adjusted to increase or decrease the amount of screen space dedicated to this top bar. When looking at studies with lots of image series, it can be helpful to increase the size of the bar, so they will wrap down instead of going offscreen. This top bar can be minimized and moved to other sides of the screen.



Regardless of what hanging protocol you are using, there is a quick way to adjust your page layout along the inner edge of the toolbar. There are many options to select from which can be placed on only the monitor you are currently selecting for, or for all your monitors. There is even a custom option where you can click and drag a box to select the layout you prefer.



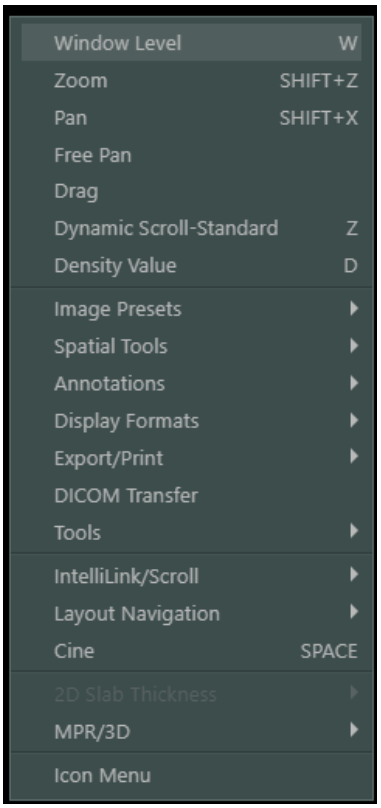


Pro tip: CTRL + scroll when hovering over a window to rapidly cycle through these.

Tools menu

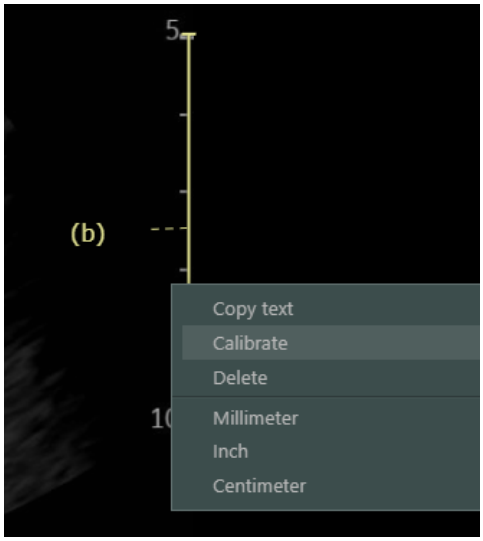


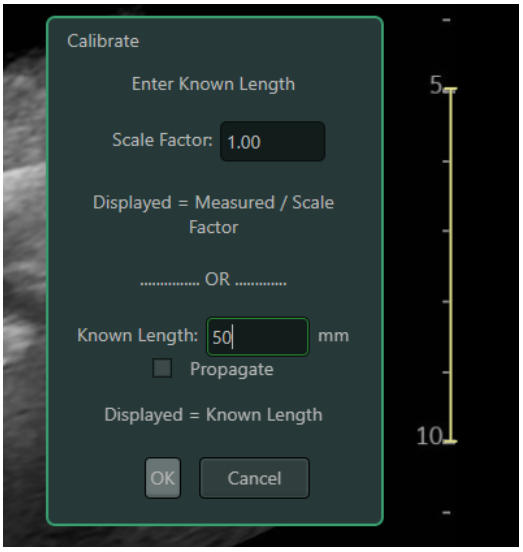
There are MANY tools available for use in FUJI. When you initially log in, the default to access the tool menu by right clicking anywhere on an image in the viewer will open the 'list' version of the tool list. The words and categories may help you find the tools you are looking for as you are learning what tools are available that you like. Once you find the tools you tend to use more regularly, switching to the 'icon' menu will make it much faster to access these tools.



The icon menu gives you a fully customizable matrix of tools that can be launched directly from using your right click and selecting the box containing the desired tool. You can right click the matrix boxes to select the specific tool you want in that box from the list. Once you get used to where the tool is on your customized matrix, getting to the tools this way will be much faster than going through the list categories each time. There are different default icon menus for different modalities as well. So, if you set your menu to have certain tools when reading a radiograph, you can set it to contain different tools when reading a CT or US. Alternatively, you can just customize one of the icon menus provided and use your mouse wheel to scroll through the different modality menus regardless of what study you are reading at the time to your customized menu and then select your tools from there.

Calibrating the ruler

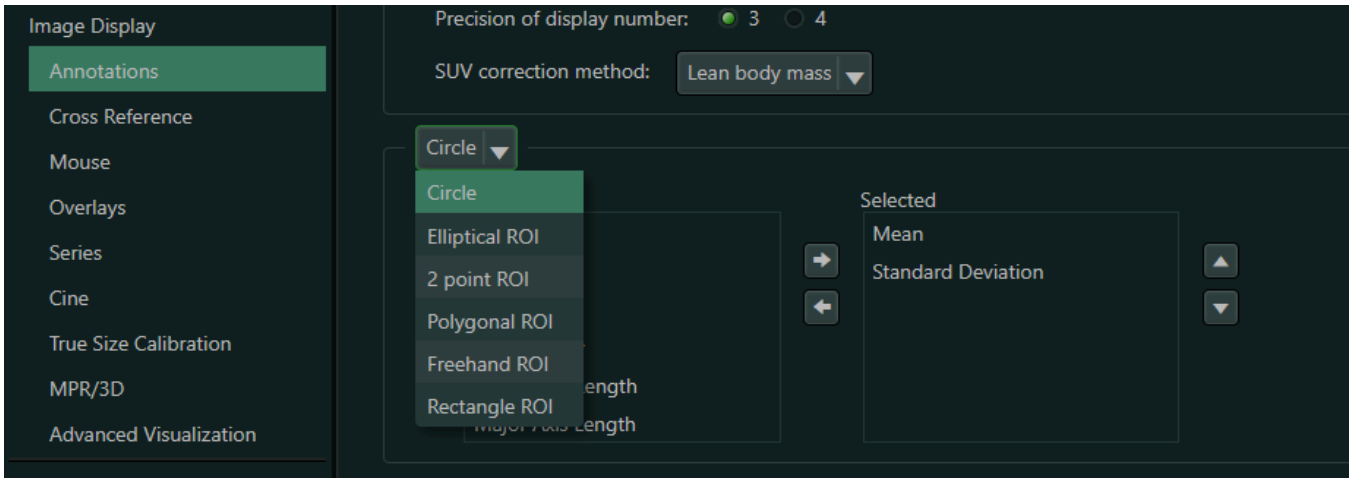




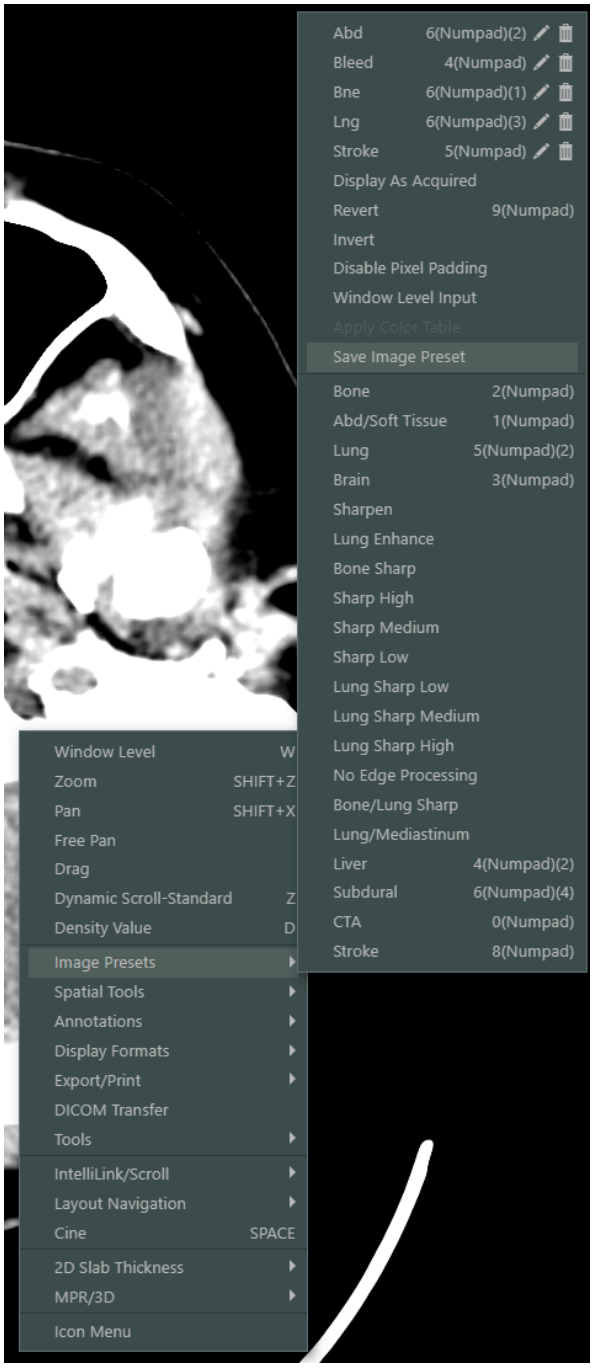
To measure things accurately in some studies (certain fluoro/US), the ruler must be calibrated. To do this, you must first draw your ruler over a known distance (a ruler in the background on fluoro or the side depth measurements on US). Then, right click on the drawn ruler and select 'calibrate'. Once the calibration menu opens, you can enter the length you measured at the bottom (in millimeters) and click okay. This will automatically adjust any other measurements you've made in the same image series as well.

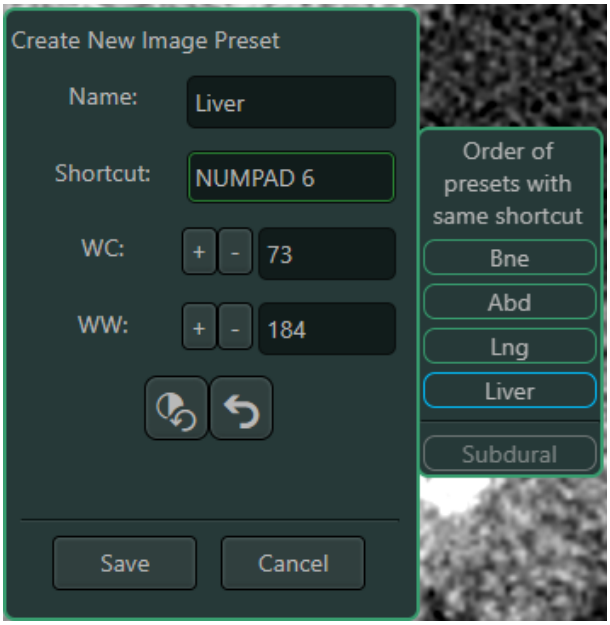
ROI Circle/annotations

The ROI annotation (by default is an ellipse) can be customized to only show desired information under "annotations" in settings. On the same menu, other annotations such as the circle can be edited to show ROI information as well.



Windowing hotkeys





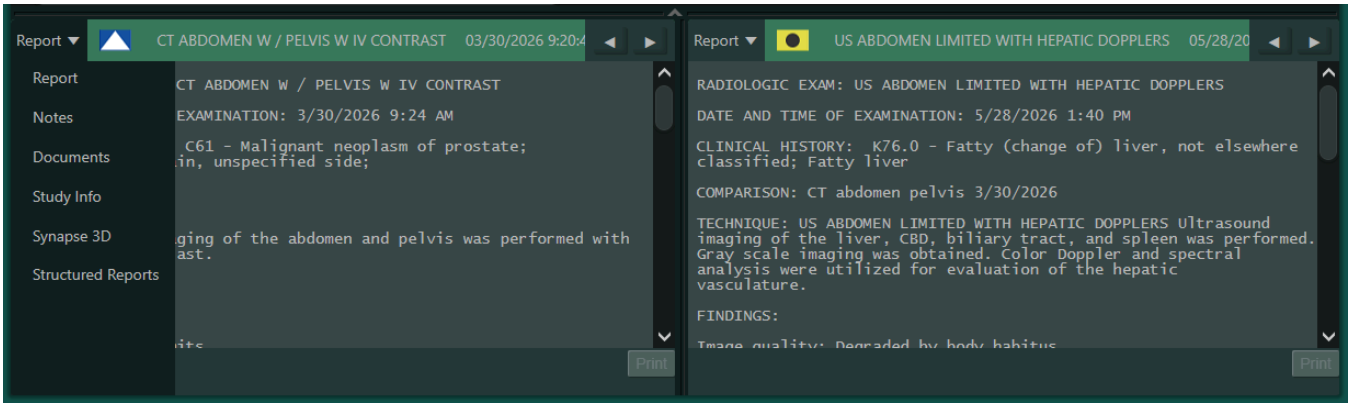
If you enter the right click menu on a window-able image series, under image presets > save image preset you can create a hotkey that will jump to that window/level setting. By manually windowing the image before doing this, the levels will be automatically entered into the ”WC” and ”WW” boxes. By default, the presets in the program are mapped to the numpad keys. If you add a preset to a key that already has presets mapped to it, the additional menu on the right will appear, allowing you to choose the order in which up to 4 different presets will cycle through as you press the same button. I use one button to cycle through my most used presets to save space on my mouse for other macros and not have to touch my keyboard to access presets. Presets make windowing MUCH faster and more convenient in FUJI since the manual windowing is very laggy.

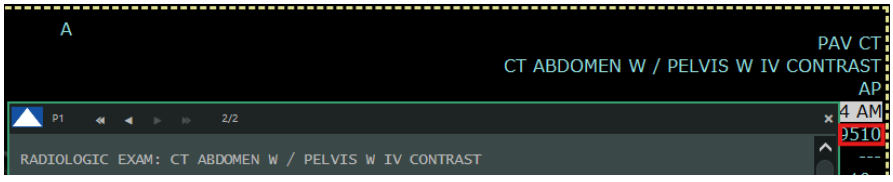
Viewing prior reports

When looking at comparison imaging or assessing a case during a call/walk-in to answer questions, there are multiple different ways to bring up and view reports to be aware of. Each option comes with its own quirks and bugs, and everyone has their own preferred way of doing this, so give these few options a try and see what you prefer.

The first option to discuss is within the 'powerjacket' itself. The powerjacket is the window that FUJI opens which lists all prior and current imaging studies a patient has available. At the bottom of this window, by default there are two panes that appear: one for the current study, and one for the selected prior study. These windows are fully size adjustable, and I often collapse the center bar to one side, so I only see the prior report here. When you are reading a study, the report window for the current study pane will be empty and useless. A way to make the current study pane useful, however, would be to set it to 'notes' which will display any tech notes input during or after the exam was performed. These notes will NOT populate in epic, so make sure you check this area before calling the techs with a question about what happened with a given study.

You can change which study's information is displayed by simply left clicking the study in the power jacket to automatically jump to your selection, or you can use the left/right arrowheads to the right upper corner of the pane to cycle through one at a time. On rare occasions, I have found outside reports in the 'structured reports' section that do not populate in the normal 'report' section, so this might be worth checking if you need to make a comparison with outside images and can't find the report in epic.

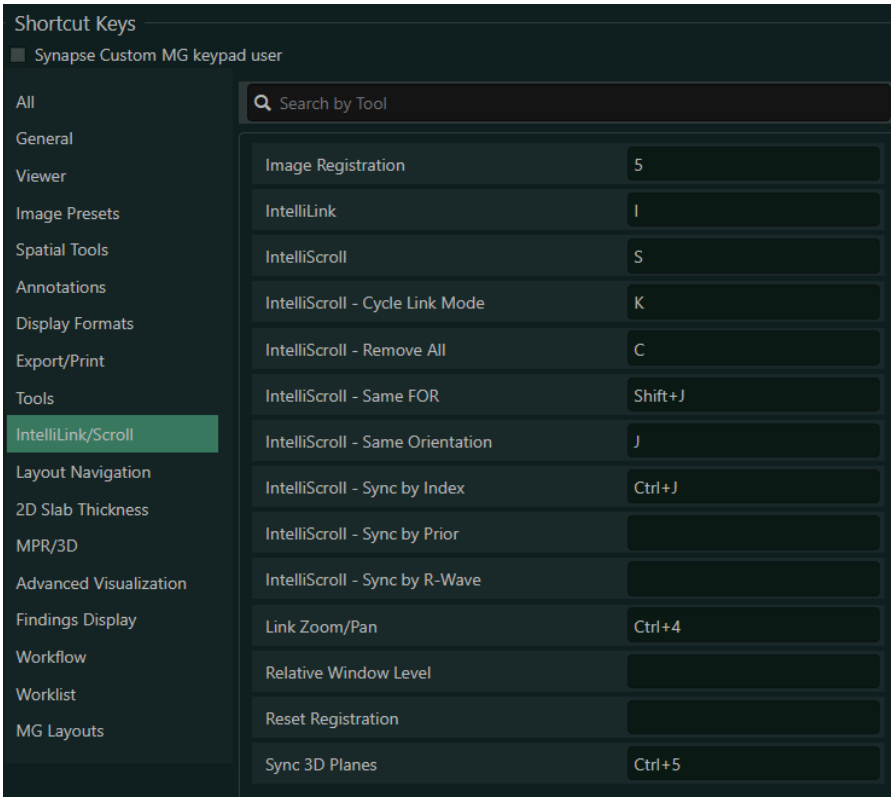




The other method to view reports is to click the MRN typed out in the upper right corner of the viewer window

(outlined in red here and obscured for confidentiality), which will open a window that hovers over your viewer and can be used to display reports of any open current or prior study. WARNING: This window is extremely finnicky and can get stuck to your cursor and be very difficult to resize since there is a 1-2 pixel window you must be on perfectly to select the border of the window to resize it.

Linking studies



Linking studies can be one of the most frustrating-to-understand aspects of using FUJI. There are many poorly labelled options listed under the "intellilink/scroll" shortcut keys in settings. Some sound like they are referring to typical image linking but aren't - at least not in the way you think. There are multiple linking types as well that are not clearly explained in the options. First off: Intellilink has nothing to do with linking studies to scroll together. This hotkey option is an auto-localizer which will jump other reconstructed sequences to the area you click on the selected sequence and place an icon where you are looking. Not 100% accurate but can be useful, for example, if you spot something on an axial and want to see where it is on the sagittal quickly.

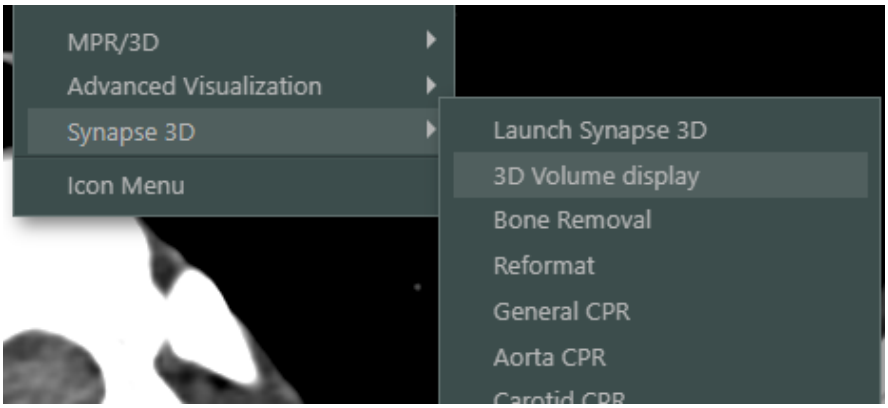
There are three main options to discuss regarding linking, or as it is referred to in FUJI, "Intelliscroll." The first is 'remove all', which very simply unlinks everything. If you are having issues with scrolling on one sequence causing another sequence to jump in an unexpected or undesired way, this hotkey (C by default) will remove all linking to stop it. Next, '**same orientation**' links all studies listed in the same direction (axial/sag/cor) between all open studies ('**same FOR**' will do this for only the selected study). The previously mentioned options will adjust automatically for slice thickness and are the most practical. '**Sync by index**' links studies 1:1 by slice, regardless of orientation or slice thickness –not really a practical implementation for this as far as I can tell.

In a practical sense, the only linking hotkeys I tend to use are 'C' for removing bad links and 'J' for same orientation linking between studies.

Linking your zooming/panning is also possible (using Ctrl+4 by default) and can be disabled using this hotkey if you find it bothersome.

Advanced use

3D reconstruction with Fuji Synapse 3D



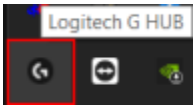
Now that 3D reconstruction has been fully implemented into FUJI, creating 3D reconstructions is surprisingly easy! Disclaimer: 3D reconstructions will look MUCH better if you use thin slices. To create a 3D recon, all you have to do is right click on the window of the desired sequence, navigate into synapse 3D, and select 3D volume display. This will start loading the 3D application within the viewer window (which will take a few moments). Once loaded, you can rotate the 3D model using left mouse button click/drag and the right mouse button click/drag up and down adjusts windowing for the density of components reconstructed.

Custom thickness MIPS

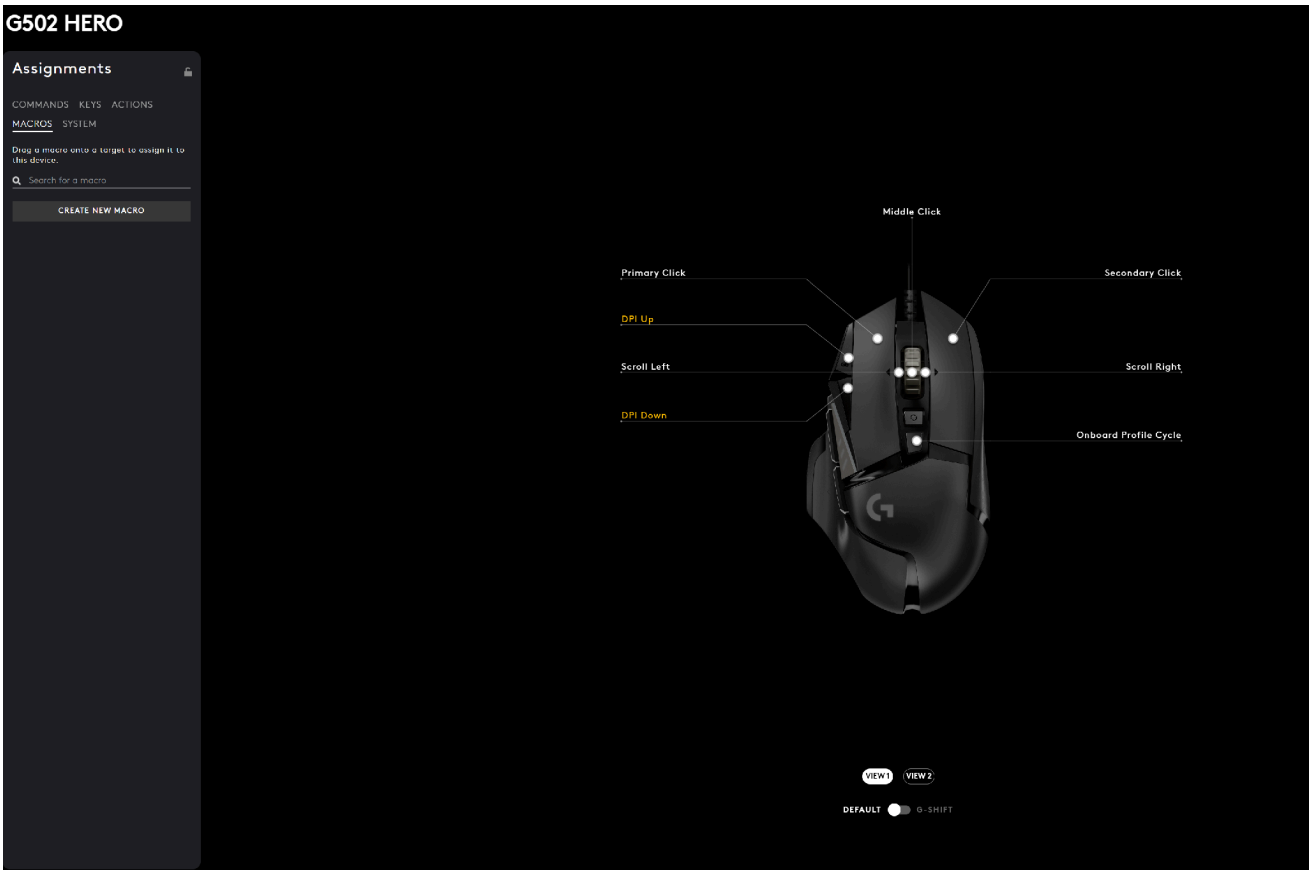
This one's easy: CTRL **+ SHIFT + mouse scroll**. This will allow you to layer slices in a MIP configuration to any level of thickness you like. Scrolling up will increase the thickness and scrolling down will decrease the thickness. Some find this so useful they do not include MIPS on some sequences in their hanging protocols, preferring to set the thickness of their own MIPS. A few ways I like to use this feature are: looking for lung nodules on studies that don't come with MIPS, finding skull fractures, and assessing skull sutures. Do ensure you have BOTH ctrl and shift pressed *before* you start scrolling. Ctrl + scroll will change your hanging protocol windows. Shift + scroll will adjust image zoom incrementally.

There is a more customizable option involving entering reconstruction mode ('3' by default). This mode allows you to create MIPS, MinIPS, AvIPS (average intensity projections) and multiplanar recons of any thickness you choose. One neat application of the AvIPS is that they can be used to essentially reconstruct a radiograph appearance of any CT scan, which can be helpful for learning what things might look like on radiography when you don't have a dedicated radiographic comparison available. However, keep in mind that annotations applied onto reconstructed images while in this mode will not be saved.

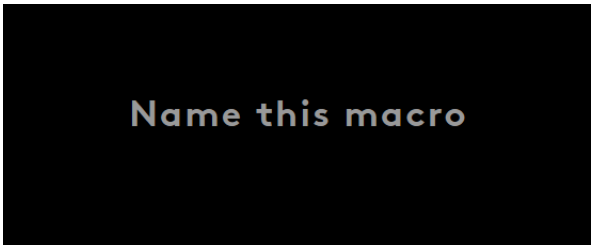
Helpful macros



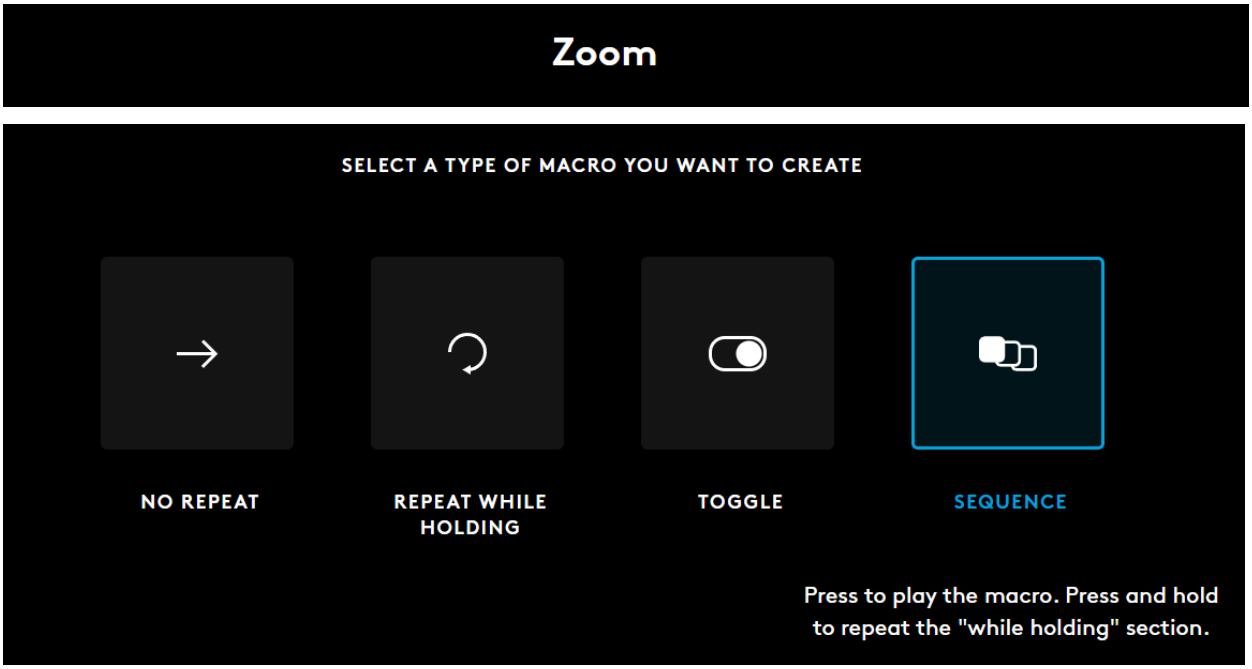
Most of our stations at UMMC are equipped with LG G502 HERO mice which are fully configurable within the LG G Hub software. The icon as demonstrated below may be found under the ‘hidden icons’ or on your desktop homescreen. If the G Hub software is not running, try searching ‘LG’ in the windows search bar. Radiology IT may be contacted to install the G Hub software if it is not available on a particular machine. Within the G Hub, you can select the mouse to enter the editing screens. There are many things you can customize about your mouse function here, but for now we will stick to the ‘macros.’ These will allow you to map complex commands and combinations of hotkeys to a single button on your mouse, which is particularly useful given the plethora of hotkeys and hotkey combinations available in FUJI. I will go into detail about setting up a macro under the first described ’zoom’ macro and simply show you the combinations required to create the later macros unless there is a different method being used. From the initial Macros tab, we will select the ’create new macro’ button to get started.



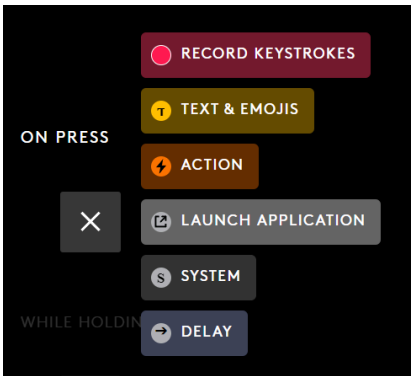
Zooming



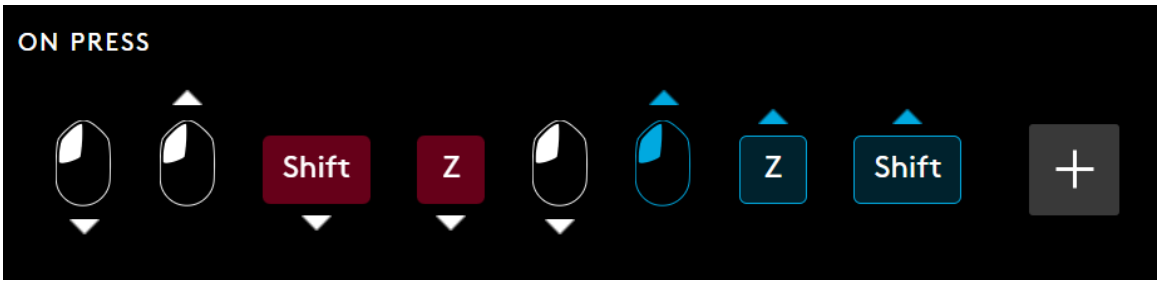
Upon entering the macro editor, you will be asked to name your macro, which for the purposes of this first example will be entitled ‘zoom.’ The purpose of this macro is to allow you to zoom in and out on any image modality by simply holding the mapped button on your mouse while you move the mouse up and down. There is not a way to zoom in FUJI on any type of image series by only using the mouse wheel unfortunately. Although there is a combination to hold which allows the mouse wheel to be used to zoom, it jumps in large increments which cannot be fine-tuned, and I found this simply slows me down more than it helps.

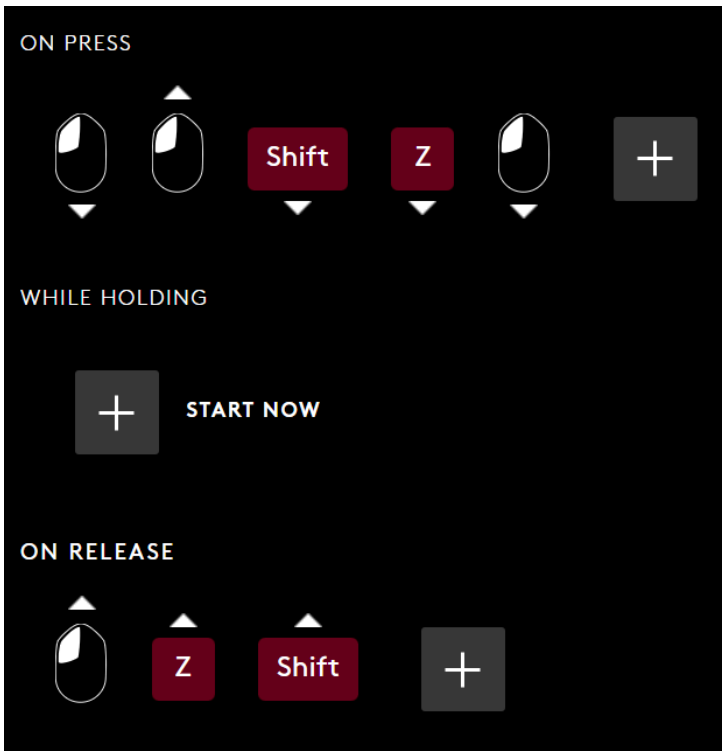


This and most of the other macros I use are created using the ’sequence’ option, which allows multiple steps during button depression, hold, and release. Although most of the macros are not that complex, I find it simpler to just use this type as it gives the most customizability unless you are specifically trying to create a very simple toggle switch or auto clicker. Keep in mind, all of the macros discussed here were created using the DEFAULT hotkey options. If you make any changes to the hotkeys involved in your settings, your macros will need to be adjusted accordingly.



To create these macros, I find it easiest to select 'record keystrokes' then you can simply perform the combination of actions you would like the macro to execute with your keyboard and mouse, and it will automatically create the macro mimicking your inputs. Note in the example below that the software documents depression and release as up and down arrows above and below the respective inputs. For this example, I clicked once, followed by the key combination Shift + Z + L mouse click and released in reverse order – mouse, Z, Shift. I have highlighted the last three release inputs documented here and in the second example you can see they have been deleted – simply select by clicking and delete with the delete key. I then re-performed the Shift + Z + L mouse click with reverse order release under the 'on release' section; this time deleting the press keys and leaving the release keys.

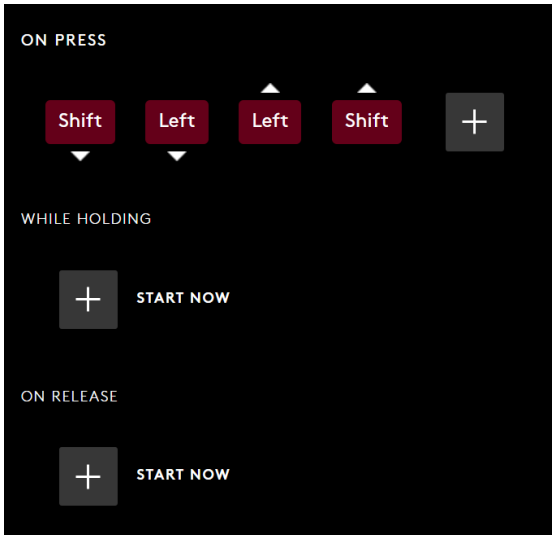




Here is what the final 'zoom' macro looks like once completed. The initial mouse click on press is technically optional. Please note that if you do not move the mouse to zoom when you press this macro, FUJI will detect the two clicks as a double click and either full screen or minimize the image series you are trying to zoom on. The alternative with the click removed will result in a capital 'Z' input into your Powerscribe or other selected window text box if you do not ensure the viewer window is selected as 'in focus' by clicking the screen manually after clicking off to another program – a problem I found much more frustrating personally and why I recommend starting with this setup. Of

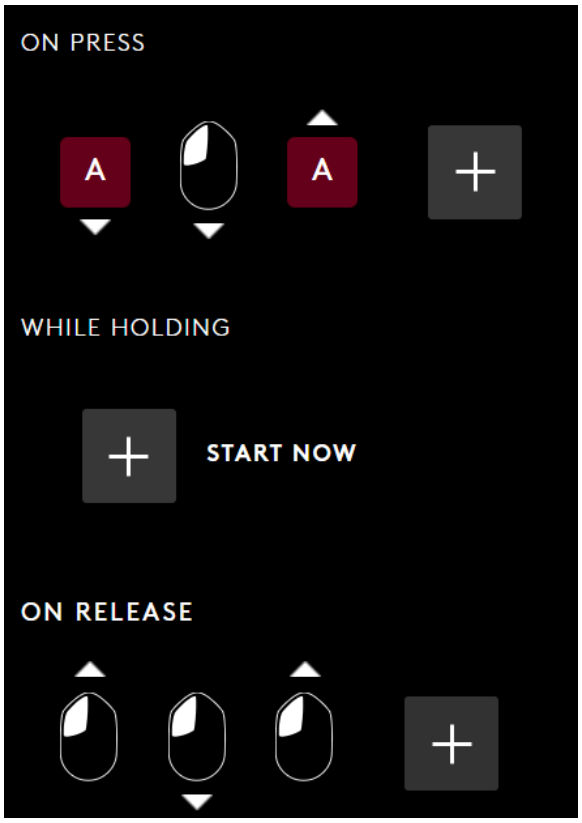
course, feel free to try this with the initial click removed to see if it works more smoothly with your personal technique.

Tab/next series



This macro will allow you to jump the currently selected viewer window to the next available series. I find it most useful reading ultrasound to 'tab' through the different cines, for example. We will again be using the 'sequence' mode and record inputs of Shift + Left arrow for tabbing to the left and in a separately named macro, Shift + Right arrow for tabbing to the right. In both circumstances, the shift button is held while the arrow key is only tapped before releasing shift. I always have these mapped to my 'scroll left' and 'scroll right' mouse buttons respectively since I don't tend to use those default functions for anything.

Arrow

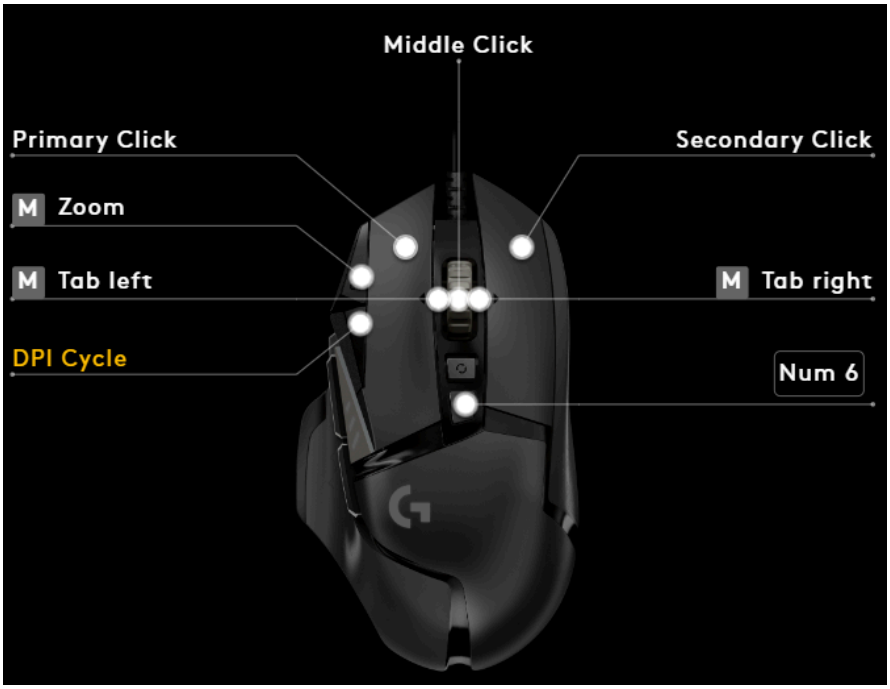


Placing arrows in FUJI can be frustrating due to the automatic text box that pops up upon placing an arrow. I find this macro useful, and it works almost flawlessly to place an arrow by using only the macro button and automatically close the text box. About 20% of the time the text box might not close in which case you will still need to click somewhere else to make it disappear, but this is the best I have managed to figure out so far. To create this macro, I did the 'on press' inputs of pressing A + L mouse, followed by releasing the mouse click and A key. I then deleted the mouse key release. For 'on release,' I simply performed 2x L mouse clicks and deleted the first down press input. This macro will allow you to use the mapped button to place an arrow on the selected window. Keep in mind, this suffers from a similar issue as the zoom macro in that if the FUJI viewer is not 'in focus' by clicking back onto the viewer after performing a task with the

mouse on another open program, it will input an ’a’ into your Powerscribe or other open textbox. Unfortunately, getting around this one with an extra click at the start of the macro is not possible because the arrow placement is done with the mouse in a still position since the arrow begins placement at the arrowhead and the tail is then drug outward – there is no way to reverse this.

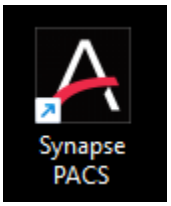
Here is an example layout of what these presented macros look like on my LG mouse. It takes me about two – three minutes to create these when I sit down at a new station that does not have them. If you're wondering why I have a button mapped to 'Num 6,' check out the section discussing windowing hotkeys here.



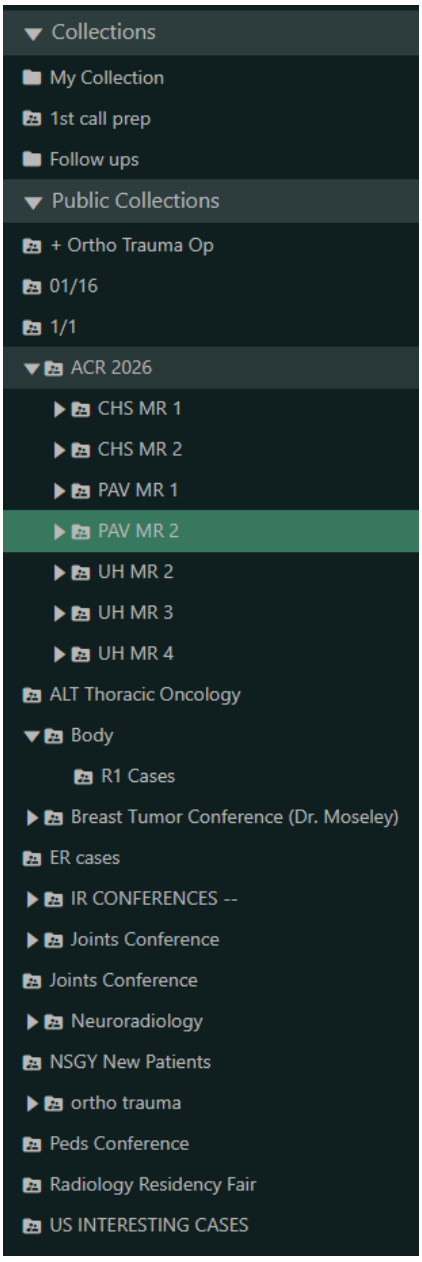


Saving cases

Call prep folder access via Synapse PACS



To get in to the call prep and other saved folders in FUJI, you will first have to launch this application on your desktop. WARNING: The application will NOT open if the FUJI viewer or powerjacket are open. If you have already launched workflow, you can still open the application as long as the rest of FUJI's programs are unopened. Once the application has launched, you will see that it is entitled 'worklist' - while we don't primarily use FUJI's built in worklist, this is also the application used to access the FUJI worklist if WFO isn't working to populate the worklist but studies are still being sent.

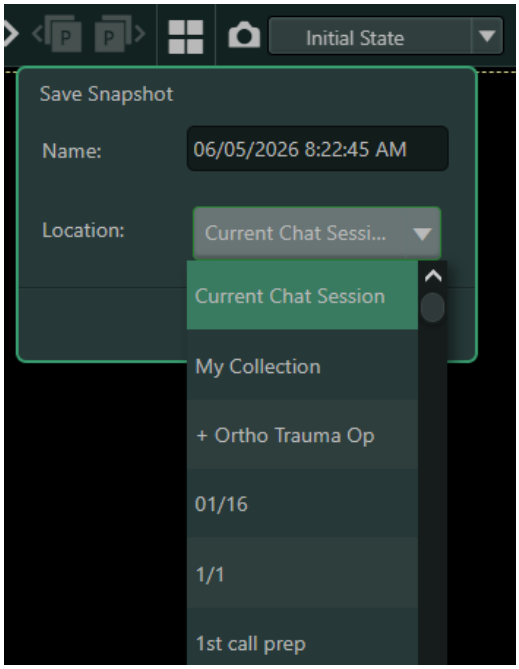


Along the left side are the different 'worklists' and if you scroll down you will see the 'collections' section which will list both your private folders and public folders you have access to under 'public collections.' You can find many useful folders here, such as the breast tumor board folder and any cases you have saved to your personal folders (we'll get to how to do that in a moment). Under Body > R1 Cases you will find a series of

cases designed to prep residents for first call.

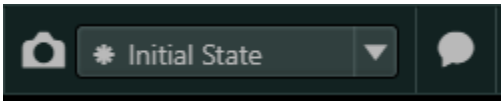


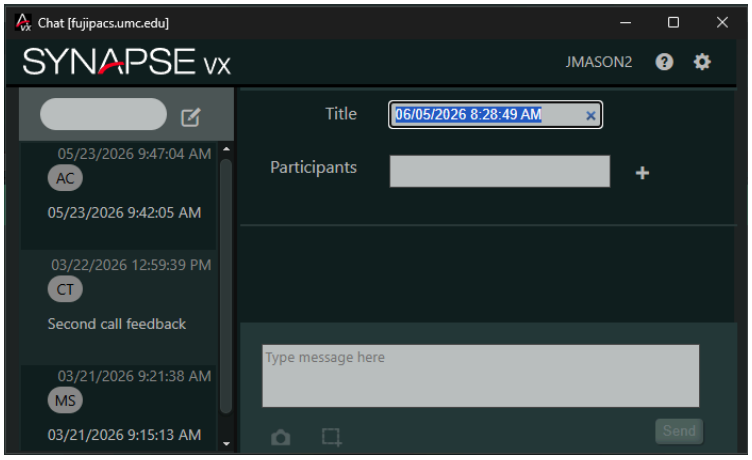
Snapshots/saving personal cases



If you right click the camera icon at the top bar of your active viewer window, this will open a window to ‘save snapshot.’ In this window you can rename the case to be whatever you want (I usually put the interesting finding, so I know why I saved the case) and then using the dropdown menu you can select what folder to save the snapshot to. Important note: whatever your current layout is for the study in your viewer windows, including the number of monitors you are currently using, will be saved EXACTLY as you have it laid out. This is usually convenient since you can make it look however you want when you pull it up initially, but it can cause issues if you are using a reading station with a different number of monitors as windows may get stretched/compressed.

Chats





If you LEFT click the camera button at the top of the client, it will do nothing unless you have an active chat. To open FUJI chat, click the chat bubble to the right of the snapshot button (this chat bubble will also flash a color when you have an unread message). Within the chat client OR within the viewer, you can left click the camera icon to prepare a snapshot to send to the person with whom you are chatting. When the recipient opens the chat snapshot, the images will open in their FUJI viewer EXACTLY how you had it laid out, making it easy to point out specific findings next to several comparisons you have already dug up in multiple different planes. The settings button within the chat window will take you directly to chat settings to adjust your color/audible notification settings.

Troubleshooting

Images not pulling up in viewer

Sometimes, on clicking ‘read’ or ‘view’ from WorkFlow Orchestrator (WFO), the yellow box at the bottom will appear – indicating that WFO has you ‘in’ the image series, but when the FUJI viewer opens, there are no images present in any of the viewer windows, no series present across the top bar with image thumbnails, and no series’ available to pick from in the FUJI powerjacket. If this sounds like your issue, then you’re in the right place. Instead of closing out of WFO and relogging back in to everything, try exiting the FUJI viewer, then exit the yellow box at the bottom of WFO. Once the powerjacket and viewer are closed and WFO is no longer telling you that you are in the exam, try re-opening the exam using the ‘view’ or ‘read’ options. I have never had to repeat this more than once to get the series to start loading. Key point: if there are exams listed in the powerjacket, the viewer may just be taking a while to load, but if the powerjacket is completely empty, this trick should work every time.

Report window stuck to mouse



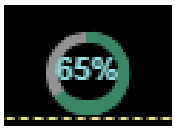
On occasion, if you use the in-viewer option to view prior reports, the window in which the reports appear (imaged above, which is accessed by clicking the in-viewer accession number label) may get ‘stuck’ to the mouse. Meaning, when you release your mouse click to let go of the window after moving it, it will continue to follow your mouse without holding down your mouse click. An exact replicable sequence of events to cause this bug has not been discovered yet, but there is a quick fix to get the report window un-stuck. Once the window is stuck, stop moving the mouse so that it rests over the top banner of the window (center of the section imaged above). Then, simply perform a regular left mouse click followed by a right mouse click, followed by another left mouse click. You should then be able to move the window wherever you want to without it becoming immediately re-stuck as well.

Windowing is not working (shortcut keys or manual)

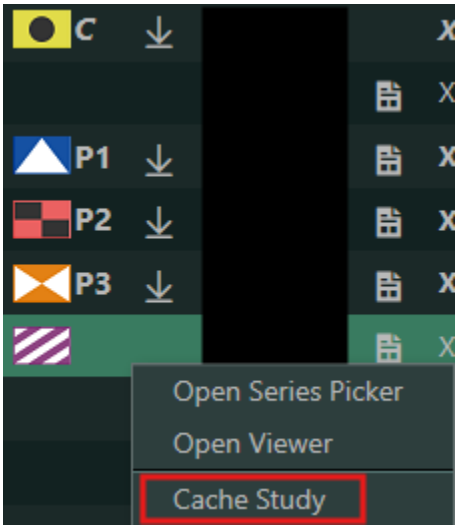
If you are using manual windowing with a mouse click and drag option, you will find that occasionally there are certain viewer windows that will not respond to manual windowing. Additionally, these windows may or may not respond to preset keys. First things first: if you are using preset keys – ensure your Num lock key is set appropriately, I’ve done this more than once and embarrassed myself with the simplicity of the solution, but this can be an easy thing to overlook when setting up at a new station after a while. If this is set appropriately but presets and/or manual windowing is not working, then try ‘rehanging’ that window by dragging

the thumbnail to that window. Once rehung, it should respond to windowing hotkeys and manual windowing gestures appropriately.

FUJI is frozen/loading slow



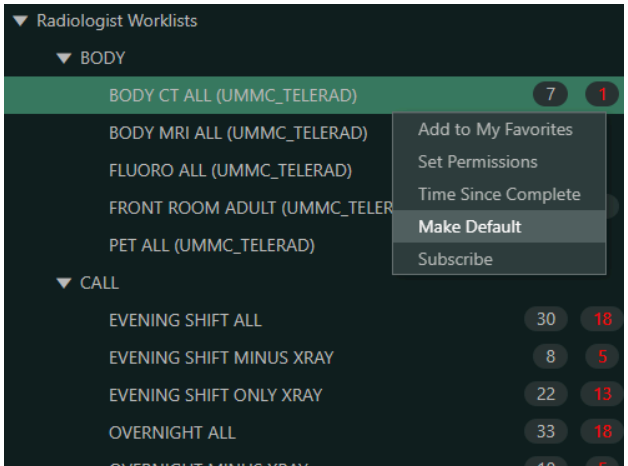
This may be the most common and obtrusive issue encountered while using FUJI. The primary question when FUJI quits responding is whether the program has crashed or is it stuck loading? Look for the green circular loading symbol on the bottom of each of your viewing windows to see. It will vanish from windows containing an image series that has completely loaded, so you must look at ALL the windows in your hanging protocol to ensure everything has loaded properly. It may often sit stuck at 0% or even 100% without responding to inputs; and while loading, it is not uncommon for the viewer to become entirely unresponsive.



A couple of things to keep in mind here: While a scrollable series is loading such as a CT, you may be able to scroll slowly, but when you reach the edge of what has loaded, the viewer will freeze until more of the study has loaded and the green circle continues to fill, which it will...eventually. When loading a prior study older than 2020, loading will take SIGNIFICANTLY LONGER (usually; and unfortunately, this is a server issue we don't have much control over - server upgrades may fix this in the future). In the power jacket, when loading a study prior to 2020, I have made it a habit to right click and cache the study. While downloading onto your local system memory, the green circle will appear in your powerjacket under the 'caching status' column if you have this added, and the downward arrow will replace it once loaded. At this point, you can add it to your comparison without any fear of freezing or waiting for more loading.

If FUJI is frozen and you do not have a loading circle anywhere, it may in fact be crashing. The first thing to try would be exiting the viewer only and reopening the study from workflow orchestrator – this may result in windows telling you the program is not responding when you try to close it, in which case you have your answer and exiting/restarting the program should resolve it.

There is a way to help reduce loading times in FUJI, and this involves subscribing to a worklist in the synapse worklist so that it will cache studies on the subscribed list in the background while you are reading. This works



best for large size studies (CT/MR) since there is a low limit on the number of studies that can be cached at once, so subscribing to a list with lots of plain films on it may not help as much. To subscribe to a synapse worklist, you will need to open the synapse client from the desktop labelled “Synapse PACS.” This worklist will not open if you have the viewer open, but you don’t have to log out of everything. Just close the viewer window if you are already logged into the workflow – it will automatically reopen when you start reading studies again. Once the FUJI worklist opens, you will find a sidebar titled ‘radiologist worklists’ where you can right click and select ‘subscribe’ on a specific worklist to begin the caching process. Unfortunately, this must be redone each time you log in to a workstation and will not be saved even if you come back to the same station after logging out. If applicable, the worklists which have ‘minus xray’ should be used to limit the number of cached studies taken by radiographs which do not typically take long to load.

Epic has vanished and only flashes for a moment when selected

It is uncertain what exactly causes this bug to occur, but when it does, there is a consistent fix! As mentioned in the heading, this fix is for if you are selecting Epic from your task bar, and it only flashes on your screen or part of your screen for a moment and then vanishes as though it were immediately minimized. When you press alt+tab to try and select Epic, it will do the same. This bug has something to do with the auto-windowing feature in windows where when you drag a window to the top of the screen (i.e. a browser window), windows will give you options to auto-snap the window to different parts of your screen, as seen in the provided figure below.



In this example, when the bug occurs, Epic will show up on one of these selections (red box). If you drag a window anywhere into the section containing Epic as a selection (in this example I dragged a browser window into the yellow box), Epic will reappear. This will likely mess with your viewer setup, but after you can see Epic again, you can reframe your windows manually including Epic, your browser, and your viewer to resolve this issue without having to log out of and back into everything. A quick way to reframe your viewer is to drag the portion of the viewer window containing the minimize, maximize, and close buttons in the upper-right corner into the far-left diagnostic monitor. Once it is there, simply press the windows key + left arrow at the same time while the window is selected, and the viewer will align to the left of the

monitor automatically. From here, simply drag the right border of the viewer window all the way across your diagnostic monitors to the right.

Rotation Specific tips & tricks

Mammo Tumor Board

I am sure we all know how to save cases in FUJI. Nevertheless, here is a quick guide on how to set up cases for tumor board.

Residents participate each week in mammo tumor board conference. Depending on the schedule, there can be 5 to 10 cases divided between the residents. The mammo attendings take time to go through each case with us. This gives them a chance to test our mammo knowledge and prepare us for oral boards while going over specifics for each case.

Just an FYI our mammo rotation is at the Pavillion, BUT tumor board meets each Thursday @4pm in-person at the Jackson Medical Mall conference center (the northeast point of the mall). Give it a Google...google maps.

Below is an example list you will receive approximately 2 days before tumor board meets. Personal notes for certain cases are highlighted, but this is shown to help you familiarize yourself with pertinent information while reading through a patients chart:

Name	MRN	Diagnosis	MD	Path	Resident
JJ	1******	New	Wings	Requested	LL
BB	123****	New	Chrissy	S26-0****	KK
PP	037****	New	Chrissy	S25-0****	LL
TT	115****	New	Chrissy	S25-1****	KK
PE	36*****	New	Plankton	S25-099**	OO
Story: Multicentric left breast IDC seen on screener 12/2050, Dx mammo 8/10/2080, transferring care out from Dr. Plankton this morning to be in Olympus. Studies: 12/17/1957 Screening mammo with 2 left breast masses 4/10/2050 Dx mammo w similar findings. 4/23/2025 biopsy On our consult we recommended formal Axillary US.					
LI	256****	New	Chrissy	S25-*****	OO
Story: 72-year-old otherwise healthy female presents after an abnormal finding on a yearly screening mammography. She underwent diagnostic mammography on March 5, 2070 which demonstrated a 7 mm mass in the right breast located 2:00 position 7 cm from the nipple. She underwent ultrasound which demonstrated an enlarged lymph node with a thickened cortex of the right axilla as well. She underwent biopsy of the mass as well as a lymph node. The mass was invasive ductal carcinoma grade 2 ER positive at 90% PR positive at 60% HER2 negative by fish and the lymph node was negative. We discussed the patient's options. We will plan on a Mag seed localized right breast lumpectomy with sentinel lymph node biopsy. We discussed the utility of sentinel lymph node biopsy given her age. She did consent to this. She will discuss the possibility of adjuvant radiation with Radiation Oncology and will also discuss her adjuvant treatment with Medical Oncology. -s/p partial mastectomy/lumpectomy and SLNB, path pending					

Studies:
Screening mammo 2/12/25 – 7mm Mass 10cmFN at 2 o clock position in lower inner quadrant.
Diagnostic mammo 3/5/50 – persists on spot views, US with 0.7cm hypoechoic mass and 2.8cm axillary node.
US biopsy and post-bx mammo 3/18/47 with similar findings.
We recommended excision also of axillary node given increased size throughout interim.

TD	400****	Re-present	Plankton	S25-07***	LL
TO	11****3	Post-op	Chrissy	S25-08***	KK
CC	445****	Post-op	Chrissy	S25-0****	OO

Story: 60-year-old male with a fungating invasive ductal carcinoma of the left breast who had been on treatment with systemic therapy for over 1 year. The patient had a decent clinical response and did not have any metastatic disease on imaging. He was in mobile and we had delayed his surgical resection to see if he would be responsive to his therapy although he was not responsive to therapy he was still not ambulating. We will discuss him at multidisciplinary tumor board and believed it was his best interest to proceed with surgery. Patient consented to a radical resection of the fungating chest wall mass as well as a sentinel lymph node biopsy and consented the procedure after voicing clear understanding of the indications, risks, and benefits of the operation. Of note, the patient was found to be covered in bedbugs when he arrived to the preoperative holding area as well as having a taco bell sauce packet stuck to his back and a TV remote within his shirt which he was unaware of.
-s/p mastectomy and SLNB w IDC, no mets on SLNB.

Studies:
Dx mammo and US 11/12/2699 – 3.4cm SA left breast mass extending to the skin.
Left breast US 9/17/2034 – 5.3cm now
Left breast 3/4/2054 – Now 3.6cm

SS	12****1	Post-op	Chrissy	S25-07***	LL
LB	36*****	Post-op	Oreo	S25-0****	KK
FG	048****	Post-op	Chrissy	5/16 - OSH	OO

Story:
-right breast lump feb 2024. Mammo and bx w TN IDC axillary adenopathy but no distant mets. Bone scan w possible sternum uptake.

s/p neoadjuvant chemo 2070.
s/p bilateral mastectomies w targeted right sentinel lymph node bx which was negative. Final path with right breast DCIS, no residual IDC.

Studies:
Dx mammo 6/07/34 w 2.0 cm 11 o clock SA right breast mass, multiple additional masses measuring up to 2.4 cm. Extensive right axillary adenopathy up to 2.8cm. US at that time with 2.7cm SA right breast mass. Probably papilloma left breast
7/5/24 Bone scintigraphy w possible sternum lesion, ill-defined sclerosis on CT likely degenerative or post-traumatic
Breast MRI 7/11/77 – similar findings of 2.3cm mass in 11o clock SA right breast, additional masses measuring up to 1.7cm, axillary adenopathy.

Post-chemo dx mammo 3/6/59 w decreased size of right breast masses and decreased right axillary adenopathy.

As stated above, these case notes are just for personal depth of understanding. It is way more than what needs to be said during tumor board. Most times the primary team (oncology or surg onc) gives an overview when introducing each case. Our responsibility is the imaging which factors into staging.

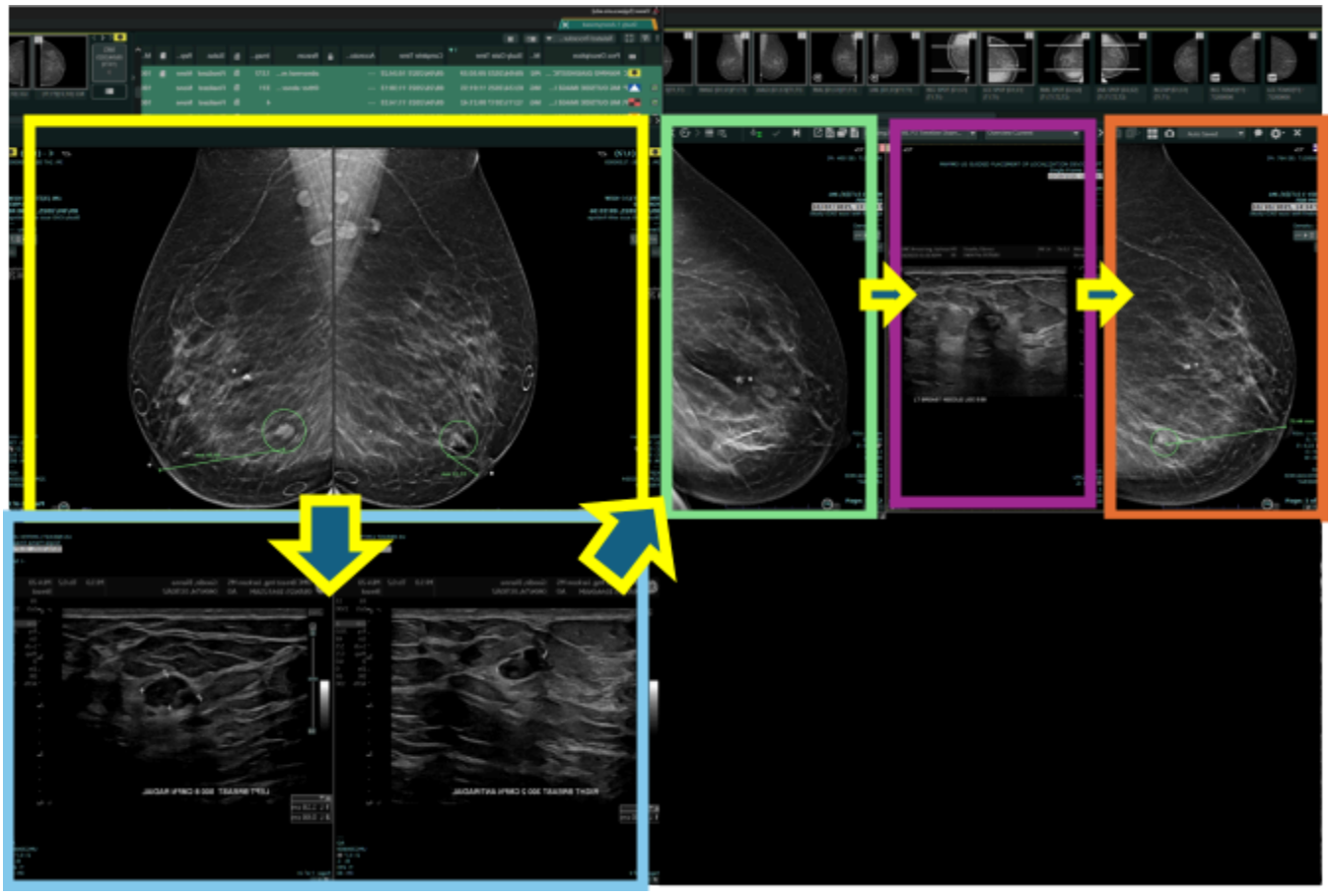
Each week there is a mix of new and repeat cases. All new cases should be prepared to present.

Repeat cases (post-surgical excision, post-neoadjuvant MRI, post PET/CT, etc.) can either be presented or passed for the week, BUT this is on a case-by-case basis (check with attending). Sometimes the primary teams talk through a few points with radiation oncology, genetics, or pathology; other times it involves everyone including us. Be sure to check for new imaging, because this can usually narrow down what you will talk about somewhat.

Most new cases present as an “area of palpable concern” or a “callback from screening”. You can generally begin your case discussing the mammography findings (simple descriptions like calcifications/mass/distortion, clockface position, and distance from the nipple), move onto the ultrasound findings when there is a correlate mass, then finish by showing the biopsy (U/S guided or stereotactic biopsy) and post biopsy marker placement. For most cases this is how the cookie crumbles. In other more complex cases, there may be an MRI and/or PET-CT to understand the extent of disease.

Here is how to format and save cases for tumor board (there are likely a few different ways of going about it – this is mine):

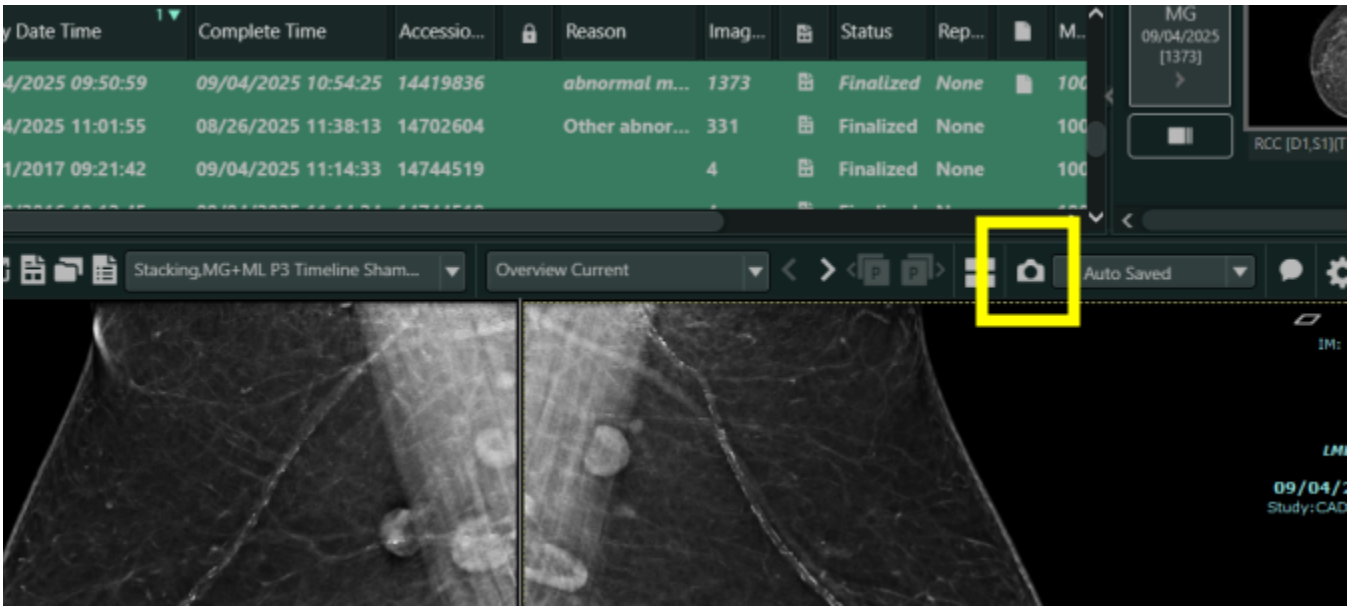
Screen 1 Screen 2



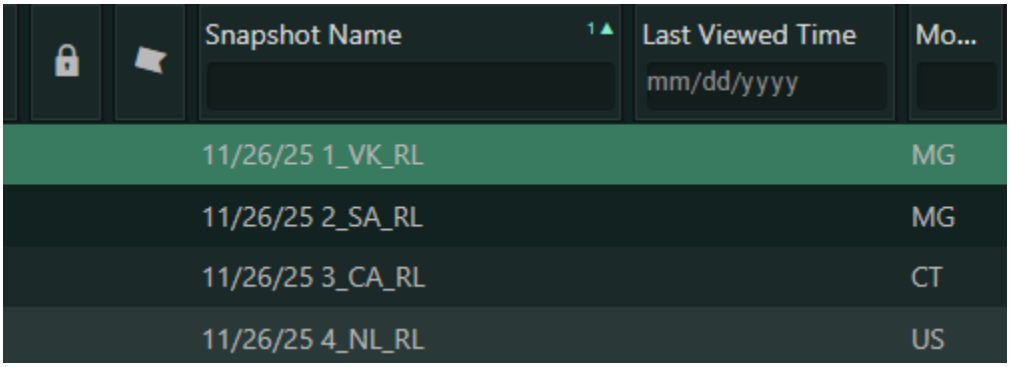
Most of the time we organize the case in chronological order. Start with the diagnostic mammo (yellow) then the ultrasound correlate mass (blue). You can add a mediolateral mammogram (green) to redemonstrate the mass in a different projection. Finally, end with the ultrasound guided biopsy (violet) and post biopsy mammo (orange) displaying clip location. Be sure to check for more advanced imaging modalities like MRI and PET-CT (if they are negative, you may not end up including them).

I would recommend saving case layouts while using mammo specific monitors; they are technically two screens in one monitor, side by side. You may be able to work around this while at home on a single screen laptop/desktop, but I think you must set monitor sensing to 2 in FUJI settings (not 4 or auto). You'll have to check me on that, but make sure the layout is correct before going to tumor board. A good time to check is right before going over cases with our attendings

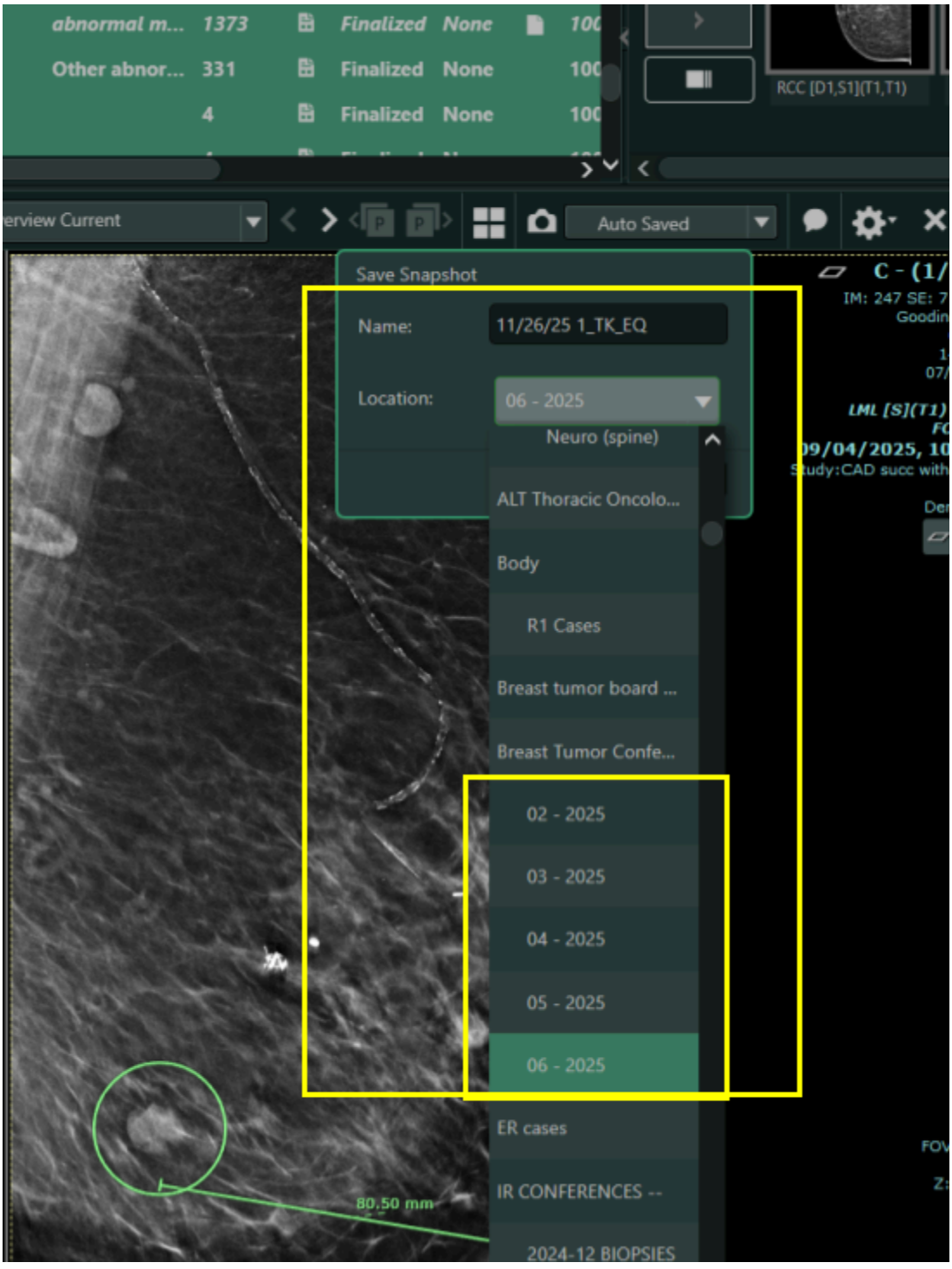
Once you have the case set up like you want...MAKE SURE to save it in the correct folder. Right-click on the camera icon and save it under the Breast Tumor Board conference subfolder:



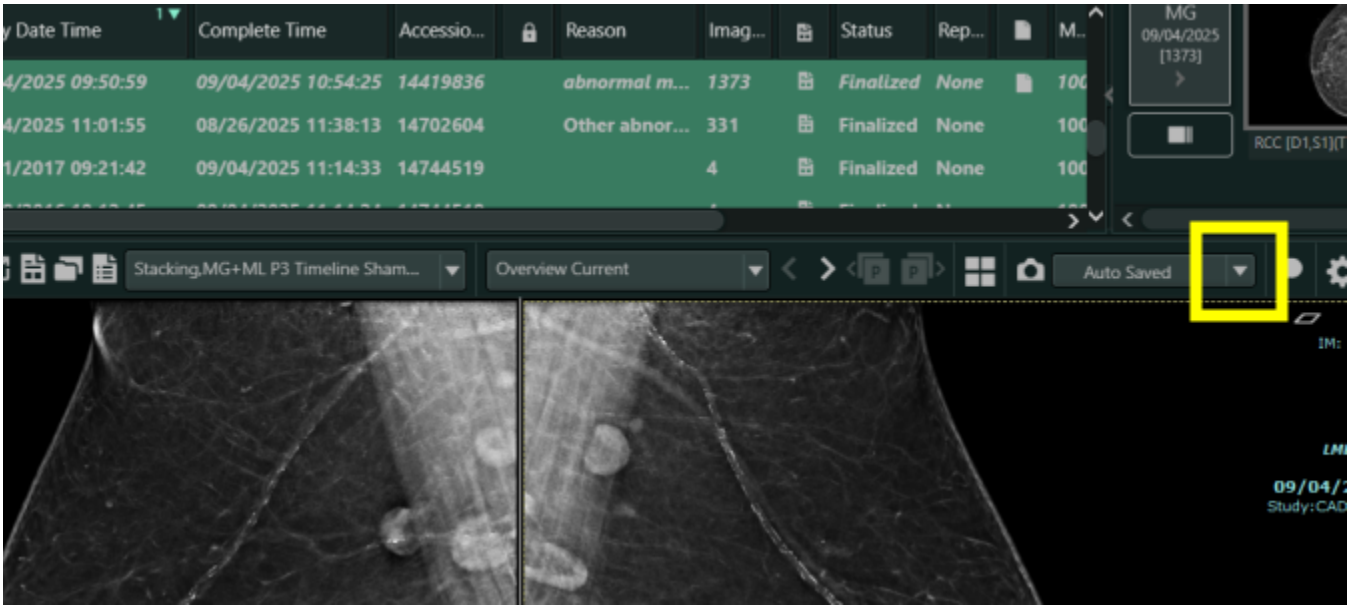
Use the following layout (date of upcoming tumor board (space) case number / patient initials / your initials) when typing in the snapshot name, so that it is easily searchable:



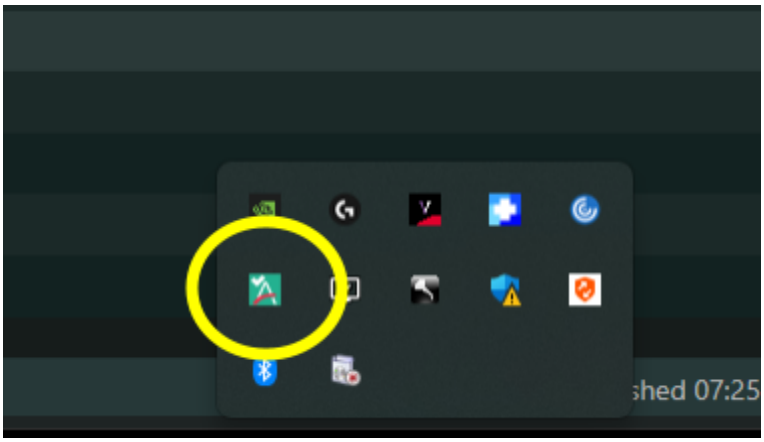
Once you right click on the camera icon, the following box will appear. Fill in the name with the correct format and search for the breast tumor board subfolders (there are millions to search through):


abnormal m... 1373 Finalized None
Other abnor... 331 Finalized None
4 Finalized None
RCC [D1,S1](T1,T1)
Auto Saved
Save Snapshot
Name:
11/26/25 1_TK_EQ
Location:
06 - 2025
Neuro (spine)
ALT Thoracic Oncolo...
Body
R1 Cases
Breast tumor board ...
Breast Tumor Confe...
02 - 2025
03 - 2025
04 - 2025
05 - 2025
06 - 2025
ER cases
IR CONFERENCES --
2024-12 BIOPSIES
80,50 mm

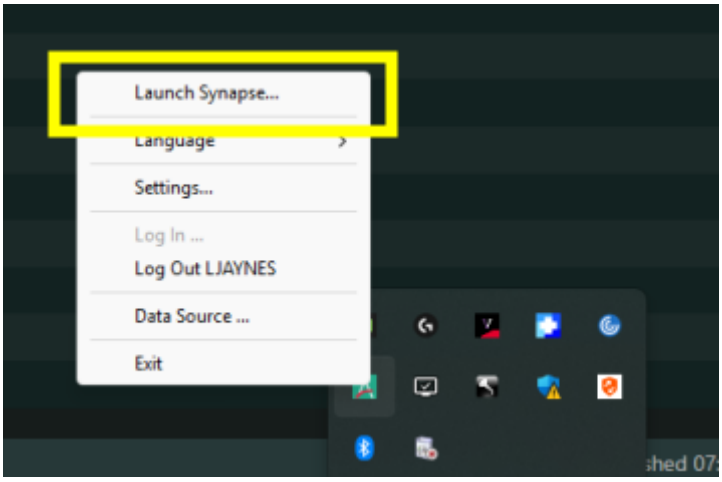
If you need to make edits to the layout, you can click this drop-down arrow and delete the layout. Then, right click the camera icon again and save it under the specific snapshot name once more.



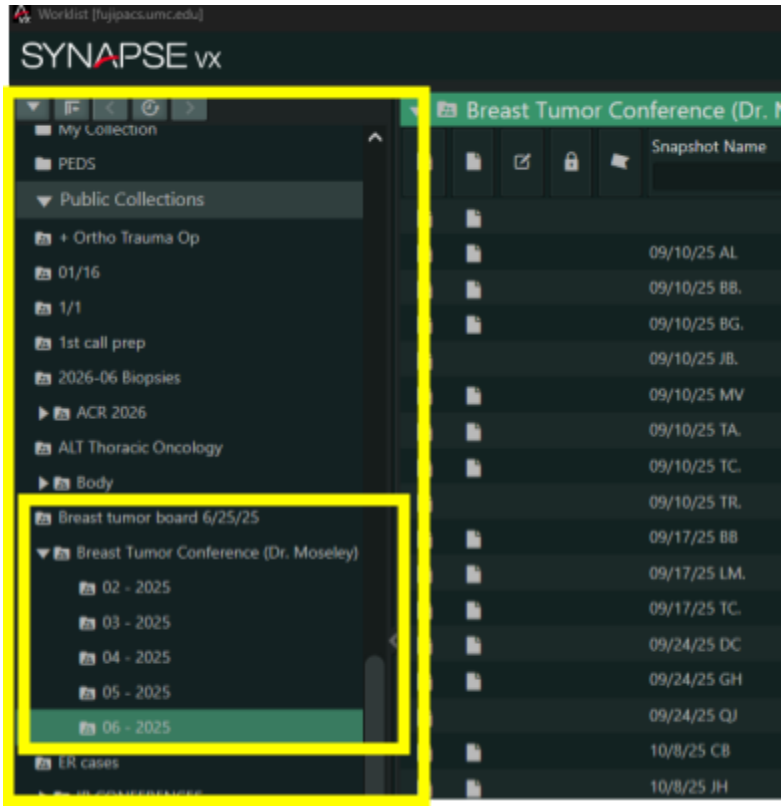
Here is how you navigate to saved cases for tumor board. First, you need to open synapse (most of us likely know, but just in case). At the bottom right of the screen you will need to right click on the icon circled in yellow (it is the A icon with a red strike through; it can be green or black).



Next, you will need to select “launch synapse” from the menu.



Once you have the synapse window pulled up, navigate to the left column. Finally, click on whichever subfolder under “Breast Tumor Conference” everyone agreed to save to for the week/month.



FYI - At tumor board there will be an added step at the onset. After you get help turning the laptop on, you will click on the synapse desktop link. It will then prompt you to log in. At that point the synapse viewer will appear but in a web browser window. You can then quickly navigate to your group's specific "Breast Tumor Conference" subfolder.