

McKesson Information Solutions



Horizon Medical
Imaging

Radiologist
Workbook



MCKESSON
Empowering Healthcare

Horizon Rad Station 11.0 (Basic Features)

As a Radiologist, do you know how to...

- Log in with your username and password
- Identify the study indicators in the In-Box and Folder Finder
(Priority, Patient Documents, Study Status, Other Studies)
- Set column display preferences in various study lists (In-Box, Folder Finder, etc.)
- Find and open studies from In-Box and Folder Finder
(Folder Finder has more search parameters for finding exams.)
- Create, organize, modify, and delete Filters
- Set user preferences (Toolbar, Image Menu, etc.)
(Users can organize advanced features on the right click menu. Make sure that the In-Box, Folder Finder, Other Apps, Close All Studies, Voice Clips, Document Scanning, Jot Pad and Rad Report icons are on the Toolbar.)
- Access Patient Documents such as reports, scanned documents
- Change the display layout of a series on the screen
- Adjust window/level and manage window/level presets
- Zoom and pan images
- Use the Annotate tools
- Open a reference study
- Flag/unflag images
- Close a study as dictated
- Access the online help

Horizon Rad Station 11.0 (Advanced Features)

As a Radiologist, do you know how to...

- Create a new stage for a display protocol
- Create a display protocol for a particular study
- Edit a display protocol for a particular study
- Apply a non-listed display protocol for a particular study
- Modify or delete display protocols
- Create alternate display protocols for a given study
- Set Hotkeys.
- Save and apply stored image presentation
- Set user preferences

(User preferences allow users to customize the operation of HMI to their needs. Configuration of keyboard shortcuts for window/level presets, auto-display of reports, and toolbar preferences.)

- Demonstrate the highlight point (double-click in CT and MR studies)
- Adjust the link alignment between different studies
- Reset link alignment
- Unlink series
- Show/hide cross reference lines
- Manage Teaching Files
- Use the magnifying glass tool on an image (optional)

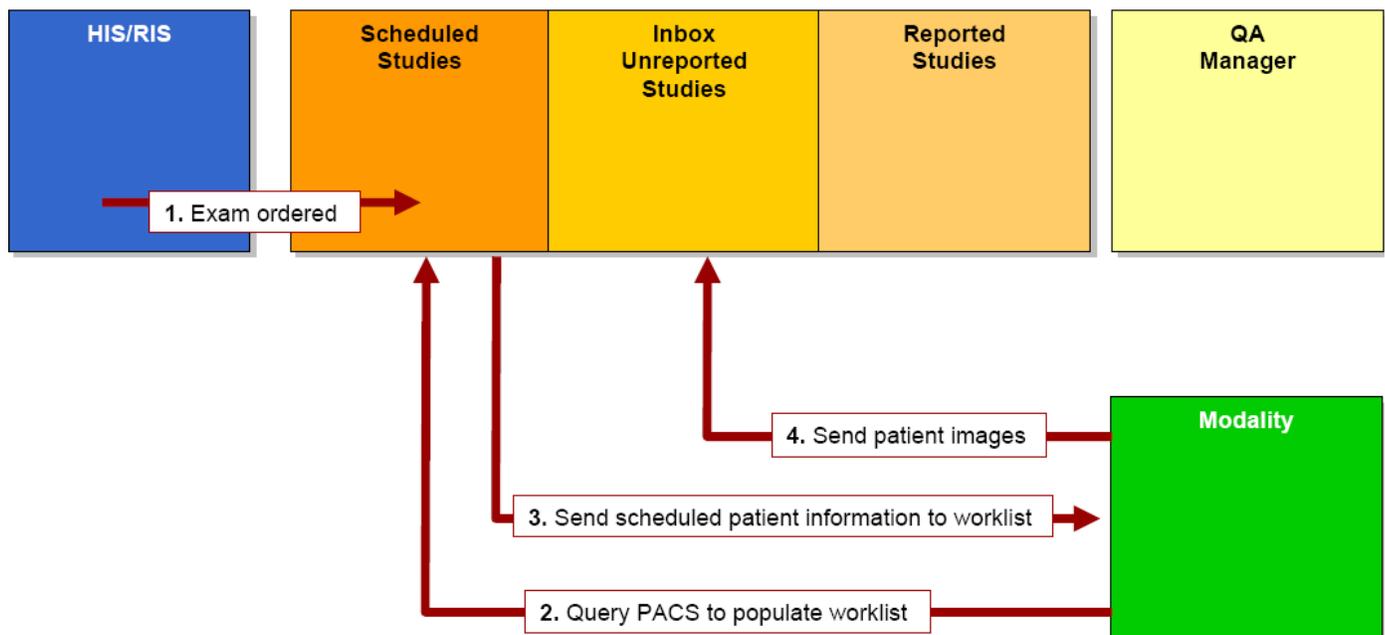
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Chapter 1 – HMI Data Flow

RIS/HIS to HMI Communication

When a radiology order is placed in the RIS/HIS, the HIR/RIS will communicate this information to HMI (PACS). This information is displayed on the Scheduled Studies List within HMI. When the modality worklist is refreshed, the modality will query HMI and receive the order from HMI. The technologist chooses the order off the worklist and starts the exam and scans the patient. Once the exam is completed, the technologist sends the images to HMI and the exam will appear in the performed studies list (inbox).



Chapter 2 – Understanding Horizon Rad Station

Logging on to HMI

1. Click CTRL + ALT + DELETE
2. Enter your User Name and Password
3. Click ENTER.



Understanding the Different Study Lists in HMI.

1. Unreported (inbox)
2. Folder Finder
3. Other lists
 - a. Schedule Studies
 - b. Recently Performed
 - c. Dictated
 - d. Recently Reported

Full Name	Patient ID	Accession	Performed on	Procedure Type	M	L	Performed By	Assigned To
Brown, Warren	85324	AC2441	14-Sep-2004 21:38	XG SPST FOR MRI CLEARA	CR	1		Main H.
Brown, Warren	85334	AC2694	07-Oct-2004 22:38	MR ANGIO NECK W/O CONT.	MR	208	Lee, Nancy	Main H.
Demko, Twp	19711225	00021958	22-Feb-2005 05:09	CR	3			
Demko, Twp	19711225	00001886	19-Mar-2005 14:21	CT PELVIS WITH CONTRAST	CT	43		
Demko, Twp	19711225	00094432	19-Jan-2005 09:20	Knee	MR	213		
Dicks, Henrietta	95141	00015781	02-Aug-2003 09:51	US	11			
Dida, William	444707	00020272	04-Oct-2003 09:17	Chest 2 Views	CR	2	Appley, Steph.	
Dida, William	444707	00020198	14-Sep-2003 14:01	Chest 2 Views	CR	2		Main H.
Dida, William	444707	03A-04L	05-Apr-2003 14:29	DX CHEST PA-LAT	SS	CR	2	
Doid, Sean	588081	00001663	04-Nov-2004 07:55	MA23	NM	8		
Elder, Jane	684601	00001728	23-Apr-2004 15:42	Osteologyprossy	ES	4		
FD-Brain-MRPT1	A1+1	6	02-Nov-2005 16:30	PT	14			
Fischer, PatientThree	F103	00001795	02-Feb-2004 10:29	MG	3			
Fischer, PatientTwo	F102	00001794	02-Feb-2004 10:28	MG	4			
Fisher, Michelle	232071	00015651	03-Aug-2003 17:45	BRAN	US	325		
Fisher, Michelle	232071	00015650	03-Aug-2003 17:38	Brain w w/o	MR	167		
Fitzpatrick, Michael	430738	00001791	10-Feb-2004 20:29	CT Head w/o	CT	62	Maib, Andrea	
Fusion, Heez	684860	00001500	14-Jan-2004 11:30	CT Scan Whole Body	CT	378		
Fusion, Heez	684860	00001500	14-Jan-2004 11:30	PET Scan Whole Body	PT	1256		
Harrison, Natasha	254488	00007612	17-Oct-2003 16:30	Chest 2 Views	OT	2		
Hoffman, Adam	1684792	00016265	26-Jul-2003 09:34	LUMBAR	CT	455		
Johnson, Mandy	160449C	00049139	19-Oct-2003 22:53	Ankle Complete	OT	1		
Lee, Andy	458901	0004723	01-Jun-2006 07:18	Arm Angio	XA	5		
Little, Doreen	148025	00021994	16-Jul-2003 16:46	Upper GI	CR	6		
Lindke, Magnus	684514	91141	17-Apr-2004 15:31	Chest 1 View	CR	1		
Lung, 4 V	IV		01-Oct-2002 15:00	POST VENT	NM	8		
Max, CR/Lat/Lateral/Study	CIMPR02	CIMPR02	01-Oct-2005 16:05	CR	2			
Max, CR/Lat/AT/Study	CIMPR04	CIMPR04	01-Oct-2005 16:05	CR	2			

Inbox (Performed)

Patient Name	Patient ID	Accession	Study ID	Today	Yesterday	Recent	Date Range
Anderson, Janice L.	RID34639	03Nov	March 10, 1942				
Anderson, Jack	99Chess at DEFAU		January 1, 1960				
ANDERSON, JACKIE	RID27021	03Nov	February 17, 1947				
ANDERSON, JACQUELINE	RID14114	03Nov	April 8, 1968				
ANDERSON, JACQUELINE	RID54266	03Nov	July 17, 1996				
ANDERSON, JACQUELYN	RID28787	03Nov	January 15, 1997				
ANDERSON, JACQUELYN S	RID34945	03Nov	November 17, 19...				
Acc.	Performed on	M	Pho.	I.	Rep.	Part.	Wor.
DR041	November 6, 20	CR	Chest	1	Samol		
DR041	June 8, 2003 22:	CR	Chest	1	Samol		
DR041	April 25, 2001 15:	CR	Chest	1	Paco50		
DR041	January 12, 2001:	CR	Chest	1	Paco50		
DR041	October 26, 200:	CR	Chest	1			
DR041	February 19, 200:	CR	Chest	1			
DR041	January 12, 1998:	CR	Chest	1			

Folder Finder

Define Properties of the Study Lists

1. Columns
2. Filters
3. Study list preferences
4. Sorting by columns
5. Icons
6. Different search criteria's within Folder Finder

Unreported Studies - Rad Station

Please select an unreported study from:

No filter set ⊞ ⚠ 🔄 ▼ 📄 Other Lists ➤ Open Study

No filter set ⊞ ⚠ 🔍 Find Study ➤ Cancel

3 Stat priority studies need review

	Full Name	Patient ID	Accession	Performed on	Procedure Types	M.	I...	Performed By	Wor...	Assigned To
	Brown, Warren	86334	AC5441	14-Sep-2006 21:38	XR ORBIT FOR MRI CLEARA...	CR	4		Main H...	
	Brown, Warren	86334	AC8594	07-Dec-2004 22:38	MR ANGIO NECK W/O CONT...	MR	208	Lee, Nancy	Main H...	
	Demo, Two	19711225	00021959	22-Feb-2005 05:09		CR	3			
	Demo, Two	19711225	00001880	10-Nov-2003 14:21	CT PELVIS WITH CONTRAST	CT	43			
	Demo, Two	19711225	00098432	19-Jan-2003 09:23	Knee	MR	213			
⚠	DeSilva, Henrietta	95141	00015781	02-Aug-2003 09:51		US	11			
⚠	Dilda, William	444707	00030273	04-Oct-2003 09:47	Chest 2 Views	CR	2	Appleby, Steph...		
	Dilda, William	444707	00029186	14-Apr-2003 14:01	Chest 2 Views	CR	2		Main H...	
	Dilda, William	444707	633A-040...	03-Apr-2003 14:29	DX CHEST PA-LAT SS	CR	2			
	Dole, Sean	5893861	00001663	04-Nov-2004 07:55	MAG3	NM	8			
	Entler, Jane	684901	00001726	23-Apr-2004 15:42	Otolaryngoscopy	ES	4			
	F7D-Brain-MRPET1	A1+1	6	02-Nov-2005 16:33		PT	14			
	Fischer, PatientThree	F1003	00001765	02-Feb-2004 10:28		MG	3			
	Fischer, PatientTwo	F1002	00001764	02-Feb-2004 10:28		MG	4			
	Fisher, Michelle	232971	00016461	10-Aug-2003 11:45	BRAIN	US	326			
	Fisher, Michelle	232971	00019350	08-Aug-2003 17:38	Brain w w/o	MR	167			
⚠	Fitzpatrick, Michael	430738	00001761	10-Feb-2004 20:29	CT Head w/o	CT	62	Malo, Andrea		
	Fusion, Hirez	684860	00001500	14-Jan-2004 11:30	CT Scan Whole Body	CT	376			
	Fusion, Hirez	684860	00001500	14-Jan-2004 11:30	PET Scan Whole Body	PT	1276			
	Harrison, Natasha	256498	00057812	17-Oct-2003 16:30	Chest 2 Views	OT	2			
	Hoffman, Adam	166479C	00018245	26-Jul-2003 09:34	LUMBAR	CT	455			
	Johnson, Mandy	165849C	00048135	19-Oct-2003 22:53	Ankle Complete	OT	3			
	Lee, Andy	458901	00004723	01-Jun-2006 07:18	Arm Angio	XA	5			
	Little, Doreen	148025	00021954	16-Jul-2003 16:46	Upper GI	CR	6			
	Locke, Magnus	684814	981441	17-Apr-2004 15:31	Chest 1 View	CR	1			
	Lung, 4 V	8V		01-Oct-2002 15:00	POST VENT	NM	8			
	Max, CRLatAsLateralStudy	CSMDP02	CSMDP02	31-Oct-2005 16:05		CR	2			
	Max, CRLatAsLATStudy	CSMDP04	CSMDP04	31-Oct-2005 16:05		CR	2			

Study List Icons

	Stat priority study		Study contains a Jot Pad diagram		Study contains quality assurance (QA) issues		Reviewed study
	High priority study		Study contains patient documentation		Other studies exist for the patient		Dictated study
	Study contains a report		Study contains a voice clip and other patient documentation		In-Progress study		Transcribed study
	Study contains a voice clip (audio message)		Other studies for the patient contain patient documentation		You have the study open		Reported study
	Study contains a scanned document		Study details are available		Another user has the study open		Needs Over-Read study

Notes:

Applying Filters and Creating Custom Filters

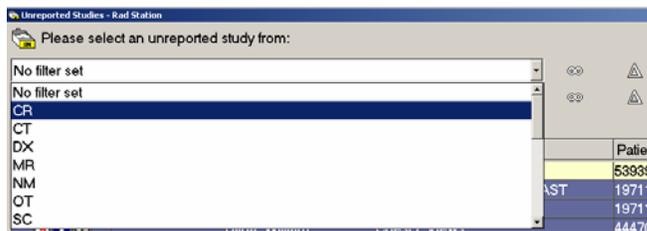
Filters allow you to narrow down the list of studies displayed in your study list. For example, if you only work with CT studies, you can set your first filter to "CT". To further narrow down the displayed studies, you may set your second filter as well.

Note: Filter sets do not carry over from one study list to another. You will need to create a new filter in each study list individually. Filter sets created in the Inbox will only be available in the Inbox, and filter sets created in the Folder Finder will only be available in the Folder Finder.

Note: Filter sets are user specific and are remembered by the system. The filter you use when you log out of HMI PACS is the filter that will be applied when you log in the next time.

Using Predefined Filters

1. Click on the arrow at the end of the first filter. A drop down list of predefined filters is displayed.

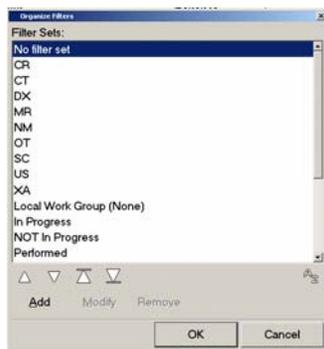


2. From the available list, select the filter you wish to apply.
3. If you wish to apply a second filter, click on the arrow at the end of the second filter.
4. From the available list, select the filter you wish to apply.
5. To reset filters to "No Filter Set", click on the infinity button corresponding to the filter you wish to reset. This will expand the list of studies to include other modalities, etc. 

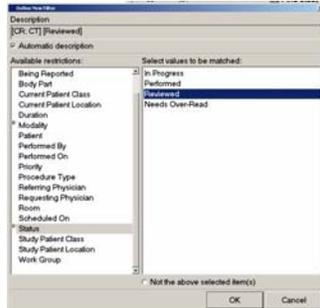
Creating a Custom Filter

The available predefined filters only contain a single restriction for a filter. Custom filters can be created to contain multiple restrictions. For example, if you wanted to view CT and MR studies that have been Reviewed, you would have to create a custom filter.

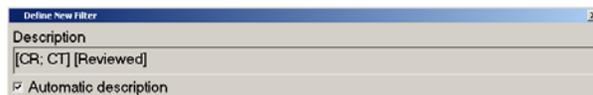
1. Click on the Define and Manage Filter button. 
2. The *Organize Filters* dialog box will be displayed, listing all the existing filters.



- Click Add. The *Define New Filter* dialog box will be displayed.



- You may either leave the HMI default name for the new filter, or you may name it manually.
 - To leave the filter name as the HMI default, ensure that the “Automatic description” box is checked off.
 - To give the new filter a custom name, uncheck the “Automatic description” box, and enter the custom name in the “Description” field.



- In the *Available Restrictions* list, single left-click on the restriction you wish to use.
- Select the value(s) for the filter restriction.
 - To select one value:
 - Single left-click on the value you wish to select.
 - To select multiple values:
 - Hold down the CTRL key on your keyboard.
 - Single left-click on each value you wish to select.

Note: You may wish to exclude the selected values from the filter. To do so, check off the “Not the above selected items” box.
- A triangle is displayed next to the restriction for which you have selected a value.

▾ Modality

- If you have chosen to use the HMI default for the filter description, the selected values will be displayed in the “Description Field”.

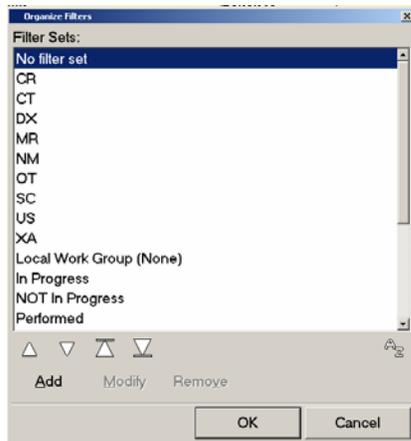
Description
[CR; CT] [Reviewed]

- To add additional restrictions, repeat steps 5 and 6.
- Click OK. The filter is added to the list of available filters in the *Organize Filters* dialog box.
- Click OK. The filter is now applied to your study list.

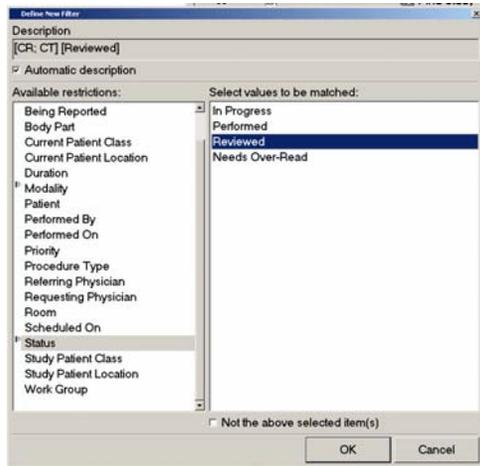
Modifying a Custom Filter

Note: Only custom filters may be modified. HMI predefined filters cannot be modified.

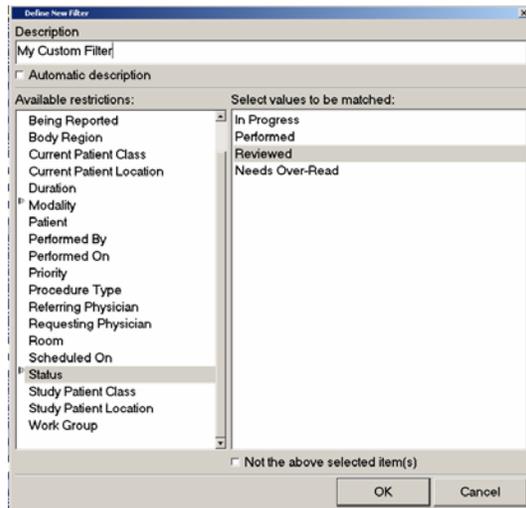
1. Click on the Define and Manage Filter button. 
2. The *Organize Filters* dialog box will be displayed, listing all the existing filters.



3. Locate the filter you wish to modify and single left-click on the name of the filter.
4. Click Modify. The *Update Filter* dialog box is displayed.



5. To rename a filter from an HMI default name to a custom name:
 - a. Uncheck the “Automatic description” box.
 - b. Enter the new name in the “Description” field.



6. To rename a filter from a custom name to an HMI default name:
 - a. Check the "Automatic description" box.
7. To change the custom name of a filter:
 - a. Highlight the existing name in the "Description" field.
 - b. Click the Backspace bar on the keyboard.
 - c. Enter the new name of the filter.
8. To modify the existing values for the filter restriction:
 - a. In the *Available Restrictions* list, single left-click on the restriction for which you wish to modify the values.
 - b. Select or deselect values to modify the restrictions.
9. To add values to the filter restriction:
 - a. In the *Available Restrictions* list, single left-click on the new restriction for which you wish to add values.
 - b. Select the value(s) you wish to add to the restriction:
 - i. To select one value:

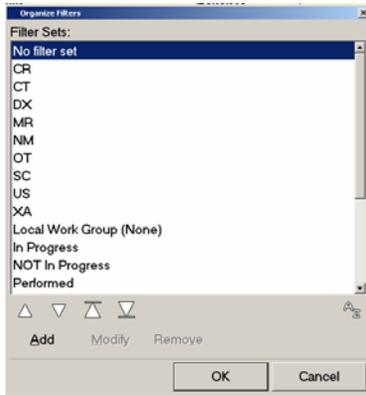
Single left-click on the value you wish to select.
 - ii. To select multiple values:

Hold down the CTRL key on your keyboard.

Single left-click on each value you wish to select.
10. Click OK. The filter is updated and is shown in the *Organize Filters* dialog box.
11. Click OK. The filter is now applied to your study list.

Deleting a Custom Filter

1. Click on the Define and Manage Filter button. 
2. The Organize Filters dialog box will be displayed, listing all the existing filters.



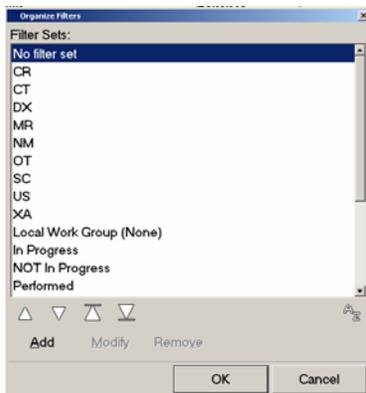
3. Locate the filter you wish to delete and single left-click on the name of the filter.
4. Click Remove. A confirmation message is displayed.



5. To delete the selected filter, click Yes.
6. The custom filter is deleted and removed from the list of available filters.

Reordering Your Filters

1. Click on the Define and Manage Filter button. 
2. The *Organize Filters* dialog box will be displayed, listing all the existing filters.



3. Locate the filter you wish to move and single left-click on the name of the filter.
4. To move the filter up by one entry in the list, click the up arrow. 

5. To move the filter down by one entry in the list, click the down arrow. 
6. To move the filter to the top of the list, click the top arrow. 
7. To move the filter to the bottom of the list, click the bottom arrow. 
8. Click OK. The next time you click on the drop down menu to set a filter, the new order will be reflected in the list.

Notes:

Chapter 3 – Teaching Files

Do you know how to ... Use the Teaching Files?

Ensure that your Teaching Files icon has been added to your toolbar. If it is not, left click on the "User Preferences" icon, locate the Teaching Files icon, left click and drag the icon to your toolbar.

1. Find the study of interested in the In-Box or Folder Finder and open the study by double clicking on it, or highlight the study and press "Open Study".
2. Left click on the Teaching Files icon and select the appropriate option from the menu:
 - a. **Create a shortcut**
 - b. **Copy study** to teaching files
 - c. **Copy series** to teaching files
 - d. **Copy image** to teaching files
 - e. **Copy selected images** to teaching files
 - f. **Copy flagged images** to teaching files (Use the Space Bar key to flag images. This latter option is only available if you have flagged images.)
3. Once you have selected one of these options, the Teaching Files application will launch and automatically highlight the folder for the user currently logged into the PACS workstation.
4. Locate the "New" button in the Teaching Files toolbar. This allows you to organize your images/studies into different Folders and Albums. Folders are typically used to organize/group studies (eg. Cancer Cases) and store shortcuts, while albums are used to store copied images. (Note: When a study is stored in a folder, an album is instantly created to hold the images.) Click on "New" and select "New Folder" or "New Album" from the menu.
5. Type in an appropriate album or folder "Description" and if desired, "Notes". At the bottom of your screen, locate the "OK" button.
6. Press the "OK" button. The shortcut/study/image is stored in the Teaching Files.
7. **Note:** If a study, series or image is copied to Teaching Files, a new study is created without patient demographics (Patient Confidentiality). Creating a shortcut will "bookmark" an exam, displaying all patient information.

Chapter 4 – Quick and Precise Registration

Do you know how to ... Link Series Between Studies through Registration

When series are in different studies for the same patient, scrolling a series does not display the same anatomical region in other linked series. You must register the series by identifying the anatomical reference points for the series you wish to align. These reference points are called registration points.

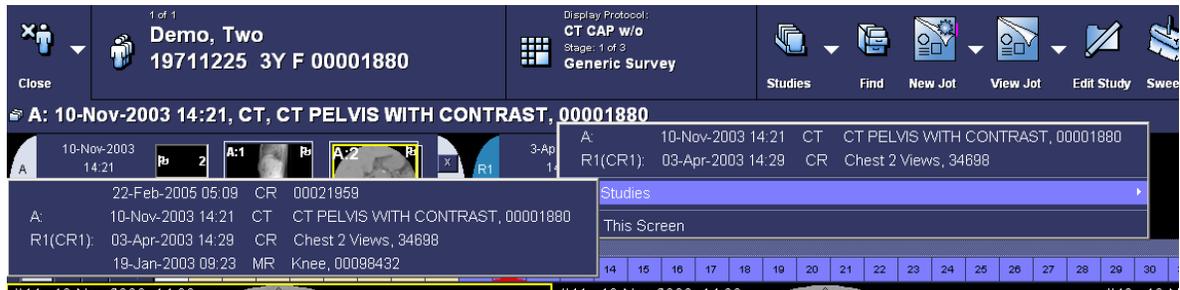
There are two types of registration:

Quick Registration – HRS uses the center of each displayed image as a registration point.

Precise Registration – Two or more registration points are identified manually.

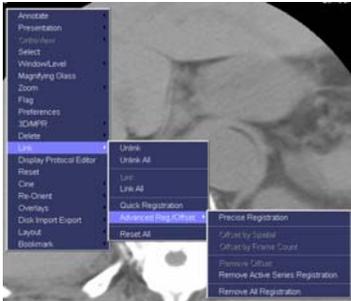
To perform Quick Registration

1. From the *Unreported Studies* list, open the study of interest. This will be the *anchor* study.
2. To compare series from the anchor study with series from a reference study, click on the Study Information Bar on the upper portion of your screen.

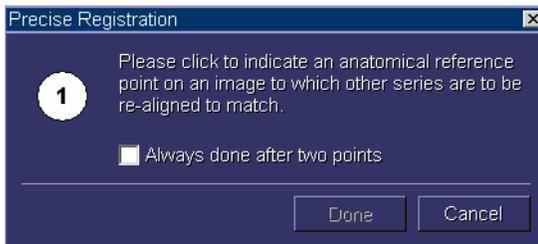


3. If the desired reference study is not displayed in the list, point to "All Studies". This will display additional studies for the patient.
4. Select the desired reference study to open by clicking on it. The study will open in a new clamshell on the toolbar. To open additional reference studies, repeat steps 2 and 3.
5. Display the series from all the desired studies that you wish to register by dragging the series down into available viewports.
6. Link all series to which you want to apply Quick Registration by clicking on the link icons corresponding to each series. 
7. For each linked series, scroll to the image whose center you wish to use as a registration point.
8. Right click on an image and in the displayed menu, point to "Link". (If "Link" is not in the right click menu, add it through the Preferences icon on the toolbar. Alternatively, you may click on the arrow next to the link icon in the viewport. )

- In the displayed menu, point to "Advanced Reg/Offset".



- In the displayed menu, select "Precise Registration".
- The *Precise Registration* dialog box will be displayed.



- Click on the series where you want to use the first registration point. The first registration point is now indicated on the image with a cross.



- Click on another series where you want use the second registration point. The second registration point is now indicated on the image with a cross.
- If you do not wish to register more points of reference, click Done in the *Precise Registration* dialog box. If you wish to register additional reference points, click on the series where you want the third, fourth, etc. registration points. Click Done in the *Precise Registration* dialog box when all desired reference points have been registered.

Precise registration is now applied, and scrolling through a series displays corresponding images in the linked series.

To Reset the Series and Remove All Registration

1. Right click on an image and in the displayed menu, point to "Link". (If "Link" is not in the right click menu, add it through the Preferences icon on the toolbar. Alternatively, you may click on the arrow next to the link icon in the viewport. )
2. In the displayed menu, point to "Advanced Reg/Offset".



3. In the displayed menu, click "Remove All Registration". Registration will be removed from all series.

Chapter 5 – Setting User Preferences

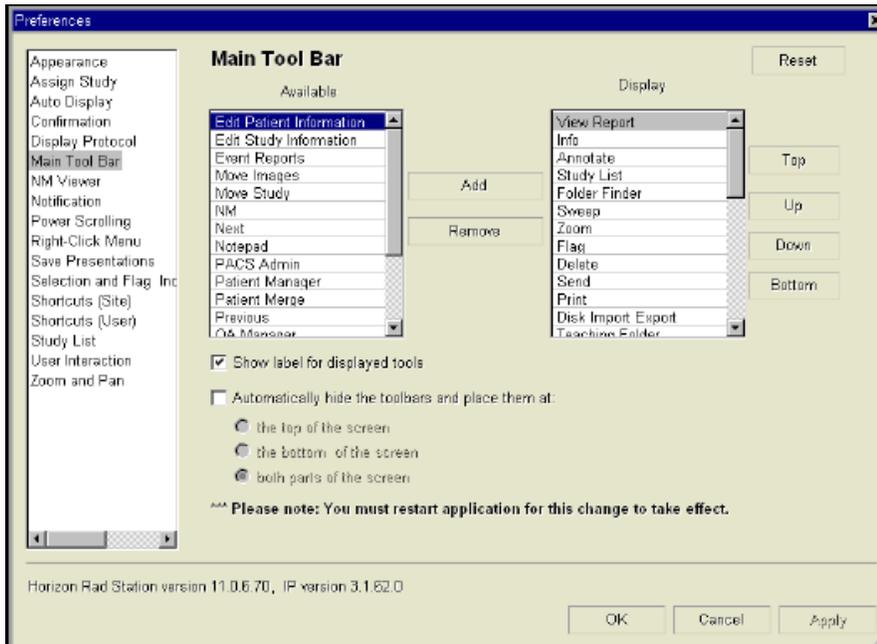
Setting Preferences

Horizon Rad Station Advanced can be customized by using preferences. You can access the preferences by clicking on the preference button on the main toolbar or right clicking on the main toolbar and selecting

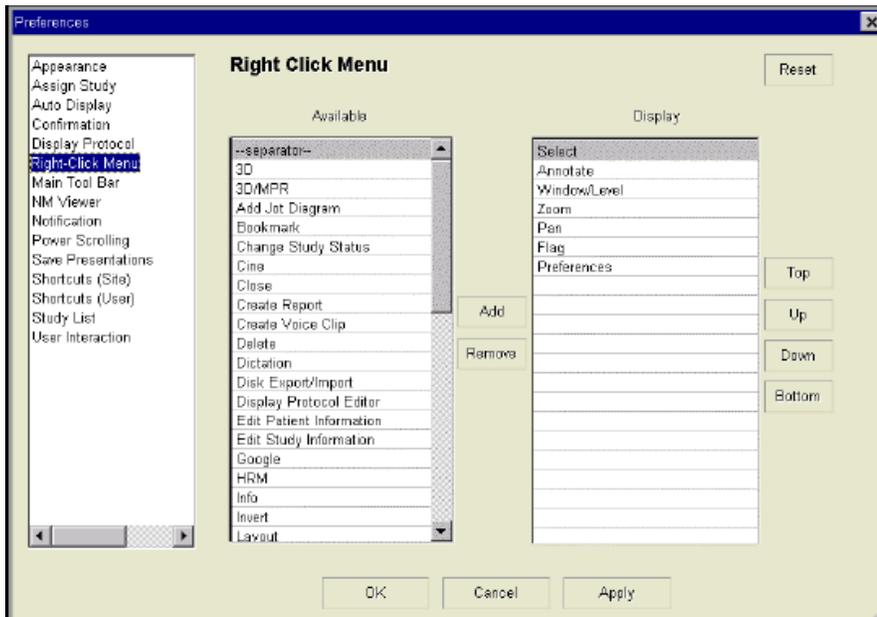


preferences.

Customize the Main Toolbar



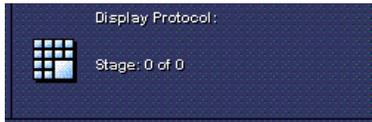
Customize the right click menu



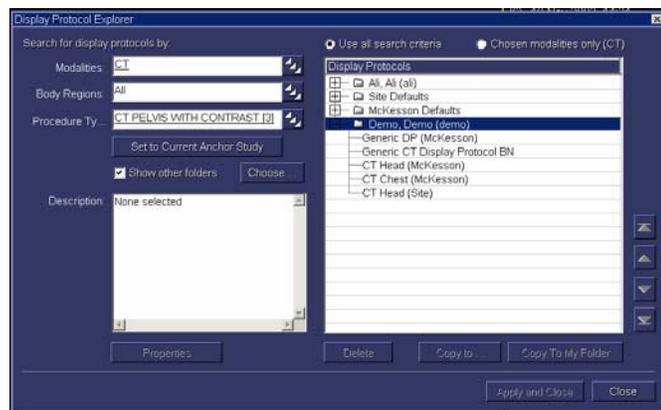
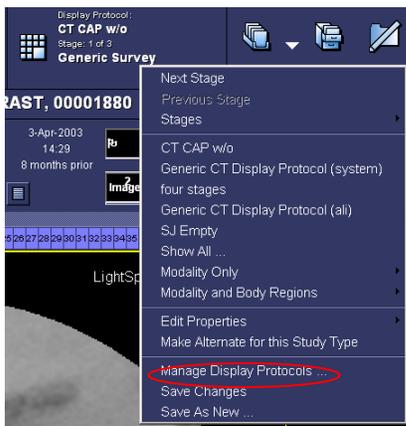
Chapter 6 – Copying DP's to Other Users

Do you know how to ... Copy Other Users' Display Protocols to Your Profile?

1. Click on the Display Protocol icon in the main toolbar.



2. From the displayed menu, select "Manage Display Protocols".



The *Display Protocol Explorer* window will be displayed.

3. On the left side of the window, you may select what types of display protocols you wish to search for.



You may search by:

- a. Modality – very general, all display protocols for the chosen modality / modalities will be displayed.
- b. Body Region – more specific
- c. Procedure Type – most specific, only display protocols for the selected procedure types will be displayed.

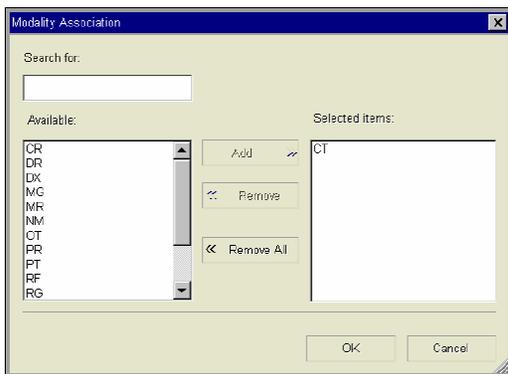
NOTE: If you select procedure type to search by, you do not have to enter a modality or body region as search criteria.

Note:

1. Each search criteria can have one or more values. If no values are specified, the criteria is set to "All". (ie. All modalities, all body regions, and all procedure types will be searched for.)

To Select Modalities:

1. Click on the expander button at the end of the "Modalities" field.  The *Modality Association* window will be displayed.



To Select One Modality:

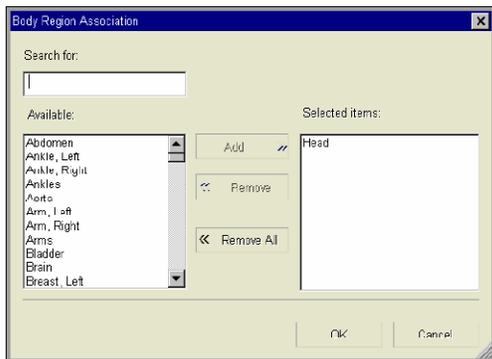
1. Single left-click on a modality in the "Available" list.
2. Click Add. The chosen modality will now be displayed under "Selected Items".
3. To remove a modality from the "Selected Items" list, select it and click Remove.
4. Click OK. The selected modality will now appear under "Modalities" in the *Display Protocol Explorer* window.

To Select Multiple Modalities:

1. Hold down the CTRL key on the keyboard.
2. Single left-click on all desired modalities in the "Available" list.
3. Click Add. The chosen modalities will now be displayed under "Selected Items".
4. To remove multiple modalities from the "Selected Items" list, select the ones you wish to remove and click Remove.
5. To remove all selected modalities, click Remove All.
6. Click OK. The selected modalities will now appear under "Modalities" in the *Display Protocol Explorer* window.

To select Body Regions

1. Click on the expander button at the end of the "Body Regions" field.  The *Body Regions Association* window will be displayed.



To Select One Body Region:

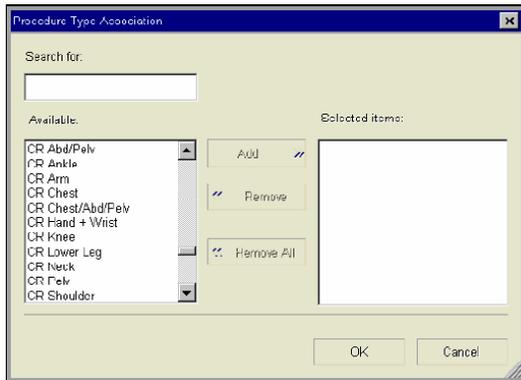
1. Single left-click on a body region in the "Available" list.
2. Click Add. The chosen body region will now be displayed under "Selected Items".
3. To remove a body region from the "Selected Items" list, select it and click Remove.
4. Click OK. The selected body region will now appear under "Body Regions" in the *Display Protocol Explorer* window.

To Select Multiple Body Regions:

1. Hold down the CTRL key on the keyboard.
2. Single left-click on all desired body regions in the "Available" list.
3. Click Add. The chosen body regions will now be displayed under "Selected Items".
4. To remove multiple body regions from the "Selected Items" list, select the ones you wish to remove and click Remove.
5. To remove all selected body regions, click Remove All.
6. Click OK. The selected body regions will now appear under "Body Regions" in the *Display Protocol Explorer* window.

To Select Procedure Types

1. Click on the expander button at the end of the "Procedure Types" field.  The *Procedure Types Association* window will be displayed.



To Select One Procedure Type:

1. Single left-click on a procedure type in the "Available" list.
2. Click Add. The chosen procedure type will now be displayed under "Selected Items".
3. To remove a procedure type from the "Selected Items" list, select it and click Remove.
4. Click OK. The selected procedure type will now appear under "Body Regions" in the *Display Protocol Explorer* window.

To Select Multiple Procedure Types:

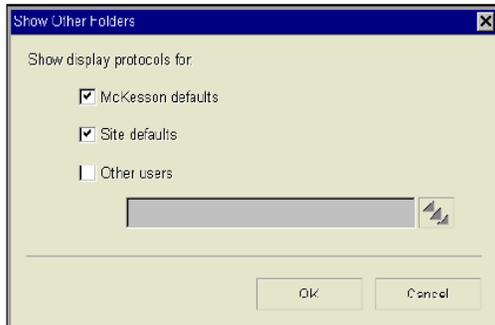
1. Hold down the CTRL key on the keyboard.
2. Single left-click on all desired procedure types in the "Available" list.
3. Click Add. The chosen procedure types will now be displayed under "Selected Items".
4. To remove multiple procedure types from the "Selected Items" list, select the ones you wish to remove and click Remove.
5. To remove all selected procedure types, click Remove All.
6. Click OK. The selected body regions will now appear under "Body Regions" in the *Display Protocol Explorer* window.

To Search Other Users' Folders for Display Protocols Matching Your Search Criteria

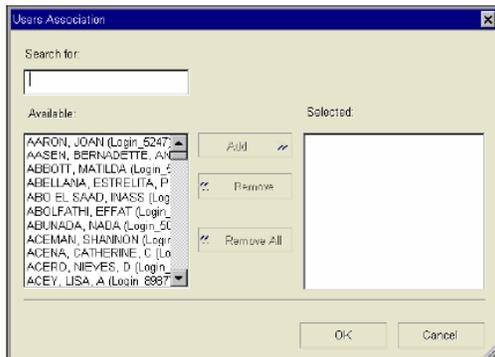
1. Ensure that the "Show Other Folders" box is checked off and click Choose.



The *Show Other Folders* window will be displayed.

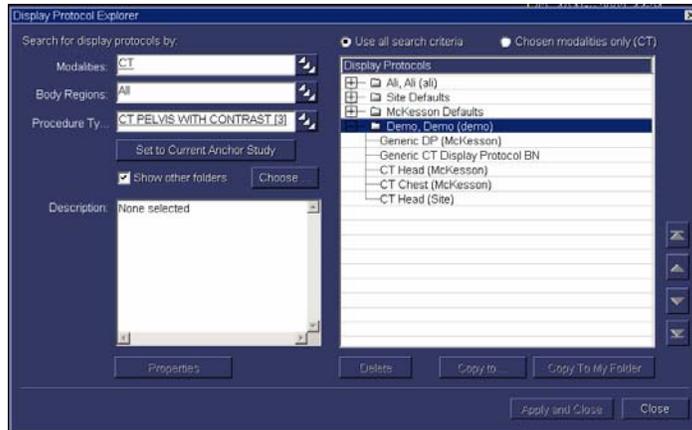


2. To include McKesson default display protocols in your search, ensure the "McKesson defaults" box is checked off.
3. To include site default display protocols in your search, ensure the "Site defaults" box is checked off.
4. To include other users' display protocols in your search, ensure the "Other users" box is checked off.
5. If you have selected other users' folders, click on the expand button.  The *Users Association* window will be displayed.



To Select One User:

1. Single left-click on a user in the “Available” list.
2. Click Add. The chosen user will now be displayed under “Selected Items”.
3. To remove a user from the “Selected Items” list, select it and click Remove.
4. Click OK. The selected user will now appear under the “Display Protocols” list in the *Display Protocol Explorer* window.

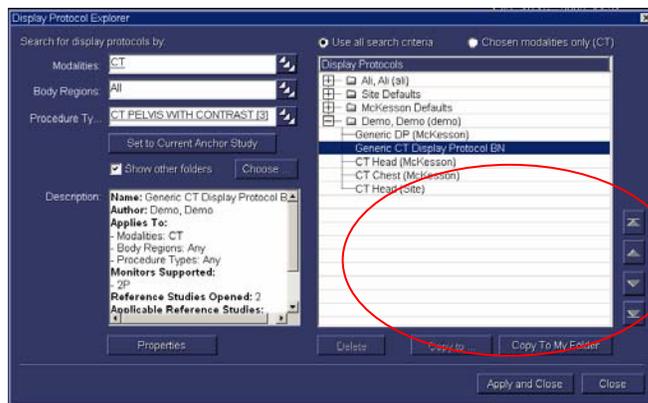


To Select Multiple Users:

1. Hold down the CTRL key on the keyboard.
2. Single left-click on all desired users in the “Available” list.
3. Click Add. The chosen users will now be displayed under “Selected Items”.
4. To remove multiple users from the “Selected Items” list, select the ones you wish to remove and click Remove.
5. To remove all selected users, click Remove All.
6. Click OK. The selected users (along with McKesson Defaults and Site Defaults if they were checked off) will now appear under the Display Protocols list in the *Display Protocol Explorer* window.

To View a Selected User's List of Display Protocols

1. Click on the plus sign next to the user's name to expand his / her folder.  McKesson Defaults The user's display protocols will be displayed.
Note: If you limited your search to specific modalities, body regions, or procedure types, only the matching display protocols will be displayed.
2. Click on a display protocol name of interest. The protocol's properties will be displayed on the left hand side of the window under "Description". For additional properties, click on the Properties button. (Once copied into your folder, you may alter the properties of the display protocol to meet your needs.)



3. To copy the selected display protocol into your own folder, click on Copy to My Folder.
4. To copy additional display protocols to your folder, repeat step 2 and 3.
Note: Display protocols followed by (McKesson) or (Site) already exist in your folder, therefore you do not need to copy them from another user's folder.
5. When done copying display protocols to your folder without applying to the study you are currently viewing, click Close.
6. To manually apply the selected display protocol to a study you are currently viewing, click on Apply and Close.

Note:

1. The copied display protocols will not be automatically set to be defaults for the types of studies they are created for. To apply a display protocol to be a default, you will have to first apply it to a study you are viewing, and check off the "Default Display for This Type of Study" box in the "Save Display Protocol As" dialog box.

Chapter 7 – Radiologist Workflow

<h1>Radiologist Workflow</h1>																									
<p>Horizon Medical Imaging™</p> <div style="margin-bottom: 10px;">  <p>1. Log on Log on to PACS with your user name and password.</p> </div> <div style="margin-bottom: 10px;">  <p>2. IN-BOX Go to the In-Box and locate the study of interest. Ensure filters are set correctly.</p> </div> <div style="margin-bottom: 10px;">  <p>3. Quality Assurance Ensure that the study has been marked as "Reviewed" by a technologist before reading. <i>If study contains a "QA" issue: DO NOT READ.</i></p> </div> <div style="margin-bottom: 10px;">  <p>4. Open Study <i>Double-click</i> on the study of interest from the study list.</p> </div> <div style="margin-bottom: 10px;">  <p>5. Review Images and Leave Prelim. Review the Images within Horizon Medical Imaging and develop your findings.</p> </div> <div style="margin-bottom: 10px;">  <p>6. Leave Dictation Leave a Dictation using PowerScribe.</p> </div> <div style="margin-bottom: 10px;">  <p>7. Close Study as Dictated <i>Single click</i> the small "X" in the top right of the screen and select "Close Study as Dictated" from the drop-down menu. Note: This step removes the study from the "Unreported Studies" list in the inbox.</p> </div> <div style="margin-bottom: 10px;">  <p>8. Quit (If Needed) Quit Horizon Medical Imaging to log off the workstation.</p> </div>	<p>Default Shortcuts</p> <p>Zoom Ctrl (keyboard) & Scroll (mouse wheel)</p> <p>Pan Shift (keyboard) & Left-click and Drag (mouse)</p> <p>Window/Level Right-click and Drag (mouse)</p> <p>Flag an image Space-bar (keyboard) or "F"</p> <p>Measure Distance D (keyboard)</p> <p>Study List Icons</p> <table border="0"> <tr><td></td><td>Reviewed study</td></tr> <tr><td></td><td>Needs Over-Read study</td></tr> <tr><td></td><td>Another user has the study open</td></tr> <tr><td></td><td>Study contains quality assurance (QA) issues and should not be dictated</td></tr> <tr><td></td><td>Other previous studies exist for the patient</td></tr> <tr><td></td><td>Study contains a scanned document</td></tr> <tr><td></td><td>Study contains a Jot Pad Diagram</td></tr> <tr><td></td><td>Stat priority study</td></tr> </table> <p>Common Icons</p> <table border="0"> <tr><td></td><td>Set the screen layout</td></tr> <tr><td></td><td>Add annotations to the image</td></tr> <tr><td></td><td>Display details about the exam</td></tr> <tr><td></td><td>View reports</td></tr> </table>		Reviewed study		Needs Over-Read study		Another user has the study open		Study contains quality assurance (QA) issues and should not be dictated		Other previous studies exist for the patient		Study contains a scanned document		Study contains a Jot Pad Diagram		Stat priority study		Set the screen layout		Add annotations to the image		Display details about the exam		View reports
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<p>Note: Some icons may need to be enabled or disabled on site or by user configurations.</p>																									
<p>MCKESSON Empowering Healthcare</p>																									

Chapter 8 – Advance Guide for HMI 11.0 Display Protocols

I. Introduction

The purpose of this document is to discuss recommendations for building display protocols in HMI 11.0 (SP4). The content of this document is intended for radiologists, PACS administrators, and other users responsible for building and maintaining display protocols.

A display protocol is a digital equivalent of a hanging protocol. It contains an ordered collection of stages through which the user can navigate to view the anchor (opened) study and any reference (comparison) studies in a useful and organized fashion.

II. Preparing A Site For Display Protocols

1. Procedure Codes

HMI determines which display protocol to apply to a study based on either body region or procedure code, depending on how the protocol was saved. If the protocol uses procedure type, then it is critical that procedure types are consistent in the RIS. For example, if a display protocol was saved for a procedure type labeled “CT Chest w/Contrast”, but the order placed is for a “Chest with Contrast”, the display protocol will not be applied to the latter exam. Multiple procedure codes for the same exam can be common at sites that have undergone recent RIS updates or site-wide changes to billing. It is recommended that users only have one choice when ordering a procedure in the RIS.

2. Body Region Associations

HMI populates its procedure code table with procedure codes sent from the RIS. Examples of procedure codes include Chest 2-View, CT Chest w/Contrast, and US Gallbladder; the procedure code table may contain a list of thousands of procedures. Each procedure code should be associated with a body region prior to go-live; a process usually performed by the PACS Administrator or someone else with administrative rights and enough clinical knowledge to know which body region is associated with what procedure. In the above examples, Chest 2-View and CT Chest w/Contrast would both be associated with the body region “Chest”. Body region associations are required for many features in HMI, including study list filters and display protocols.

For example, if body region associations have been set up, a display protocol can be saved to automatically apply to all CR Chest exams simply by selecting “CR” as a modality and “Chest” as a body region. If body region associations have not been set up, the user would have to select “Chest 1-View”, “Chest 2-View”, “Chest Decub”, and perhaps a dozen more procedures from a list of thousands of procedure codes, which may not even be in alphabetical order depending on how they were labeled in the RIS.

3. Standardizing Modality Series Descriptions

When a display protocol is created, image and series placement are saved based upon DICOM properties in the image and/or series. For example, a CT Chest Axial series may be recognized by the properties “Image Type”, “View”, and “Contrast”, which is information sent by the modality automatically.

However, under some circumstances, it is possible that these properties are not used, and series description is used instead. In these instances, series description must be consistently and uniquely labeled for each modality of the same type for the entire site. For example, if there are two CT scanners from different vendors, both scanners must be configured to send the same series description for the CT Chest Axial series mentioned above. The label is arbitrary, but is sensitive to characters, spaces, and even capitalization. Common labels would be “Axial” or “AX”; the exact label does not matter as long as both CT scanners use the same labeling consistently.

III. Creating a Display Protocol

The following is a step-by-step guide to creating display protocols in HMI 11.0 (SP4):

1. Choose the right study:

Open the study of interest along with any comparison studies you would like to save with the display protocol. It is important to choose representative studies when building display protocols. For example, it is not recommended to build a display protocol using a trauma study or an abnormal procedure containing images that are not normally captured.

It is also important to choose a study captured on a modality that is used regularly. For example, it is not recommended to build a display protocol on a study captured on a mobile unit that makes infrequent visits, or a modality that will be replaced in the near future.

2. Make changes starting with a blank screen:

The recommended first step to creating a new display protocol is to start with a blank screen by dragging all the series loaded into viewports off the screen. There are two reasons for this:

a) By default, the “Generic Display Protocol” associates the property “Display Any Series” with each viewport. Dragging a series into a viewport from the thumbnails will replace the “Display Any Series” property with the properties for that series. If this step is not performed, the display protocol will not show any changes the next time it is applied.

If series are dragged from viewport to viewport (instead of from the thumbnails), the “Display Any Series” property will be swapped. If this Display Protocol is saved, there will be no change at all to the original presentation.

b) Dragging and dropping a thumbnail into a viewport will replace the “Display Any Series” property with the properties of the dropped series. However, since each viewport may have displayed a series of images to begin with, it is possible to lose track of which viewports are populated with series that were dragged down from the thumbnail bar.

What happens when a thumbnail is “drag and dropped” into a viewport?

As you hover the mouse cursor over a thumbnail, a popup box appears listing the properties of that series. Some of these properties are asterisked. This functionality was implemented in HRS 11.0 (SP3 + PTF-12).

The properties with an asterisk are determined to be the smallest set of criteria that can be used to uniquely identify that series from the others in the study. For each thumbnail, every property is examined to see if all other thumbnails have the same value for this property. If this is the case, the property is ignored; otherwise, it is asterisked.

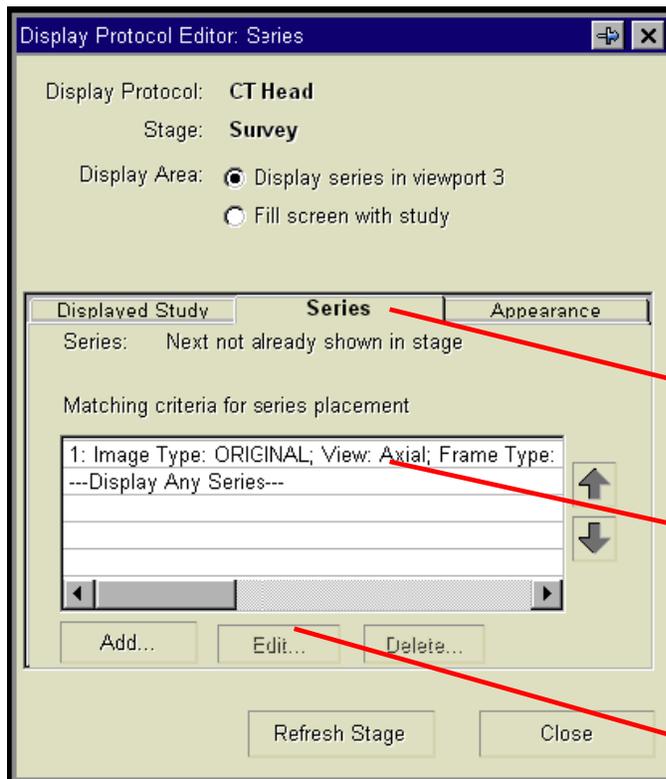
When the thumbnail is dropped into a viewport, those image or series properties that are asterisked will be associated with the viewport. You can verify this by opening the Display Protocol Editor to view the specific matching criteria for that viewport.

After making changes to series and image layout, make any other presentation changes such as Window/Level, Zoom/Pan, Image Orientation, and Series Linking status before continuing.

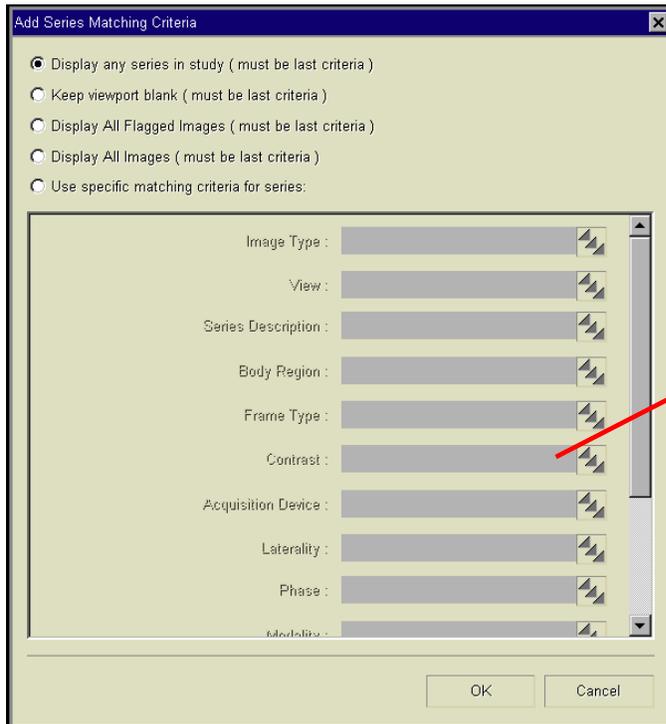
3. Correcting series placement with the Display Protocol Editor:

The “drag and drop” method of building display protocols will save matching criteria for the opened study. However, it will likely need to be extended constantly to accommodate for slight variations in matching criteria due to differences in properties from different modality vendors or different acquisition protocols.

Rather than extending the display protocol every time it hangs incorrectly, it is important to use the Display Protocol Editor to correct the series matching criteria immediately.



- a) Invoke the Display Protocol Editor by clicking the Display Protocol Button > select **Edit Properties** > select **Series Placement and Appearance**.
- b) *Note: the Display Protocol Editor button can be added to the right-click menu.*
- c) Click on the viewport of interest.
- d) Click the **Series** tab.
- e) A list of matching criteria for the selected viewport appears. There is a separate line for each set of matching criteria. Note that a thumbnail will drop in this viewport if it matches any one set of criteria. Click on the matching criteria of interest.
- f) e) Click the **Edit** button to invoke the **Series Matching Criteria** screen.



a) This window allows the user to specify which DICOM properties are desired for series display in the selected viewport.

The pick list can be used to select from a predefined set of criteria. For example, under the “Contrast” field, the pick list will show the options “Yes” and “No”. If contrast is not important for the display protocol, simply remove the options and leave the field blank.

It is important to scroll through the list of criteria to ensure that each field is populated with the desired criteria for series placement.

The following is a list of recommended matching criteria to save in a viewport (all other matching criteria can usually be ignored):

- **CR: *Projection*** is the only property that is normally required for a CR protocol. Most protocols require only AP, the lateral and the oblique projection images to be placed properly. On occasion, some radiologists simply use the “All Images” sequence for their protocol.
- **CT: *View, Image Type* and *Contrast*** are the only useful properties currently available for CT.
- **MR: *View, Image Type, Echo Type, Contrast, Pulse Sequence* and *Diffusion Coefficient*** are the only available properties that are useful for building protocols. The larger number of properties allows more flexibility in building MR protocols.
- **MG: *Image Type, MG Projection, Intent, Laterality* and *MG Implant Displacement*** are the most important properties for MG protocols.

When are series descriptions used for series placement?

When no properties can uniquely identify a series, then series description is used as matching criteria instead. This is indicated by the fact that when you hover the mouse cursor over that thumbnail, you'll see that series description is the only property that is asterisked.

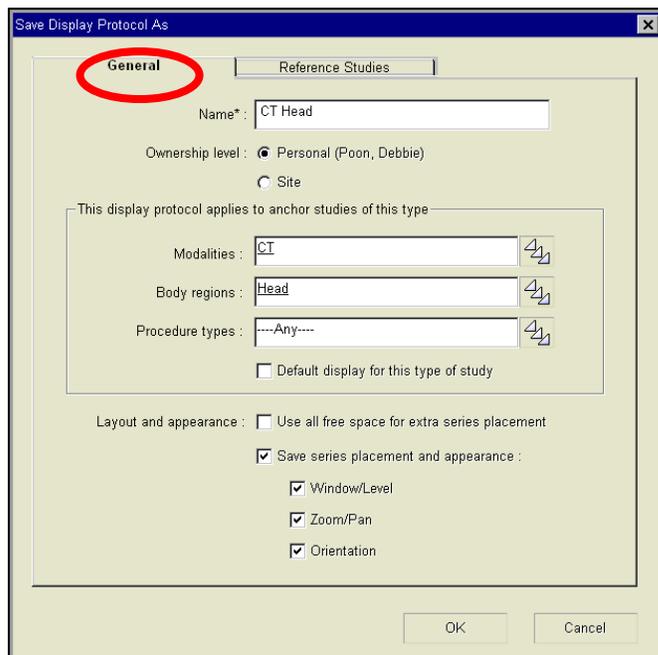
It is recommended to avoid using series description as matching criteria whenever possible. Series descriptions are subject to differences between vendors and technologist manual entry. If the series description saved in a display protocol differs from the series description sent in subsequent studies, even by a single character or space, the display protocol will not hang images correctly.

4. Save the Display Protocol:

Click on the Display Protocol Button and select **Save As New** from the dropdown menu.



a) The Save Display Protocol As window is displayed at the General properties tab:



b) In the **Name** field, enter the name of the display protocol. It is recommended that the name contain user initials, modality, and scope for identification later, e.g. "CT Head – JD"

c) Specify the ownership level of the display protocol (administrator's only).

d) Specify the applicability rules, which determine which modality, body region, and procedure types the display protocol applies to.

e) *Note: It is good practice to add procedure types that have similar series, e.g. CT Abdomen and CT Stone Survey have different series and thus they should have different display protocols.*

f) Specify whether the display protocol applies automatically by checking **Default display protocol for this type of study**.

g) Specify which properties to save with the **layout and appearance** checkboxes.

- h) g) If you would like to automatically load comparison studies, click on the **Reference Studies** tab:

- i) Check the **Open reference studies automatically** checkbox.
- j) Click on the **Maximum Reference Studies to Open** dropdown, and specify the maximum number of reference studies that should be opened.
- k) Specify the applicability rules, which determine which modality, body region, and procedure types the display protocol will try to open.
- l) *Note: Specified body region will load any associated procedure types, e.g. if CR is specified for modality and Chest is specified for body region, the protocol will load Chest 1-View, Chest 2-Views, Chest Portable, etc.*
- m) Specify additional rules to determine whether study statuses or date should be considered when opening reference studies.

- n) l) Click **OK** to save the display protocol.

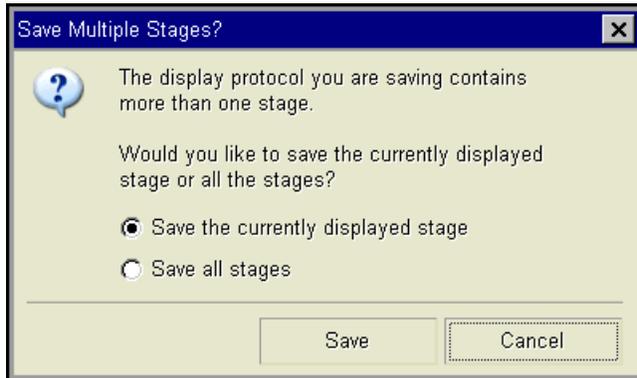
5. Update a Display Protocol

It is possible to edit the properties of a display protocol if changes need to be made (alternatively, it is also possible to overwrite the display protocol with a new one using the same name).

- a) Open the study of interest, and make sure the display protocol you would like to edit is already applied. The name of the currently applied display protocol is written on the Display Protocol Button:



- b) If the General or Reference Studies properties of the Display Protocol need to be edited, click on the Display Protocol button and select **Edit Properties > Anchor/Reference Study Properties**.
- c) Modify the series and image layouts and presentation settings such as Window/Level, Zoom/Pan, Image Orientation, and Linking status.
- d) Click the Display Protocol Button and select **Save Changes** from the dropdown menu.
- e) If the display protocol contains multiple stages, the **Save Multiple Stages** warning is displayed:



- i. Specify whether to save the layout and presentation settings of the current stage by selecting option box **Save the currently displayed stage**.
- ii. Specify whether to save the layout and presentation settings of ALL the stages by selecting option box **Save all stages**.

f) Click Save.

6. Extending a display protocol:

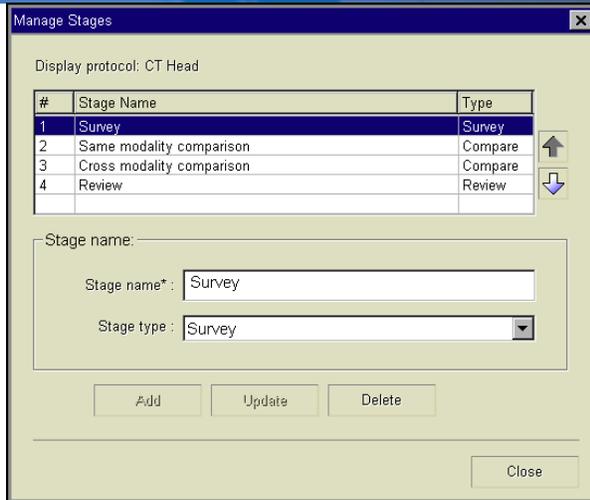
Any series subsequently dropped into the viewport will add matching criteria to that viewport. For example, if an “Axial Pre” series is dragged into a viewport and saved, then an “Axial Post” is dropped into the viewport and saved again, that viewport will search for both “Axial Pre” and “Axial Post” in the future. This is called “extending” a display protocol, which can be used to accommodate variations in series properties from different modality vendors.

Any changes made to the protocol need to be saved by clicking on the Display Protocol Button and selecting Save Changes.

7. Adding or Deleting Stages:

Display protocol stages can be interpreted as display protocols within display protocols. Each stage can specify different ways in which images are displayed and in what viewports they are placed on the screen.

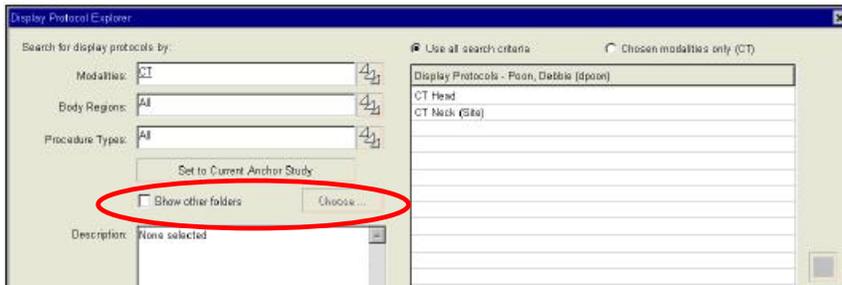
- a) Open the study of interest along with any comparison studies you would like to save with the display protocol. The first stage is always applied when an exam is first opened.
- b) Navigate to other stages by clicking on the Display Protocol Button and selecting **Next Stage** or **Previous Stage**.
- c) Modify the series and image layouts and presentation settings such as Window/Level, Zoom/Pan, Image Orientation, and Linking status for each stage (remember to navigate to a stage before making changes to it).
- d) If you would like to add or delete stages, click on the Display Protocol Button and select **Manage Stages** from the dropdown menu. The Manage Stages window appears listing the McKesson default stages:



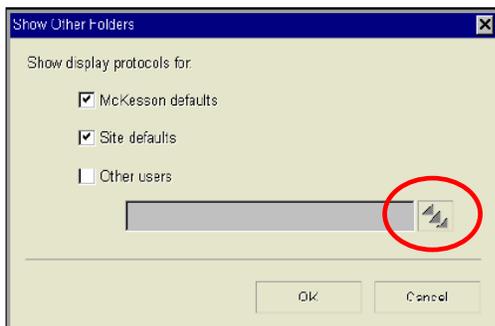
- i. To modify the name of a stage, select the stage of interest from the list and type in a new name in the **stage name** box.
- ii. Click on the **stage type** dropdown and select the context in which the stage is used.
- iii. Click the **Update** button to save the changes.
- iv. To add a stage, enter a stage name and stage type, then click the **Add** button.
- v. To delete a stage, select the stage of interest, then click the **Delete** button.
- vi. Click the **Close** button to finish.

8. Sharing Display Protocols:

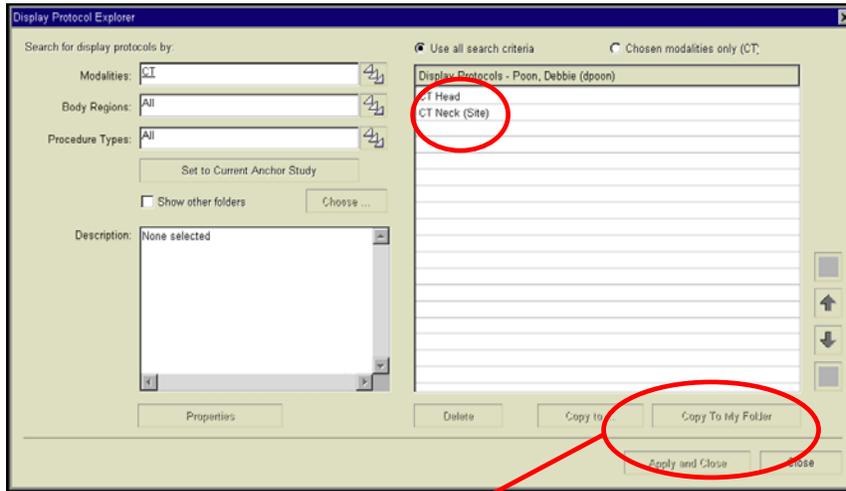
- a) Click on the Display Protocol Button and select **Manage Display Protocols** from the dropdown menu. The following window pops up displaying the available display protocols.
- b) Check the **Show Other Folders** checkbox and click the **Choose** button.



- c) The following popup box appears. Click the picklist button to select the user from whom you want to copy a display protocol and click **OK**.



- d) Select the display protocol of interest from the menu on the right. Lists can be expanded by clicking on the + signs.



- e) Click the **Copy To My Folder** button to copy the display protocol to your own profile.
- f) Click the **Apply and Close** button to save and close the Manage Display Protocols window.

IV. Frequently Asked Questions

1. How does Horizon Rad Station determine which Display Protocol to use when I open a study?

When creating a display protocol, you can associate the protocol with up to three properties: modality, body region, and procedure type. Modality should always be assigned. Either body region or procedure type can be assigned; it is not required to have both. Body region is set up by your administrator and is recommended for simplicity. For example, if a protocol is assigned to “CT” and “Chest”, the display protocol will automatically apply to CT Chest w/Contrast, CT Chest wo/Contrast, and CT Chest w & wo/Contrast. If you desired separate protocols for all three procedure types, then you would ignore body region and assign the protocol to procedure type instead.

2. How are thumbnails placed in viewports?

When a display protocol is applied to a study, the thumbnails are evaluated for placement in the same order in which they appear on the bar. For each thumbnail, the *first viewport with matching criteria* is chosen for placement; this is the first series with all the properties specified as matching criteria for the viewport. Currently, each sequence is placed in the first viewport that satisfies the matching criteria. The ranking of the matching criteria does not play a part in series placement into viewports.

3. What happens when you swap the contents of two viewports?

Swapping two viewports swaps the matching criteria associated with each viewport. The results of swapping the contents are dependent on the actions performed prior to the swap.

Case #1: The generic protocol is applied and the contents of two viewports are swapped

Results: This action simply results in swapping the same property “Display Any Series”. When the protocol is saved, the changes made are not noticed. For this reason, this practice should be avoided while creating protocols.

Case #2: One of the two viewports involved in the swap had a thumbnail dropped into it. For example, viewport #1 had a thumbnail dropped into it and is now associated with a set of properties, while viewport #2 is still associated with “Display Any Series”.

Results: Swapping these two viewports will swap the properties as expected; saving the protocol and re-applying it will result in viewport #2 displaying the expected series; though the same is not necessarily true of viewport #1. To avoid confusion, it is best practice to always drop series from the thumbnail bar.

Case #3: Both viewports involved in the swap had a thumbnail dragged into them

Results: This is the best scenario to work with. The set of image properties associated with each viewport are exchanged. When this protocol is saved and re-applied, the results are as expected (i.e. the series appear in the viewports in which they were expected to appear).

4. What happens when the same series is dropped into different viewports?

The same thumbnail can be dropped into multiple viewports. For example, this may be used for CT where the radiologist wants to see a Chest exam with Abdomen, Lung, and Mediastinum window/levels at the same time.

Once multiple viewports are associated, the specific matching criteria for the viewports *cannot be updated or deleted*. If the viewports are associated with slightly undesirable matching criteria that may not consistently work, simply add a new set of matching criteria to the first viewport of this collection. This association can be removed by clicking on the “Break” button in the “Series” tab of the Display Protocol Editor.

5. What is Clinical Series Mapping?

Clinical Series Mapping (aka. sequencing) encompasses four separate processes:

a) Identification of Image Content

Information related to image properties such as view, projection, pulse sequence, contrast, etc. is found in the DICOM header of the image; however, the exact DICOM tag that has information related to a specific property is not always the same. The first step in sequencing a study is to search through the DICOM header and extract as much information as possible. The extracted information is used to populate the McKesson-specific DICOM tags (one for each property, identified by the group number 3711).

The purpose of the exercise above is two-fold:

- I. The properties extracted are used later to group images into series; the idea is that a series is made up of images with similar properties
- II. The properties extracted are used by the Display Protocol Editor to determine which series populates a particular viewport on HRS

b) Grouping of Images into a Series

The basic purpose of grouping is to ensure that images with a set of similar properties are clustered together. For a study of a particular modality, a specific set of splitting criteria are applied one at a time and the end result is a set of series or groups, all of which have the same image properties. Some commonly used splitting criteria include DICOM Series UID, View, Contrast, etc.

c) Sorting of Images in a Series

Commonly used sorting criteria include anatomical slice location, acquisition time and image number.

d) Sorting Series

The process is very similar to sorting images in a sequence. Commonly used sorting criteria in this case would be series number, series date or time and the recently created “thumbnail group” property. A direct consequence of sorting series is the order in which thumbnails appear on HRS.

6. How do display protocols work for different monitor configurations?

A display protocol can be adapted to behave differently depending on the number of available active monitors. The recommended approach to use this feature is to build the protocol on the configuration with the lowest number of monitors, and then adapt the protocol to configurations with more monitors. When you build a protocol on a 2-monitor configuration and open it on a 4-monitor workstation, the protocol opens up showing the first two monitors with series placed and the last two monitors with blank viewports.

However, when a protocol is built on a 4-monitor workstation and then opened on a 2-monitor workstation, the software will revert to the “generic display protocol” until the custom protocol has been extended for the other configuration. This behavior may be unintuitive to users, as it will appear as though the display protocol is not working.

To extend a protocol for a different monitor configuration, apply the display protocol on a different monitor configuration, alter the viewports as desired, and use the “Save Changes” feature to update the protocol. This protocol will now work for both monitor configurations.

7. What is the purpose of “Stage Type”?

SP4 brought a feature enhancement where a stage can be skipped if no relevant images or studies are found for a particular Stage Type. The following stages can be skipped assuming that the Stage Type is correctly set:

- a) The “Survey” stage where all visible viewports are set with the “Blank Viewport” property is skipped. Basically, if you drag everything off the screen and saved the changes, this stage would be skipped.
- b) The “Comparison” stage with no relevant open comparison studies is skipped. If you have a comparison stage that is set up to display images of a CT reference study, but no relevant CT reference studies are found, such a stage would be skipped.
- c) The “Comparison” stage that has a relevant comparison study open, but does not have any viewports configured to show a series from the relevant prior, will be skipped. If such a stage has at least one viewport configured to show a certain series from the relevant reference study, then this stage will not be skipped, even if there are no series in the comparison study that match the criteria specified in the viewport.

Stage skipping can be turned off in Preferences under the "Display Protocol" tab.

V. Troubleshooting Scenarios

The following section deals with some common scenarios where previously created display protocols fail. As an example, we will use a two monitor display protocol created for a “CR Chest 2-View” (frontal and lateral views) study using the drag and drop method on a perfectly sequenced study. The following are scenarios where this protocol can fail:

1. Missing DICOM properties

Description: There is a lateral image on the thumbnail bar but this image does not appear in the viewport as expected. The empty viewport will list the properties with which it is associated.

Explanation: Looking at the DICOM header, you may find that the property “Projection Type” does not exist. This usually indicates that the projection type was not found anywhere in the DICOM header.

Action: Drag down the lateral image and save the display protocol. Take a look through the DICOM header and see if you find the projection type anywhere. If not, this is a modality problem; keep an eye out to see if all studies from a particular device are like this or if it’s just a rare occurrence. If you do find a projection type value somewhere, inform a member of the McKesson team to make a script change.

2. Incorrect DICOM properties

Description: As in the previous example, there is a lateral image on the thumbnail bar but this image does not appear in the viewport as expected. The empty viewport will list the properties with which it is associated.

Explanation: Even though the image is visually identified as a lateral image, the DICOM header incorrectly states that this image is “AP”.

Action: An incorrect DICOM tag is typically caused by technologist error or incorrect modality configuration. It is also possible that the projection is stored correctly in another DICOM tag. A member of the McKesson team should be notified to investigate the problem, but this usually cannot be corrected in PACS.

3. Variations of expected property values

Description: Once again, there is a lateral image on the thumbnail bar but this image does not appear in the viewport as expected. The empty viewport will list the properties with which it is associated.

Explanation: The viewport was saved with the projection type “Lat” which is the most common form of representation, but for this study, HRS extracted “Lateral” or “Late” or “LL” (short for “Left Lateral”).

Action:

1. verify what value the lateral image has for projection type in its DICOM header. After verifying that it is just a variation of syntax and not an incorrect value, there are two possible courses of action to take:
2. Drag down the thumbnail to the viewport and “Save Changes”. This viewport will now look for both variations of the value “lateral”. The criteria can be verified using the Display Protocol Editor.
3. Open the Display Protocol Editor and manually add the variations to the specific matching criteria dialog. You do not necessarily have to choose from the default values in the pick list; you can type the values in the dialog box as well, separating values with a semicolon.

4. Sequence with specified properties is not available

Description: A viewport remains blank after a display protocol is applied to a study. The empty viewport will list the properties with which it is associated.

Explanation: The viewport expects a sequence with certain properties but such a sequence is not found in the study.

Action:

There are two possibilities for this error: either such a sequence does not exist in the study or the matching criteria in the viewport is so constrained that none of the sequences in the study are considered a fit for that viewport. If the former is the case, the sequence expected has not been sent to PACS. To troubleshoot the latter, hover the mouse cursor over the thumbnails that have not been placed in a viewport and check to see how the matching criteria of the viewport can be reduced to “fit” the desired sequence. For example, the viewport may be looking for a body region of “Chest” which was not sent by the modality. This property should be removed from the display protocol using the Display Protocol Editor.

5. Improper Series Placement

Description: The viewport in question was not populated by the expected series.

Explanation: There are a few possible causes for this:

- a) Not enough properties were set as matching criteria, so a thumbnail that comes before the expected series is chosen for placement into the viewport.
- b) The expected thumbnail may have been chosen for placement in a different viewport.
- c) The same series might be acquired twice as the patient was not in a favorable position for the first series; in this case, you'll have two series with identical properties. The first thumbnail will be chosen for placement even though this is the series that the radiologist does not want to see.
- d) The study may have more thumbnails than viewports; by the time the series in question is evaluated for placement, all viewports have been filled with previously occurring thumbnails.
- e) Owing to mislabeled properties (stemming from incorrect DICOM info), the properties of a thumbnail did not match with the matching criteria of a viewport.

Action: A good understanding of (1) how thumbnails are placed into viewports and (2) how Display Protocol editor is used to increase/decrease the matching criteria associated with the viewport is required to identify the source of the problem and the potential solution.

VI. Display Protocols Building

Display Protocol Building

1. Choose The Right Study:

Open the study of interest along with any comparison studies you would like to save with the display protocol. It is important to choose representative studies when building display protocols.

2. Start with Blank screens:

The recommended first step to creating a new display protocol is to start with a blank screen by dragging all the series loaded into viewports off the screen

1. Click on the Viewport icon and select a 1 x 1 View.
2. Left click on the 1 x 1 image in the viewport and while holding down the left mouse button, drag the image back up to the thumbnail gallery
3. Repeat step #2 for all of the monitors

This should result in all of the Diagnostic monitors having a blank screen

3. Drag Thumbnails (Series) Down To Populate Viewports

Dragging and dropping a thumbnail into a viewport will replace the "Display Any Series" property with the properties of the dropped series.

To drag and drop a series to the desired viewport:

1. Left click and hold down the left mouse button on the desired thumbnail or series
2. While holding the left mouse button down, drag the thumbnail to the desired viewport
3. Once the thumbnail is over the desired viewport, release the left mouse button and the thumbnail will "Drop" into the viewport
4. Repeat these steps until all of the viewport are filled as desired

4. Correcting Series Placement Using The Display Protocol Editor:

The "drag and drop" method of building display protocols will save matching criteria for the opened study, however, it will likely need to be extended constantly to accommodate for slight variations in matching criteria due to differences in properties from different modality vendors or different acquisition protocols.

Rather than extending the display protocol every time it hangs incorrectly, it is important to use the Display Protocol Editor to correct the series matching criteria immediately.

1. Invoke the Display Protocol Editor by clicking the Display Protocol Button > select Edit Properties > select Series Placement and Appearance.
2. Click on the viewport of interest.
3. Click the Series tab. *(Note that a thumbnail will drop in this viewport if it matches any one set of criteria)*
4. Click on the matching criteria of interest.
5. Click the Edit button to invoke the Series Matching Criteria screen.

5. Adding or Deleting Stages (If necessary):

Display protocol stages can be interpreted as display protocols within display protocols. Each stage can specify different ways in which images are displayed and in what viewports they are placed on the screen.

1. Open the study of interest along with any comparison studies you would like to save with the display protocol.
2. Navigate to other stages by clicking on the Display Protocol Button and selecting **Next Stage** or **Previous Stage**.
3. Modify the series and image layouts and presentation settings such as Window/Level, Zoom/Pan, Image Orientation, and Linking status for each stage (remember to navigate to a stage before making changes to it).

If you would like to add or delete stages, click on the Display Protocol Button and select **Manage Stages** from the dropdown menu. The Manage Stages window appears listing the McKesson default stages

6. Save the Display Protocol

Click on the Display Protocol Button and select **Save As New** from the dropdown menu.

VII. Viewport Image Criteria

Viewport Image Criteria

The following is a list of recommended matching criteria to save in a viewport
(all other matching criteria can usually be ignored)

Modality	Selection Criteria
CR/DR/RF (Plain Film)	<ul style="list-style-type: none"> • Projection • Series Description*
CT	<ul style="list-style-type: none"> • View • Image Type • Contrast • Series Description*
MRI	<ul style="list-style-type: none"> • View • Image Type, • Echo Type, • Contrast, • Pulse Sequence • Diffusion Coefficient • Series Description*
Ultrasound	<ul style="list-style-type: none"> • Image Type • Series Description*
Mammography	<ul style="list-style-type: none"> • Image Type, • Projection • Intent • Laterality • MG Implant Displacement • Series Description*

*NOTE: Series Description should only be used when all other criteria match

