

medDream

Hanging protocols v2 setup manual for MedDream viewing functionalities version 8.9.1

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Hanging protocols configuration

Hanging protocols configuration defines the fields per conditions group, that will be displayed in the drop-down tags list. If the configuration file "hangingProtocolsConfig.json" is not available, the default configuration file "hangingProtocolsConfig.json" is created, and the default configuration is loaded at system start.

The hanging protocol configuration may be changed only by manual editing of the "hangingProtocolsConfig.json" file. To load the changed configuration, the system should be restarted.

Tags used in Hanging protocol conditions

The tag in the hanging protocol condition may be identified by custom name, like "modalities_in_study", further named as custom tags, or by the 8-digit DICOM tag with scope prefix, like "study.00080070":

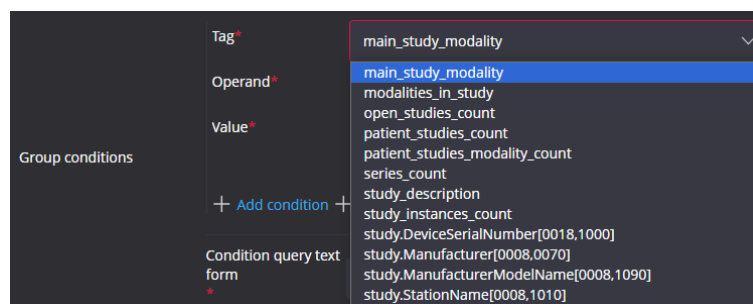


Figure 1. Tags example in Group conditions Tag list

The custom tags identify the data, that is retrieved and used for study loading, image display or other system functions, like history window opening. If the protocol contains only the custom tags, the additional data should not be retrieved, and applying the hanging protocol works quicker.

For getting the data of the DICOM tag other than custom tag, the metadata (DICOM tags) of the particular instance should be retrieved and checked, when applying the hanging protocol.

The next sections provide the tags of the default configuration and explain tags and their usage.

Tags of the default configuration

The section lists the tags, that are created and stored in "hangingProtocolsConfig.json" by default.

Group conditions default configuration tags:

1. main_study_modality
2. modalities_in_study
3. open_studies_count
4. patient_studies_count
5. patient_studies_modality_count
6. open_studies_modality_count
7. series_count
8. study_description
9. study_instances_count
10. study.DeviceSerialNumber[0018,1000]
11. study.Manufacturer[0008,0070]
12. study.ManufacturerModelName[0008,1090]
13. study.StationName[0008,1010]
14. series_description

15. series.ViewCodeSequence[0054,0220]
16. series.ViewPosition[0018,5101]
17. series_SOP_class_UID

Study conditions default configuration tags:

1. main_study_modality
2. modalities_in_study
3. open_studies_count
4. patient_studies_count
5. patient_studies_modality_count
6. open_studies_modality_count
7. series_count
8. series_description
9. series_SOP_class_UID
10. series_transfer_syntax_UID
11. study_description
12. study_instances_count
13. study.AcquisitionDeviceProcessingDescription[0018,1400]
14. study.DeviceSerialNumber[0018,1000]
15. study.InstitutionName[0008,0080]
16. study.Manufacturer[0008,0070]
17. study.ManufacturerModelName[0008,1090]
18. study.StationName[0008,1010]
19. series.FrameLaterality[0020,9072]
20. series.ImageLaterality[0020,0062]
21. series.Laterality[0020,006X]
22. series.ViewCodeSequence[0054,0220]
23. series.Laterality[ALL], included metadata: imageLaterality; attribute.00200060, frameLaterality
24. series.ViewPosition[ANY], included metadata: viewPosition, protocolName, attribute.0008103E, attribute.00540220, attribute.00540220/00080121, "attribute.00540220/00540222, attribute.00540220/00540222/00080121"

Patient (prior) studies conditions default configuration tags:

1. modalities_in_patient_study
2. patient_study_description
3. scroll_step
4. study_date_filter



NOTE! Only the listed tags are currently supported in Prior conditions.

Other (viewer) studies conditions default configuration tags:

1. modalities_in_open_study
2. open_study_description
3. scroll_step
4. study_date_filter



NOTE! Only the listed tags are currently supported in Other conditions.

Series conditions default configuration tags:

1. matched_series_number

2. scroll_matched_series
3. series_description
4. series_instances_count
5. series_modality
6. series_number
7. series_SOP_class_UID
8. series_transfer_syntax_UID
9. series.AcquisitionDeviceProcessingDescription[0018,1400]
10. series.AnatomicRegionSequence[0008,2218]
11. series.BodyPartExamined[0018,0015]
12. series.BreastImplantPresent[0028,1300]
13. series.ContrastBolusAgent[0018,0010]
14. series.FrameLaterality[0020,9072]
15. series.ImageLaterality[0020,0062]
16. series.Laterality[0020,006X]
17. series.ImageType[0008,0008]
18. series.PatientOrientation[0020,0020]
19. series.PrimaryAnatomicStructureSequence[0008,2228]
20. series.ProtocolName[0018,1030]
21. series.RotationDirection[0018,1140]
22. series.SeriesNumber[0020,0011]
23. series.ViewCodeSequence[0054,0220]
24. series.ViewPosition[0018,5101]
25. series.Laterality[ALL], included metadata: imageLaterality; attribute.00200060, frameLaterality
26. series.ViewPosition[ANY], included metadata: viewPosition, protocolName, attribute.0008103E, attribute.00540220, attribute.00540220/00080121, "attribute.00540220/00540222, attribute.00540220/00540222/00080121

Instance conditions default configuration tags:

1. instance_number
2. instance_SOP_class_UID
3. instance_transfer_syntax_UID
4. instance.AcquisitionDeviceProcessingDescription[0018,1400]
5. instance.AnatomicRegionSequence[0008,2218]
6. instance.BodyPartExamined[0018,0015]
7. instance.BreastImplantPresent[0028,1300]
8. instance.ContrastBolusAgent[0018,0010]
9. instance.ImageLaterality[0020,0062]
10. instance.ImageType[0008,0008]
11. instance.Laterality[0020,006X]
12. instance.PatientOrientation[0020,0020]
13. instance.PrimaryAnatomicStructureSequence[0008,2228]
14. instance.ProtocolName[0018,1030]
15. instance.RotationDirection[0018,1140]
16. instance.SamplesPerPixel[0028,0002]
17. instance.ViewCodeSequence[0054,0220]
18. instance.ViewPosition[0018,5101]
19. matched_instance_number
20. number_of_frames
21. scroll_matched_instance
22. instance.Laterality[ALL], included metadata: imageLaterality; attribute.00200060, frameLaterality
23. instance.ViewPosition[ANY], included metadata: viewPosition, protocolName, attribute.0008103E, attribute.00540220, attribute.00540220/00080121, "attribute.00540220/00540222, attribute.00540220/00540222/00080121

DICOM tags

In general, any tag from the DICOM file may be retrieved and returned with instance metadata. However, saving the time and data space, the limited amount of data is retrieved. Part of the metadata is built in metadata, and is always returned. The other part is configurable, and returned by default configuration. The configurable metadata may be added, or removed. See install manual for description, how to change the returned instance metadata. See section about Changing hanging protocol configuration for explanation, how to use the tags, that were added to instance metadata, in hanging protocols.

The default list of instance metadata is provided in table below:

DICOM attribute tag and name	Variable(s) in instance metadata (with data retrieve and access path)
Built in instance metadata	
00080008 Image Type	imageType
00082218 Anatomic Region Sequence	anatomicRegion
00180015 Body Part Examined	bodyPartExamined
00181030 Protocol Name	protocolName
00181140 Rotation Direction	rotationDirection
00185101 View position	viewPosition
00200011 Series Number	seriesNumber
00200020 Patient Orientation	patientOrientation
00200062 Image Laterality	imageLaterality
00209072 Frame Laterality	frameLaterality
Instance metadata, extended by default configuration	
00080070 Manufacturer	attribute.00080070 attribute.00500010/00080070
00080080 Institution Name	attribute.00080080
00081010 Station Name	attribute.00081010
00081090 Manufacturer's Model Name	attribute.00081090 attribute.00500010/00081090
00082228 Primary Anatomic Structure Sequence	attribute.00082228
00180010 Contrast Bolus Agent	attribute. 00180010
00181000 Device Serial Number	attribute.00081000 attribute.00500010/00081000
00181400 Acquisition Device Processing Description	attribute.00181400 attribute.00189506/00181400 attribute.52009229/00189412/00181400 attribute.52009230/00189412/00181400
0020,006X Laterality	"attribute.00200060"

00280002 Samples Per Pixel	attribute.00280002
00281300 Breast Implant Present	attribute. 00281300
00540220 View Code Sequence	attribute.00540220 attribute.00540220/00080121 attribute.00540220/00540222 attribute.00540220/00540222/00080121
00185101 SeriesDescription	attribute.0008103E



NOTE! If multiple path values are configured, and the data is returned from several pathes, the system requires at least one corresponding value in case of positive operator (like contain, =), and no one corresponding value in case of inverted operator (like not_contain, !=).

In case when Sequence is configured as instance metadata attribute, the system concatenates all the data from the first level data tags into one string type attribute, and returns this string in metadata. In the sequence contains child sequences, the data from these sequences are not retrieved automatically. You need to add the child sequence explicitly, and the concatenated string with child sequence data attribute values will be returned as additional attribute. Example:

- View Code Sequence in DICOM file:

- (0054,0220)	SQ		View Code Sequence
(0008,0100)	SH	R-10206	Code Value
(0008,0102)	SH	SNM3	Coding Scheme Designator
(0008,0104)	LO	antero-posterior	Code Meaning

- Returned values in instance metadata:

```

▼ attributes: {00080070: "0", 00081090: ""Definium 6000"", 00080080: "",...}
  00080070: "0"
    ...
  00540220: "R-10206\\SNM3\\antero-posterior"
    ...
  00540220: "R-10206\\SNM3\\antero-posterior"

```



NOTE! The ACR BI-RADS Equivalent value will be added in addition to the code value in the View Code Sequence of the mammography image, if one of the following view codes is present: R-10224; R-10226; R-10228; R-10230; R-10242; R-10244; R-102D0; R-1024A; R-1024B. Example: if the view code "R-10228" is found, the substring "R-10228 (LM)" will be added to the metadata string.



NOTE! The string type should be used for handling the concatenated sequence string and it is recommended to use the "contain" and "not_contain" operators in the sequence case.

When regular DICOM tag is used in hanging protocol configuration and hanging protocol, there should be the scope defined for the tag. The scope is defined as prefix before the tag, for example "study.00181010".

The following scope prefix's may be used:

- "study." prefix is used for retrieving the metadata from the representative main series instance. The main series of the study is the first series having the main study modality;

- “series.” prefix is used for retrieving the data from the representative instance of each series in the study;
- “instance.” Prefix is used for retrieving the data from each instance.



NOTE! The representative series instance is either first, or middle instance, depending on what instance is configured and used for thumbnail creation.

The scope prefix affects the hanging protocol conditions executions, as explained:

- If “series.” scope is used in Study conditions, the system checks representative instance of each series, and indicates the conditions as true depending on the used operator. For regular operators, like “contain”, “=”, the condition is evaluated as true, if at least one series match the value. For inverted operators, like “not_contain”, “!=”, the condition is indicated as true, if all the series match the value. Examples:
 - If Study conditions has condition “series.0008103E contain “tomo””, the condition is evaluated as matched, if at least one series in study contains description with word “tomo”.
 - If Study conditions has condition “series.0008103E not_contain “tomo””, the condition is evaluated as matched, if no one series in study contains description with word “tomo”.
- Tags with “instance.” scope are not supposed to be used in Group conditions, Study conditions, or Series conditions.

Custom tags in Group, Study, Series and Instance conditions

The custom tags do not have the scope prefix and general rules of execution. The condition execution depends on the tag, operator, and conditions type (Group condition, Study condition, Series condition, or Instance condition). The section has the alphabetic list of custom tags with input type for the tag in the brackets near the name, and the additional description of condition.



NOTE! Prior study conditions and Other study conditions has separate list of custom tags and execution rules, and these are explained in separate section.

- **instance_number** [numeric]: instance level data, equals to the instance number in the series, as sorted in the Viewer window. Conditions execution explanation:
 - Instance level tag “instance_number” is not supposed to be used in Group conditions or Study conditions.
 - Instance level tag “instance_number” is not supposed to be used in Series conditions, use the series_instances_count custom tag, if count of the instances in the series is required.
 - Set value to “-1”, if want to open the middle instance in the series.
 - **instance_SOP_class_UID** [string]: instance level data, retrieved from the DICOM tag 00080016. Conditions execution explanation:
 - Instance level tag “instance_SOP_class_UID” is not supposed to be used in Group conditions, Study conditions, or Series conditions.
 - **instance_transfer_syntax_UID** [string]: instance level data, retrieved from the DICOM tag 00020010. Conditions execution explanation:
 - Instance level tag “instance_transfer_syntax_UID” is not supposed to be used in Group conditions, Study conditions, or Series conditions.
-

- **matched_instance_number** [numeric] - the number starting from the 1 may be entered, and it indicates, which instance, that meets the other instance conditions, should be used. Conditions execution explanation:
 - Instance level tag “matched_instance_number” is not supposed to be used in Group conditions, Study conditions, or Series conditions.
 - When series conditions are specified, the instance is searched for and taken from the series found according to the series conditions. Otherwise, the instance is searched for in the entire study.
- **main_study_modality** [string]: study level data, the modality from the series modalities, which the algorithm identifies as main. Unlike modalities_in_study, that contains all series modalities list, only one modality is defined as main.
- **matched_series_number** [numeric] - the number starting from the 1 may be entered, and it indicates, which series, that meets the other series conditions, should be used. Conditions execution explanation:
 - Series level tag “matched_series_number “ is not supposed to be used in Group conditions, Study conditions, or Instance conditions.
- **modalities_in_study** [string]: study level data, list of modalities of the series of the study. Each modality is included one time. The modalities of not displayable series, like presentation states (PR), key objects (KO), segmentations (RTSTRUCT) are not included in the modalities_in_study.
- **number_of_frames** [numeric]: instance level data, retrieved from DICOM tag 00280008. Conditions execution explanation:
 - Instance level tag “number_of_frames” is not supposed to be used in Group conditions, Study conditions, or Series conditions.
- **patient_studies_count** [numeric]: count of patient studies. The current study is included into the count.
- **patient_studies_modality_count** [numeric]: count of patient studies, having the same modality as main modality of current study. The current study is included into the count.
- **open_studies_count** [numeric]: count of studies, that are opened in Viewer window. The current study is included into the count.
- **open_studies_modality_count** [numeric]: count of studies with the same modality as main modality of current study, that are opened in Viewer window. The current study is included into the count.
- **scroll_matched_instance** [numeric]: used for enabling scrolling through all the instances, that match the instance conditions. If scroll_matched_instance condition is used in instance conditions, the system creates a kind of virtual series from all the study instances, that match the instance conditions, in the same order as they are ordered in study. The first instance is opened by default, but **matched_instance_number** condition may be used to open the other instance. If scroll_matched_instance condition is used in instance conditions, the series conditions may be not defined, and is ignored, if defined.
- **scroll_matched_series** [numeric]: used for enabling moving to the next matching series, when scrolling images in the viewport. If scroll_matched_series condition is used in series conditions, the system automatically opens the first image of the next series, that matches the series conditions, when to the end of the current series is reached.
- **series_count** [numeric]: count of the displayable series of the study. The not displayable series, like presentation states (PR), key objects (KO), segmentations (RTSTRUCT), are not included in the count. The displayable secondary captures series are included into count.
- **series_description** [string]: series level data, retrieved from DICOM tag 0008103E. Conditions execution explanation:
 - If series_description tag is used in Study conditions or Group conditions, the system checks each series, and indicates the conditions as true depending on the used operator. For regular operators, like “contain”, “match” the condition is evaluated as true, if at least one series description in the study match the value. For inverted operators, like “not_contain”, “not_match”, the condition is indicated as true, if all the series description in the study match the value.
- **series_instances_count** [numeric]: count of all the instances in the series. Conditions execution explanation:

- Tag “series_instances_count” not supposed to be used in Group conditions or Study conditions.
- **series_modality** [string]: series level data, retrieved from DICOM tag 00080060. Conditions execution explanation:
 - Tag “series_modality” not supposed to be used in Group conditions or Study conditions, use the modalities_in_study custom tag, if modalities of all series are needed.
- **series_number** [numeric]: series level data, equals to the series place number in the Viewer window. Conditions execution explanation:
 - Tag “series_number” is not supposed to be used in Group conditions or Study conditions, use the series_count custom tag, if count of the series in the study is required.
- **series_SOP_class_UID** [string]: instance level data, for series it is retrieved from the DICOM tag 00080016 of the representative instance of the series. Conditions execution explanation:
 - If series_SOP_class_UID tag is used in Study conditions or Group conditions, the system checks each series, and indicates the conditions as true depending on the used operator. For regular operators, like “contain”, “match” the condition is evaluated as true, if at least one series description in the study match the value. For inverted operators, like “not_contain”, “not_match”, the condition is indicated as true, if all the series description in the study match the value.
- **series_transfer_syntax_UID** [string]: instance level data, for series it is retrieved from the DICOM tag 00020010 of the representative instance of the series. Conditions execution explanation:
 - Series level tag “series_transfer_syntax_UID” is not supposed to be used in Group conditions.
 - If series_transfer_syntax_UID tag is used in Study conditions, the system checks each series, and indicates the conditions as true depending on the used operator. For regular operators, like “contain”, “match” the condition is evaluated as true, if at least one series description in the study match the value. For inverted operators, like “not_contain”, “not_match”, the condition is indicated as true, if all the series description in the study match the value.
- **sop_instance_UID** [string]: instance level data, for series it is retrieved from the system returned study structure taking from any representative instance of the series. Conditions execution explanation:
 - Series level tag “sop_instance_UID” is not supposed to be used in Group or Instance conditions.
 - The purpose of the attribute (condition) is to identify the virtual (created by the system from multiframe image for example) series, for which the instance UIDs are constructed with the “.” symbol in UID. In study conditions the purpose is to identify study, that contains or not contains the virtual series: for operator “contain” the condition is evaluated as true, if at least one series is virtual, and for “not_contain” the condition is indicated as true, if all the series are not virtual.
- **study_description** [string]: study level data, retrieved from DICOM tag 00081030.
- **study_instances_count** [numeric]: count of all the instances in the displayable series of the study. The not displayable series, like presentation states (PR), key objects (KO), segmentations (RTSTRUCT), instances are not included in the count. The displayable secondary captures series instances are included into count.

Custom tags in Prior study conditions and Other study conditions

Prior study conditions and Other study conditions has separate list of custom tags and execution rules, that are explained in this section. See Custom tags section for custom tags, that are used in other conditions.



NOTE! Tags, that may be used in Prior study conditions and Other study conditions, are limited to the Custom tags, that are listed in this section.



NOTE! If patient history functionality is disabled in the system or for the user, the system treats the current study as the only patient study when executing the prior study conditions.

Prior study conditions

The complete patient studies list consists of the studies, that are displayed patient history window, excluding the primary study, for which the hanging protocol is initially applied. Prior study conditions are the rules for selecting the Prior studies from the whole patient studies list. The studies that meet the Prior study conditions are automatically sorted by study date, starting from the oldest. Custom tags to be used in the Prior study conditions:

- **modalities_in_patient_study** [string]: study level data, list of modalities of the series of the study.
- **patient_study_description** [string]: study level data, retrieved from DICOM tag 00081030.
- **scroll_step** [numeric]: used for adding the iteration through Prior studies. If scroll_step condition is used, the system displays the Next comparison study button in the Viewer for opening the next study from the Prior studies list, in case more than one study is found in the Prior studies list. Note, that number of opened prior studies may be limited by setting the "Maximum number of comparison studies" parameter in hanging protocol. Set scroll_step to 1, if you need to navigate through the comparison studies one by one. Setting the scroll_step to 2, omits one study and opens the next after it. The process is cyclic.
- **study_date_filter** [dateTime]: used for filtering the prior or other studies according to study date.



NOTE! Currently the system supports only variable @primary_study_date to be used in study date filter.

Other study conditions

The complete other studies list consists of the studies, that are opened in the Viewer window. In general, this function is foreseen for cases, when several studies are opened in the Viewer. The first study in the Viewer window is treated as primary study, for which the hanging protocol is applied. The Other study conditions may be used for selecting Other studies from the rest of the studies, that are opened in the Viewer window. The studies, that meet the Other study conditions, are sorted in the same order, as they are listed in the Viewer window toolbar. Custom tags to be used in the Other study conditions:

- **modalities_in_open_study** [string]: study level data, list of modalities of the series of the study.
- **open_study_description** [string]: study level data, retrieved from DICOM tag 00081030.
- **scroll_step** [numeric]: used for adding the iteration through Other studies. If scroll_step condition is used, the system displays the Next comparison study button for opening the next study from the Other studies list, in case more than one study is found in the Other studies list. Set scroll_step to 1, if you need to navigate through the comparison studies one by one. Setting the scroll_step to 2, omits one study and opens the next after it. The process is cyclic.
- **study_date_filter** [dateTime]: used for filtering the prior or other studies according to study date.



NOTE! Currently the system supports only variable @primary_study_date to be used in study date filter.

Editing hanging protocols configuration

The hanging protocol configuration may be changed only by manual editing of the "hangingProtocolsConfig.json" file.

The structure of "hangingProtocolsConfig.json" is as follows:

```
{
```

```

    "groupConditions": [{...}, {...}, ...],
    "studyConditions": [{...}, {...}, ...],
    "priorStudyConditions": [{...}, {...}, ...],
    "otherStudyConditions": [{...}, {...}, ...],
    "viewportSeriesConditions": [{...}, {...}, ...],
    "viewportInstanceConditions": [{...}, {...}, ...]
  }

```

Each conditions array holds the tags list of the corresponding conditions group of the hanging protocols settings. The tags in the drop-down list are listed in the same order, as they are placed in the array.

Each object in the array describes one tag in the tags list, either custom tag, or DICOM tag. The structure of the tag object is as follows:

- Example of the custom tag of the string type object:

```

{
  "name": "modalities_in_study",
  "inputType": "string",
  "operations": [
    "match",
    "not_match",
    "begins_with",
    "end_with",
    "contain",
    "not_contain"
  ],
  "path": []
}

```

- Example of the DICOM tag of the numeric type object:

```

{
  "name": "instance.SamplesPerPixel[0028,0002]",
  "inputType": "numeric",
  "operations": [
    "=",
    ">",
    "<",
    ">=",
    "<=",
    "!="
  ],
  "path": [
    "attribute.00280002"
  ]
}

```

- Example of the DICOM tag of the dateTime type object:

```

{
  "name": "study_date_filter",
  "inputType": "dateTime",
  "operations": [
    "=",
    ">",
    "<",
    ">=",
    "<=",
  ],
  "path": []
}

```

- Description of the attributes of the tag object:

- “name” is the unique name of the tag, which is displayed in the drop-down tags list. The name of the custom tag must be from the list of allowed custom tags. The name of the DICOM tag must comply the required format, starting from one of the scope prefix, and ending of 8 digits string.
- “inputType” may be either “string”, or “numeric”, or date`Time`. The input type for the custom tags is provided in the section with the custom tags’ description. The input type for the DICOM tags is selected based on the tag type, and how you want the system to validate the value. If the DICOM data may be converted to numeric type, and you want to use the numeric validation, like “>”, the “numeric” input type should be used. Use the “string” input type otherwise. Note, that for DICOM sequence, the concatenated string of all the data tags from the first sequence level is built, and therefore only the “string” input type should be used.
- “operations” array includes the list of operation, that is displayed for the tag in the drop-down operations list. The examples above have the complete list of operations for the “string” input type, and “numeric” input type, and “date`Time`” input type. You may add less operation to the array, if some are not needed, but only the operation from the listed may be used.
- “path” array has the value of the instance metadata attribute, where the particular data should be searched. The “path” should not be added for the custom tag, and is required for the DICOM tag. The path values for DICOM tags, that are included in instance metadata by default configuration, is provided in section with default DICOM tags description. For the built-in metadata, the system search for the data is hardcoded, and you can provide only the instance metadata attribute value. For the extended metadata, you can configure where to search for the DICOM tag value (see Install manual for additionalMetadataTags configuration), and you can configure the several paths, for example to check in shared multi-frame sequence, and per-frame sequence. In such cases, the found values will be stored in corresponding metadata attribute, and all these metadata attributes should be provided in the “path” array in order the system check all of them. Conditions execution with multiple paths:

For regular operators, like “contain”, “=”, the condition is evaluated as true, if at least one of the several paths has data and match the value.

For inverted operators, like “not`_`contain”, “!=”, the condition is indicated as true, if at least one of the several paths has data and all the returned values the value.

In case no data is returned, the condition is indicated as false.

The bellow described changes of the “hangingProtocolsConfig.json” is save and simple:

- You can remove not used tags from the drop-down tags list bey removing the corresponding tag object from the corresponding array.
- In default hanging protocols configuration, all the operations are listed for each tag. You can remove not needed operation for the tag by removing the string from the “operations” array.



NOTE! Tags order in the configuration has no effect, as system sorts the tags in expandable list according to the name.

Examples of default and changed hanging protocol configuration are provided in the figures below.

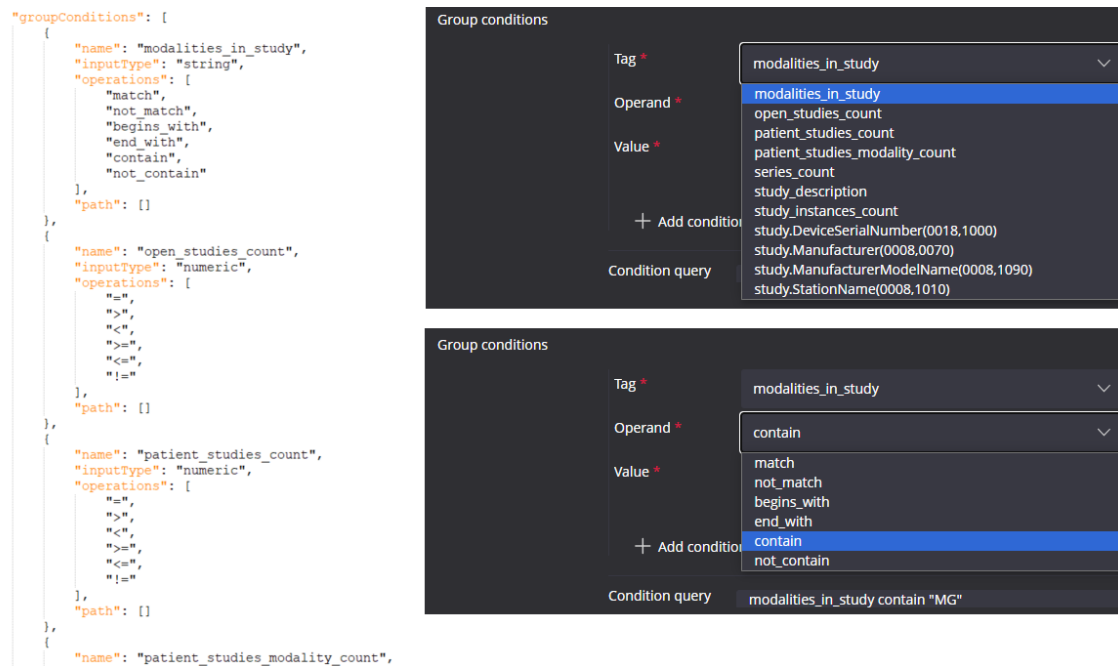


Figure 2. Default Group conditions configuration

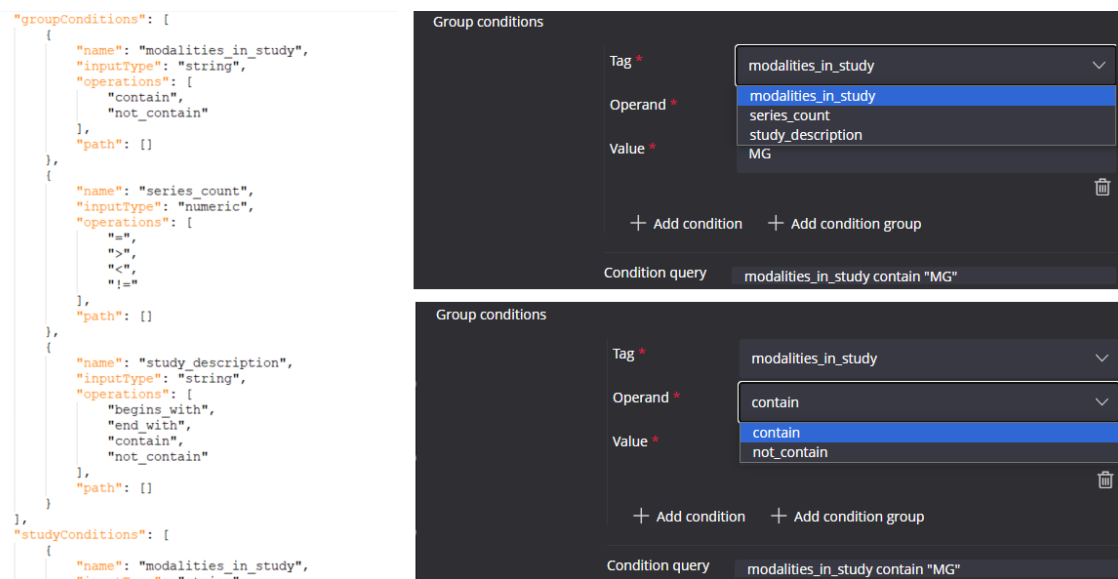


Figure 3. Changed Group conditions configuration

It is also possible to add the additional tags for Group conditions, Study conditions, Series conditions, or Instance conditions by extending the instance metadata and adjusting the hanging protocols configuration. However, these changes are more complex, requires additional analysis, and it is recommended to contact the support or integration staff in such case.

Hanging protocol settings

NOTE! The system may be configured to run either the Hanging protocol version V1 or the Hanging protocol version V2 and the corresponding version is displayed in the Hanging protocols settings page. See install manual for instructions, how to change the configuration.

On **Hanging protocol** tab, you can create new hanging protocols, review and modify existing hanging protocols. The window below lists the hanging protocols, which are provided in default hanging protocols json file.

NOTE! The file hangingProtocolsV2.json with default version V2 hanging protocols is included in build package. If the file is deleted, the system will automatically recreate the file with few protocols, but not all the default protocols.

Figure 4. Hanging protocol settings

NOTE! All the data changes that are done in Hanging protocol list, group and protocol child windows (like create group window, create protocol window) are saved in the temporary storage. That means the changes are not accessible to the other users and would be lost in case of program accidental close. The permanent data saving is done only when the **Save settings** is done.

NOTE! The hanging protocols are stored separately from the other system settings.

NOTE! The hanging protocols of version 2 are stored separately from the hanging protocols of the first version. You will not damage the protocols of the first version, if trying the Hanging protocols V2 functionality.



NOTE! Note that the user with the administrator right can modify only the global hanging protocols, which, after saving, are shared by all users. See the install manual on how to configure the hanging protocols per user group or user.

Hanging protocols applying settings

Apply HP on initial study open in Viewer *	Auto	Menu	No
Apply HP on initial study close in Viewer *	Auto	Menu	No
Apply HP on studies change in Viewer *	Auto	Menu	No

Figure 5. Hanging protocol applying settings

The hanging protocol applying settings defines when and how the system executes the conditions for selecting the applicable hanging protocols and applies the hanging protocol:

- If **Auto** option is selected, the protocol conditions are executed, and the first protocol from the applicable protocols list is automatically applied.
- If **Menu** option is selected, the first study that is opened in the empty Viewer window is treated as initial study, and the hanging protocol conditions is executed protocol conditions are executed, and the applicable protocols list is built, but hanging protocol is not applied automatically. The user may select and apply the hanging protocol in the hanging protocol modal or drop-down menu.
- If **No** option is selected, the hanging protocol conditions for the case is not executed.

The hanging protocol conditions may be executed or re-executed upon the described events:

- The setting **Apply HP on initial study open in Viewer** allows to execute and apply the hanging protocol for the initial study, which is the first study, that is opened in the empty Viewer window. The default value for **Apply HP on initial study open in Viewer** setting is **Auto**, and this is common hanging protocol usage mode.
- The setting **Apply HP on initial study close in Viewer** allows to re-execute the hanging protocols conditions, if the user closes the initial study (first study in the Viewer thumbnail bar). The default value for this setting is **No**. The system re-executes and applies the hanging protocols for the study, that became the first study in the Viewer thumbnail bar, if **Auto** or **Menu** option is selected for **Apply HP on initial study close in Viewer** setting.
- The setting **Apply HP on studies change in Viewer** allows to re-execute the hanging protocols conditions, if the user closes any of the studies in the Viewer window. The option is useful for hanging protocols with Other studies conditions applied. The default selection for this setting is **No**.



NOTE! The system does not prevent from setting the **Apply HP on initial study open in Viewer** to **No**, but applying the hanging protocol on initial study close or studies change. However, such behavior would be hardly understandable by user, and such configuration is not recommended.

Hanging protocols list

The system has three lists of hanging protocols, serving the different purposes:

- The main list is the first in the settings window and contains the protocols that are applied when opening the study in Viewer.

- The 'HP for Comparison study' list is placed below the main list and contains the comparison study protocols that may be applied as sub-protocol inside the main protocol (see section 'Enable comparison protocol in panel').
- The 'HP for Study drag' list is placed below the 'HP for Comparison study' list and contains the protocols that are applied for the study when its header is dragged to the viewport.

If not specified otherwise, the below described hanging protocol list features apply to all three lists

The Hanging protocol list is two level expandable list with the hanging protocol group in the first level and the hanging protocols of the group in the second level.

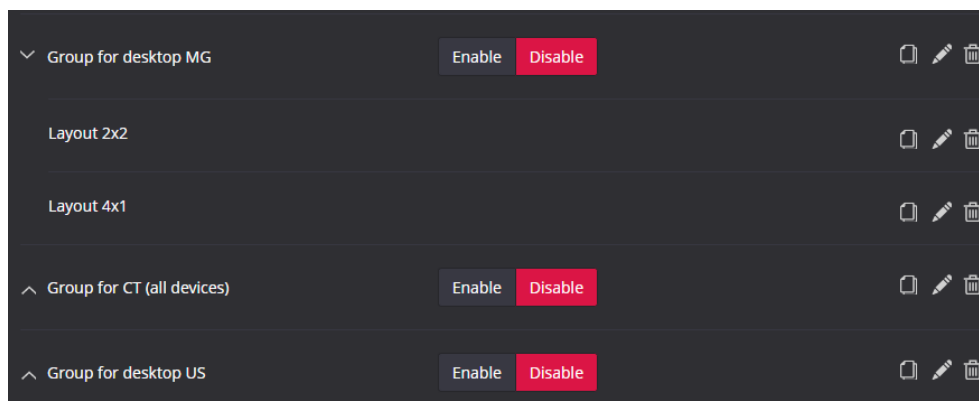


Figure 6. Hanging protocols list

You can perform the following in the hanging protocols list:

- To expand or collapse the list of group's protocols with chevron icon at the left of group's name.
- To enable the group's protocols by selecting the Enable/Disable buttons. The disabled groups and its protocols are not used for automatic or manual apply.



NOTE! The 'HP for Study drag' protocols list has only one protocols group, that is recreated empty and disabled by default. This list does not have group management (create, copy, edit, delete) functions, only possibility to enable or disable the group.

- The Copy, Edit, and Delete icons-buttons at the end of each group's and protocol's line provides access to group's or protocol's data review and edit:
 - clicking the **Copy** icon makes the copy of hanging protocol or group of protocols. The protocol is placed at the end of the group protocols list and postfix "-copy" is added to the name of the copied protocol. The group is placed at the end of the group list and postfix "-copy" is added to the name of the copied group and all its protocols;
 - Clicking the **Edit** icon at the end of group line opens the **Edit group** window with group data filled in the entry fields. You can review and edit the group's data. See detail fields description in Create hanging protocols group section;
 - Clicking the **Edit** icon at the end of protocol line opens the **Edit protocol** window with protocol data filled in the entry fields. You can review and edit the protocol's data. See detail fields description in Create hanging protocol section;
 - Clicking the **Remove** icon at the end of group or protocol line deletes the item. If the group is removed, all the protocols of this group are also deleted.
- The drag-and-drop functionality for changing the order of groups in the same protocols list and for changing the order of protocols in the same protocols group. To change the place of the group or protocol item, press the right mouse button on the item and drag the item to the desired place. The items order is important in automatic hanging protocol apply: the first group, that meets the group conditions, is chosen and the first protocol of this group, that meets the study conditions, is applied.

Create hanging protocols group

Clicking the **Add new group** button above the Hanging protocols list opens the **Create group** window:

Figure 7. Create hanging protocol group window

NOTE! The group creating functionality is not applicable for the 'HP for Study drag' protocols list.

NOTE! The 'HP for Comparison study' list group has only name description and enabling attributes available in the group window.

To create a new hanging protocol group:

- Enter the required group name in **Name** field. The group name is used for protocol identification and is shown to the users in MedDream viewer.
- If you need, enter the group description in **Description** field. The group description is only visible in settings.
- Select the **Devices** for which the group's protocols should be applied. Clicking the button with device name enables or disables selection.

NOTE! The device settings may be used only by web browsers based on Chromium. And Window management should be allowed in the MedDream site Privacy and security settings for getting access to device information.

NOTE! If no one device is enabled, or device information may not be received from the browser, the protocol group is treated as applicable for any devices.

- Specify the Group conditions. The conditions entry is described in Enter the conditions section.
- Enable the **Skip if other group has applicable HP** option, if you want the group to be disabled in case there is other group with applicable protocols already found for the study.

- Activate hanging protocol group by selecting Enable or Disable buttons in the **Active** field. The disabled groups and its protocols are not used for automatic or manual apply.
- Click the **Create** button when all the group data is entered. The **Create group** window is closed, the entered group data is saved in temporary storage and is shown at the end of hanging protocol list on Hanging protocol setting tab.

Quick save HP group

The Quick save HP feature may be enabled in the system which allows the user to create the hanging protocol from the layout and images in the Viewer window. The system groups automatically created quick save hanging protocols by the main modality of the primary study and assigns to the corresponding quick save HP group. If the corresponding group does not exist, the system automatically creates it and places at the top of the protocols list.

The screenshot shows the 'EDIT GROUP' window for a 'Quick save HP for modality CT' group. The window contains the following fields and controls:

- Name:** Quick HP for CT
- Description:** (Empty text field)
- Devices:** A row of buttons: Mobile, Tablet, Desktop, 1 display, Desktop, 2 displays, Desktop, 3 displays, Desktop, 4 displays.
- Group conditions:**
 - Tag:** main_study_modality
 - Operand:** match
 - Value:** CT
 - Buttons:** + Add condition, + Add condition group, and a trash icon.
- Condition query text form:** main_study_modality match "CT"
- Skip if other group has applicable HP:** Enable (selected), Disable
- Active:** Enable (selected), Disable
- Buttons:** Update (highlighted in red), Close

Figure 8. Quick save hanging protocol group edit window

The automatically created quick save HP group has the read only Quick save HP for modality and Name fields. Based on this information the system assigns the new quick save hanging protocols to the group. This data is not used when applying the hanging protocols.

By default, the system creates the group condition for main modality of the study to match the quick save HP group modality. The user can edit the group conditions and the other attributes for the quick save group as described in parent section and save the updated group data. The saved group and protocol information is further used when applying the hanging protocols.

NOTE! If Quick save HP feature is disabled in the system, the system will automatically ignore the quick save HP groups despite the group is marked as active. However, the quick save groups and protocols in the group can still be viewed and edited in Hanging protocols v2 settings page. If you want some of previously saved quick save hanging protocols to be used after disabling the Quick save HP feature, assign the particular protocol to the regular (not quick save HP) group, or make a copy of the whole quick save HP group with all the protocols.

Enter the conditions

Condition is an expression that could be evaluated as true or false and is used for automatic selecting the applicable Hanging protocols. Condition consist of custom tag or DICOM tag that by default is evaluated against the entered static value according the specified 'operand'. An example of condition: 'Modalities in study contains 'MG''. By default, the entered conditions are joined to final rule using AND operand, that means all conditions should be met. The conditions grouping and setting different operator currently is allowed only for Study conditions (see section "Combine Study conditions").

NOTE! For all the conditions except Study conditions, the system curently supports only AND operator for joining conditions into executable rules.

NOTE! The system supports entering the variable instead of the statis value for the condition of the String type. Currently supported variables: 1. `@primary_study_main_modality` variable should be used for the main modality of the initial study. 2. `@primary_study_date` should be used in study date filter for the date and time of the initial study.

The system allows to enter the ecexution rules in Condition query text form editor field, or by entering each condition using the condition entry fields.

Figure 9. Hanging protocol condition's entry fields

If the user clicks the **+Add condition**, the system displays the **Tag**, **Operand** and **Value** fields for new condition entry. The system automatically selects the first value of the Tag and Operand expandable list, and displays the corresponding text expression in the condition query entry field.

To enter the condition using conditions entry fields:

- select DICOM or custom tag in Tag drop-down list. The list of tags for each conditions type is defined by hanging protocol configuration, and the tags are sorted alphabetically by name;
- select the evaluation operand in Operand drop-down list. The operands list for a particular tag depends on the tag type and is taken from the hanging protocol configuration;
- enter the value in Value field. The string value should be entered for string tag, and the numeric value should be entered for numeric tag.

NOTE! See detailed tags description and conditoyions execution descritpion in hanging protocol configuration section.

To remove the entered condition, click the **Remove** icon below the condition entry fields.

All the actions in with the condition entry fields are immediately reflected in **the Conditions query text form** and vice versa. You can enter or edit the conditions directly in the form.

Combine Study conditions

System provides the following possibilities for Study conditions entry:

Elementary condition in top-level rule

Condition group in in top-level rule

Study conditions

All conditions in group combined with OR

All conditions and condition groups in top-level rule combined with AND

Tag

Operand

Value

Tag

Operand

Value

Tag

Operand

Value

Tag

Operand

Value

Tag

Operand

Value

+ Add condition

+ Add condition group

Combining conditions using

Combining conditions using

Show all condition connectors

Condition query text form

open_studies_count > 1 && (modalities_in_study contain "CT" || modalities_in_study contain "PT" || modalities_in_study contain "MR")

Figure 10. Study condition's entry

- Adding multiple elementary condition or one level (not nested) condition groups to the rule. The controls for the top-level rule conditions or condition groups adding are placed at the bottom of the rule conditions entry fields, above the query form.
 - Clicking the **+Add condition** adds the fields for entering the elementary condition. See the parent section for details on how to fill the fields, edit or delete the condition.
 - Clicking the **+Add condition group** adds the new group. By default, the group is empty and you should use the **+Add condition** located at the bottom of the group to add conditions to this group. See the parent section for details on how to fill the fields, edit or delete the condition inside the group. The Delete button located at the bottom of the group may be used to delete the group.
- To select the AND and/or OR operator to combine the conditions in the group and in the top-level rule.
 - If more than one condition is added to the group, the **Combining conditions using** field is displayed at the bottom of the group, near the **+Add condition** field. You can set the same operator to combine all the conditions inside the group by clicking the "&&" or "||" option in **Combining conditions using** field. If the same operator is applied for the whole group, it is highlighted: **Combining conditions using && ||**.

- If more than one condition/condition group is added to the top-level rule, the **Combining conditions using** field is displayed on the right of **+Add condition** field for the top-level rule. You can set the same operator to combine all the elementary conditions and condition groups inside the top-level rule by clicking the “&&” or “||” option in **Combining conditions using** field for the rule. If the same operator is applied for the rule group, it is highlighted.
- You can mark the **Show all condition connectors** box to set the “&&” or “||” operator separately between any entities. It is possible to change the condition combine operator for conditions inside the group, as well as for the top-level rule conditions/condition groups. If the different operators are used inside the group or top-level rule scope, the highlighting is automatically removed from the corresponding “Combine conditions using” field.

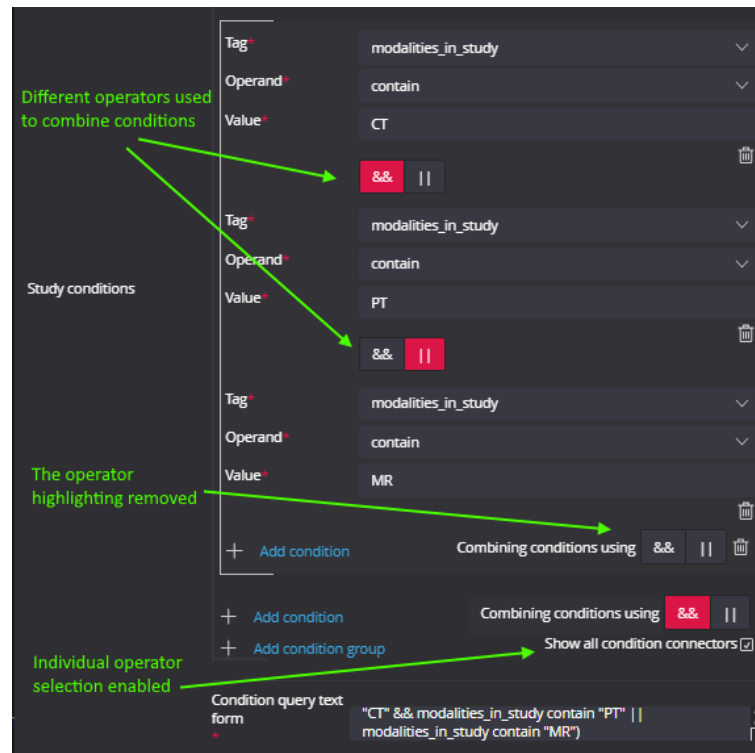


Figure 11. Changing combine operators in Study conditions

Create hanging protocol

Clicking the **Add new protocol** button on Hanging protocol settings tab opens the **Create protocol** window:

Figure 12. Create protocol window

To create a new hanging protocol:

- Select the group of the hanging protocol in **Group** drop-down list.



NOTE! The system allows the protocol to for 'HP for Comparison study' list or 'HP for Study drag' list by selecting the Group from this list when editing the hanging protocol. If the protocol from main list with more than one panel is selected the 1x1 panel is moved.

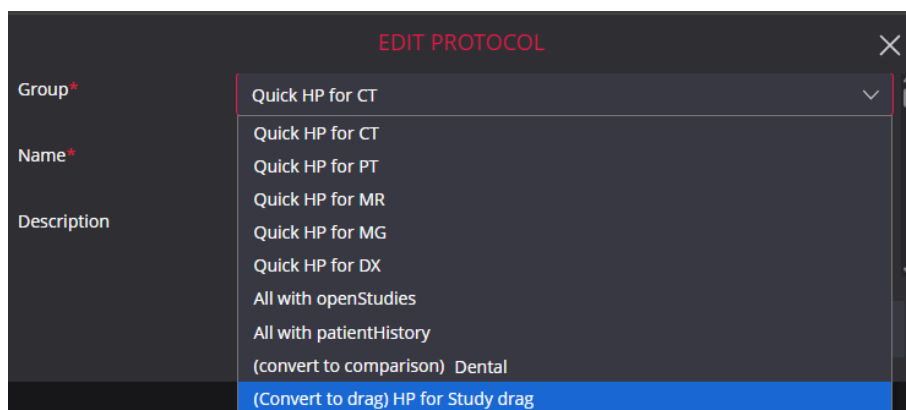


Figure 13. Move protocol to other list in Edit protocol window

- Enter the required protocol name in **Name** field. The protocol name is used for protocol identification and is shown to the users in MedDream viewer.
- If needed, enter the protocol description in **Description** field.
- Define the number and layout of panels for the protocol by selecting from the **Panels** drop-down list. The selected number of panels will be added at the end of the window.



NOTE! The layout of panels selection is not available for 'HP for Comparison study' and 'HP for Study drag' protocols. These protocols apply in one panel, and the layout is automatically set to 1x1 Panel.

- Select **Link scrolled series** option which you want to be set in the Viewer window when this hanging protocol is applied. If any option is selected, the hanging protocol does not change the Link scrolled series selection in Viewer window.
- Select **Sync actions** option which you want to be set in the Viewer window when this hanging protocol is applied. If any option is selected, the hanging protocol does not change the Sync actions selection in Viewer window.
- Specify the **Study conditions**, that will be used to select whether the protocol should be applied to the study. See description of condition entering in the Enter the conditions section.
- Select either the **Prior conditions** and related options, or the **Other conditions**, if you want the image from other studies to be displayed for comparison, and enter the conditions for comparison studies selection. For more detailed description of using comparison studies in hanging protocols see section Enter comparison studies data.



NOTE! The comparison studies data entry is not available for 'HP for Comparison study' and 'HP for Study drag' protocol.

- Specify the hanging protocol layout, image selection and display data for each panel of the selected hanging protocol panels layout. The expandable subsections for each panel are displayed at the bottom of the window. See next sections for panel layout and viewport data entry.
- Click the **Create** button when all the protocol and views data is entered. The Create protocol window is closed, a new protocol is saved in temporary storage and is shown as the last protocol of selected group in protocols list on Hanging protocol settings tab.

Enter panel layout



NOTE! The layout of panels selection is not available for 'HP for Comparison study' and 'HP for Study drag' protocols.

NOTE! The panel is identified by number [row number]x[column number], that is identifier “1x2” indicates the panel in the first row and second column. The arrow near the panel indicator can be used to expand or collapse the data entry fields for the panel.

The regular layout or overview layout may be selected for the panel.

To specify the regular layout for the panel:

The figure shows two screenshots of the '1x1 Panel' settings interface. The top screenshot shows the 'Layout columns' field set to 2, with a red box highlighting the input field and its dropdown arrow. The bottom screenshot shows the same interface with the 'Layout columns' field set to 2, also with a red box highlighting the input field and its dropdown arrow. Both screenshots show the 'Overview layout protocol', 'Quadrant zoom protocol', and 'Comparison study protocol' settings, all set to 'Disable'.

Figure 14. Entering regular layout for panel

- Keep the **Overview layout protocol** setting value **Disabled**, if creating a regular panel layout. Overview layout description see further in the section.
- Keep the **Quadrant zoom protocol** setting value **Disabled**. Quadrant zoom protocol description see in the section “Enable quadrant zoom in panel”.
- Keep the **Comparison study protocol** setting value **Disabled**. See comparison study protocol description in the section “Enable comparison protocol in panel”.
- Define the layout by entering the number of columns in **Layout columns** field and the number of rows in **Layout rows** field. The selected number of viewports will be added to the Views section.
- Specify the image selection and display data for each viewport of the selected layout as described in the next section “Enter viewport data”.

Overview layout may be used for quick reviewing of the series or the images of the study and/or comparison study in the panel. The Prior study conditions or Other study conditions for viewing the comparison studies in overview layout should be entered as described above.

NOTE! The possibility to navigate through the comparison studies list is supported and may be used in panel with overview layout.

To specify the overview layout for the panel, the following data should be entered:

- The **Overview layout protocol** setting value should be set to **Enabled** for the panel. The system automatically hides the Layout rows and Layout columns settings and creates View with only one 1x1 viewport.
- The **Overview layout** should be selected from the expandable list. The field is automatically displayed at the top of the 1x1 viewport data entry section. The value *1x1 Overview layout* is selected by default, and this means that one series or image is displayed per overview layout page.



NOTE! The system does not execute the series and instance conditions for the panel/viewport with overview layout and displays all the series or images in a row.

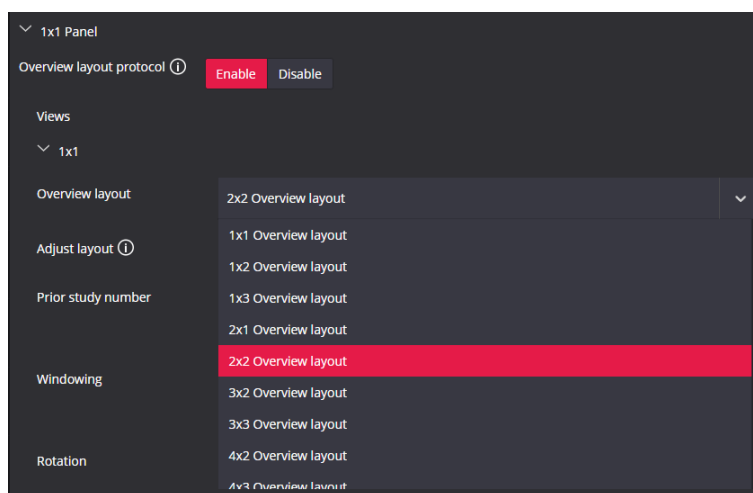


Figure 15. Selecting the Overview layout for the panel/viewport

- The **Adjust layout** setting may be changed. If set to **Enable**, the system automatically selects the 1x1 Overview layout for the panel, if the study has only one applicable series or image to display.
- The **Prior study number**, or **Other study number** may be entered, if the panel has to display the series of the comparison study in overview layout.



NOTE! The comparison studies data entry is not available for 'HP for Comparison study' and 'HP for Study drag' protocol.

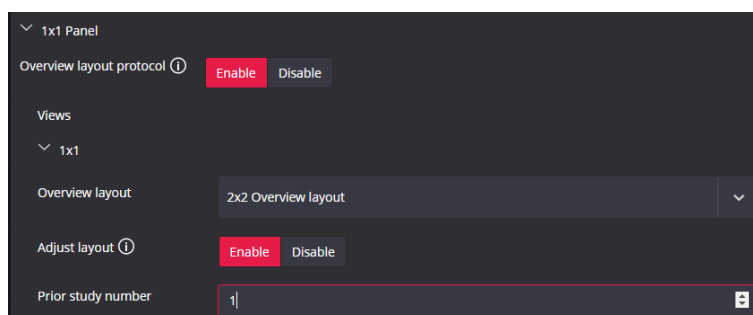


Figure 16. Viewport data entered for the panel/viewport with overview layout

When applying the hanging protocol, the system creates the selected overview layout in panel. The series, starting from the first series of the study or of the comparison study, are opened in the created overview layout. The first or the middle instance of the series, the one which is configured to be opened by default, is opened and default presentation parameters, like windowing, alignment, are applied.



NOTE! Opening all the study images instead of the series in Overview layout may be configured for particular modalities.

Enable quadrant zoom in panel

Quadrant zoom may be enabled in the Panel to automatically start the Quadrant zoom function when opening the hanging protocol.

NOTE! The quadrant zoom may be activated only in one panel of the protocol. The system asks for confirmation, if you try to enable the Quadrant zoom in the protocol which already has the panel with quadrant zoom enabled.

NOTE! The layout may not be selected for the panel with quadrant zoom, and the layout entry fields are hidden.

If the **Quadrant zoom protocol** setting value is set to **Enabled**, the system automatically applies 1 row and 2 columns regular layout for the Panel and adds the 2 viewports to the Views section:

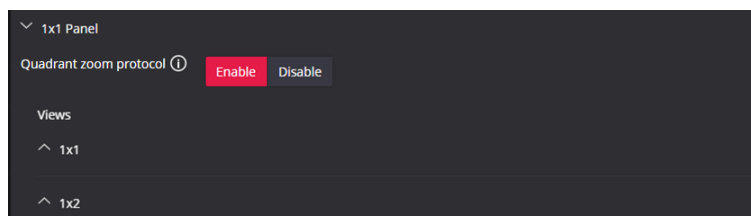


Figure 17. Selecting the Quadrant zoom for the panel

Specify the image selection and display data for each viewport of the panel with quadrant zoom enabled described in the next section Enter viewport data. Note, that quadrant zoom may be applied only for mammography images of the identical size and aligned to the center line of layout. The system automatically sets the proper alignment for each viewport. The system also hides the MPR option selection as it is not applicable for the quadrant zoom.

Enable comparison protocol in panel

The sub-protocol from the 'HP for Comparison study' list may be selected for the comparison study.

NOTE! At least one group should be created in the 'HP for Comparison study' list, and the required protocols should be created in this group in advance.

If the **Comparison study protocol** setting value is set to **Enabled**, the system automatically changes the panel attributes entry window for Comparison study data entry and protocol selection:

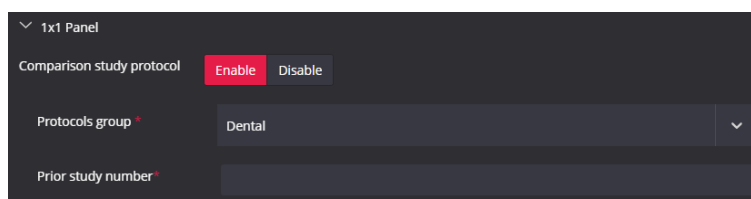


Figure 18. Selecting the Comparison protocol for the comparison study

- Select the protocol group from the drop-down list, that contains all the groups created in the 'HP for Comparison study' list. The protocol from this group will be selected for the comparison study based on the study conditions of this protocol.
- Enter the **Prior study number**, or **Other study number**. The system automatically adjusts the label, depending on the selected conditions.

Enter viewport data

NOTE! The viewport is identified by number [row number]x[column number], that is identifier "1x2" indicates the view in the first row and second column. The arrow near the viewport indicator can be used to expand or collapse the data entry fields for the view.

Figure 19. Entering viewport settings in hanging protocol

The following data may be entered for the viewport:

- The **MIST MPR** automatically starts the MPR in the viewport. The selected MPR function will be started, if the multiplanar reconstruction may be done for the selected series. The sub-layout viewports will be automatically created in the viewport, if Oblique or Dental reconstruction is selected.

If any MPR option except PET is selected, the system displays options for selecting **MPR series in Viewer** that may be used for MPR generation. The default selection is No, and the system selects series according to the series conditions. However, you can set to generate MPR from series in the Active viewport or enlarged series.

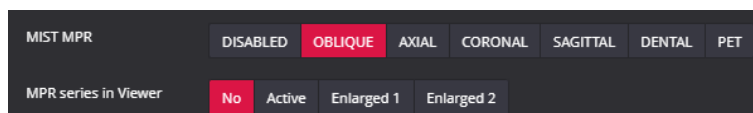


Figure 20. Setting MPR series in Viewer for MPR generation

If MPR option PET is selected, there is not possible to select the MPR series in Viewer, and background series is always selected either based series and instance conditions, or from comparison studies list based on prior/other study number. In addition, the PET series conditions must be entered to select the top series for fusion. The series for fusion is selected from the same study as background series.

Figure 21. Viewport data entry for MIST MPR PET

- The **Prior study number**, or **Other study number** for selecting the comparison study from Prior studies or Other studies list, depending of which conditions are entered for the protocol. Leave the fields empty, if the viewport is not supposed to display the comparison study instance. For detailed description of using comparison studies in hanging protocols see section Enter comparison studies data.



NOTE! The comparison studies data entry is not available for 'HP for Comparison study' and 'HP for Study drag' protocol.

- Enter the **Windowing Width** and **Center**, if you need the particular values to be applied. The default windowing will be applied at instance opening, if the fields are left empty.

- Change the **Rotation**, **Flip**, **Scale**, and **Alignment** according to your needs. Use the Zoom option of the **Scale** field, if you need the images to be identically scaled in all viewports. The system will display the entry field for entering the scale factor:

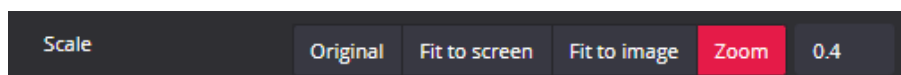


Figure 22. Entering image scale factor

NOTE! **Fit to Image** scaling is applicable only for mammography images. If the other image type is opened in the viewport, the system automatically selects the Fit to screen scaling instead of Fit to image.

- Specify the **Series conditions**. See description of condition entering in the Enter the conditions section. If the series conditions are entered, the system first finds the meeting series in the initial study, or comparison study, and then searches for the instance in the series that match the series conditions.

NOTE! The series conditions may not be entered, and then the system searches for the instance in all the series of the study, starting from the first series.

- Specify the **Instance conditions**. See description of condition entering in the Enter the conditions section. The instance conditions must be entered. The image will not be searched and opened, if instance conditions are not entered.

Enter comparison studies data

NOTE! The comparison studies data entry is not available for 'HP for Comparison study' and 'HP for Study drag' protocol.

If not specified otherwise, the Series conditions and Instance conditions are evaluated with data of the initial study (first study in the Viewer window) and finds and displays the images of this study. To display the image from the other study, the following data should be entered:

- Conditions for finding the applicable comparison studies should be entered in the Create protocol window:

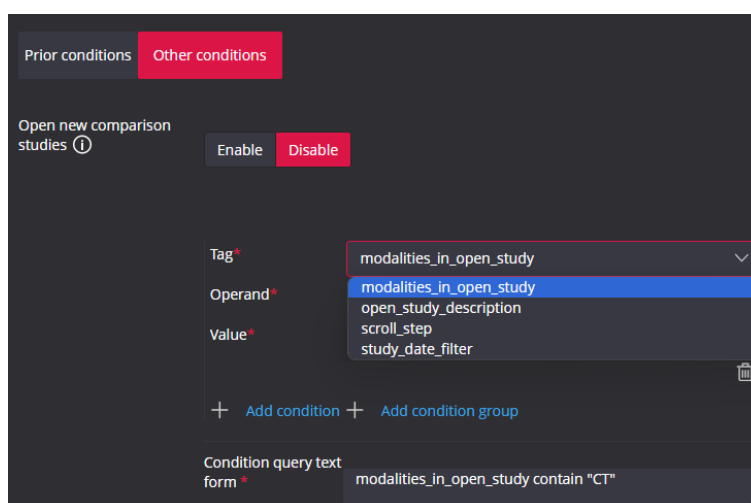


Figure 23. Entering comparison studies conditions in Create protocol window

- Select what type of comparison studies you want to use, by clicking the **Prior conditions**, or **Other conditions** button. The selected button is highlighted, and the tags for the selected conditions type will be displayed, when entering the conditions.



NOTE! The system allows entering either **Prior conditions**, or **Other conditions** for one hanging protocol, but not both.

- Enter the conditions for comparison studies selection. See hanging protocol configuration section for detailed description of the tags and execution rules for the prior and other study conditions.
- **Open new comparison studies** parameter is applicable for **Other conditions** case, and should be enabled, if you need the studies, that are added to the Viewer window, to be automatically opened in the hanging protocol. By default, the option is disabled.
- The parameters for handling the Prior studies list, which is used when scroll_step condition is entered, may be set:

Figure 24. Entering prior studies handling parameters in Create protocol window

- Set the **Maximum number of comparison studies** if you want to limit the list of used prior studies to a particular number. The default value is “0”, and all the studies, that patient’s historical studies, that meet the Prior conditions, are used and displayed for comparison.
- **Show all prior studies thumbnails** should be enabled, if you want all the prior studies, starting from the latest at the top, to be displayed in the Thumbnails bar. **Expand all prior studies thumbnails** should be enabled, if you want all the prior studies descriptions to be expanded in the Thumbnails zone. By default, these options are disabled, and the system displays and expands in the thumbnail zone only the Prior studies, that are currently viewed in the Viewer window.
- The **Prior study number**, or **Other study number** should be entered, if the viewport should display the instance of the comparison study. The system automatically adjusts the label, depending on the selected conditions:

Figure 25. Entering comparison studies number in in the viewport data

- The number starting from the 1 may be entered, and it indicates, which study from the comparison studies list should be used.



NOTE! The possibility to navigate through the comparison studies list and navigation step is defined in Prior study conditions or Other study conditions.

- The series conditions, and instance conditions should also be entered as described in Enter viewport data section, and are used for selecting the instance to display in comparison study.

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