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# Hanging protocols v2 setup manual

# for

# MedDream viewing functionalities

# version 8.6.0

The document describes the configuration and setup of Hanging protocol v2 for MedDream Viewing functionalities.

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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 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":

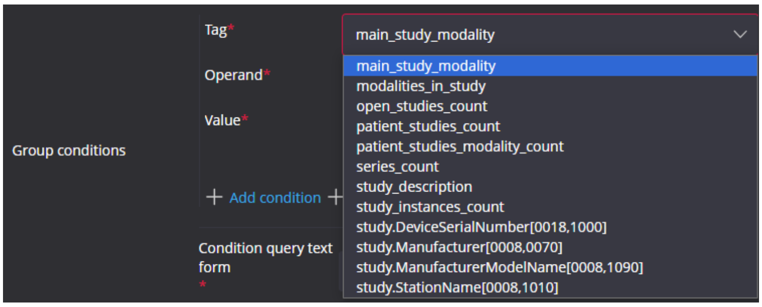


*Figure 1. Tags example in Group conditions Tag list*

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. series_count
7. series_description
8. series.ViewCodeSequence[0054,0220]
9. series.ViewPosition[0018,5101]
10. study_description
11. study_instances_count
12. study.DeviceSerialNumber[0018,1000]
13. study.Manufacturer[0008,0070]
14. study.ManufacturerModelName[0008,1090]

15. study.StationName[0008,1010]

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. series_count
7. series_description
8. series_SOP_class_UID
9. series_transfer_syntax_UID
10. series.FrameLaterality[0020,9072]
11. series.ImageLaterality[0020,0062]
12. series.Laterality[0020,006X]
13. series.ViewCodeSequence[0054,0220]
14. study_description
15. study_instances_count
16. study.AcquisitionDeviceProcessingDescription[0018,1400]
17. study.DeviceSerialNumber[0018,1000]
18. study.InstitutionName[0008,0080]
19. study.Manufacturer[0008,0070]
20. study.ManufacturerModelName[0008,1090]
21. study.StationName[0008,1010]

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.ImageType[0008,0008]
17. series.Laterality[0020,006X]
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]

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

# 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<br>attribute.00500010/00080070 |
| 00080080 Institution Name | attribute.00080080 |
| 00081010 Station Name | attribute.00081010 |
| 00081090 Manufacturer's Model Name | attribute.00081090<br>attribute.00500010/00081090 |
| 00082228 Primary Anatomic Structure Sequence | attribute.00082228 |
| 00180010 Contrast Bolus Agent | attribute. 00180010 |
| 00181000 Device Serial Number | attribute.00081000<br>attribute.00500010/00081000 |
| 00181400 Acquisition Device Processing Description | attribute.00181400<br>attribute.00189506/00181400<br>attribute.52009229/00189412/00181400<br>attribute.52009230/00189412/00181400 |
| 0020,006X Laterality | "attribute.00200060" |
| 00280002 Samples Per Pixel | attribute.002800002 |
| 00281300 Breast Implant Present | attribute. 0028130 |
| 00540220 View Code Sequence | attribute.00540220<br>attribute.00540220/00080121<br>attribute.00540220/00540222<br>attribute.00540220/00540222/00080121 |

⚠ **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 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.
- **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.

- **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 trough Prior studies. If scroll_stepp 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 trough Other studies. If scroll_stepp 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 handing 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 dateTime. 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 “dateTime” 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.

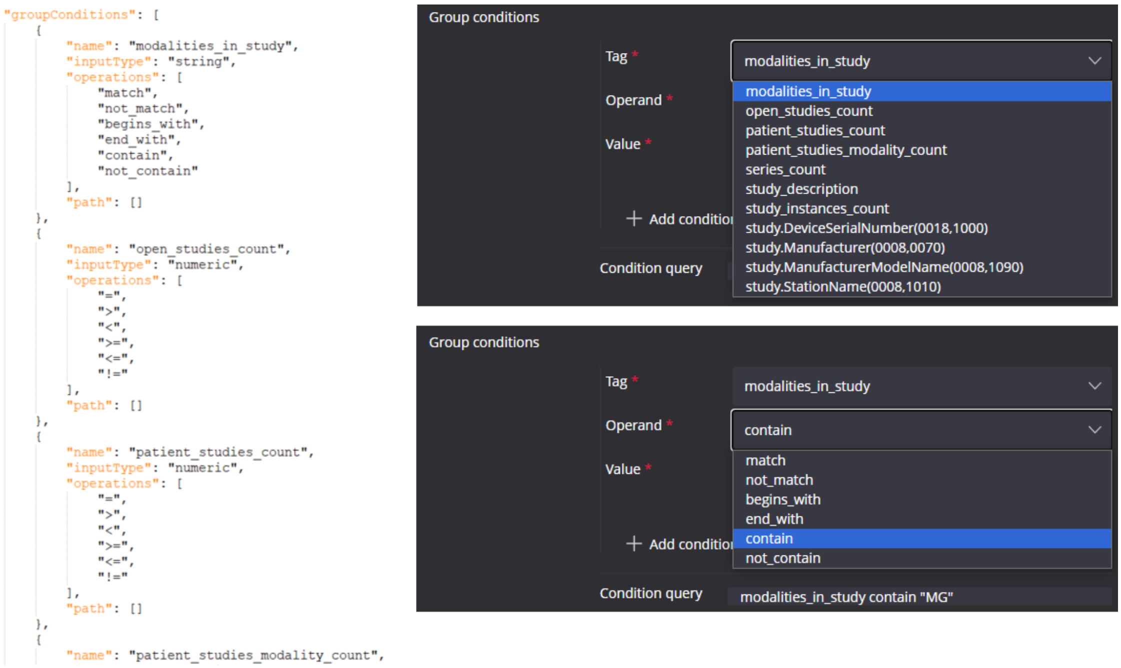


*Figure 2. Default Group conditions configuration*

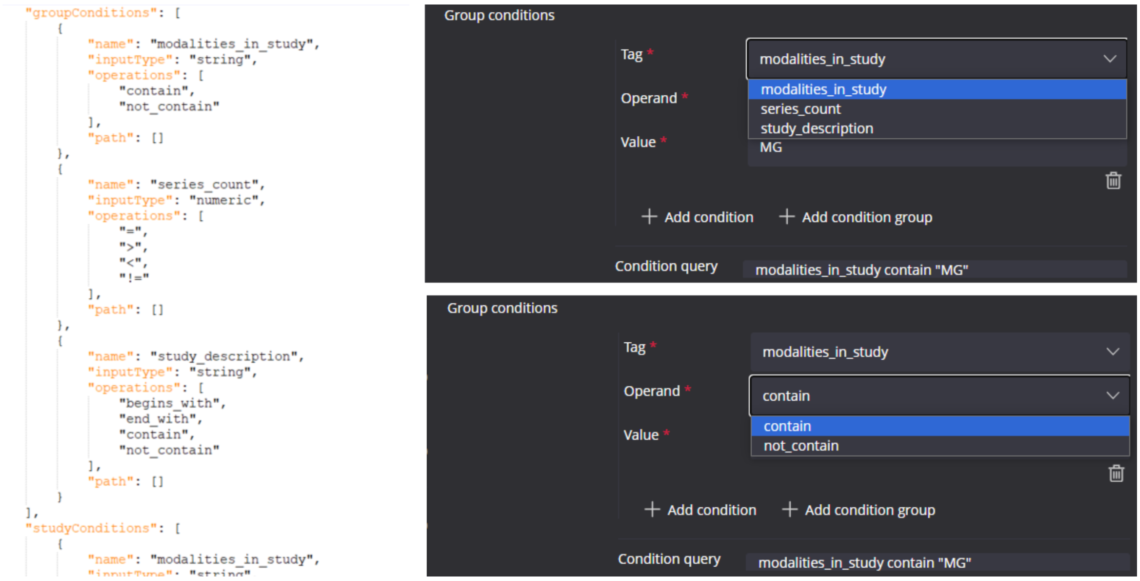

*Figure 3. Changed Group conditions configuration*

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!** By default, the system runs the first version of the Hanging protocols, and version number V2 is not displayed in the Hanging protocols settings page. See install manual for instructions, how to change the configuration and run the Hanging protocols version 2.

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 no all the default protocols.

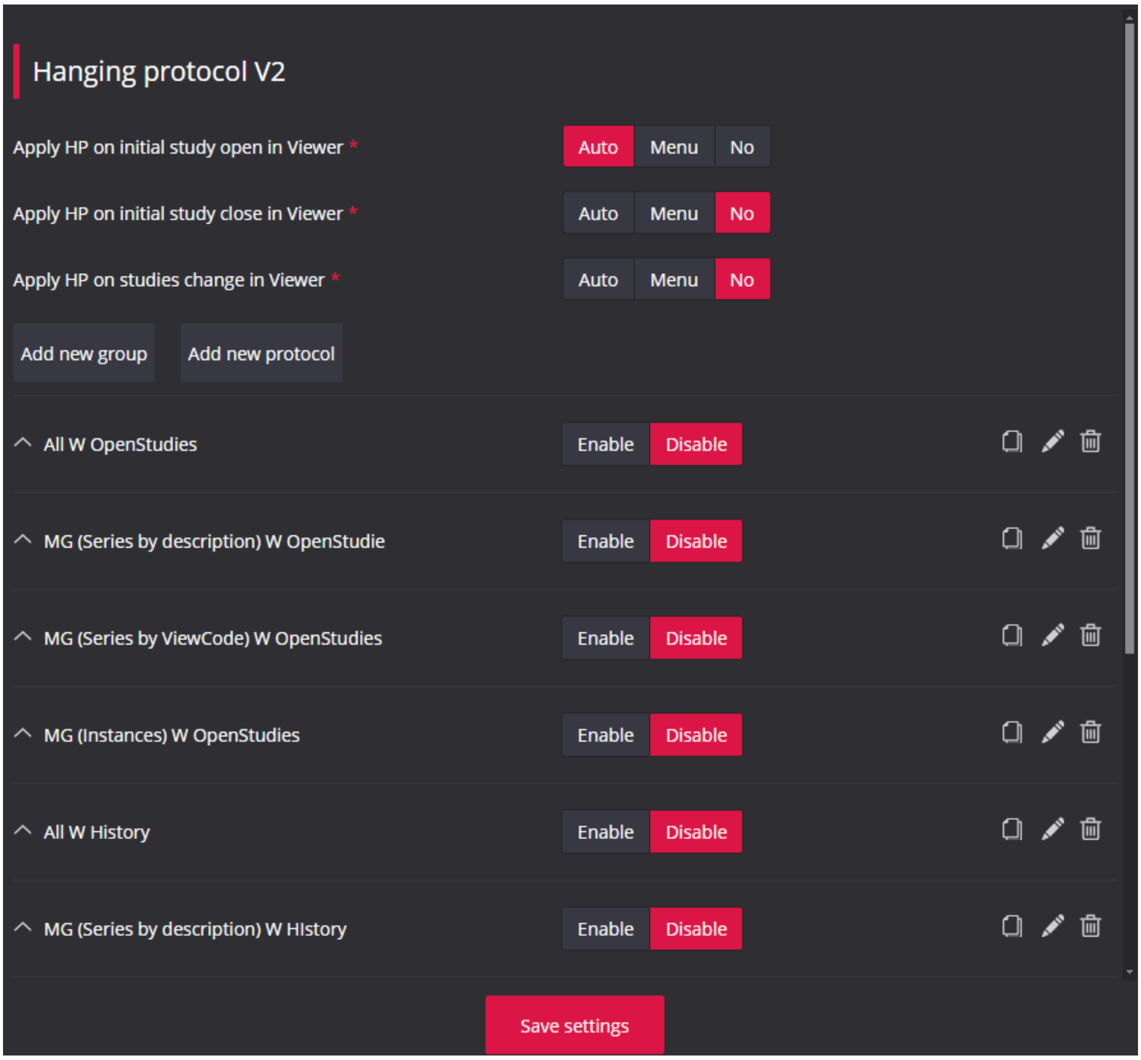


*Figure 4. Hanging protocol settings*

⚠ **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

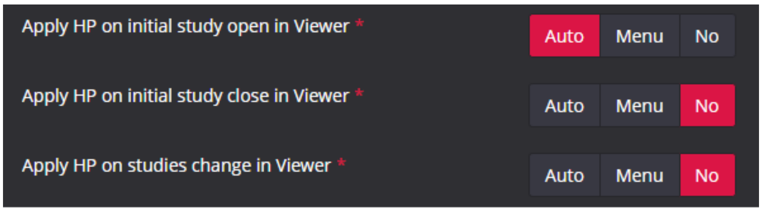


*Figure 5. Hanging protocol applying settings*

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, ant 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 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.

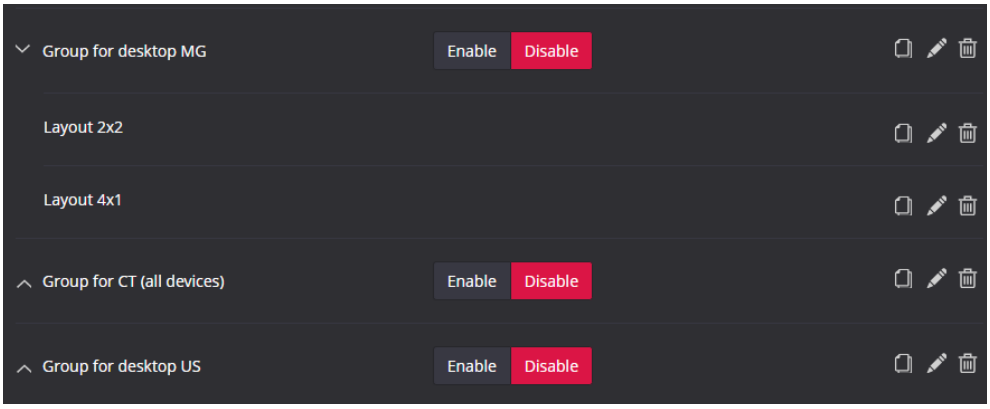


*Figure 6. Hanging protocols list*

You can perform the following in the hanging protocols list:

- To expands 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.
- 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 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 group in the list and for changing the order of protocols in the 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 on Hanging protocol tab opens the **Create group** window:

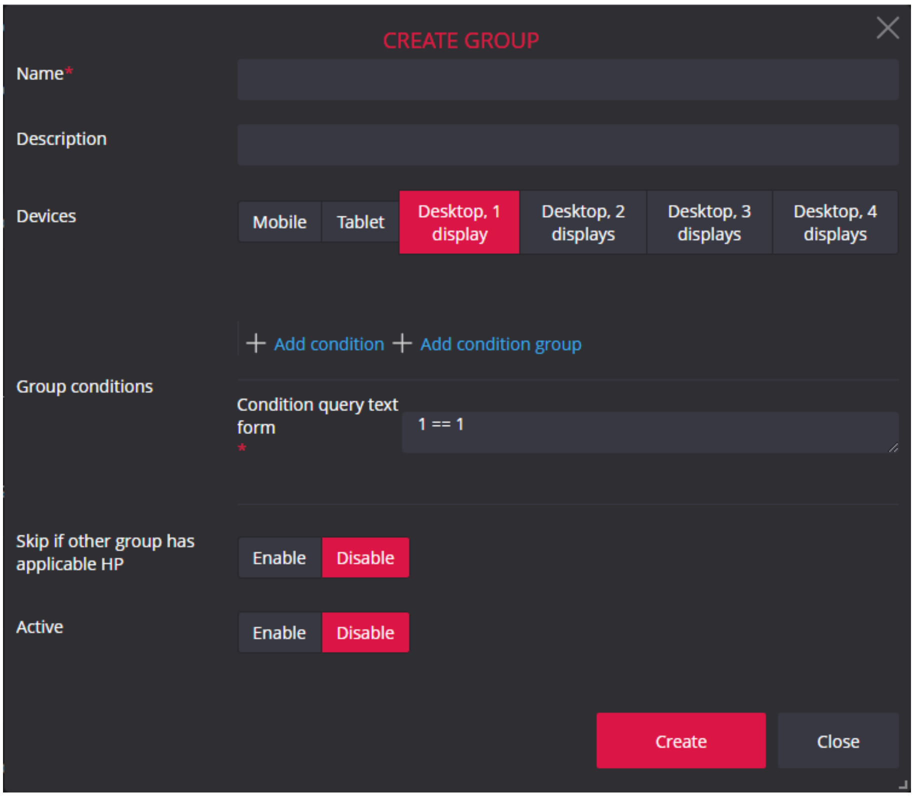


*Figure 7. Create hanging protocol group window*

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.

# 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’’. Several conditions are joined using AND operand, that means all conditions in the group should be met.

**NOTE!** The system curently supports only AND operator for joining conditions and conditions groups into executable rules. Therefore using the +**Add condition group** button and grouping the conditions into groups has no effect on rules execution, and **+Add condition** button is sufficient for defining the conditions

**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.

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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.

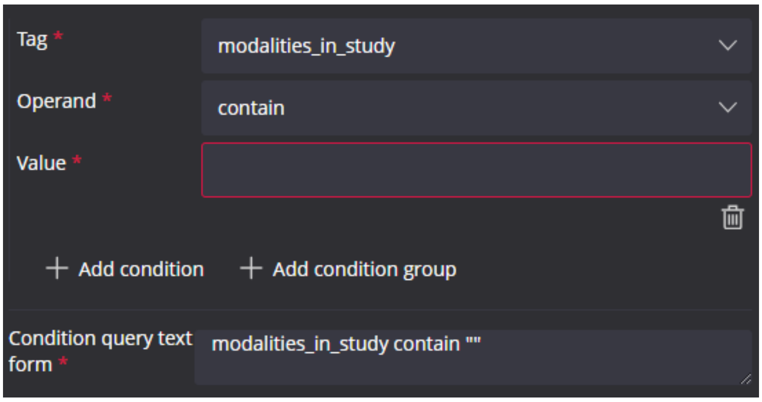


*Figure 8. Hanging protocol condition’s entry fields*

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 condityions execution descritpion in hanging protocol configuration section.

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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.

# Create hanging protocol

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

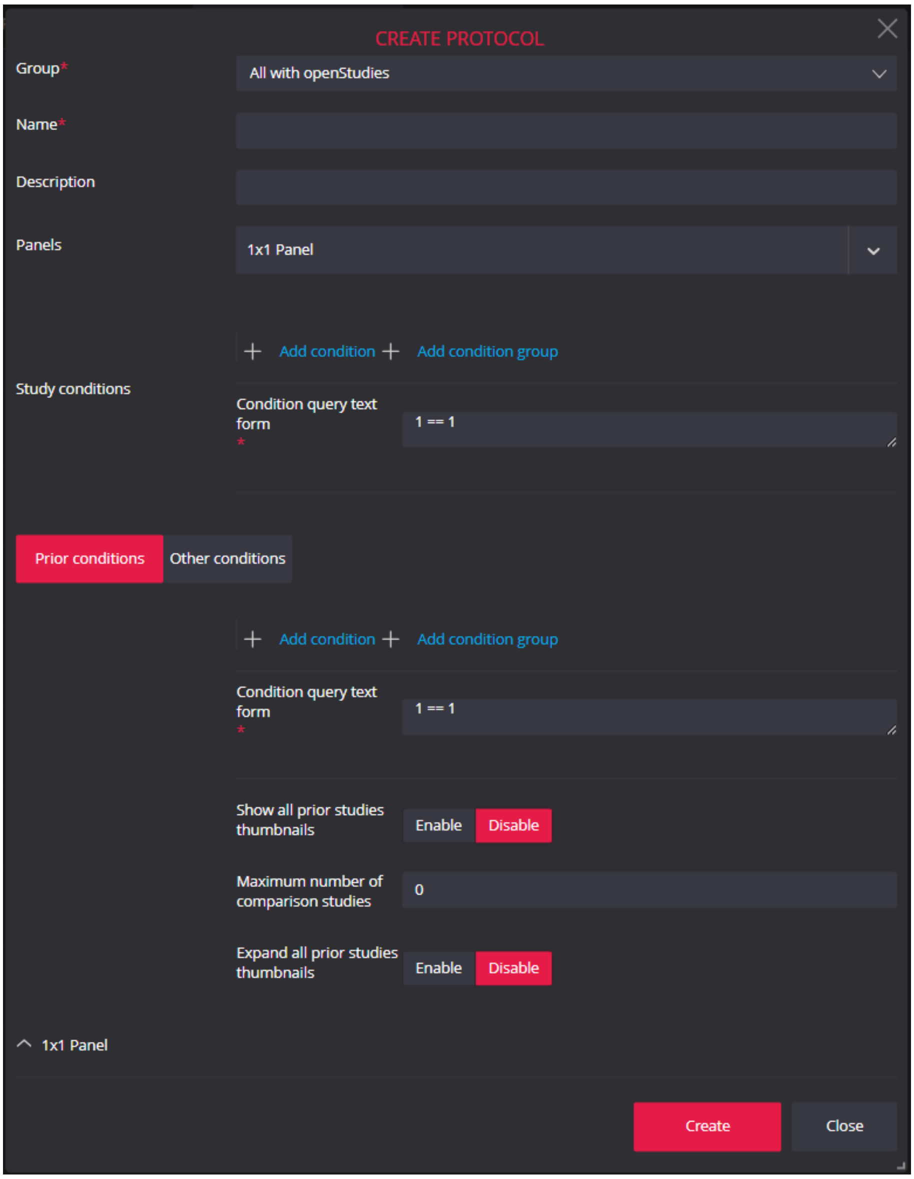


*Figure 9. Create protocol window*

To create a new hanging protocol:

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

- 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 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:

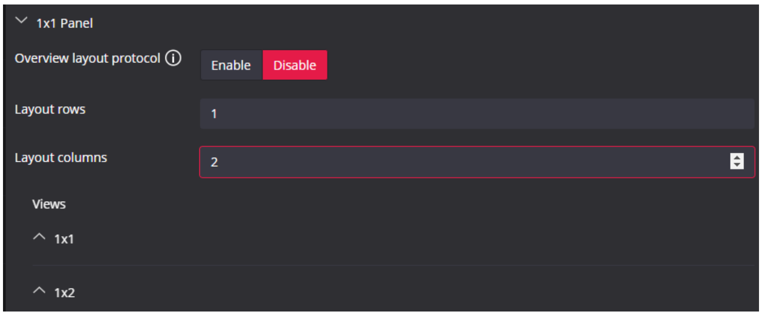


*Figure 10. Entering regular layout for panel*

- Keep the **Overview layout protocol** setting value **Disabled**, if creating a regular panel layout. Overview layout description see further in the section.
- 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.

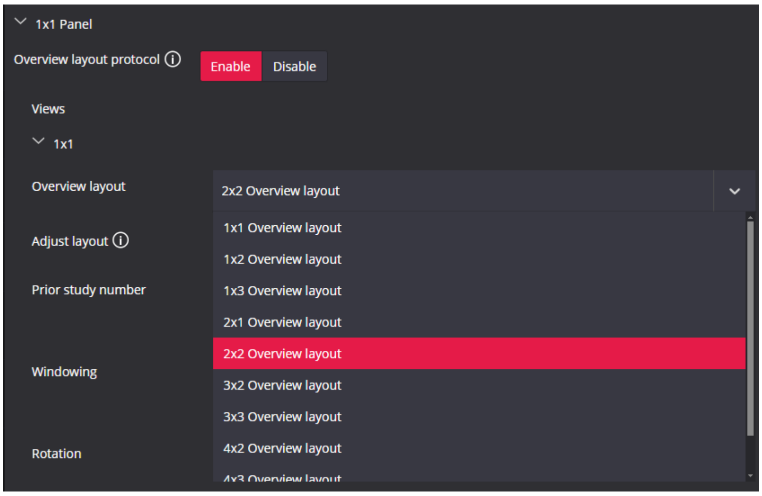


*Figure 11. Selecting the Overview layout for the panel/viewport*

- 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.

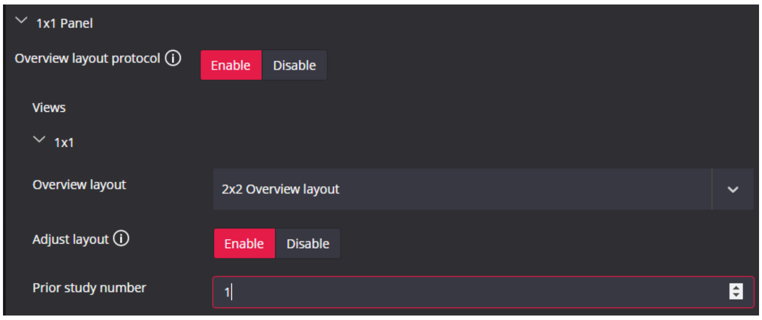


*Figure 12. Viewport data entered for the panel/viewport with overview layout*

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.

# 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.

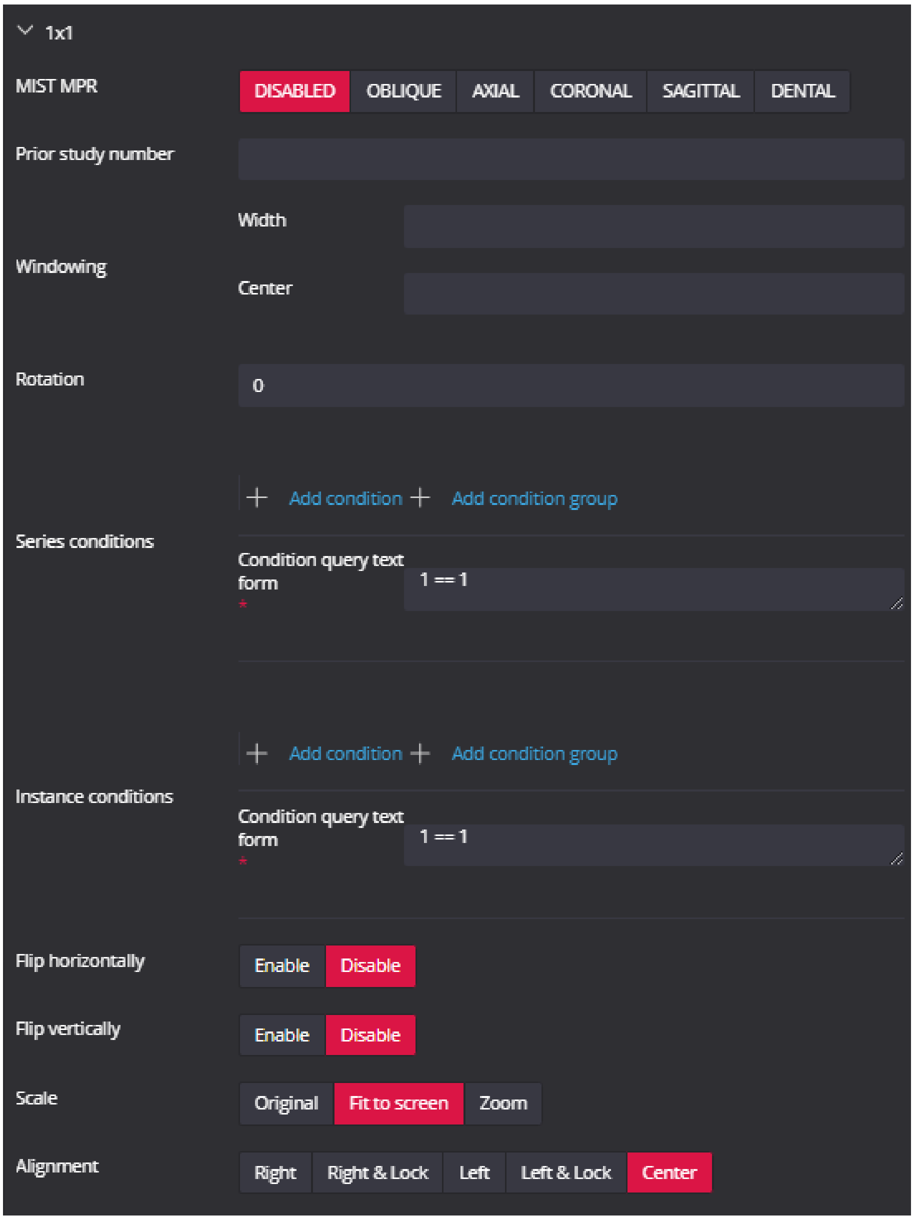


*Figure 13. Entering viewport settings in hanging protocol*

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 the MPR function 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.

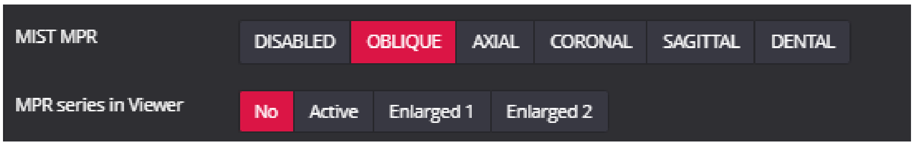


*Figure 14. Setting MPR series in Viewer for MPR generation*

Note, that multiplanar reconstruction may not be done and is automatically disabled, if the multi-series layout is selected in the viewport.

- 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.
- 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 15. Entering image scale factor*

- 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

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:

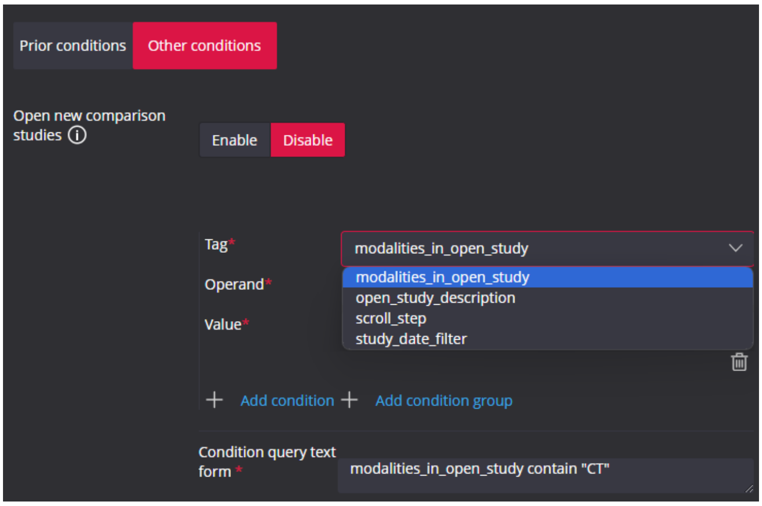


*Figure 16. Entering comparison studies conditions in Create protocol window*

- 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:

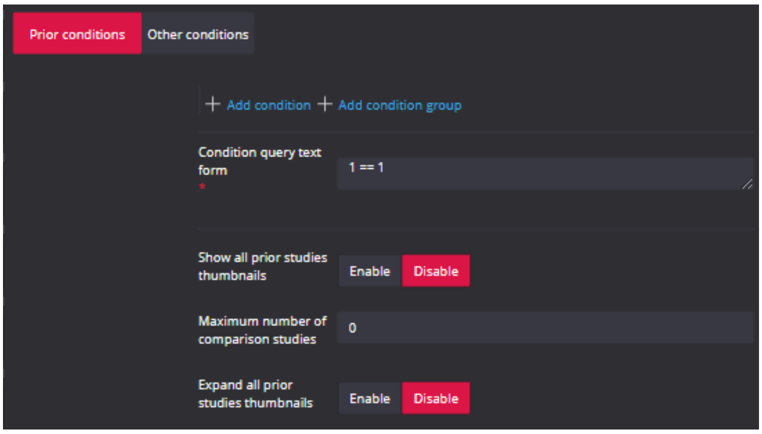


*Figure 17. Entering prior studies handling parameters in Create protocol window*

- 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 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:

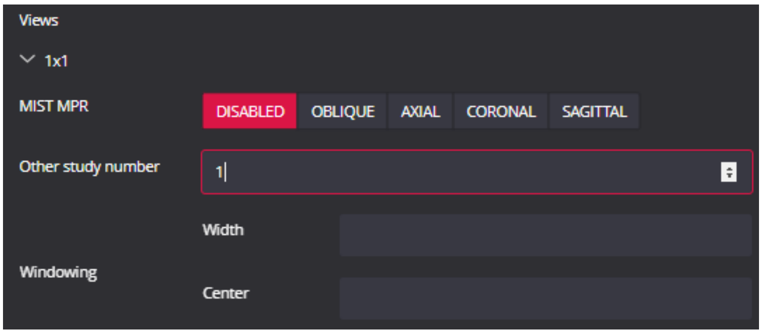


*Figure 18. Entering comparison studies number in in the viewport data*

– 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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