

VI. Setting up and acquisition

Proper setup of an acquisition is critical to ensure optimal data collection. This chapter provides the information needed to manage your study data, determine acquisition parameters and set up the physical aspects of your acquisitions. Please note acquisition cannot be started directly from the top menu, it opens automatically as result of the procedures described in this chapter.

1. Data management - worklist page

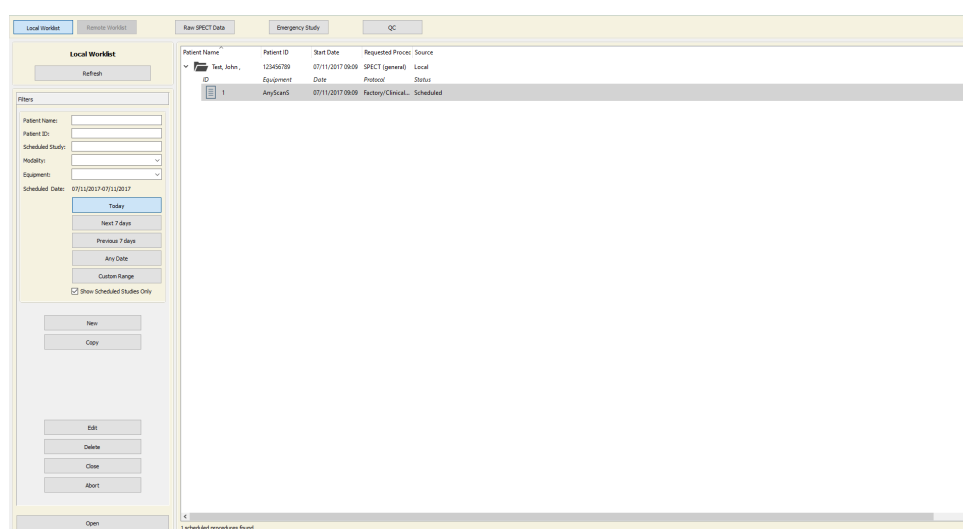



Figure 58. - Worklist page


The worklist page can be accessed by pressing the  icon in the Main Menu. Worklist used to present information about scheduled and ongoing imaging procedures to the operator. On the worklist page you can create new scheduled procedures, view and edit scheduled procedures created earlier and manage ongoing procedure states. Each procedure may contain several procedure steps, which are displayed under procedures. To display procedure steps of a procedure double click on the procedure. Acquisition software can execute procedure steps by selecting a procedure and pressing **[Open]** to execute it. In data management the following sections are available:

- **[Local Worklist]**: list of local scheduled and ongoing procedures (see [Local worklist](#))
- **[Remote Worklist]**: list of remote scheduled and ongoing procedures (see [Remote worklist](#)).
- **[Raw SPECT Data]**: reconstruction and post-reconstruction of an earlier procedure (see [Tera-Tomo 3D SPECT reconstruction](#)).
- **[Emergency Study]**: urgent study of a patient in case of emergency (see [Emergency study](#)).
- **[QC]**: list of quality control procedures (see [Quality control and Maintenance](#)).

1.1. Local worklist

Local worklist made up of scheduled and ongoing procedures, which were created by a Nucline operator i.e. does not originate from the configured **Remote Worklist Server**. This list is saved in the configured **Local Server** database.


To access the **Local Worklist**:

1. Press the  icon to activate the **Worklist Main Page**.
2. Press [**Local Worklist**] to enable the **Local Worklist**.

1.1.1. Creating a new scheduled procedure

The acquisition software allows the operator to input information for procedures to be performed immediately or later.

To create a new scheduled procedure:

1. Press the  icon to access the **Worklist Main Page**.
2. Press [**New**] from the vertical menu on the left-hand side of the screen to access the **New Study** information form.
3. Fill in the relevant **Patient** information.

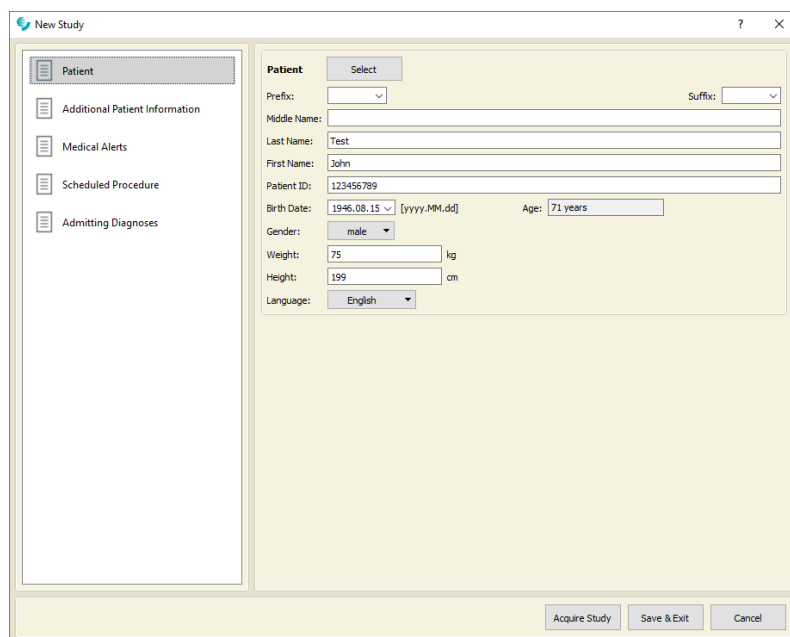
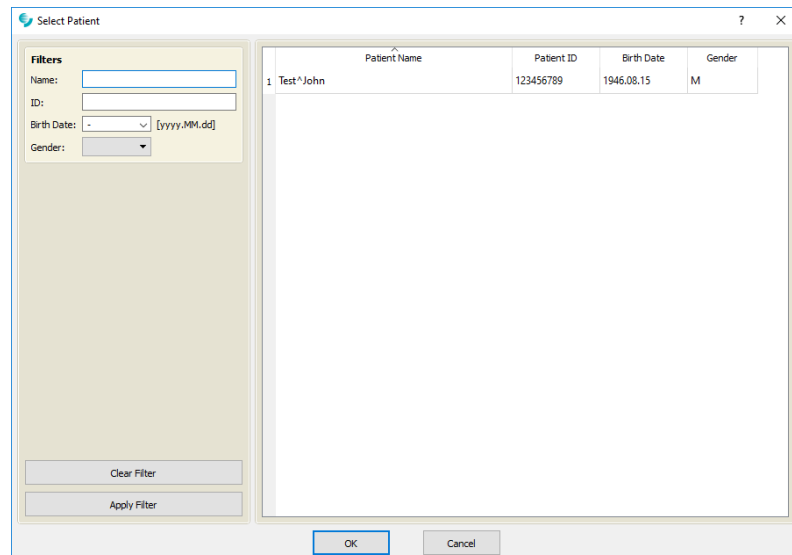


Figure 59. - New study

By default the **Last Name** and **Birth Date** must be specified (could be changed in **Study Management**). Please note that **Patient ID** numbers are not generated automatically. Please fill in **Gender** with a proper value as it will always be written to images and other result with a default value even if you do not provide a value.

You can fill in patient information automatically with an already existing patient data by pressing [**Select**] button.

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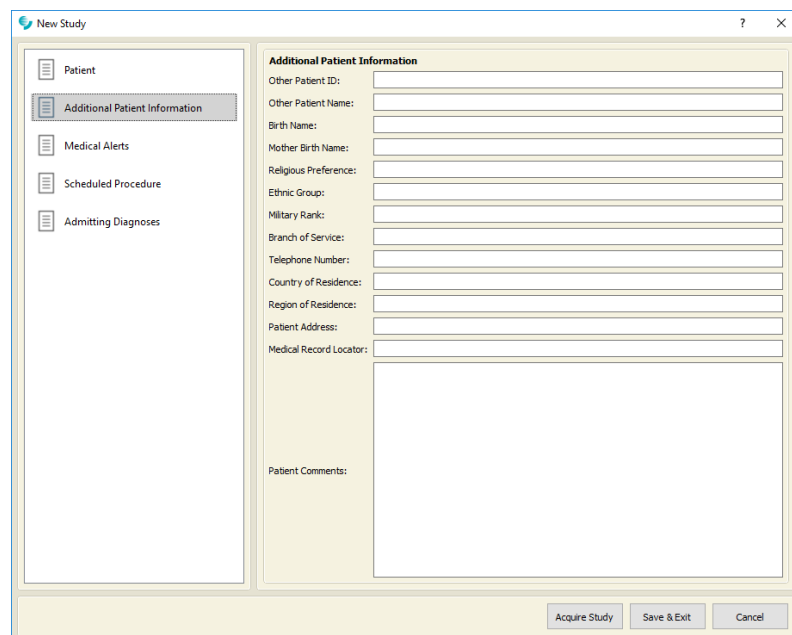
The 'Select Patient' dialog box features a 'Filters' section on the left with input fields for Name, ID, Birth Date (with a dropdown and format [yyyy-MM-dd]), and Gender. Below these are 'Clear Filter' and 'Apply Filter' buttons. The main area is a table with columns: Patient Name, Patient ID, Birth Date, and Gender. It contains one entry: '1 Test^ John', '123456789', '1946.08.15', and 'M'. At the bottom are 'OK' and 'Cancel' buttons.

	Patient Name	Patient ID	Birth Date	Gender
1	Test^ John	123456789	1946.08.15	M

Figure 60. - Select Patient

You can use the **Name**, **ID**, **Birth Date**, **Gender** filters to narrow the patient list. Press **[Apply Filter]** after editing filter fields. To reset filter values press **[Clear Filter]**. Select the desired patient from the list and press **[OK]**.

4. Optionally fill in Additional Patient Information, **Medical Alerts** and **Admitting Diagnoses** information by selecting the appropriate page.



The 'New Study' dialog box has a sidebar on the left with a tree view containing 'Patient', 'Additional Patient Information' (selected), 'Medical Alerts', 'Scheduled Procedure', and 'Admitting Diagnoses'. The main area is titled 'Additional Patient Information' and contains several text input fields: Other Patient ID, Other Patient Name, Birth Name, Mother Birth Name, Religious Preference, Ethnic Group, Military Rank, Branch of Service, Telephone Number, Country of Residence, Region of Residence, Patient Address, and Medical Record Locator. Below these is a large 'Patient Comments' text area. At the bottom are 'Acquire Study', 'Save & Exit', and 'Cancel' buttons.

Figure 61. - Additional Patient Information

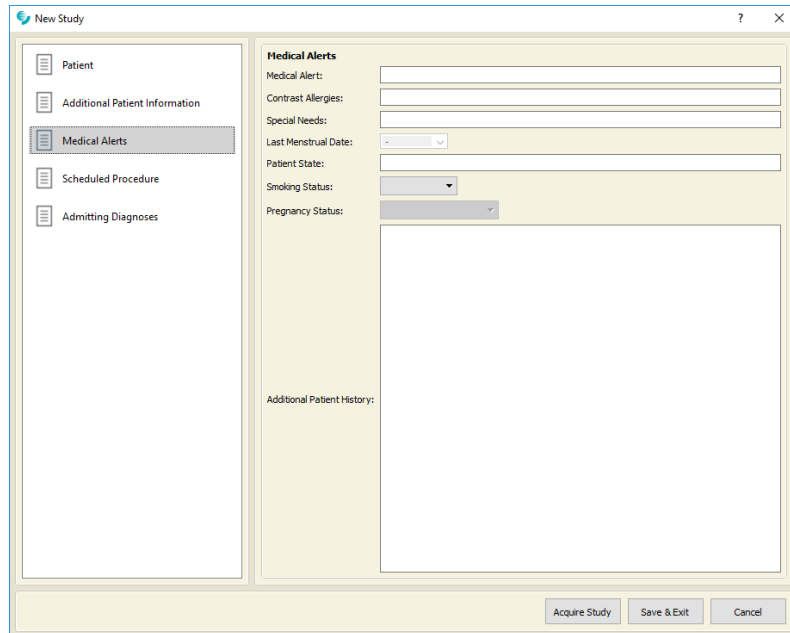


Figure 62. - Medical Alerts

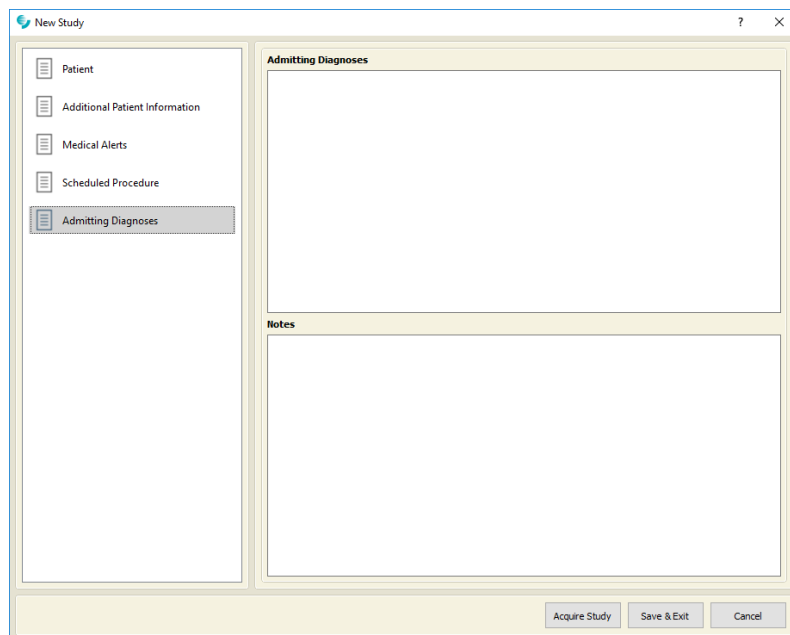


Figure 63. - Admitting Diagnoses

5. Add scheduled procedure steps i.e. protocol(s) to the procedure.
 - Press **[Scheduled Procedure]** in the vertical menu on the left-hand side of the screen. In the **Scheduled Procedure Steps** field press **[New]**.
 - A new window will appear with list of predefined protocols available for selection. For information on creating new protocols, see [Protocol editor](#) section. Here you can choose the type of scan to be performed.

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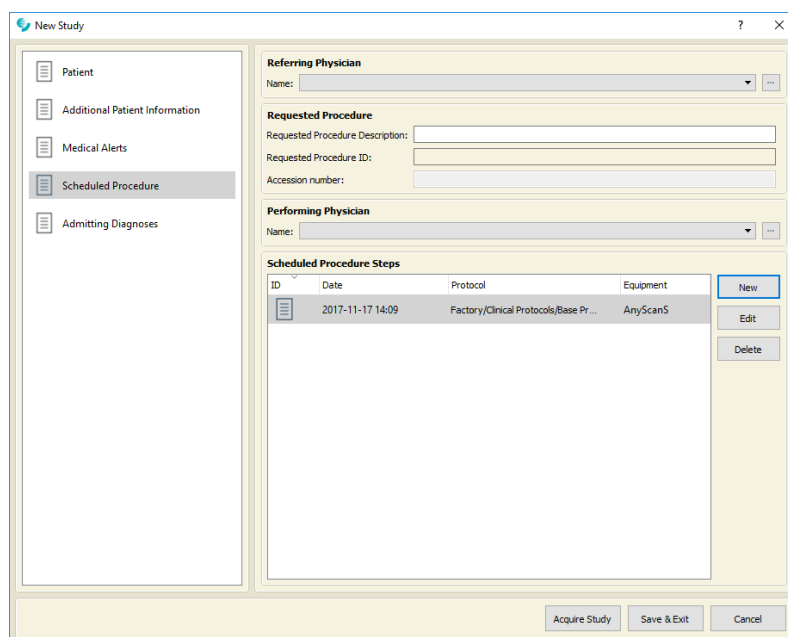


Figure 64. - Scheduled Procedure

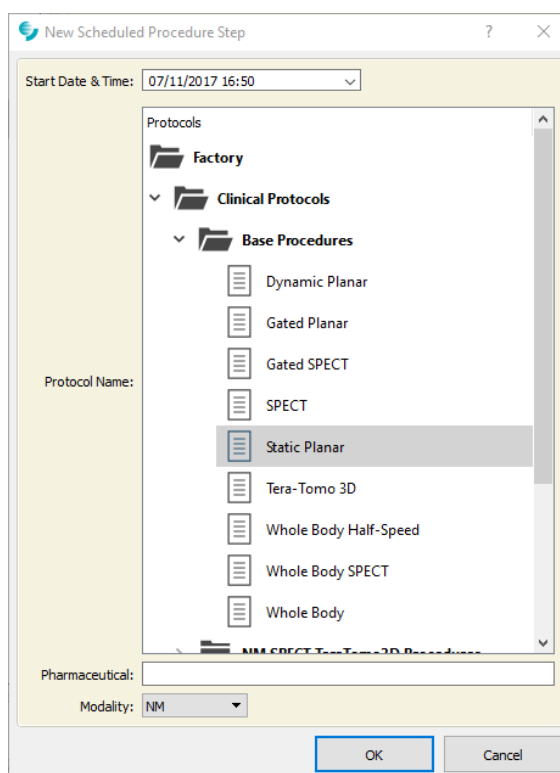


Figure 65. - New Scheduled Procedure Step

- Highlight the desired protocols and press **[OK]**.
- Enter any relevant information in the other fields as desired.
- **Requested Procedure ID** is automatically generated and cannot be changed (only during an emergency study). **Accession Number** is automatically generated or can be specified by the operator depending on the configuration. If no value specified for **Accession Number** one will be automatically generated.

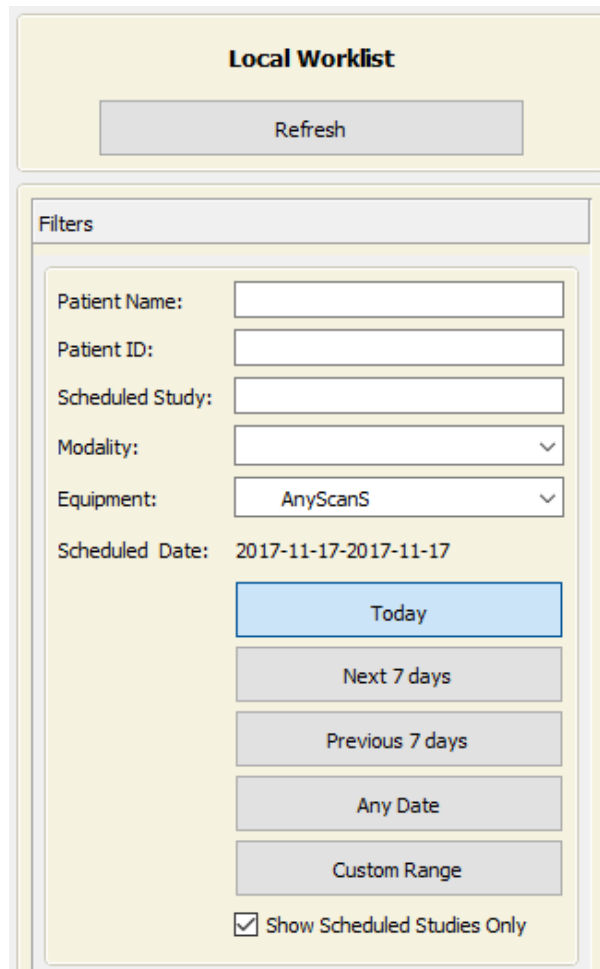
6. If the procedure step is to be carried out later press **[Save And Exit]**, to execute the procedure immediately press **[Acquire Study]**.

Once you have completed and saved the new procedure information it will appear in the **Local Worklist**.

You can also create a new procedure by pressing **[Copy]** from the vertical menu options on the left-hand side of the screen. It will create a new procedure with the same parameters as the original one only the procedure identifiers will be different. Highlight the procedure you wish to copy by clicking on the procedure then press **[Copy]**.

1.1.2. Finding a procedure

From the **Worklist Main Page** you can search for a particular procedure using the various filters.



The screenshot shows the 'Local Worklist' interface. At the top, there is a 'Refresh' button. Below it is a 'Filters' section. The filters include:

- Patient Name: [Text Input]
- Patient ID: [Text Input]
- Scheduled Study: [Text Input]
- Modality: [Dropdown Menu]
- Equipment: [Dropdown Menu, currently showing 'AnyScanS']
- Scheduled Date: 2017-11-17-2017-11-17

 Below the date field are five buttons: 'Today' (highlighted in blue), 'Next 7 days', 'Previous 7 days', 'Any Date', and 'Custom Range'. At the bottom of the filters section is a checkbox labeled 'Show Scheduled Studies Only' which is checked.

Figure 66. - Local Worklist

To find a procedure enter the appropriate information to **Patient Name**, **Patient ID**, **Scheduled Study**, **Modality**, **Equipment** and **Scheduled Date** then press **[Refresh]** or the **Enter** key.

Scheduled Study filters for scheduled protocol code sequence's code meaning value. **Equipment** filters for scheduled station's application entity title. Press the **[Today]** or

[**Next 7 Days**] or [**Prev 7 Days**] or [**Any Date**] or [**Custom Range**] button to display the procedures that was scheduled for appropriate date. Please note that all procedure steps of a given procedure are always displayed independently of filters specified.

1.1.3. Editing a procedure

To edit procedure information:

- Highlight the procedure you wish to edit by clicking on the procedure.
- Press [**Edit**] from the vertical menu options on the left-hand side of the screen.
- Modify information. Please note that not all attributes of procedures can be modified if you have already completed the procedure partially or fully. Especially patient attributes cannot be modified after procedure execution.
- Press [**Save & Exit**].

Edit remote procedures in the same way as you edit **Local Worklist**, the only difference is that not all the attributes can be edited. Please note that after refreshing the remote worklist your modifications may be discarded because remote worklist changes takes precedence over local modifications.

NOTICE

Editing a remote scheduled procedure may cause integration problems in the hospital information system.

1.1.4. Deleting a procedure

To delete a procedure or a procedure steps from your **Local Worklist**:

1. Highlight the procedure(s) or the procedure step(s) with a single-click.
2. Press [**Delete**] from the vertical menu options on the left-hand side of the screen.

Deleting remote procedures is not feasible, only the local copy, which is saved in **Local Server** database, is deleted. Next time you refresh the remote worklist the deleted procedure step will reappear if it is still in the remote worklist.

1.1.5. Managing procedure step states

Procedures steps will automatically close and will not appear in the **Local Worklist** after the execution. Procedure steps can also be closed or aborted manually by pressing [**Close**] or [**Abort**] from the vertical menu options on the left-hand side of the screen.

When modality performed procedure step functionality is switched on (see **MPPS Server** configuration) the procedure step related MPPS is also closed or aborted. In the abort case, you have to supply the procedure discontinuation reason.

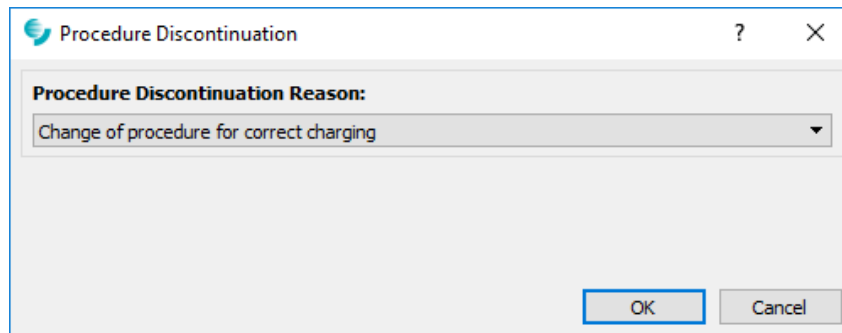


Figure 67. - Procedure discontinuation reason


Select the appropriate procedure discontinuation reason then press **[OK]**, if you press **[Cancel]** no procedure discontinuation reason will be provided in the related MPPS.

You can display closed and aborted procedure step by unchecking **[Show Scheduled Studies]**.

1.2. Remote worklist

Remote worklist made up of scheduled and ongoing procedures, that originate from the configured **Remote Worklist Server** typically from a hospital information system. The **Remote Worklist Server** maintains this list but it is saved in the configured **Local Server** database. Each time the **[Refresh]** is pressed the current procedure steps, which satisfy the filters, are queried from the **Remote Worklist Server** and saved in **Local Server** database. After refreshing all remote procedure steps are displayed, which are in **Local Server** database (which satisfy the current filters). It may be different from the current procedure steps list maintained by the **Remote Worklist Server**. By default all the procedure steps which were ever returned from the **Remote Worklist Server** are kept in **Local Server** database. This behavior can be changed to keep only those procedure steps which are currently in the **Remote Worklist Server** worklist in order to keep displayed remote procedure steps view in sync with the remote worklist. Remote procedure steps, which were executed, are never removed from the **Local Server** database automatically after refresh.

To access the **Remote Worklist**:

1. Press the  icon to activate the **Worklist Main Page**.
2. Press **[Remote Worklist]** to enable the Remote Worklist.

1.2.1. Copying a new scheduled procedure

Creating a remote worklist item is not possible, but you can make a copy of a remote scheduled procedure by pressing **[Copy]**. It will make a local procedure copy which you can find in **Local Worklist**.

1.2.2. Finding a procedure

From the **Worklist Main Page** you can search for a particular procedure using the various filters.

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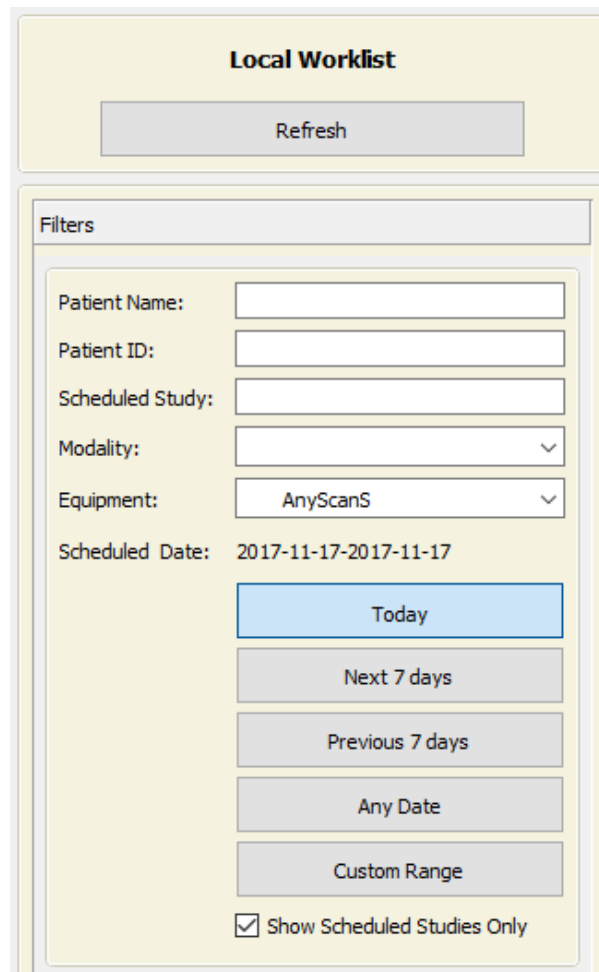


Figure 68. - Local Worklist

To find a procedure enter the appropriate information to **Patient Name**, **Patient ID**, **Scheduled Study**, **Modality**, **Equipment** and **Scheduled Date** then press **[Refresh]** or the **Enter** key.

Scheduled Study filters for scheduled protocol code sequence's code meaning value. **Equipment** filters for scheduled station's application entity title. Press the **[Today]** or **[Next 7 Days]** or **[Prev 7 Days]** or **[Any Date]** or **[Custom Range]** button to display the procedures that was scheduled for appropriate date. Please note that all procedure steps of a given procedure are always displayed independently of filters specified.

1.2.3. Editing a procedure

To edit procedure information:

- Highlight the procedure you wish to edit by clicking on the procedure.
- Press **[Edit]** from the vertical menu options on the left-hand side of the screen.
- Modify information. Please note that not all attributes of procedures can be modified if you have already completed the procedure partially or fully. Especially patient attributes cannot be modified after procedure execution.
- Press **[Save & Exit]**.

Edit remote procedures in the same way as you edit **Local Worklist**, the only difference is that not all the attributes can be edited. Please note that after refreshing the remote worklist your modifications may be discarded because remote worklist changes takes precedence over local modifications.

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Deleting remote procedures is not feasible, only the local copy, which is saved in **Local Server** database, is deleted. Next time you refresh the remote worklist the deleted procedure step will reappear if it is still in the remote worklist.

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Procedures steps will automatically close and will not appear in the **Local Worklist** after the execution. Procedure steps can also be closed or aborted manually by pressing **[Close]** or **[Abort]** from the vertical menu options on the left-hand side of the screen.

When modality performed procedure step functionality is switched on (see **MPPS Server** configuration) the procedure step related MPPS is also closed or aborted. In the abort case, you have to supply the procedure discontinuation reason.

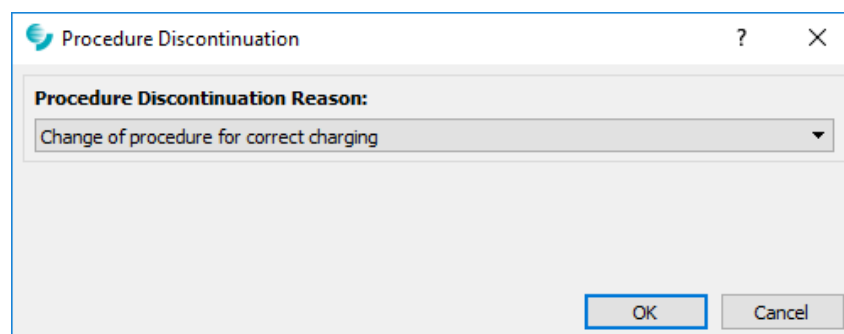


Figure 69. - Procedure discontinuation reason

Select the appropriate procedure discontinuation reason then press **[OK]**, if you press **[Cancel]** no procedure discontinuation reason will be provided in the related MPPS.

You can display closed and aborted procedure step by unchecking **[Show Scheduled Studies]**.

1.3. Emergency study

Emergency Study

Use this button only in case of urgency. You can start a study without predefining any information. In this case **Patient Name** will be *Emergency*.

NOTICE

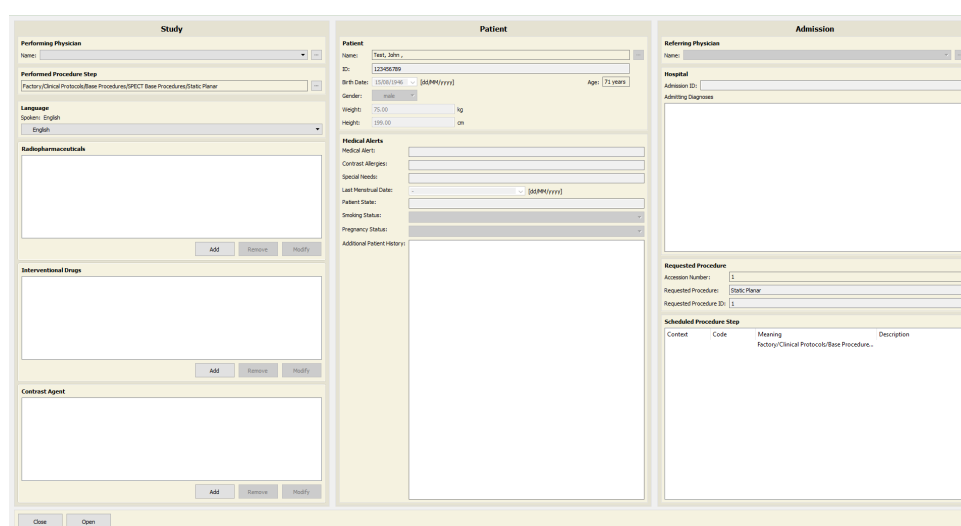
If DICOM file has been generated you can only change the Patient Name in the **Study Browser's Edit Data** window.

1.4. Selecting a study for acquisition

When you are ready to begin an acquisition, you may choose an existing study file or you can make a new study folder as previously described. To begin work with a study:

1. Select a study from your worklist page by highlighting the folder with a single click. If a study has more than one set of protocols, you may need to select an individual protocol set before continuing to the next step. This is done by pressing the ► icon to the left of the Patient name.
2. Press **[Open]** in the lower left hand corner of the screen.
3. The next screen (**Protocol Cover Page**) will display the information about the study that was previously entered.
4. When **[Open]** is pressed, the acquisition page for that procedure will be displayed.

1.4.1. Protocol cover page main panels



The screenshot displays the 'Protocol Cover Page' interface, which is divided into three main panels: Study, Patient, and Admission.

- Study Panel:** Contains fields for 'Performing Physician' (Name), 'Performed Procedure Step' (Factory/Clinical Protocols/Base Procedures/DECT Base Procedures/Static Planar), 'Language' (Spoken: English, Written: English), 'Radiopharmaceuticals' (with Add, Remove, Modify buttons), 'Interventional Drugs' (with Add, Remove, Modify buttons), and 'Contrast Agent' (with Add, Remove, Modify buttons). At the bottom are 'Close' and 'Open' buttons.
- Patient Panel:** Contains fields for 'Patient' (Name: Test, John), 'ID' (123456789), 'Birth Date' (12/12/1946), 'Age' (72 years), 'Gender' (Male), 'Weight' (75.00 kg), 'Height' (170.00 cm), 'Medical Alerts' (Medical Alert, Contrast Allergy, Special Needs, Last Menstrual Date, Patient Status, Smoking Status, Pregnancy Status, Additional Patient History).
- Admission Panel:** Contains fields for 'Referring Physician' (Name), 'Hospital' (Address ID), 'Admission ID', 'Admission Diagnosis', 'Requested Procedure' (Accession Number: 1, Acquired Procedure: Static Planar, Requested Procedure ID: 1), and 'Scheduled Procedure Step' (a table with columns: Content, Code, Meaning, Description, and a row for 'Factory/Clinical Protocols/Base Procedure...').

Figure 70. - Protocol cover page

- **Study panel**

At the top you can define the **Performing Physician** of the study.

In the **Performed Procedure Step** you can select protocols for the study. In case of a remote study the protocol could be mapped to Nucline with the **Protocol Mapper** function. For further details on the usage of **Protocol Mapper** see [Protocol mapper](#).

In the **Language** subpanel you can choose or modify the spoken language.

There are 3 additional subpanels where you can define the injected materials. In each panel you find following buttons:

- **[Add]**: you can add an element to the list with the adequate dialog.
- **[Remove]**: you can remove the current element from the list.
- **[Modify]**: you can modify the current element with the adequate dialog.

The panels are:

- **Radiopharmaceuticals**
- **Interventional Drugs**
- **Contrast Agent**

You can add such materials to the study later on the **Acquisition Screen**, too.

Important: if you define injected materials on the **Protocol Cover Page**, all acquisitions of the protocol will contain the information about them. If you add such materials later on the **Acquisition Screen** of an acquisition plugin, the already finished acquisitions will not contain these materials, only the later executed acquisitions.

- **Patient panel**

Information about the patient could be found and filled here. In every acquisition by default the **Weight** and **Height** of the patient must be filled (if not defined earlier and could be changed in **Study Management**). In the **Additional Patient History** you can type additional information as a free text.


Important: some information of the **Patient** is not editable.

- **Admission panel**

This panel explains the admission history and requested procedures of the patient.

Important: some information of the **Admission** is not editable.

2. Transfer manager

Transfer Manager's role is to reliable transfer acquisition data to **Local Server**, to configured **Store Servers** and to **Dose Server** destinations. The transfer manager page can be accessed by pressing the  icon in the main menu. **Transfer Manager**'s icon will reflect **Transfer Manager** current state: It will blinking yellow if the **Transfer Manager** or any configured destination server is switched off. It will blinking red if transfer to one or more

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configured destination server has failed. To actualize **Transfer Manager**'s information shown you have to press **[Refresh]**, it will not be refreshed automatically.

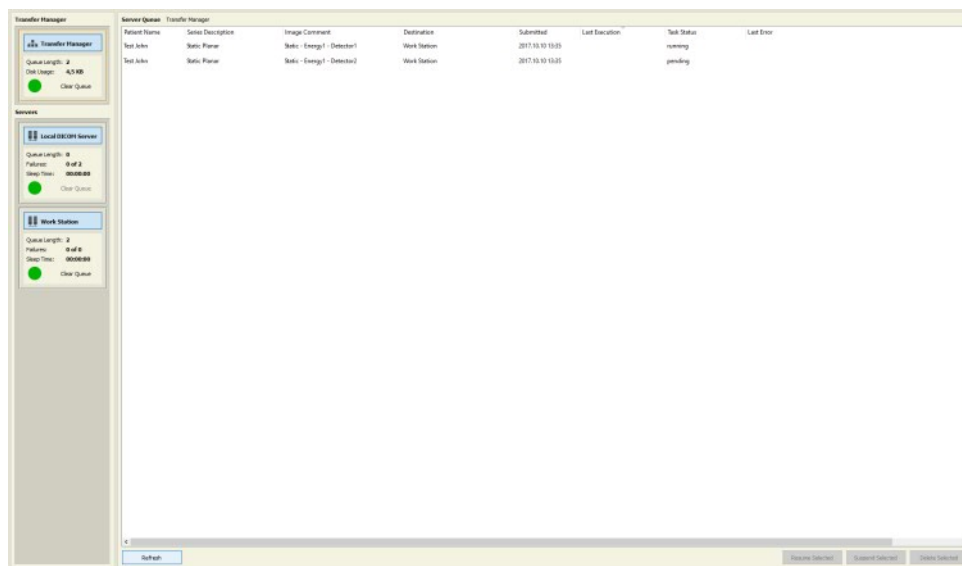


Figure 71. - Transfer Manager

2.1. Server panels

Left side vertical toolbar contains a panel for the **Transfer Manager** on the top and a sever panel for the **Local Server** and for each configured **Store Servers** and **Dose Servers**. The **Server Queue** shows the ongoing transfer tasks of **Transfer Manager** or transfer tasks to the selected server. A server panel can be selected by clicking its panel.

Transfer Manager can be disabled/enabled by checking/unchecking **[Transfer Manager]** button. Transfer to a specific server can be disabled/enabled in a similar way by checking/unchecking the button which label is the desired server name.

After an unsuccessful transfer to a server the next transfer to that server will be delayed. Delay time is increased after each unsuccessful transfer, its current value is shown as **Sleep Time** on each server's panel.

2.2. Transfer tasks

Each task is about to transfer an instance to the desired destination. Tasks are described by the transferred instance's patient name, series description and image comment.

Transfer task status can be one of the following:

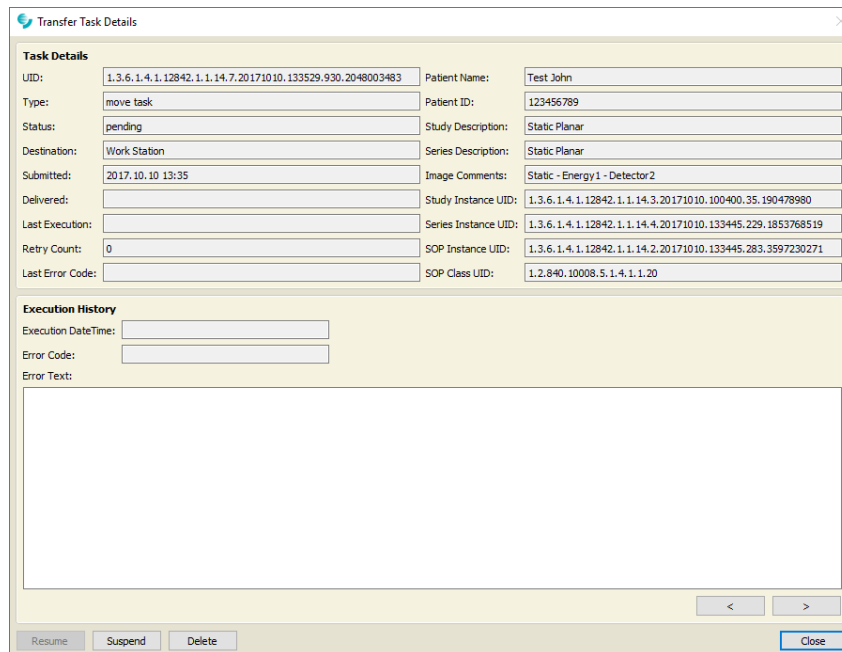
- **Pending:** Task has not been processed yet, waits for execution.
- **Running:** Currently executed task.
- **Suspended:** Currently disabled task which will not be executed while suspended.
- **Transient Failure:** Task execution failed and will be tried later.
- **Permanent Failure:** Task execution failed and will not be tried again, user intervention required.
- **Delivered:** Task successfully finished.

You can manually suspend i.e. disable execution of tasks except the running one. To suspend a task select it then press **[Suspend]**. Permanently failed tasks cannot be suspended as their execution are disabled.

To resume a task execution select it then press **[Resume]**, task status will be set to pending. This is the only way to enable re-execution of a permanently failed task.

You can eliminate task(s) from **Task Manager**'s queue. To delete a task select it then press **[Delete]**. Please note that deleting a task which destination is the **Local Server** results in permanent data loss so make sure you do not need the data which is transferred by the deleted task.

To check out a particular task details double click on it, a new **Transfer Task Details** dialog appears. The execution history of the task can be analyzed by pressing **[<]** and **[>]**. You can also resume, suspend and delete the task here by pressing **[Resume]**, **[Suspend]** and **[Delete]** respectively.



The dialog box titled "Transfer Task Details" contains the following information:

Task Details	
UID:	1.3.6.1.4.1.12842.1.1.14.7.20171010.133529.930.2048003483
Type:	move task
Status:	pending
Destination:	Work Station
Submitted:	2017.10.10 13:35
Delivered:	
Last Execution:	
Retry Count:	0
Last Error Code:	
Patient Name:	Test John
Patient ID:	123456789
Study Description:	Static Planar
Series Description:	Static Planar
Image Comments:	Static - Energy 1 - Detector2
Study Instance UID:	1.3.6.1.4.1.12842.1.1.14.3.20171010.100400.35.190478980
Series Instance UID:	1.3.6.1.4.1.12842.1.1.14.4.20171010.133445.229.1853768519
SOP Instance UID:	1.3.6.1.4.1.12842.1.1.14.2.20171010.133445.283.3597230271
SOP Class UID:	1.2.840.10008.5.1.4.1.1.20

Execution History

Execution DateTime:

Error Code:

Error Text:

Navigation buttons: < >

Action buttons: Resume Suspend Delete Close

Figure 72. - Transfer Task Details

3. Study browser

Study Browser is a tool to operate with various PACS, DICOM servers, folder and other data repositories. The tool is used for loading, transferring, deleting, filtering and general browsing in the selected data repository. Study browser organizes data into a three-tiered hierarchical system: Studies, Series and Instances.

Studies: A study is a collection of images and/or other objects that are logically related for the purpose of diagnosing a patient.

Series: For each protocol, or type of acquisition, performed within a study, a series is created. Series are listed as sub-folders. To access data at the series level simply click on the **>** icon to the left of the Study.

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Instance: An image or other object that is created within a series. To access information at the instance level simply click on the [>] icon to the left of the series name.

Please note that the top level items in study browser are studies so a specific patient may appear multiple times as he/she may have more than one study.

Pressing the **[View]** button starts **Image Viewer** application. This application could be InterView Fusion or other software depending on your system configuration and licencing. For further information on the **Image Viewer** please consult the application's user manual.

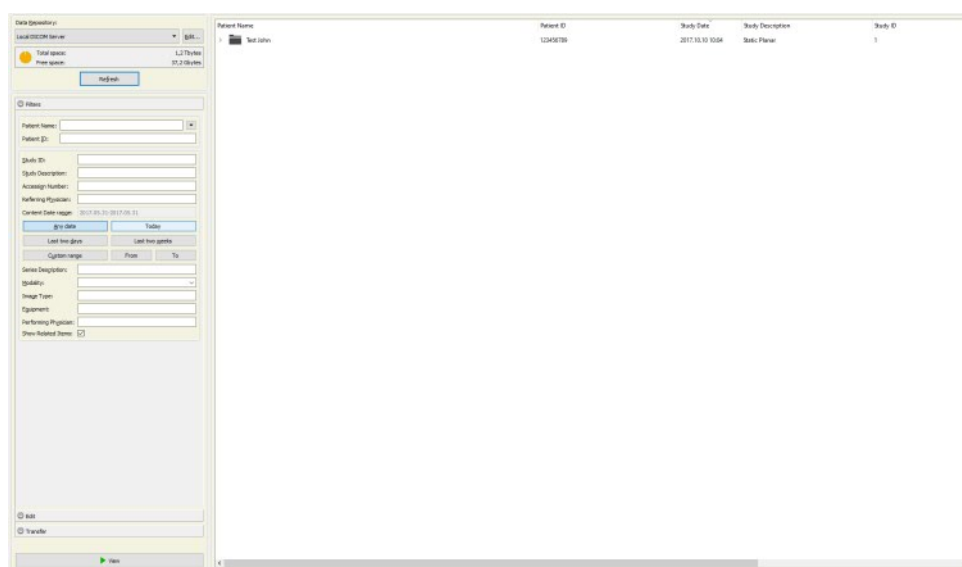
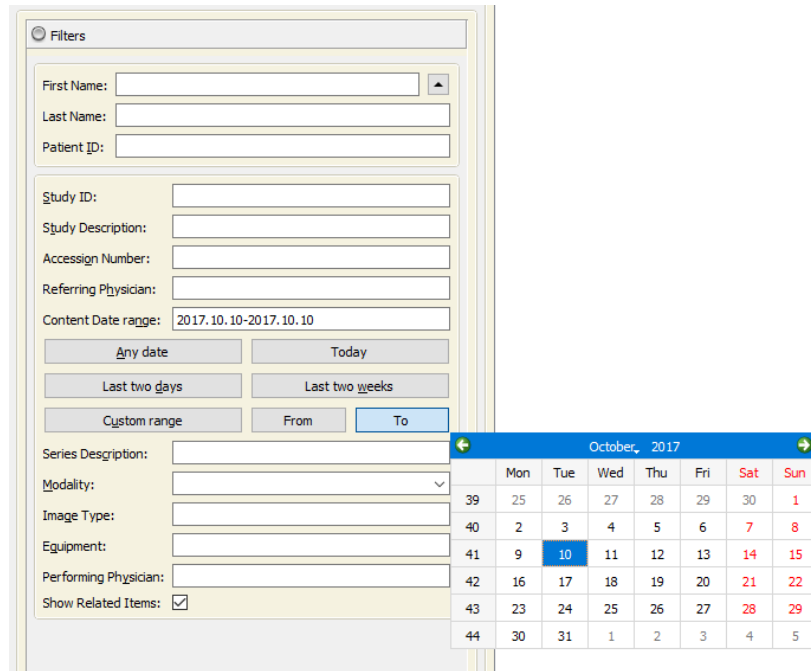


Figure 73. - Study Browser

3.1. Filters

Filtering data in the current data repository is available for several key patient or acquisition based DICOM attributes on the **Filter** tab. Applying filters is done with the **[Refresh]** button or by pressing the **Enter** key.

Please note that some filters may not work if the connected server does not support the used filter or relational queries.



October, 2017							
	Mon	Tue	Wed	Thu	Fri	Sat	Sun
39	25	26	27	28	29	30	1
40	2	3	4	5	6	7	8
41	9	10	11	12	13	14	15
42	16	17	18	19	20	21	22
43	23	24	25	26	27	28	29
44	30	31	1	2	3	4	5

Figure 74. - Filters

Patient name filtering mode can be “**Simple**” or “**Detailed**” (see below). In simple patient name filtering mode only one **Patient Name** field is shown, the string entered there will be searched in the entire patient name. In detailed patient name filtering mode you can create a filter for the first name and for the last name separately. Patient name filtering is case insensitive, all the other filters are case sensitive.

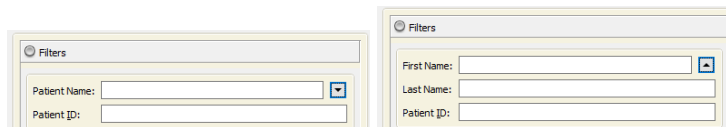


Figure 75. - Simple/Detailed filters

Series Description, **Image Type**, **Equipment**, **Performing Physician** filters are disabled if the selected repository does not support relational queries. **Equipment** field filters for manufacturer’s model name. If **Show Related Items** is checked then study browser will show all existing series and instance items under study and series items. If **Show Related Items** is not checked then it will just show series and instance items, which satisfy the currently specified filters.

3.2. Edit

Editing selected data may be done with the controls on the **Edit** tab. Data editing works only if the selected data repository is a Mediso DICOM server type.

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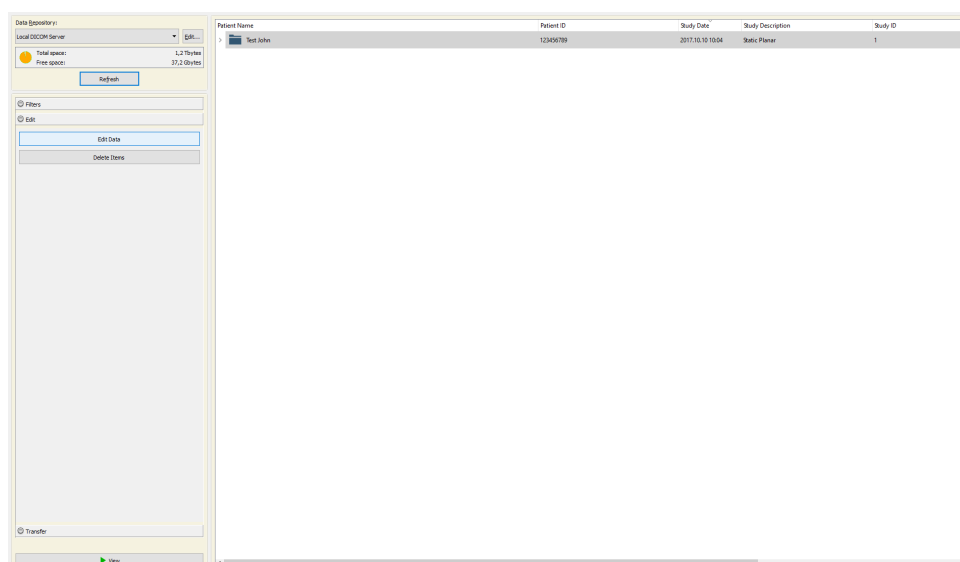
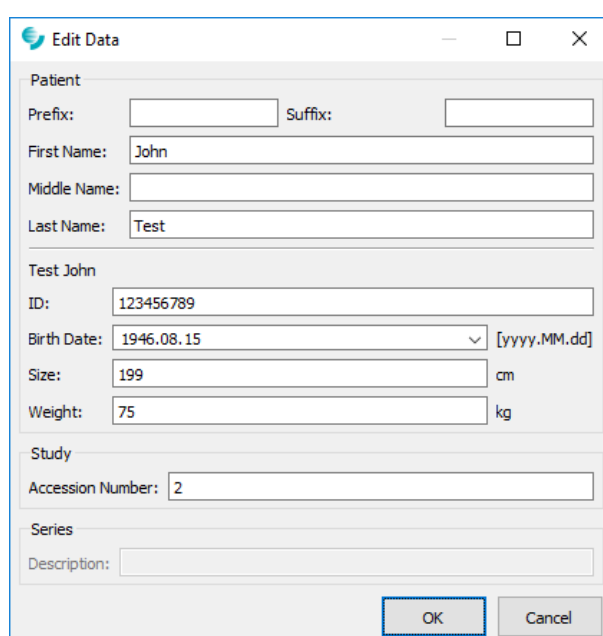


Figure 76. - Edit

Pressing the **[Edit Data]** button opens a dialog to change the selected Patient data information (e.g. fixing a few of the miss-typed patient data) at the particular DICOM server.



The 'Edit Data' dialog box is shown, containing the following fields:

- Patient**
 - Prefix:
 - Suffix:
 - First Name:
 - Middle Name:
 - Last Name:
- Test John**
 - ID:
 - Birth Date: [yyyy.MM.dd]
 - Size: cm
 - Weight: kg
- Study**
 - Accession Number:
- Series**
 - Description:

At the bottom right, there are 'OK' and 'Cancel' buttons.

Figure 77. - Edit Data

Please note that editing an instance's patient, study or series information will change the edited information in all instances, which belongs the same patient, study or series. Editing information may cause information integration problems through connected DICOM servers so please do the same editing in all connected data repositories where the same data is reside.

[Delete Items] button deletes the selected DICOM instances. Deleting works only if the selected data repository is a Mediso DICOM server type.

3.3. Transfer

Data transfer between selected repositories is managed on the **Transfer** tab. Press the **[Start Transfer]** button to transfer the selected DICOM data to the selected **Target Repository**. Transfer to **DIAG** repositories does not work.

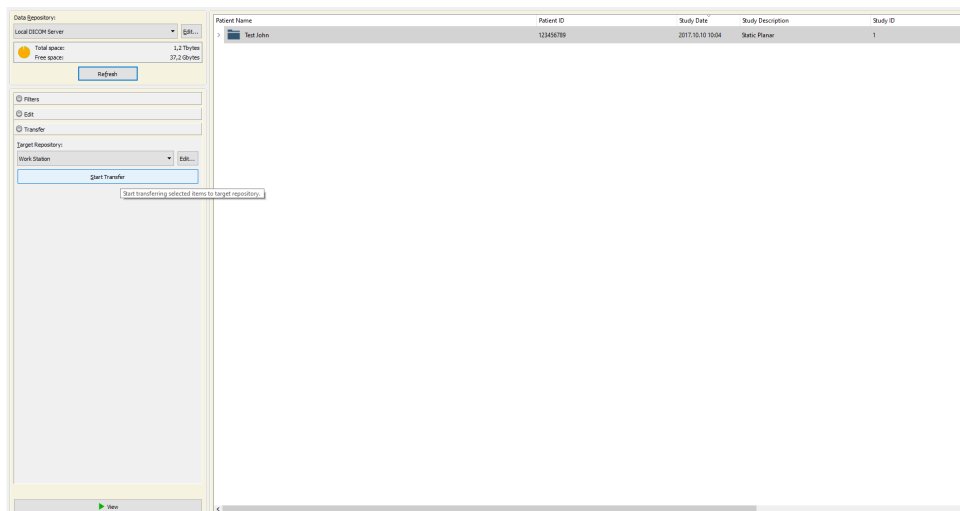


Figure 78. - Data transfer

3.4. Data repositories

Study Browser may have several configured data locations, both DICOM servers and other local or network folders. By pressing the **[Edit...]** button the **Data Repositories** dialog appears where DICOM server locations and data locations may be configured.

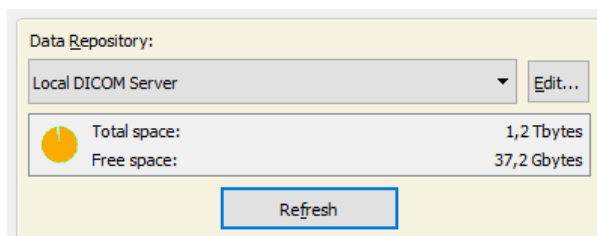


Figure 79. - Data repository

VI. Setting up and acquisition

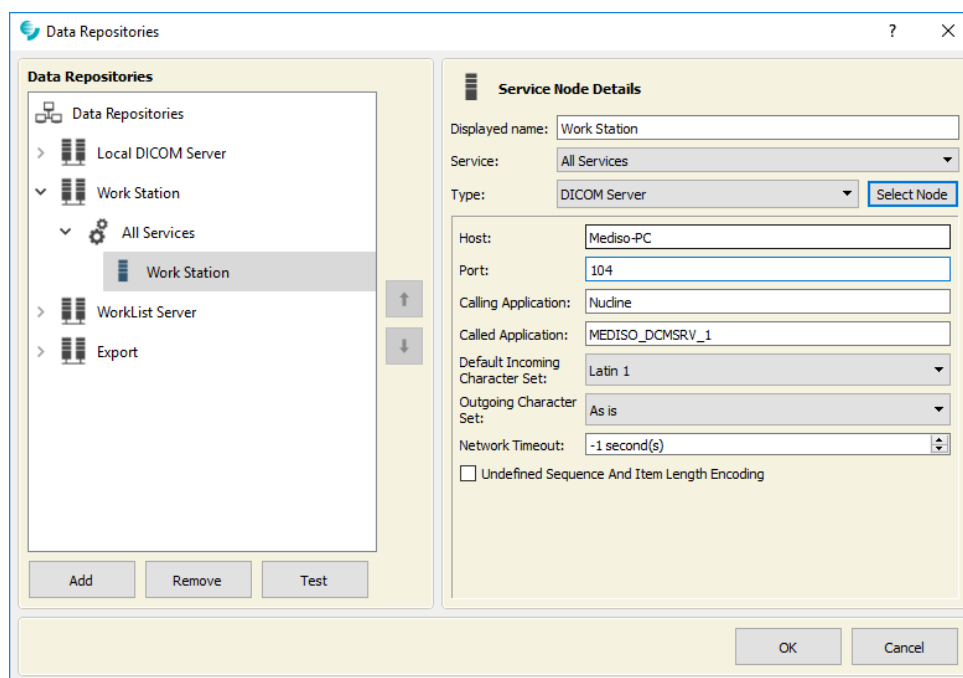


Figure 80. - Data repositories

To add a new data repository select the **Data Repositories** in the dialog and press the **[Add]** button. A dialog will appear for the name of the repository. On the right side of the dialog there is the **[Type]** selector combo box to define the type of the repository **DICOM Server**, **DIAG**, **DICOM File Set** or **Data Folder**.

- **DICOM Server** repository type: It is for servers, which can communicate through DICOM protocol such as Mediso DICOM Servers, PACS, HIS etc. It is necessary to specify the **Host**, which is the TCP/IP address of the server, **Port**, **Calling**, and **Called Application** (which are the calling and called application entity titles respectively) values.
- **DIAG** repository type: It is for DIAG Processing Software data repositories. Please enter the 'adat' (data) and 'kepek' (images) locations into the appropriate fields. Cannot be a transfer destination repository.
- **DICOM File Set** repository type: It represents a local or a network folder where the data is stored with an accompanying DICOMDIR file. Enter the data location into the **Folder** field.
- **Data Folder** repository type: It represents a local or a network folder where the data is stored. Enter the data location into the **Folder** field. Exported data files are created with a .dcm extension.

For **DICOM Servers**, **DICOM File Sets**, **Data Folders** repository types you can change the DICOM sequence encoding mode. To use explicit sequence encoding mode uncheck the **Undefined Sequence And Item Length Encoding** otherwise undefined sequence encoding will be used.

For **DICOM Servers**, **DICOM File Sets**, **Data Folders** repository types you can change the character set in which the data is encoded by setting the **Default Incoming Character Set** to

the appropriate value. This setting is used only in such situations when the specific character set is missing from the DICOM dataset i.e. it cannot be used to override existing encoding information.

For **DICOM Servers**, **DICOM File Sets**, **Data Folders** repository types you can change the character set in which the data are transferred by setting the **Outgoing Character Set** to the appropriate value.

For **DICOM Servers** you can change the network timeout value by entering the appropriate value into **Network Timeout** field. -1 timeout means that the default timeout value will be used which is 5 minutes.

After selecting a repository there is an option to disable auto-query by unchecking the **Auto Query On Study Browser Open** option.

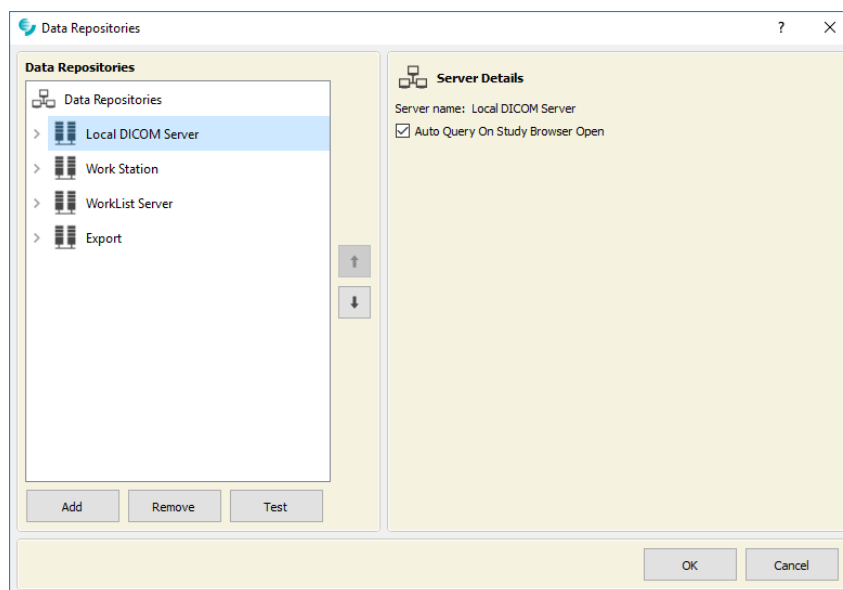


Figure 81. - Auto Query On Study Browser Open

4. Acquisition screen

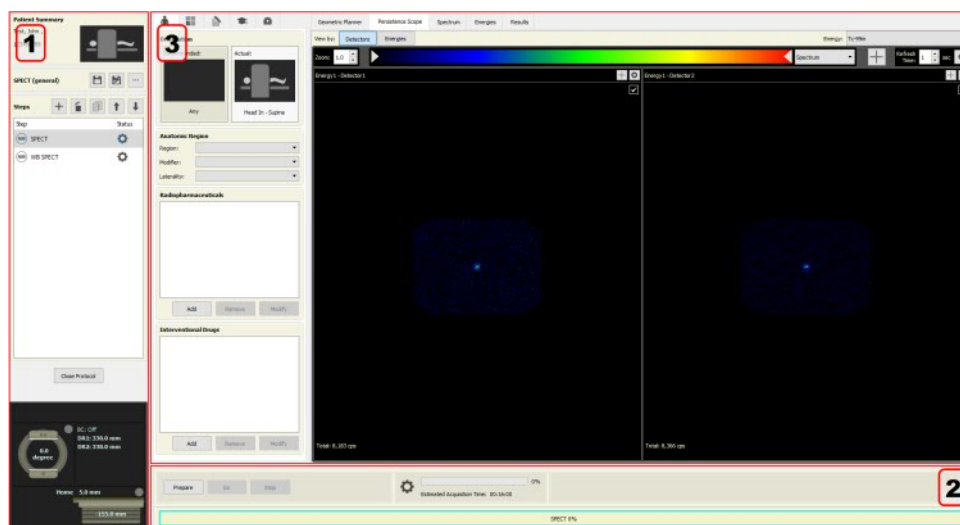


Figure 82. - Acquisition screen

This form is the user interface during the acquisitions.




It contains logically 3 main panels.

1. **Protocol Information Panel**
2. **Control Panel**
3. **Acquisition Panel**



4.1. Protocol information panel




This panel (left column of the screen) contains information about the loaded protocol. It displays Patient Summary, protocol name, the protocol steps of the loaded protocol, and at the bottom you can see a status window which visualizes the main parts of the hardware elements of the modalities and the gantry.

Right to the protocol name there are function buttons:

- **[Save Protocol]**  : you can update the loaded protocol from the runtime form with the runtime modified parameter set
- **[Save As Protocol]**  : you can create a new protocol from the runtime form with the runtime modified parameter set
- **[Open Another Protocol]**  : you can leave the loaded protocol and open another one

At the top of the protocol step panel there are function buttons:

- **[Merge Protocol]**  : you can merge the steps of an existing protocol into the current loaded protocol.
- **[Remove Protocol Step]**  : you can remove the current protocol step from the list.

- **[Copy Protocol Step]**  : you can copy the current protocol step under a unique name.
- **[Move Protocol Step Up]**  : you can move the current protocol step one level up.
- **[Move Protocol Step Down]**  : you can move the current protocol step one level down.

In the panel there is the list of the protocol steps (with modality icon, name and status columns). One of them is always active (current protocol step). The order of the protocol steps in the list is not a processing order, the procedure can be started at any step. The sole exception if there is a chain of protocols: the first one (* marked) is the only one could be started and the following steps (🕒 marked) are automatically initiated.

The current protocol step can be renamed with double click on the name of it if it was not executed already.

In the **Control** and **Acquisition** panels (see [Control panel](#) and [Acquisition panel](#)) you can see information always about the current protocol step.

With the **[Close]** button you can leave the protocol and close the acquisition screen.

4.1.1. Small Status Screen of the SPECT

It is the quick review scheme of the SPECT. It appears on every acquisition screen on the bottom left part of the screen.

The semantics of the icons are:

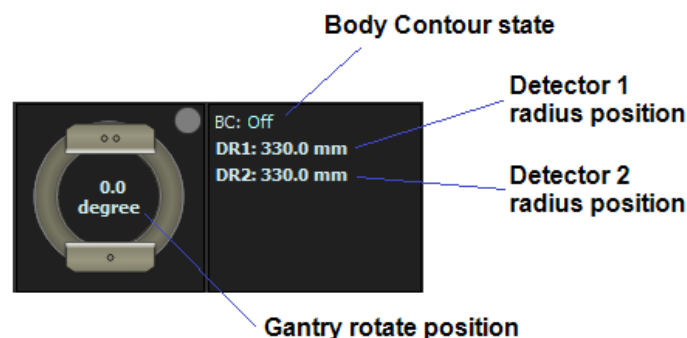


Figure 83. - The semantics of the icons

4.2. Control panel

The Control panel is at the bottom of the acquisition screen. It contains information about the current protocol step.

On the left you find control buttons for initializing and executing the current acquisition:

- **[Prepare]**: Before starting an acquisition you must validate the parameters and move the gantry to the initial position. Until you did not initialized the acquisition with the Prepare button, the other buttons are not enabled.

VI. Setting up and acquisition

- **[Go]**: start the acquisition (enabled only after successful initialization).
- **[Stop]**: stop the acquisition (if necessary).

In case of connected protocol steps **[Prepare]** validates the parameters of the whole protocol step chain, and **[Go]** starts the execution of the whole protocol step chain.

Right to the control buttons you can see the status icon of the current acquisition (same as in the protocol step panel) and the progress information: estimated time before executing the acquisition and remaining time and percentage value of the progress during the acquisition.

On the right you can see actual status or error messages of the system (scanning, reconstruction in progress, etc.).

In the bottom part of the control panel the acquisition time line is displayed. It is useful in case of connected protocol steps.

4.3. Acquisition panel

The content of the Acquisition panel can be totally different in case of different protocol step types. This panel visualizes always the acquisition UI of the current protocol step.

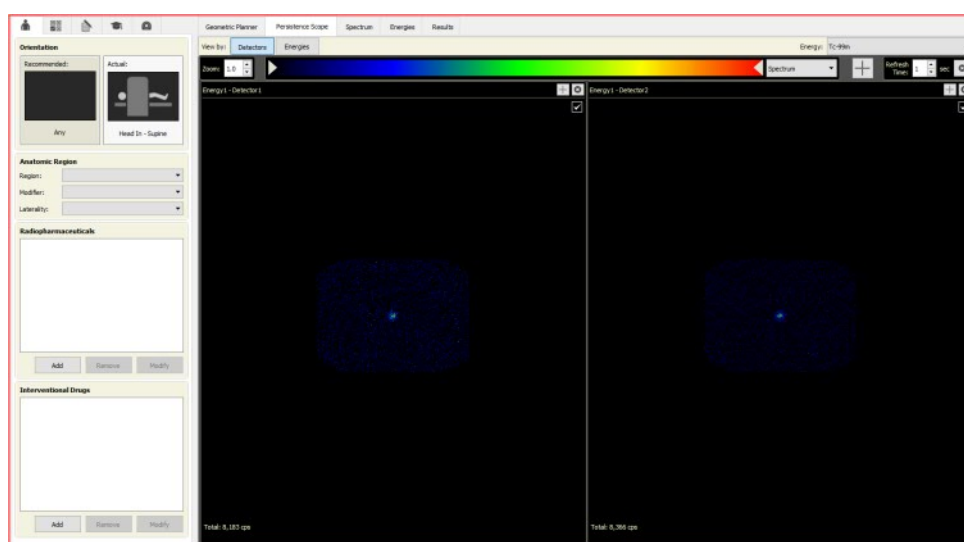


Figure 84. - Acquisition panel

The Acquisition panel has 2 main parts:

- **Parameter Editor** (left column): Various panels allow to enter different parameters to customize acquisition conditions. Protocol Editor should be used to save predefined parameters differing from factory default settings.
- **Image View**: This panel displays viewers to help graphically control acquisition. By default, the **Persistence Scope** viewer is displayed showing live images of patient.

4.3.1. Parameter editor

Patient

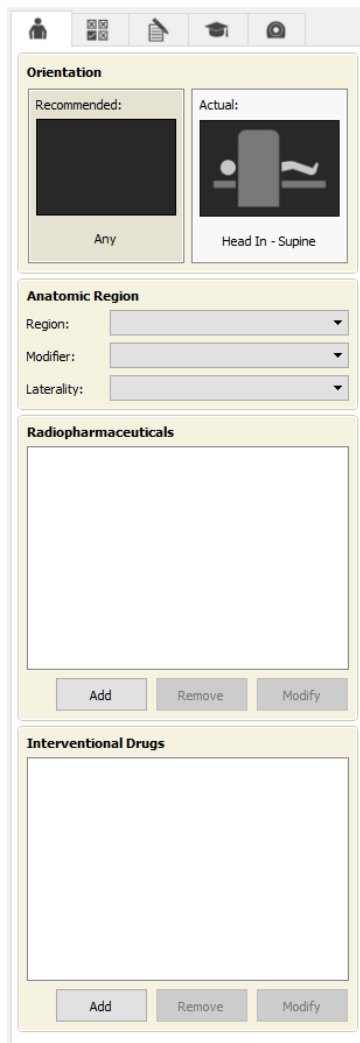


Figure 85. - Patient tab

Select here actual patient orientation, patient anatomic region being examined. The Orientation depends on the selected Detector Configuration mode. Selecting patient orientation will automatically have transferred to all protocol steps.

Here you can **[Add]**, **[Remove]** or **[Modify]** the **Radiopharmaceuticals** and **Interventional Drugs**.

The radiopharmaceuticals tab allows you to enter information about the type of agent injected into the patient and details such as injection volume, time of injection, route of injection and any other relevant information. Information on the type of radionuclide and the activity/dose used can also be entered. This tool is useful for keeping records of what procedures were carried out for a particular study.

For some evaluation procedures (like SUV calculation), the accurate patient information (e.g. sex, weight, height) and radiopharmaceuticals data (e.g. type, administered dose, administration date and time) are required.

VI. Setting up and acquisition

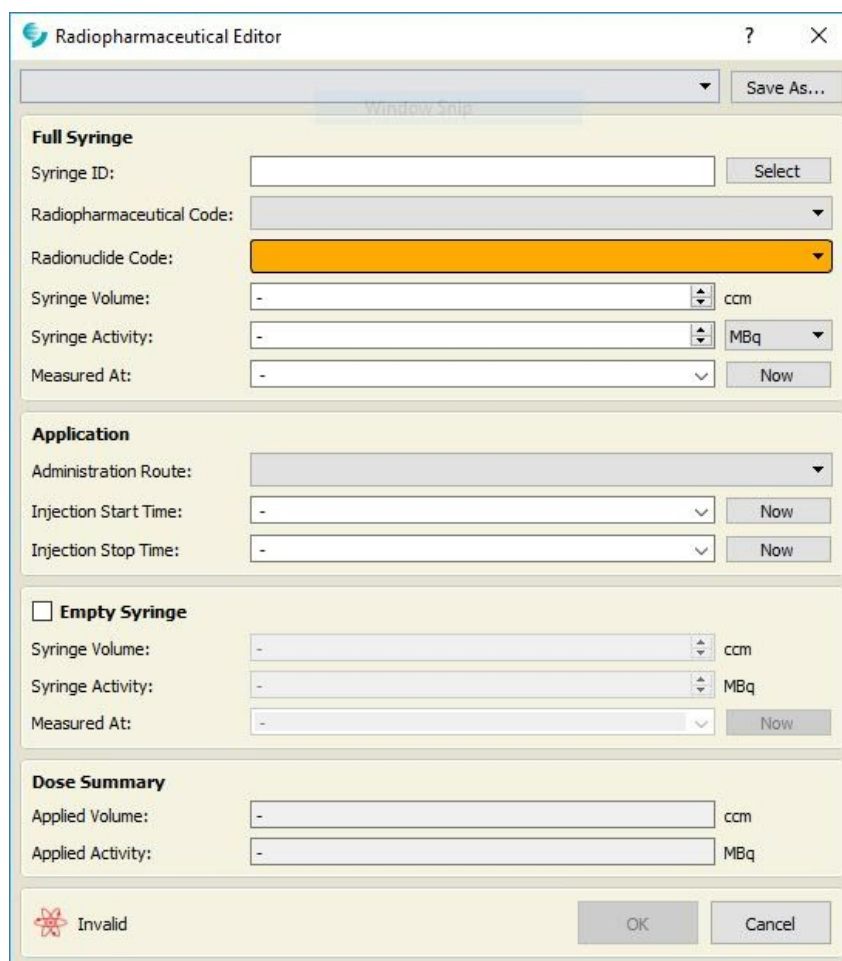


Figure 86. - Radiopharmaceutical Editor

Radiopharmaceutical:

- **Radiopharmaceutical Code:** name of the tracer
- **Radionuclide Code:** applied isotope
- **Administration Route:** Identifies the administration route for the radiopharmaceutical
- **Injection Start Time:** starting time of entering the tracer
- **Injection Stop Time:** At continuous dosing this is the end time of entering the tracer. At one-shot dosage set this field to the same time as the start time (optional).

Full Syringe:

- **Syringe ID:** Identifier of the syringe.
- **Syringe Volume:** The volume of the tracer in the syringe.
- **Syringe Activity:** Measured Activity of the full syringe.
- **Measured At:** The time, when the Syringe Activity was measured.

Press [**Select**] to choose the previously saved (in the **Syringe Editor**) syringe.

Empty Syringe:

- **Syringe Volume:** The remaining tracer volume.
- **Syringe Activity:** The remaining tracer activity.
- **Measures At:** The time, when the Empty Syringe Activity was measured.

Dose Summary:

- **Applied Volume:** The difference between the Full Syringe and the Empty Syringe.
- **Applied Activity:** Applied activity, considering the degradation.

There is also an option to enter information on any additional intervention drugs used in the study, including volume, route and time of injection.

Press **[Save As...]** button to save the form. The previously saved forms can be loaded from the drop-down menu.

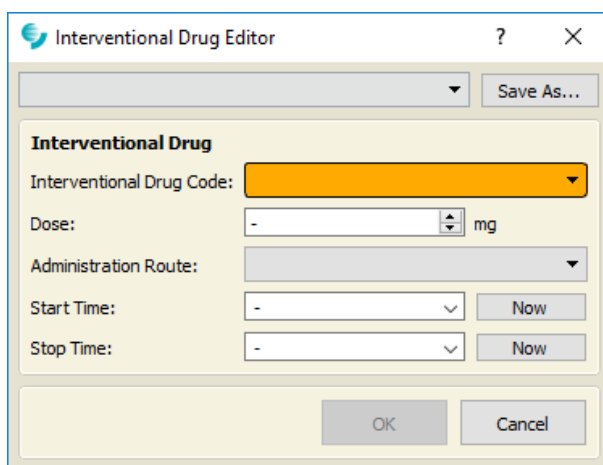


Figure 87. - Interventional Drug Editor

- **Interventional Drug Code:** name of the drug
- **Dose:** applied volume
- **Administration Route:** Identifies the administration route for the drug.
- **Start Time:** starting time of entering the drug
- **Stop Time:** At continuous dosing this is the end time of entering the drug. At one-shot dosage set this field to the same time as the start time (optional).

Press **[Save As...]** button to save the form. The previously saved forms can be loaded from the drop-down menu.

VI. Setting up and acquisition

Prepare

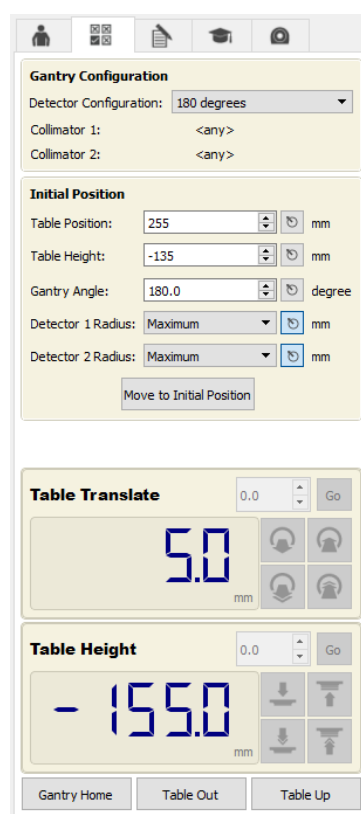


Figure 88. - Prepare tab

This panel used to prepare patient position before acquisition is ready to start.

Detector Configuration: select one of possible head configuration: 90 Degrees, 102 Degrees, 180 Degrees

Collimator 1, 2: displays required collimator by this examination.

Initial Positions: enter here all positions need to positioning patient before acquisition start.

Move To Initial Position: press this button to move patient to required position entered into fields above.

Gantry Controls: These are standard gantry controls, they allow easy adjustment of the positioning of the patient and the patient prior to imaging.

Routine

Slightly different views can be found at this tab for different acquisition types.

- **Acquisition Mode:** When a detector head is selected for acquisition (any combination of the detectors) images from that selected heads will be collected and saved during acquisition. Images will be stored separately for each head but especially for **SPECT** acquisitions the system merges images into one file.
- **Gantry, Patient Table, Scan Range, Rotation And Dynamic Options:** In these panels you can define the patient and gantry positions during acquisition. In **Rotation** panel of **SPECT** and **Whole Body SPECT** protocol **Scan Mode** control enables selecting

between **Step And Shoot** and **Continuous** acquisition mode. **Scan Mode** defines how detector rotation is performed during acquisition. In **Step And Shoot** acquisition mode at each angular position detectors are in fixed position while building the image. At **Continuous** mode detectors continuously rotate and collect all gamma events to the same image under a given scan arc. In **Dynamic Options** panel of **SPECT** and **Gated SPECT** protocol the **Number Of Scans** defines the repetition number of the same scan (like at **Whole Body SPECT**).

- **Termination Conditions:** define here conditions which will terminate acquisition.
- **Phases:** this panel used by Dynamic acquisition, same as like **Termination** condition for other panels. Defines how to acquire series of images and when to stop the process.
- **Scan Range:** this panel used by **Whole Body** acquisition. Not only contains the patient and gantry positions during acquisition but defines acquisition end (termination conditions) with controls **Scan Length** and **Scan Speed**. This panel is used by **Whole Body SPECT** acquisition too and contains **Number Of Scans** which defines the scan length by number of **FOVs**, **Direction** for patient table movement and **Scan Direction** of head rotation. **Fitting Mode** defines the method how images of separate **FOVs** are joined to form a final image (**Iris**: using iris definition to eliminate missing field at corner cut, **Fixed**: uses setting definition for overlapping **FOVs**).
- **Start Control:** used when more protocol steps are executed automatically one after another. Define here the start condition for a selected protocol step.

Advanced

Frames

Frame options determine how the projection data is saved. You may define the following:

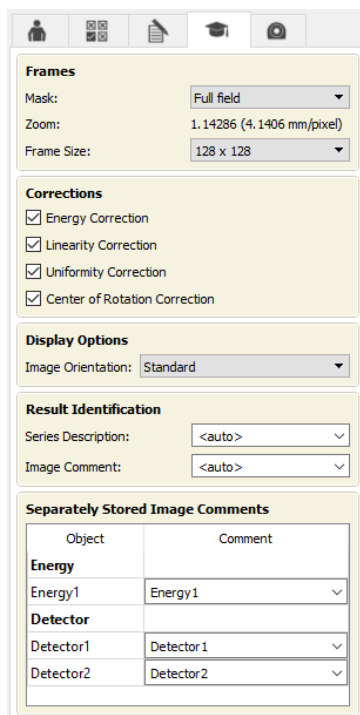
Mask: This function allows you to image with the detector's full field or only a portion of it. The selected area can be at the center, top or bottom part of the detector. The default parameter is **Full Field**.

Zoom: For a given frame size, the zoom function decreases the field of view (FOV), thus zooming into the middle of that FOV. Zoom value can be modified by choosing a different **Mask**.

Zooming can be performed when the projection of the object on the detector is relatively small in comparison to the detector FOV. Thus, after the zoom, the image has more pixels in the region of interest. Note that the zoom does not increase the intrinsic resolution.

It is generally favorable to increase the Frame Size instead of increasing zoom. By doing so, similar mm/pixel values can be achieved without the risk of crop artifacts. The final volume-of-interest can be flexibly decreased and the irrelevant regions can be cropped during the reconstruction or the post-processing phase.

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Frames

Mask: Full field

Zoom: 1.14286 (4.1406 mm/pixel)

Frame Size: 128 x 128

Corrections

☒ Energy Correction

☒ Linearity Correction

☒ Uniformity Correction

☒ Center of Rotation Correction

Display Options

Image Orientation: Standard

Result Identification

Series Description: <auto>

Image Comment: <auto>

Separately Stored Image Comments

Object	Comment
Energy	
Energy1	Energy1
Detector	
Detector1	Detector1
Detector2	Detector2

Figure 89. - Advanced tab

CAUTION



Zoom should be set with great care in order to avoid truncation of the image. When too large value is set, some of the organs or body parts could be cropped from the image, which leads to artifacts on the reconstructed image or even parts of the target organ can go missing.

Frame Size: This parameter dictates how the FOV should be discretized, namely, the matrix size of the digital data.

Corrections

These parameters describe what corrections will be applied to the data. In general, all of these values should be left on unless a calibration measurement calls for something else. You may enable the following corrections:

Energy: Controls the calibration of the energy estimation of measured gamma rays; should always be turned on.

Linearity: Corrects for non-linear artifacts inherent to the position-estimation process; should always be turned on.

Uniformity: Corrects for any crystal or electronic non-uniformity across the FOV of the detector; should always be turned on.

Center Of Rotation: Adjusts the position of the center of the detector with respect to the axis of rotation as the camera rotates. Does not need to be turned on during planar

measurements, though it may be best to leave this correction on at all time in the spirit of consistency (set this option always to on state for SPECT acquisitions).

Display Options

Image Orientation: Standard or Native. Defines how image is displayed in **Persistence Scope** view (This selection has no influence to the saved image orientation).

- **Standard:** patient is displayed always with head up, left/right side as would be visible from detector.
- **Native:** do not apply any image rotation and flip while displaying in **Persistence Scope**.

Result Identification

Series Description: This text will be added to DICOM image. Text will be displayed in image browser under **Series Description** column. [**<Auto>**] means use protocol step name for series description.

Image Comment: This is a general image comment. The text will be added to DICOM image combined with **Separately Stored Image Comment**. [**<Auto>**] means use acquisition type name for image comment (**Static, Gated, Dynamic, SPECT, Whole Body**).

Separately Stored Image Comments – This text will be added to DICOM image combined with general image comment. Enter here the text for image comment of a separately stored image. These texts will be used to create image comment for each separately stored image and will be added to general image comment. Finally, image comment will have the following format: <General image comment> - <Image comment by energy> - <Image comment by detector> (example: Static – Energy1 – Detector1).

Image ID added to DICOM image is generated automatically as a short version of Image comment. Image ID is built in following format: <Energy> - <Phase> - <Detector> <Acquisition type> (example: E1-D1 SP). Image ID is displayed in image browser under Instance Description column.

Gating tab

Gating panel defines conditions used during ECG acquisition. Displayed only at Gated Planar and Gated SPECT acquisition.

R-R Interval (msec): this value is the actual ECG interval of patient being examined. During acquisition the value could be changed entering a number to this control or using [**Auto**], [**<<**] or [**>>**] buttons.

R-R Tolerance (%): Defines R-R range. Inside this interval all heart beats are accepted during acquisition.

Skip Beats: The number of heart beats fell into accepted interval but skipped just after rejected beats.

Number Of Time Slots: Defines the number of time intervals between two heart beats. For each such interval an image will be created and saved with acquired data.



VI. Setting up and acquisition

[Auto], [<<] or [>>] buttons: Pressing these buttons automatically measures or modifies R-R Interval value.

Clear Button: Press this button to clear the contents of R-R monitor and R-R histogram.

Automatically Adjust R-R Interval: Check this option to allow program to automatically follow R-R Interval.

ECG signal monitoring buttons:

-  Indicates the presence of ECG signal.
-  Indicates the R-R interval is in or out of tolerance range.

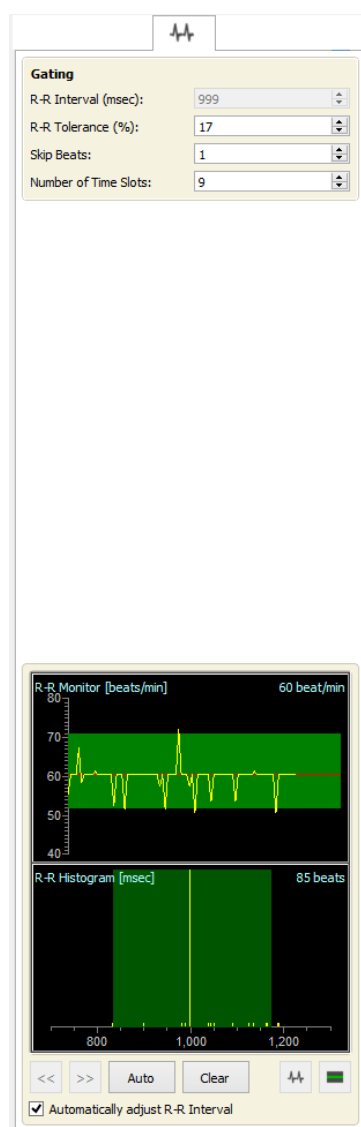


Figure 90. - Gating tab

Marker

This panel contains the list of markers placed to the image in **Persistence Scope**. These markers will be saved together with image then the image processing program InterView is able to display them. At this panel selected marker could be deleted pressing **[Delete]**

button. Adding and positioning marker on image is possible in **Persistence Scope** with marker tool buttons.

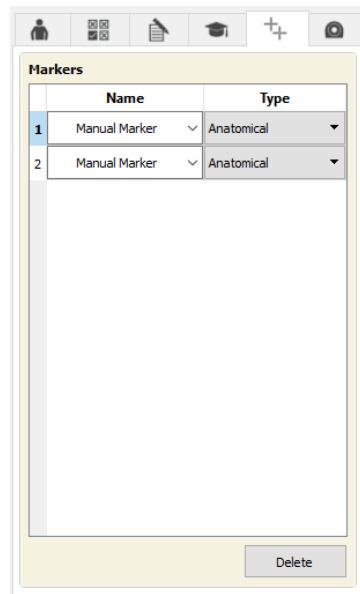


Figure 91. - Marker tab

Gantry tab

Proper positioning of the gantry, patient bed and table height greatly impacts image quality. Access to the standard gantry controls is provided in the acquisition screen so you can easily adjust the positioning of the gantry and patient prior to imaging. You can adjust:

Gantry Rotate: Rotates the gantry (heads) around the patient in a clockwise or anti-clockwise direction.

Detector Radius: Moves the detector head in and out (closer to or away from patient).

Table Translate: Moves the patient table in and out of the system (axial).

Table Height: Moves the table height up and down.

Table Home: Pulls out the table fully, and lowers to the bottom position.

Table Out: Pulls out the table fully.

Table Up: Moves the table height to COR position.

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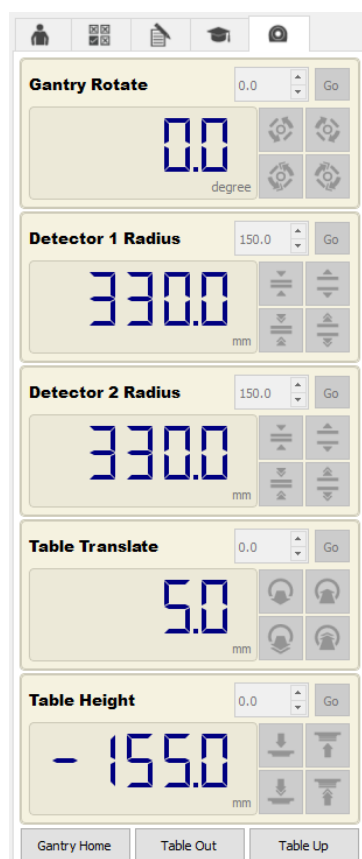


Figure 92. - Gantry tab

4.3.2. Image viewer

This panel consists of 5 different tabs which are activated according to protocol type or the state of the protocols.

Geometric planner

This tool is used to graphically select the scan able area of patient (in other words adjusting patient table positions). The blue rectangle shaped area is the graphic representation of **Table Position** and **Table Height** from **Routine** tab of **Parameter Editor**. This can be moved and resized with the mouse.

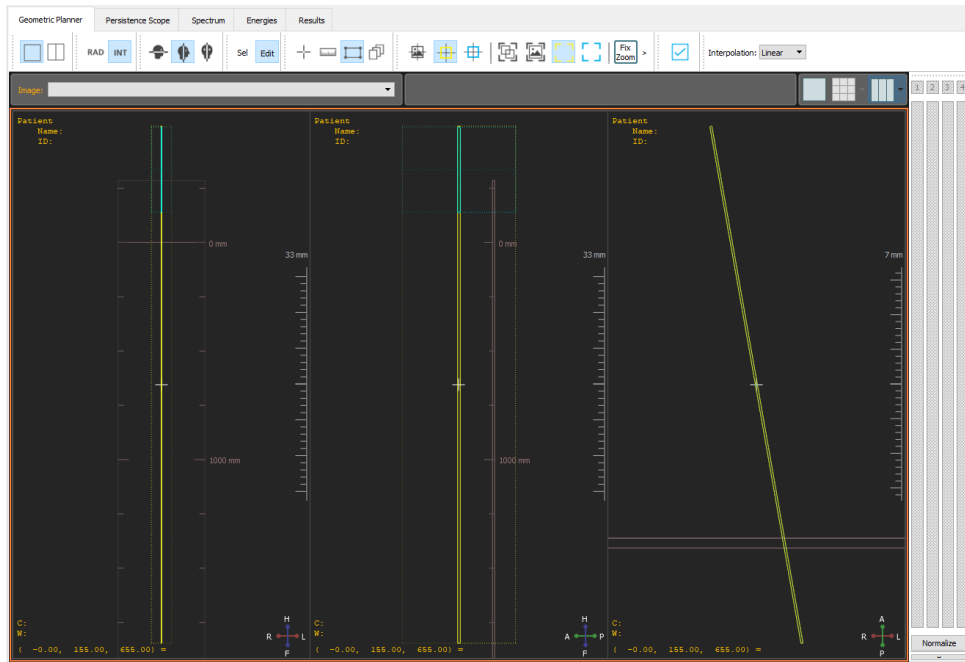


Figure 93. - Geometric Planner tab

Following controls could be used from **Geometric Planner** toolbar.

- [Single Panel] / [Double Panel]
- Radiology [RAD] / Interventional Radiology [INT]
- [Axial] / [Coronal] / [Sagittal]
- Selection Mode [Sel] / Edit Mode [Edit]
- [Scan Box Layer] / [Cursor Layer] / [Ruler Layer]
- Move Camera
- Scan Box Visibility Settings
- Interpolation Toolbar
- [Planar Viewer] / [Tiled Viewer] / [Orto Viewer]

Presistence scope

Displays live image of patient, this tab is displayed by default when protocol is opened.

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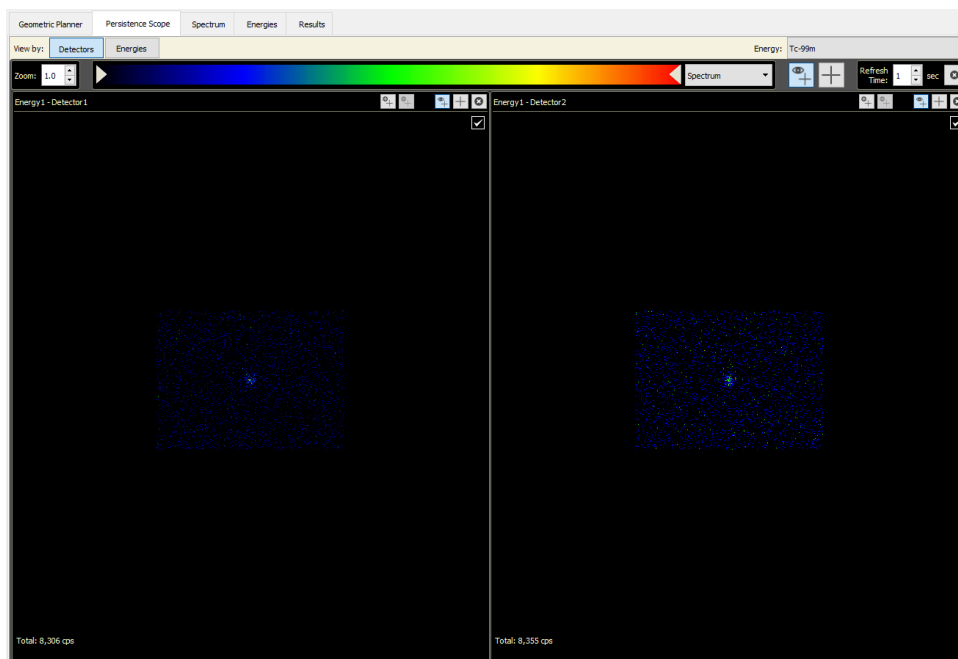


Figure 94. - Persistence scope

View By [Detectors]: press this button if you would like to see the live image feed of all detectors. On the right side of this toolbar line the energy images could be selected.



View By [Energies]: press this button if you would like to see all energy images of one detector. On the right side of this toolbar line the detector could be selected.




Zoom: increases/reduces the **Persistence Scope** live image size. This size has no influence to acquired and saved DICOM image size (size of saved DICOM image is selectable in **Parameter Editor, Advanced Tab, Frame Size**).

Spectrum: select one of predefined color scheme used to display image in **Persistence Scope**.

Refresh Time: the time rate at which **Persistence Scope** image is deleted automatically. Selecting **INF** never deletes Persistence Scope image.

Persistence scope toolbar

- **Persistence Scope Name:** identical with image comment, editable in **Parameter Editor, Advanced** tab.
- **Add Marker Button** : adds marker to **Persistence Scope** image. Marker is added to the image center but the marker could be moved anywhere in the image by mouse. Markers are strongly connected and belongs to patient orientation (**Parameter Editor, Patient** tab). Changing patient orientation will hide markers added at previous patient orientation. Markers are visible in all protocol steps if they have the same patient orientation selected. Markers are stored with the acquired image. Set marker parameters (**Name – Type**) on the **Markers** tab (see in Marker section).
- **Delete Marker Button** : deletes selected marker

- **Show/Hide Markers Button** : displays or hides markers. Even markers are hidden they will be saved to DICOM image.
- **Cross Hair Button** : draws to lines to show image center
- **Clear Persistence Scope Button** : pressing this button clears live image.

Spectrum

Displays live spectrum of gamma rays registered by detectors. Furthermore, displays energy windows used in Energy map with different colors.

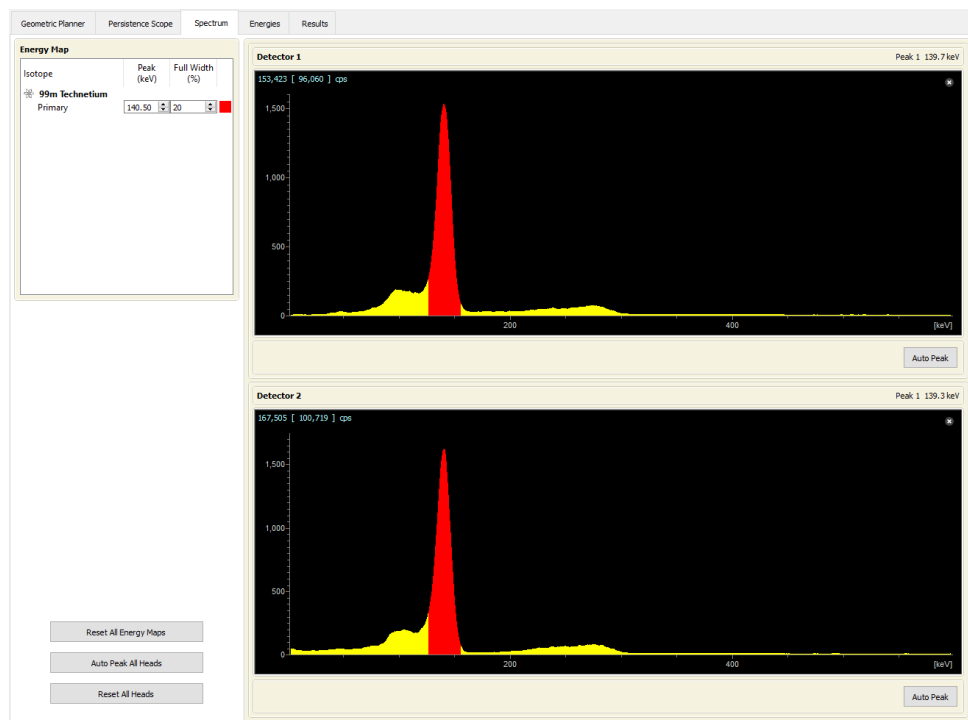


Figure 95. - Spectrum tab

Isotope: Identifies the classification of the isotope used.

Peak: Defines the energy peak for the relevant isotope.

Full Width: This field identifies the size of the energy window, calculated as a function of the peak energy. Namely, a 20% energy window for Tc^{99m} will be +/-14.1 keV around 140.5 keV. See the [Energy Map editor](#) section for more on defining energy window parameters.

Energy windows values are editable (**Peak** and **Full Width**) for the opened acquisition. Modified Peak and Full Width values are applied only to active (opened) acquisition step. If the same Energy map is used in other protocol step, they remain unchanged.

[Reset All Energy Maps]: press this button to revert edited values of energy window (**Peak** and **Full Width**) to their original state.

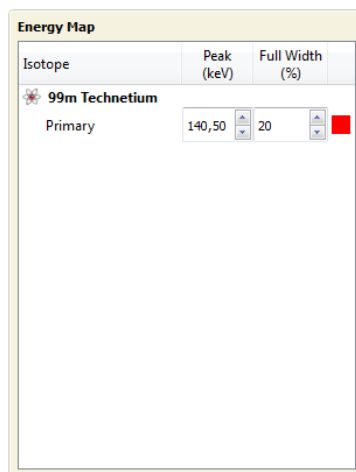
Auto Peak: Finds the center of the spectrum peak as defined in **Energy Map Editor** (Auto-peak column) then set the spectrum to match these target position. This operation applies to one detector only. Press **[Auto Peak]** if this is the first acquisition with a particular isotope, if

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this isotope has not been imaged for an extended period of time (weeks) or if the spectrum does not appear to align properly with the shaded energy regions.

[Auto Peak All Heads:] do the same as **[Auto Peak]** but for all heads in the same time.

[Reset All Heads]: If you have pressed **[Auto Peak]** or **[Auto Peak All Heads]** button but you would like to return the spectrum to the position it was in the moment you entered to the acquisition protocol, press **[Reset All Heads]** button. When one of **[Auto Peak]** or **[Auto Peak All Heads]** button is pressed the detector must be exposed with radiation of selected isotope. When one of **[Auto Peak]**, **[Auto Peak All Heads]** or **[Reset All Heads]** button is pressed spectrum is moved in all acquisition steps.



Isotope	Peak (keV)	Full Width (%)
99m Technetium		
Primary	140,50	20

Figure 96. - Energy map

Energies

Allows selecting Energy map and editing Images of Energy map. Each image in Images list will produce a separate picture during acquisition.

In the **[Energy Map]** field, the predefined isotope (chosen during study selection) is present, along with information about the isotope including its peaks and peak width (For detailed information see previous section).

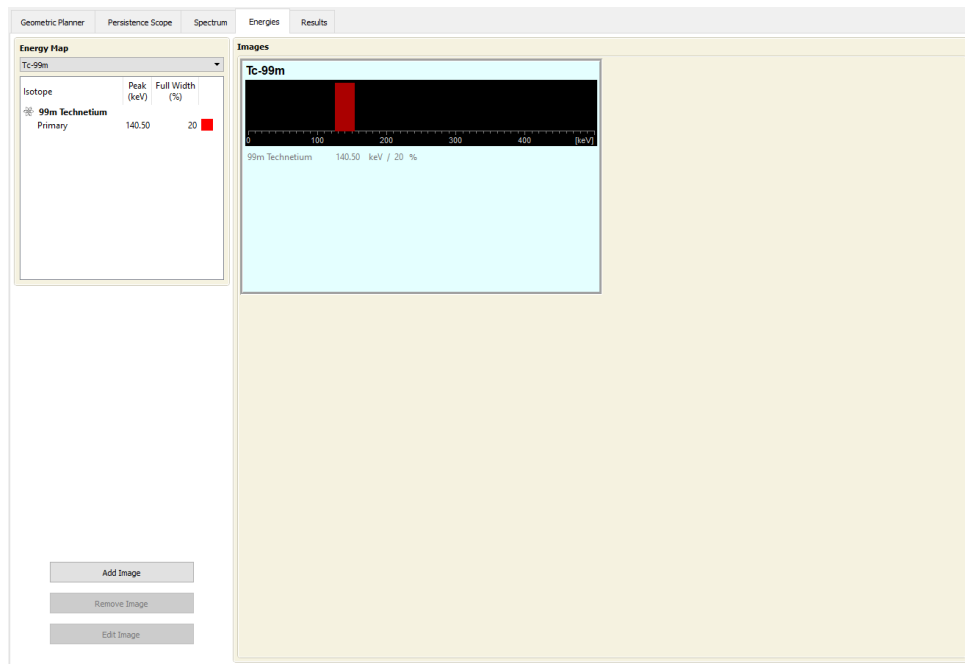


Figure 97. - Energies tab

If you decide to change energy maps (i.e., for a new isotope or combination of isotopes), they can do so by selecting the new energy map from this drop down menu. The new energy map, containing the isotope of interest, will then be displayed in the energy map.

For multi-isotope studies, information on all isotopes will appear in the energy map.

For each acquisition new frames can be added to the study. This is useful when acquiring dual isotope studies and when using isotopes with more than one energy peak.

To add images, press **[Add Image]** button. Pressing this button displays **Image Setup** dialog box to create a new image. In **Image Setup** dialog box edit the **Image Name** and select the energy window you intend to belong to image.

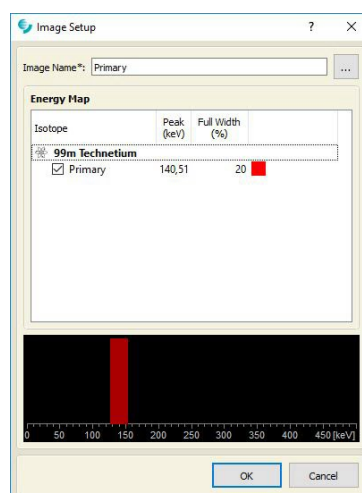


Figure 98. - Image Setup

If an isotope has two energy peaks, these can be split into two different frames by highlighting an individual peak and pressing **[OK]**.

VI. Setting up and acquisition

The new image will then appear in the **Images** field.

Likewise, this can also be used to separate energy peaks from different isotopes.

To remove a frame, highlight the frame and press **[Remove Frame]**.

[Edit Image]: pressing this button displays **Image Setup** dialog box for a selected image. In **Image Setup** dialog box edit the **Image Name** and select the energy window you intend to belong to image.

Results

Displays the acquired image.

Immediately following the end of the acquisition the monitor is automatically switching to Results tab.

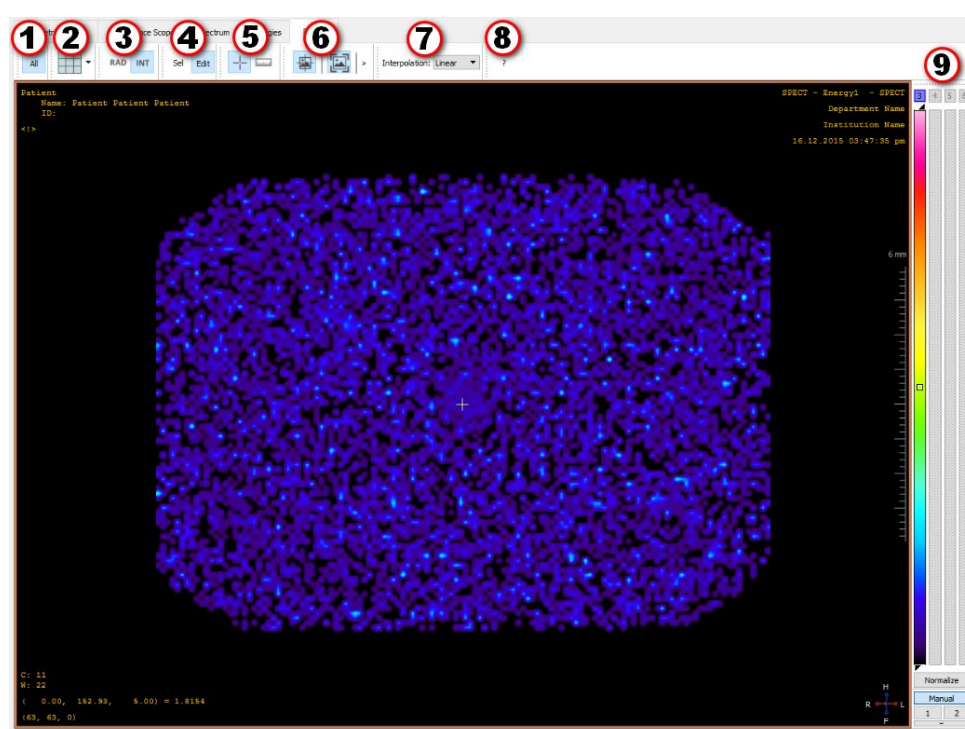


Figure 99. - Results tab

Results toolbar functions.

1. **Layout Toolbar** (All – displays all images)
2. **Viewer Type Toolbar**
3. **Display Convention Toolbar:** **[Rad]** – Radiology; **[INT]** – Interventional Radiology
4. **Mode Toolbar:** Selection or Edit mode
5. **Layer Toolbar:** Cursor or Ruler
6. **Focus Toolbar:** Move camera to the center of image/ Move camera center and zoom to fit the image
7. **Interpolation Toolbar:** Nearest, Linear, Cubic
8. **Hotkeys**
9. **Palette Toolbar**

When you performing a Dynamic acquisition the view is already switched to **Time Activity Curve Viewer (TAC)** tab at the acquisition start. Displays Time Activity Curve of ROIs (Region Of Interest) for selected Detector and Energy image.

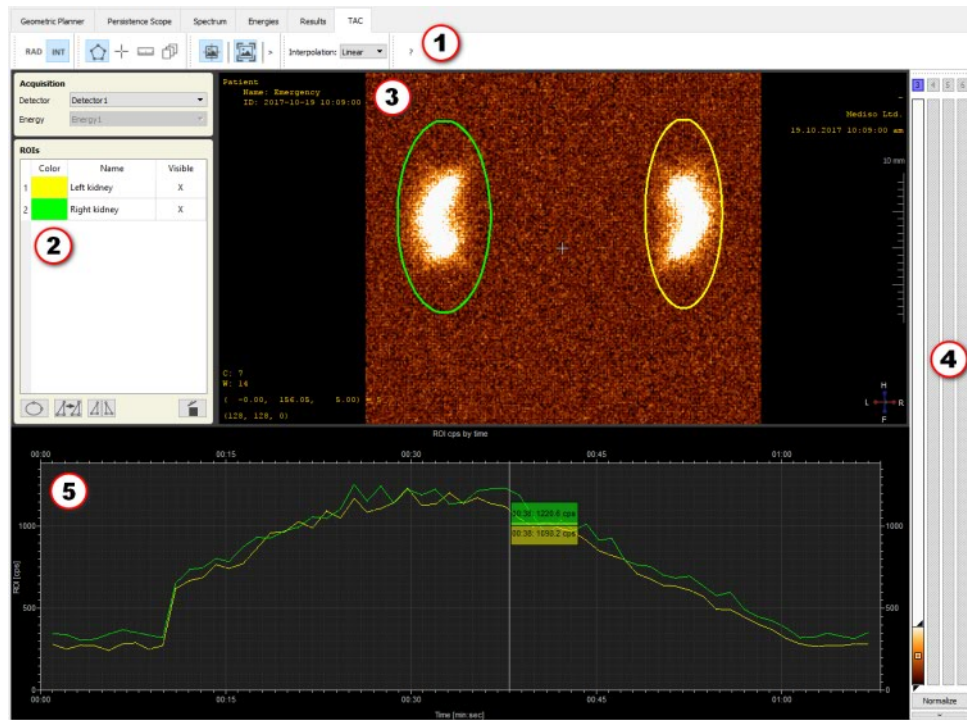


Figure 100. - Time Activity Curve viewer

TAC Panels And Functions.

1. Image Toolbar
2. ROI list and toolbar (Create, Copy, Delete functions)
3. Summed image with ROIs
4. Summed image spectrum
5. TAC of ROIs

VII. Performing an acquisition

This chapter provides instructions on performing SPECT acquisitions.

NOTICE

The detector's high voltage should be on for at least 24 hours before acquiring images. If the power is off for short time periods (10 to 30 minutes), then the power should be restored for a comparable time (10 to 30 minutes) prior to performing acquisitions. If the power is off for more than 1 hour, wait at least twice the time (maximum 24 hours) before using the camera. To ensure that the high voltage is on, keep the Main Power Switch on the rear of the Gantry switched ON at all times.

1. Performing a SPECT acquisition

CAUTION



Mediso recommends to follow local regulations and guidelines (e.g. EANM). These guidelines may include information for the whole protocol, e.g. for SPECT cardiac examinations:

- The patient must be informed about the procedure, empathizing to lay motionless.
- For better image quality it is recommended to lay down the patient on the patient table 6-10 minutes prior the acquisition.
- Use positioning accessories (e.g. arm rest) for patient comfort and better image quality.
- After acquisition check for motion in cine mode and if motion is ≥ 2 pixels, repeat the acquisition.

1. Go to Local Worklist, press **[New]** button. Enter required data according to [Local worklist](#).
2. Add patient information and fill the Radiopharmaceutical Editor.
3. Select Scheduled Procedure, Press **[New]** button then select **SPECT** study from **SPECT Base Procedure** from **Factory** protocol set (**User** and **Favourites** protocol sets are also available). The same procedure need to be done for **Static Planar**, **Dynamic Planar**, **Gated Planar**, **Gated SPECT**, **Dynamic SPECT**, **Dynamic Gated SPECT**, **Whole Body**, **Whole Body SPECT**, **Pinhole SPECT** and **Gated Pinhole SPECT** acquisitions.

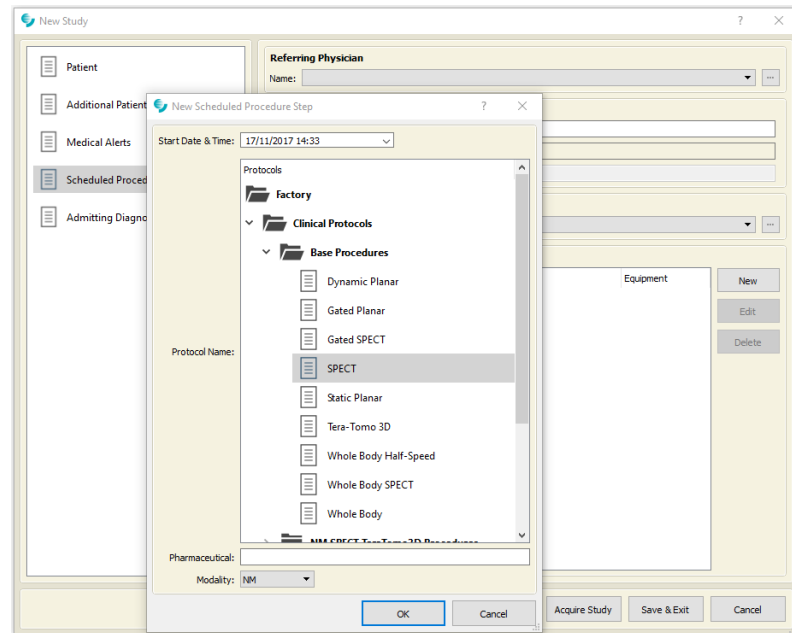


Figure 101. - Select study

4. Press the **[OK]** button, then press **[Acquire Study]** button.

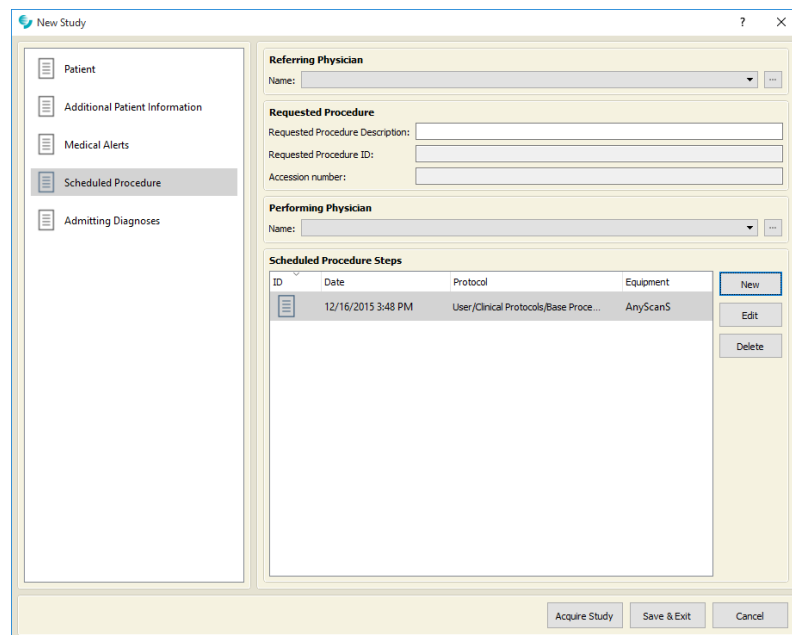


Figure 102. - Acquire study

5. Press the **[Open]** button on the left corner of the next screen.

VII. Performing an acquisition

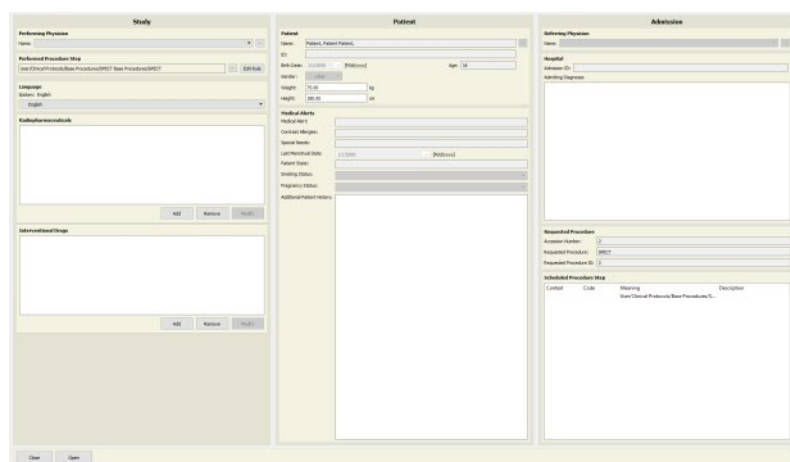


Figure 103. - Open

6. The **SPECT Acquisition** screen opens.

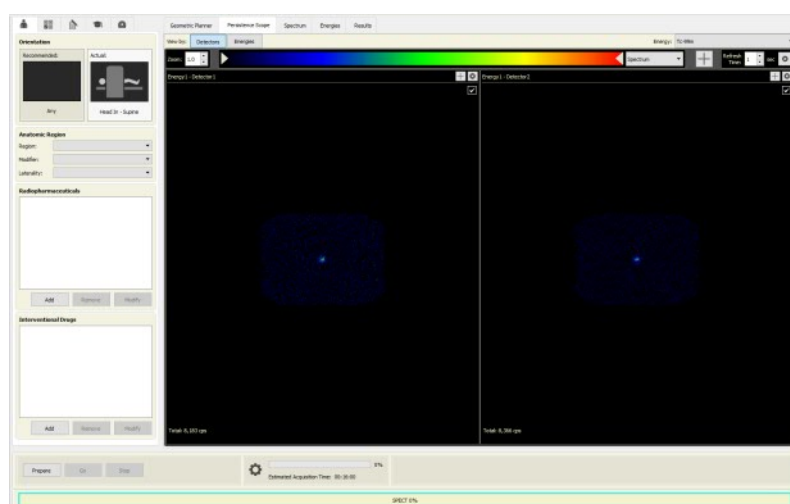




Figure 104. - SPECT Acquisition

7. Verify all acquisition parameters in **Parameter Editor** panels walking through all tabs (See description of **Parameter Editor** panel). Adjust **Patient Orientation** at **Patient** panel .
8. Change to **Prepare** panel pressing icon . Move patient table to position at which patient could easily lay to the table. Use Gantry handcontroller for this purpose or press **[Table Out]**, or **[Gantry Home]**. Position patient on the table according to choice in **Patient** panel.

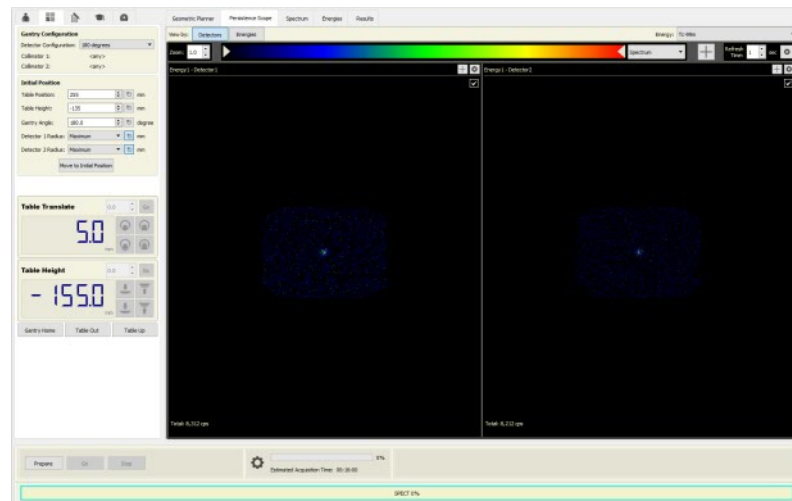



Figure 105. - Prepare panel

9. Press **[Move To Initial Position]** button. Patient table is moving to required position.
10. Scroll to the tab **Routine** . Patient is already moved to the right position so select **As Is** mode for the next parameter fields: **Table Position** and **Table Height**. On the **Routine** tab choose between **Scan Mode** options, **Step And Shoot** or **Continuous** and adjust the **Number Of Scans**. It is recommended to set all **Detector Radius** to **Body Contour**.

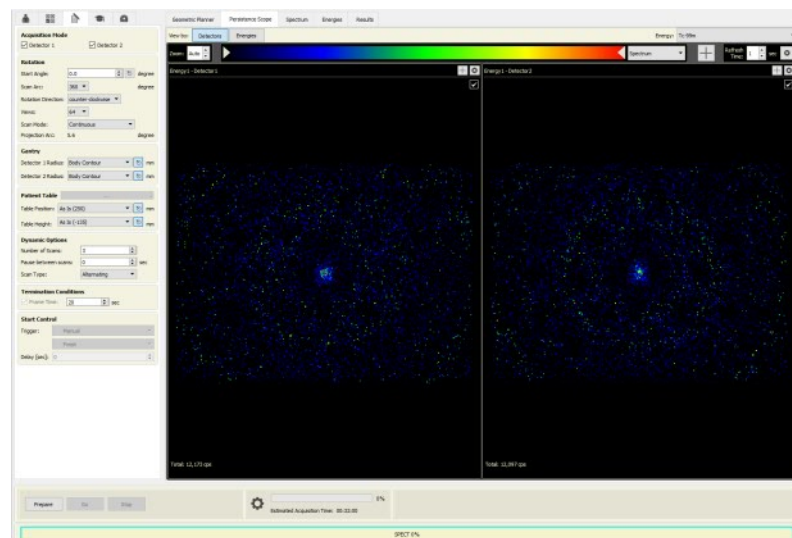


Figure 106. - Routine tab

VII. Performing an acquisition

11. Press **[Prepare]** button in Control bar. The Gantry Positioning dialog is opened and by pressing **[Start]** starts some table and detector moving.
12. Acquisition is ready to start. Verify on **Persistence Scope** the patient position and verify gamma ray energy in **Spectrum Viewer**. Press **[Go]** in Control bar to start acquisition.
13. After the acquisition, the **Image** view is changed from **Persistence Scope** to **Results**.

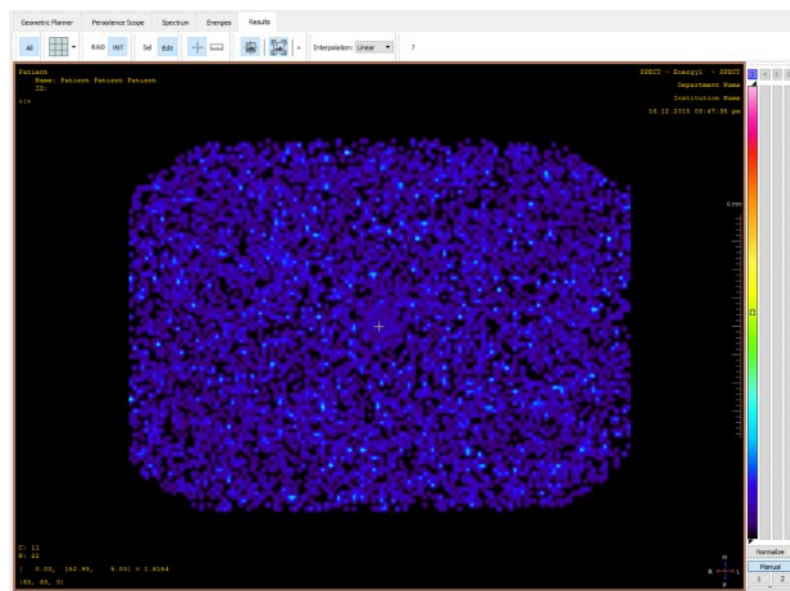



Figure 107. - Result after acquisition

14. When acquisition is finished change to **Prepare** panel pressing  icon. Move patient table to position at which patient could easily get up out of bed. Use Gantry handcontroller for this purpose or press **[Table Out]**, or **[Gantry Home]**.
15. When acquisition is finished acquired images are automatically saved.

1.1. Functions during a SPECT acquisition

While the acquisition is in progress you will be able to view the data on your acquisition monitor as it is collected. The status bar in the lower portion of the screen will alert you of the current operations of the camera, any recent errors or further instructions. Not only you can see the data being acquired, but also monitor the position of the gantry and patient table.


During the acquisition you will be able to view the data on the screen in several formats. You may make the following selections:

- **Head Selection:** You can view data from a single detector at a time or from all detectors simultaneously.
- **Isotope Selection:** You can view data from different isotopes when acquiring dual isotope scans.
- **Color Scale:** Color scales can be selected from the drop-down menu.

During the acquisition it is recommended:

- Monitor the object to ensure that its position has not changed.
- Check the progress of the acquisition. Any errors will result in an error message appearing in the status bar in the lower portion of the screen.
- Observe proper radiation safety measures, namely ensure there are no open sources of radioactivity (other than patient). Keep yourself and the camera out of range from any sources of radioactivity not involved in the data acquisition.

1.2. Gated acquisition

Set **Internal ECG** in the **Configuration**  page, **Camera Configuration – ECG** window. This function is password protected!

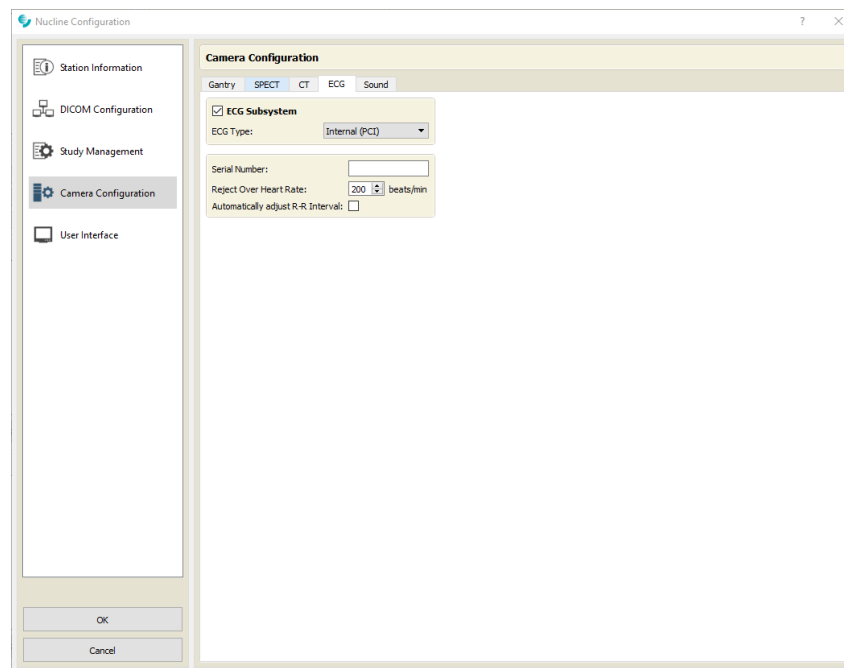



Figure 108. - Set internal ECG

The AnyScan S system has an integrated 5 electrode ECG unit. Press the  icon to access the **ECG** parameters.

VII. Performing an acquisition



Figure 109. - ECG parameters

Options:

- **Auto Channel Scan:** Automatically switch between the channels.
- **Sound:** Heart sound on/off.
- **Calibrate:** Emits and displays a square wave signal.

NOTICE

These parameters are only available at the acquisition station!

- **Gain:** amplifies the input signal.
- **Filter:** can be used for environmental noise filtering.
- **Speed:** sets the signal speed (ECG interval length) display on the monitor.

NOTICE

These parameters are also available in the Gantry monitor!



Figure 110. - Gantry monitor – ECG parameters

1.2.1. Performing a Gated acquisition

1. Go to Local Worklist, press **[New]** button. Add to the Worklist patient, enter required data.
2. Select **Scheduled Procedure**, Press **[New]** button then select **Gated Planar** study from **SPECT Base Procedure**. Press the **[OK]** button, then press **[Acquire Study]** button.
3. When **Gated Planar** study is opened verify all acquisition parameters in **Parameter Editor** panel (See description of **Parameter Editor** panel).
4. Prepare patient and connect the ECG equipment to support the acquisition. Depending on the ECG device the following lead placements are recommended (local regulations and guidelines takes precedence):
 - **3 electrode ECG:** left shoulder (LA/L), right shoulder (RA/R), left abdomen (LL/F).
 - **4 electrode ECG:** as 3 electrode placement + left leg (V/C).
 - **5 electrode ECG:** as 4 electrode placement + right leg (RL/N).


CAUTION



It is mandatory to attach all connected ECG electrodes.

Abdomen placement can vary horizontally depending on anatomical characteristics of the patient.

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5. In **ECG Channels** window set the ECG channel.
6. Return to the Acquisition menu by clicking on the  icon.
7. Open **Gating** panel and verify that ECG signal is arriving to Nucline program and histogram displays correct values. Press [**<<**], [**>>**] or [**Auto**] to set the optimal R-R interval.

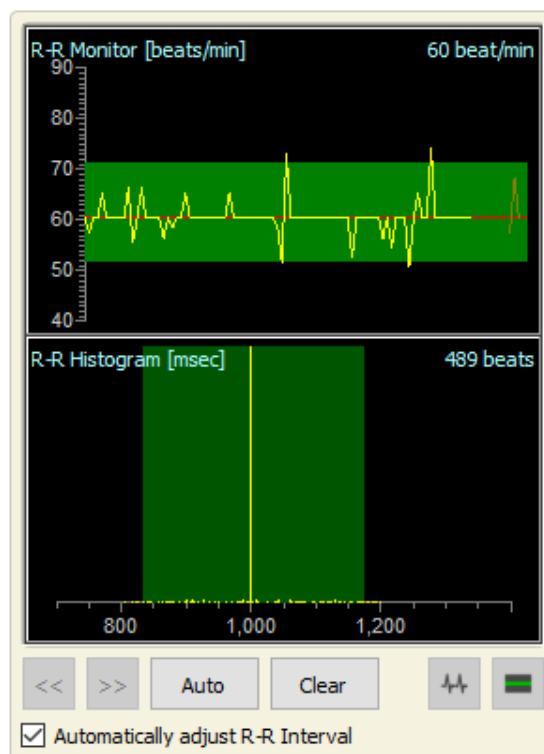


Figure 111. - Gating panel

8. Press the [**Prepare**] then [**Start**] button.

NOTICE

If ECG signal is not available or it is out of range a warning sound is played and the acquisition can not be started.

9. Press the [**Go**] button to start the acquisition.
10. Follow the ECG signal and histogram during acquisition. If heart beat is falling out from the interval use **Automatically Adjust R-R Interval** or press [**<<**], [**>>**] or [**Auto**] buttons.

1.3. List Mode acquisition

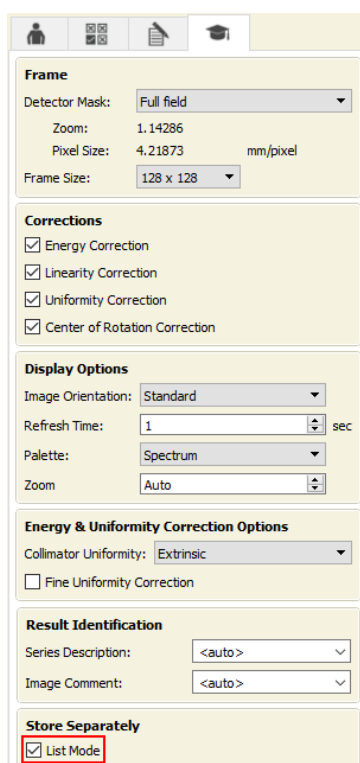
List Mode acquisition is intend to record raw data for further reprocessing with modified acquisition conditions. The function is enabled for following acquisition types:

- Pinhole SPECT,
- Gated Pinhole SPECT,
- Semi Stationary SPECT,
- Static Planar,
- Dynamic Planar,
- SPECT,
- Gated SPECT,
- Whole Body SPECT.

First three acquisition type used by pinhole collimators while others with parallel collimators.

1.3.1. Acquisition

Enable List Mode raw data collection and saving in **Parameter Editor's Advanced** panel by checking **List Mode** checkbox in **Store Separately** group.



The screenshot shows the 'Parameter Editor's Advanced' panel with the following settings:

- Frame**
 - Detector Mask: Full field
 - Zoom: 1.14286
 - Pixel Size: 4.21873 mm/pixel
 - Frame Size: 128 x 128
- Corrections**
 - ☒ Energy Correction
 - ☒ Linearity Correction
 - ☒ Uniformity Correction
 - ☒ Center of Rotation Correction
- Display Options**
 - Image Orientation: Standard
 - Refresh Time: 1 sec
 - Palette: Spectrum
 - Zoom: Auto
- Energy & Uniformity Correction Options**
 - Collimator Uniformity: Extrinsic
 - ☐ Fine Uniformity Correction
- Result Identification**
 - Series Description: <auto>
 - Image Comment: <auto>
- Store Separately**
 - ☒ List Mode

Figure 112. - List Mode selection

List Mode raw data is stored separately as DICOM image beside regular image. The raw data is always collected for selected detectors.

1.3.2. Processing List Mode raw data

Select **Worklist** icon in **Main Menu**, then press the button **[Raw SPECT Data]**. Select in the browser those images whose **Series Description** contains **List Image**. Then select in **Processing Protocols** panel the List Mode processing protocol. If there is no **List Mode**

Patient Name	Patient ID	Study Date	Study Description
Emergency, .	2018-04-12 15:19:41	12/04/2018 15:19	Emergency
Series #	Equipment	Series Date	Series Description
2	AnyScan SC	12/04/2018 15:20	SPECT - List image - Detector 1
3	AnyScan SC	12/04/2018 15:20	SPECT - List image - Detector 2

Processing Protocols

Name

- User
 - Clinical Protocols
 - SPECT List Mode Processing

Figure 113. - List Mode processing

Press **[Prepare]** and **<Go>** to start reprocessing List Mode raw data. At the end of processing the result image is saved to regular DICOM image under the same patient with new series number.

2. Tera-Tomo 3D SPECT reconstruction

The SPECT acquisitions collected in the past can be reconstructed with the Tera-Tomo reconstruction module integrated into Nucline.

2.1. Selection of the measurement

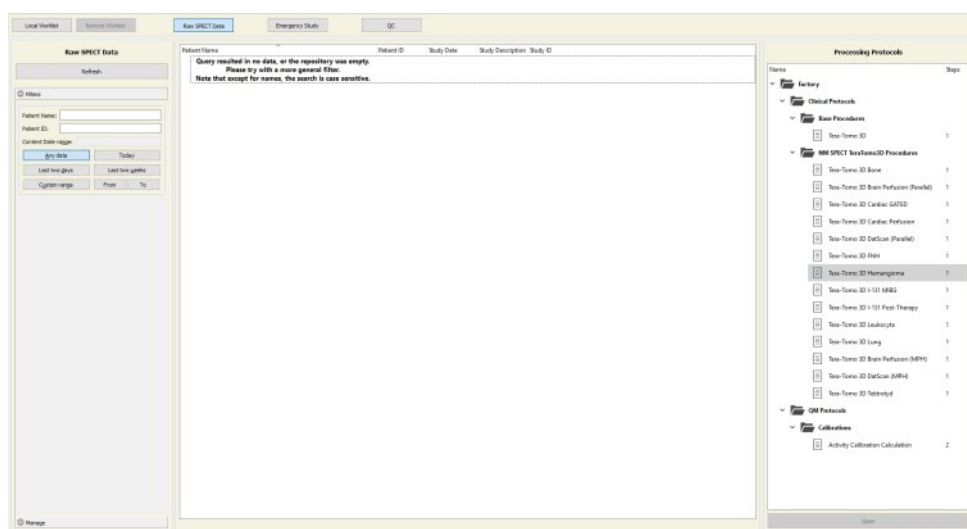


Figure 114. - Raw SPECT data form

In order to start the reconstruction, first one have to select the previously acquired SPECT image from the Local Server. The source of these images could be a procedure containing

several procedure steps. SPECT images residing on other DICOM servers first have to be copied to the Local Server or they have to be reconstructed with InterView XP.

1. Press the **[Raw SPECT Data]** button on the **Worklist** page.
2. Select one or more SPECT acquisition(s) from a single study to be reconstructed.
3. Additionally, a CT image can be selected from the same acquisition series. (Optional, required for attenuation and scatter corrections)
4. Select one of the preconfigured Tera-Tomo 3D protocols from **Processing Protocols / Factory / Clinical Protocols / NM SPECT TeraTomo3D Procedures** list or choose **Processing Protocols / Factory / Clinical Protocols / Base Procedures / Tera-Tomo 3D** protocol for default settings. User defined reconstruction protocols will also appear on this list.
5. Press **[Open]**.

2.2. Protocol cover page main panels

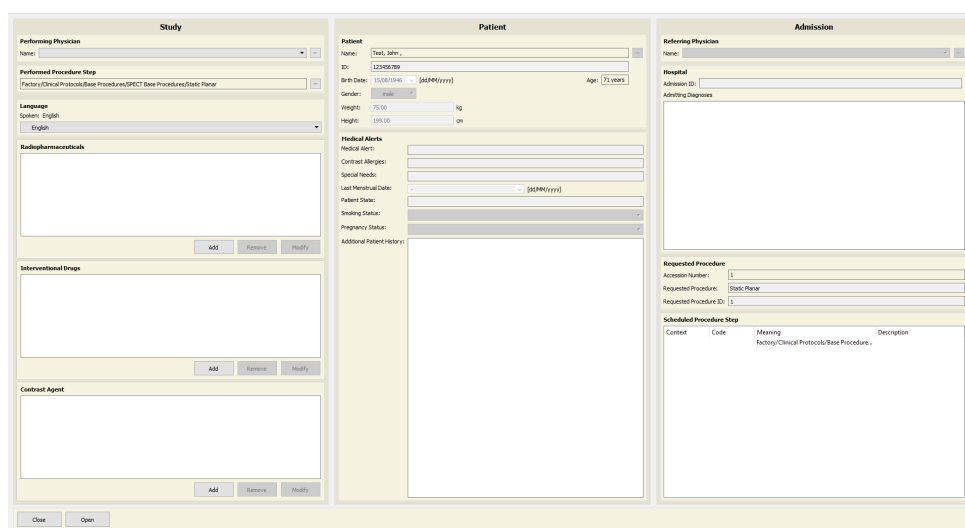


Figure 115. - Protocol cover page

• Study panel

At the top you can define the **Performing Physician** of the study.

In the **Performed Procedure Step** you can select protocols for the study. In case of a remote study the protocol could be mapped to Nucline with the **Protocol Mapper** function. For further details on the usage of **Protocol Mapper** see [Protocol mapper](#).

In the **Language** subpanel you can choose or modify the spoken language.

There are 3 additional subpanels where you can define the injected materials. In each panel you find following buttons:

- **[Add]**: you can add an element to the list with the adequate dialog.
- **[Remove]**: you can remove the current element from the list.
- **[Modify]**: you can modify the current element with the adequate dialog.

The panels are:

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- **Radiopharmaceuticals**
- **Interventional Drugs**
- **Contrast Agent**

You can add such materials to the study later on the **Acquisition Screen**, too.

Important: if you define injected materials on the **Protocol Cover Page**, all acquisitions of the protocol will contain the information about them. If you add such materials later on the **Acquisition Screen** of an acquisition plugin, the already finished acquisitions will not contain these materials, only the later executed acquisitions.

- **Patient panel**

Information about the patient could be found and filled here. In every acquisition by default the **Weight** and **Height** of the patient must be filled (if not defined earlier and could be changed in **Study Management**). In the **Additional Patient History** you can type additional information as a free text.

Important: some information of the **Patient** is not editable.

- **Admission panel**

This panel explains the admission history and requested procedures of the patient.

Important: some information of the **Admission** is not editable.

2.3. Role selection

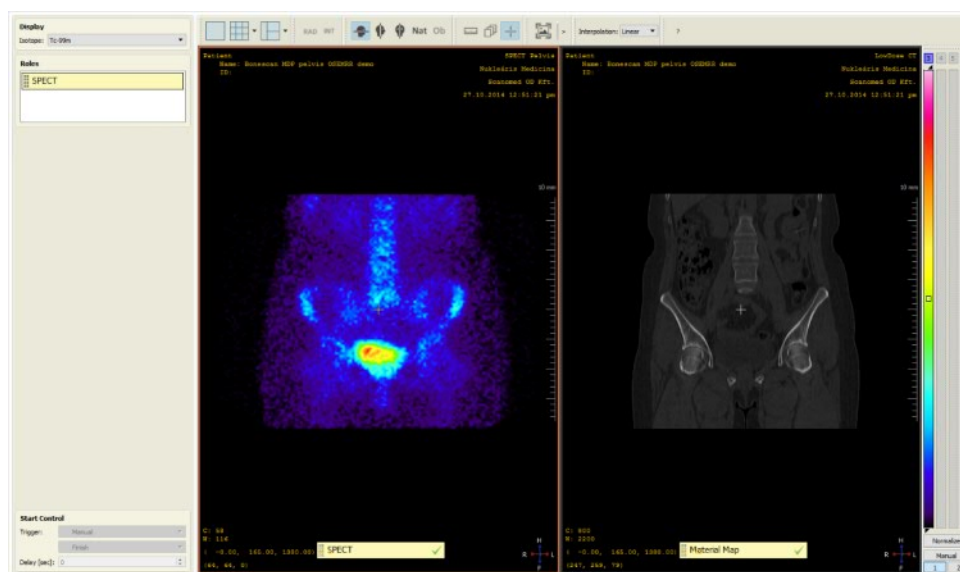


Figure 116. - Role selection page

During the reconstruction – either from **RAW SPECT Data** or as the final step of an acquisition – roles should be selected. These roles are **SPECT** and **Material Map** roles, and should be selected by dragging the **SPECT** and **Material Map** labels to the corresponding viewers. **SPECT** role selection is mandatory, but **Material Map** is optional, could be assigned to an MR or CT image.

After the role selection, you can proceed to the **Attenuation Map** page if **Material Map** label is assigned. by clicking the **[Next]** button.

During the procedure the following controls are available:

- **[Stop]**: Interrupts the current reconstruction.
- **[Back]**: Moves to the previous procedure step.
- **[Next]**: According to the current settings proceeds to the next procedure step .
- **[Auto Run]**: Processes all the auto-proceed enabled procedure steps.

To use the **[Auto Run]** feature, for each procedure step in the [Protocol editor](#) the **Enable Auto-Proceed** option must be checked.

Previous steps can be reached by selecting the appropriate tab at the top of the page.

2.4. Attenuation map

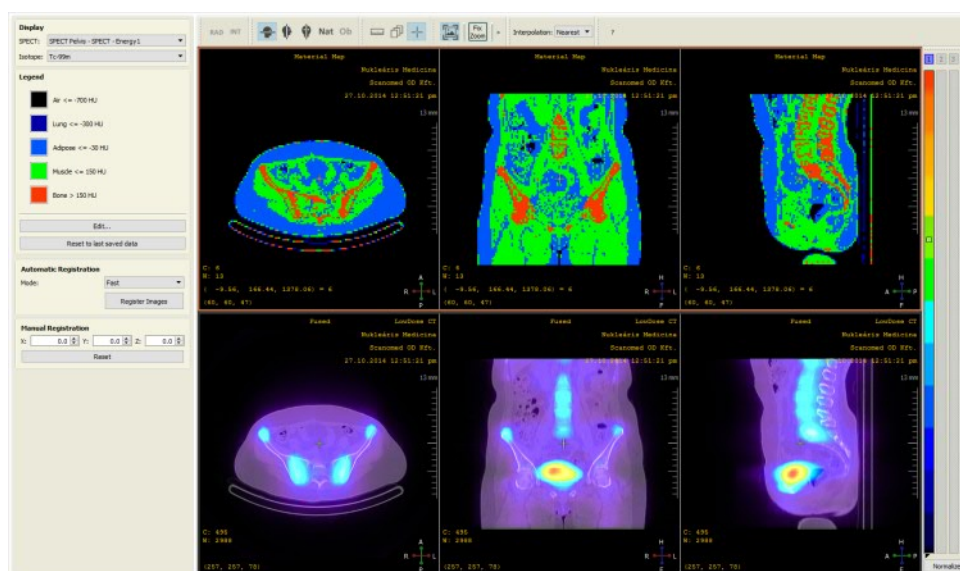


Figure 117. - Attenuation map page

The purpose of the Attenuation map page is to segment the loaded CT image and create the material map that will be used for attenuation and scatter correction calculations during the reconstruction.

During the loading phase of the page a preview reconstructed image is created in a couple of seconds. The process can be aborted by pressing the **[Stop]** button.

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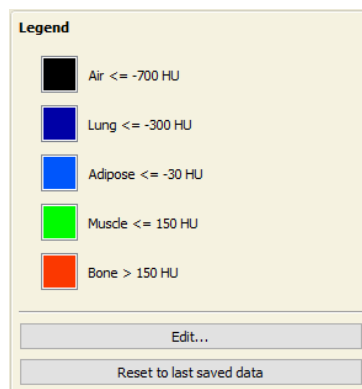


Figure 118. - Default material list

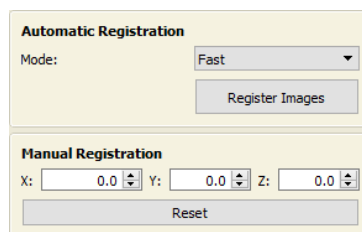


Figure 119. - Registration options

A default set of materials is offered, but you are able to modify it by clicking the **[Edit]** button. After that it is possible to add new materials to the list and also to remove existing ones. The threshold of each material can be modified by editing the corresponding HU limit. User can restore the last saved segmentation thresholds by clicking the **[Reset To Last Saved Data]** button. Most of the cases, when the CT image is HU calibrated, no manual modification of the material data is needed.

The co-registration of the CT and SPECT images can be checked in the bottom viewer section. If the two images or not registered you should start a registration process by the **Automatic Registration** or the **Manual Registration** options. With **Automatic Registration** the software tries to align the two images with the selected algorithm. **Manual Registration** moves the CT image by the supplied mm values.

NOTICE

In case of **Pinhole SPECT** and **Gated Pinhole SPECT** the **Automatic Registration** and **Preview Image** functions are not available.

After configuring the attenuation map, you can proceed to the next procedure step by clicking the **[Next]** button. Previous steps can be reached by selecting the appropriate tab at the top of the page.

2.5. Reconstruction

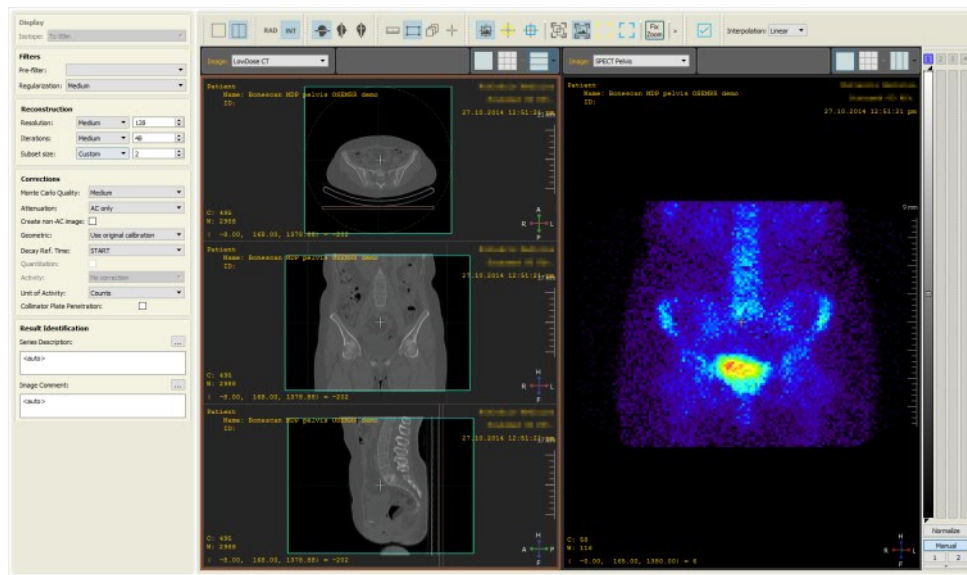


Figure 120. - Reconstruction page

User can fine-tune the reconstructed image quality through a number of options on the Reconstruction page.

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Filters	
Pre-filter	Projection images can be filtered to reduce the noise on the reconstructed image.
Regularization	Low / Medium / High Noise on the reconstructed image can be reduced by choosing a higher regularization level. High- resolution images require lower regularization. Optimized settings are available for certain acquisition types.
Reconstruction	
Resolution	Low / Medium / High / Custom Number of voxels in the reconstructed image in transaxial direction. Higher settings can lead to finer details on the reconstructed image, but also increases the noise. High resolution reconstructions also take significantly longer time to complete.
Iterations	Low / Medium / High / Custom Number of voxels in the reconstructed image in transaxial direction. Higher settings can lead to finer details on the reconstructed image, but also increases the noise. High resolution reconstructions also take significantly longer time to complete.
Subset size	Low / Medium / High / Custom / Maximum Higher subset settings reduce the reconstruction time. Too high settings can however introduce artifacts on the image. Example: 1 subset with 40 iterations = 2 subsets with 40 iterations $\text{Time}(1 \text{ subset with } 40 \text{ iterations}) > \text{Time}(2 \text{ subsets with } 40 \text{ iterations})$
Corrections	
MC Quality	Low / Medium / High / Very High Monte Carlo quality sets the number of photons used in the forward and backprojection steps. Low settings can be used when fast reconstructions are needed with the downside of noisier images.
Attenuation	None / AC only / AC + SC If CT image was loaded, attenuation and scatter correction can be enabled. Both settings lead to longer reconstructions.
Create non-AC image	Creates both the AC and non-AC images.

Geometric	Geometric calibration data can be loaded either from the acquisition DICOM file (Use original calibration), or from the current calibration data in the Nucline database (Use latest calibration). The latter option should only be selected in special cases when the geometric calibration process was carried out after the given SPECT acquisition.
Decay Ref. Time	Isotope decay correction can be applied with different reference times: start of acquisition (START), time of drug administration (ADMIN), or it can be disabled (No decay correction).
Quantitation	If enabled, the reconstructed image will contain quantitatively correct voxel values with Bq/ml unit (AC or AC+SC is needed). Otherwise the reconstructed image is normalized to the sum of counts in the acquisition image.
Activity	Activity correction factor can be applied to the image either from the acquisition DICOM (Use original calibration), or from the current calibration data in the Nucline database (Use latest calibration).
Unit of Activity	Counts: The sum of voxels in the result image is normalized to the sum of pixels in the original acquisition. Bq/ml: The result image voxel values contain the activity concentration of the isotope distribution. (Quantitation has to be enabled.)
Collimator Plate Penetration	Reconstruction simulates the penetration of high-energy photons through the aperture plate. (Multi-pinhole only.)
Result Identification	
Series Description	Series description can be created manually by typing in the text box or from a predefined list. For the later press the [...] to open the Series Description Editor window. In both cases some information can be generated by the software using various tags (e.g. <Reg>, <Res>, <S>, etc.)
Image Comment	Image comment can be created manually by typing in the text box or from a predefined list. For the later press the [...] to open the Image Comment Editor window. In both cases some information can be generated by the software using various tags (e.g. <Reg>, <Res>, <S>, etc.)

The volume of the reconstruction can be selected by resizing and moving the scanbox on the viewer plane. It is usually advisable to acquire full frame images without zoom (with an appropriate pixel size), and select the volume of interest here, during the reconstruction process, or later during the post-processing stage (see [Advanced](#)).

After configuring the reconstruction, you can proceed and start the reconstruction by clicking the **[Next]** button. After reconstruction is finished, results are automatically shown on the **Post-Filter** page. Reconstruction process can be aborted by clicking the **[Abort]**

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button, from that point results can be overwritten by starting a new reconstruction. Previous steps can be reached by selecting the appropriate tab at the top of the page.

2.6. Post-filter

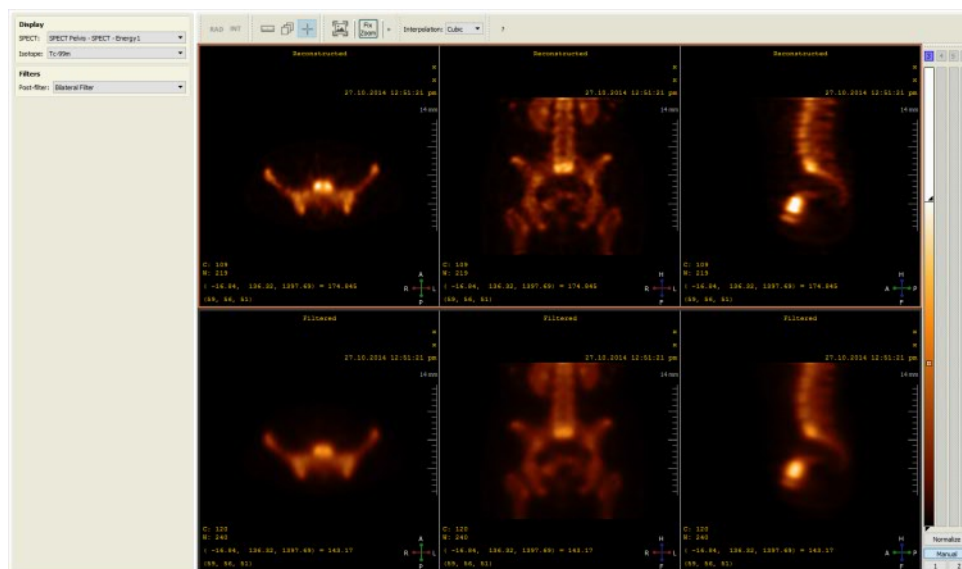


Figure 121. - Post-filter page

Post-filter can be applied on the reconstructed image.

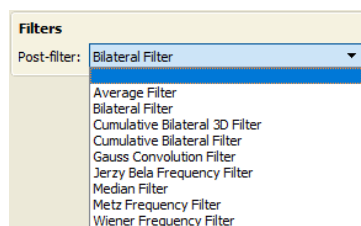


Figure 122. - Post-filter list

After the filter selection, you can proceed to the **Results** page by clicking the **[Next]** button. Reconstruction process can be aborted by clicking the **[Abort]** button, from that point results can be overwritten by starting a new reconstruction. Previous steps can be reached by selecting the appropriate tab at the top of the page.

2.7. Results page

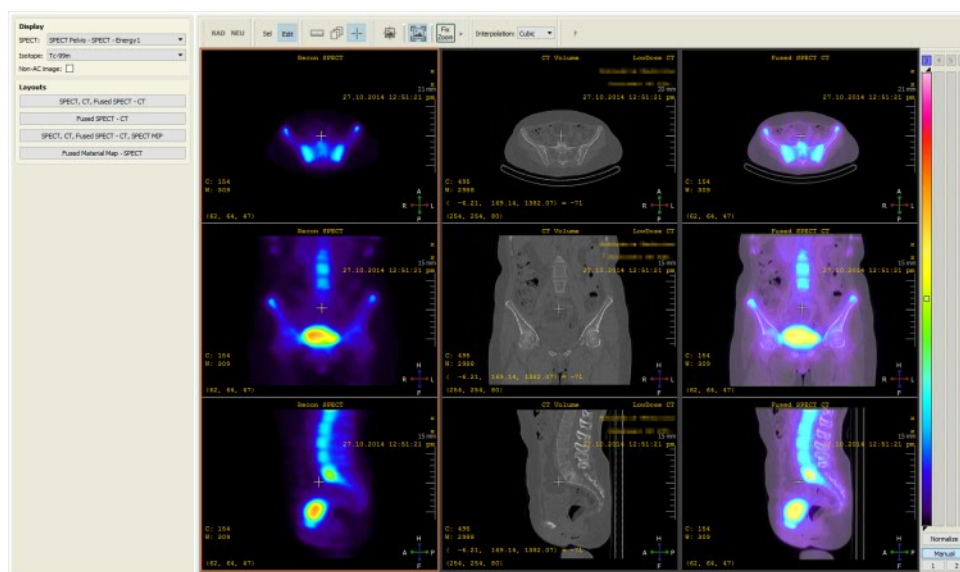


Figure 123. - Results page

Result image can be viewed in a configurable viewer on the **Results** page, and can be saved to the DICOM server. If multiple results exist, you can choose the image to be viewed with the Display options. The overall layout of the page can be modified by choosing from the four predefined arrangements in the **Layouts** options.

On the results page the following controls are available:

- **[Abort]**: Interrupts the current reconstruction, results can be overwritten by starting a new reconstruction.
- **[Back]**: Moves to the previous procedure step.
- **[Save]**: Saves the reconstructed images but the reconstruction can be repeated with different settings.
- **[Save&Finish]**: Saves the reconstructed images.

Previous steps can be selected by clicking on the appropriate tab at the top of the page.