

# **Medic**

## **USER'S MANUAL**

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This manual describes how to use the Medic system to process and document nuclear medicine image studies.

**Ver 1.1**

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# 1.0 Introduction

The Medic system is a Nuclear Medicine Image Processing and Documentation System. It can import images in DICOM format either via a network communication or as DICOM files stored in a folder. It is using its own database which can be placed on a server for multiuser application or on a stand-alone workstation. Reports created in the system can be sent to a PACS system as DICOM SECONDARY CAPTURE, printed on printer or stored as an .jpg image. The system configuration are shown in fig. 1.

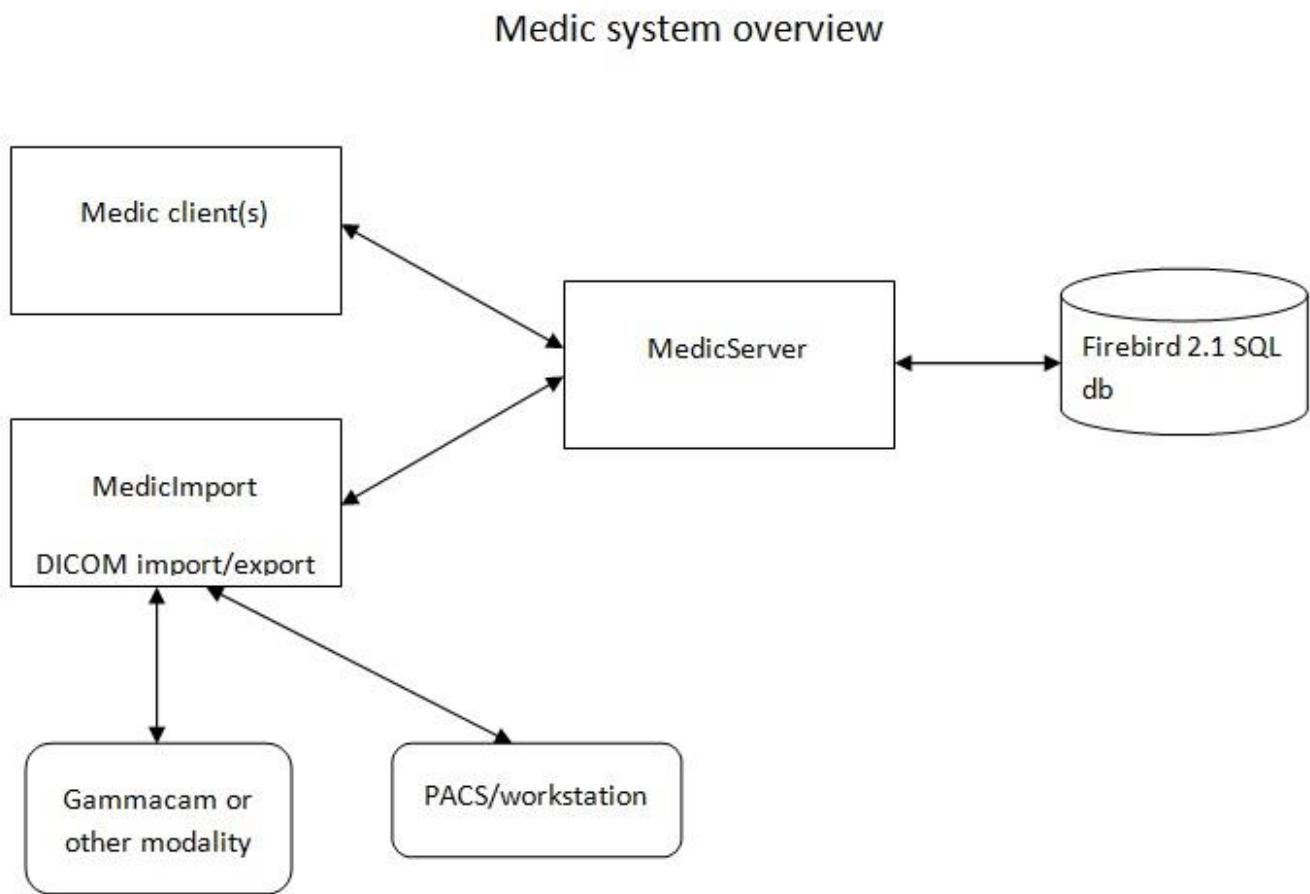


Fig. 1.1

## 1.1 Configuration

The configuration of the Medic system are stored in a configuration file (default name medic.ini located in the c:\medic folder). The details of the content of the configuration file are described in section 6.0.

## 2.0 Main Window

The main window is show in fig. 2.1

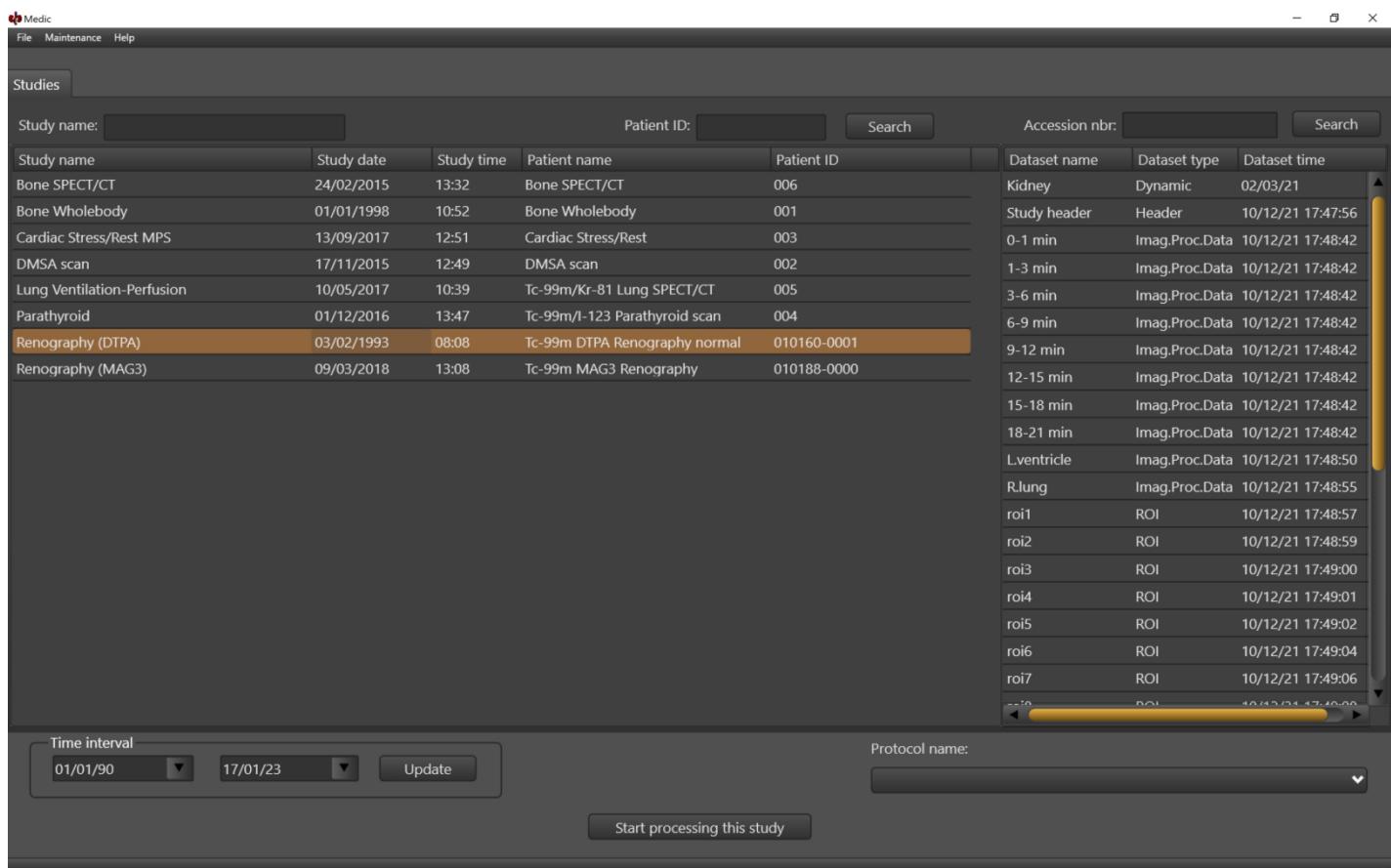


Fig. 2.1

In the left side of the window there are a list of studies in the selected time interval. If a specific study is selected a list of datasets contained in this study are shown in the list to the right. The study list can be filtered according to Study name, Patient ID and Accession nbr. To start processing a study either double-click a study (to start manual processing) or select a processing protocol from the “Protocol name” drop-down box where protocols related to the selected study are listed and press “Start processing this study”.

In the top of the window are the main menu. From the Maintenance menu it is possible to: create new colormaps, create predefined ROI(region of interest), create study protocol relations, delete studies, delete datasets, delete protocols, delete colormaps, delete predefined ROI, edit study/patient data, edit study header, edit dataset name, show dataset info, edit processing protocols, edit study protocols relation, edit Medic setup, import dataset (Medic format), import colormap form Medic file, import colormap from bin file, import protocols, export processing protocols, export colormaps, export datasets (in Medic format), export datasets in DICOM format.

## 2.1 Creating new colormaps

To create a new colormaps in the system (or edit an existing colormap) select Maintenance->Create->Colormap and the dialog in fig.2.2 is shown.

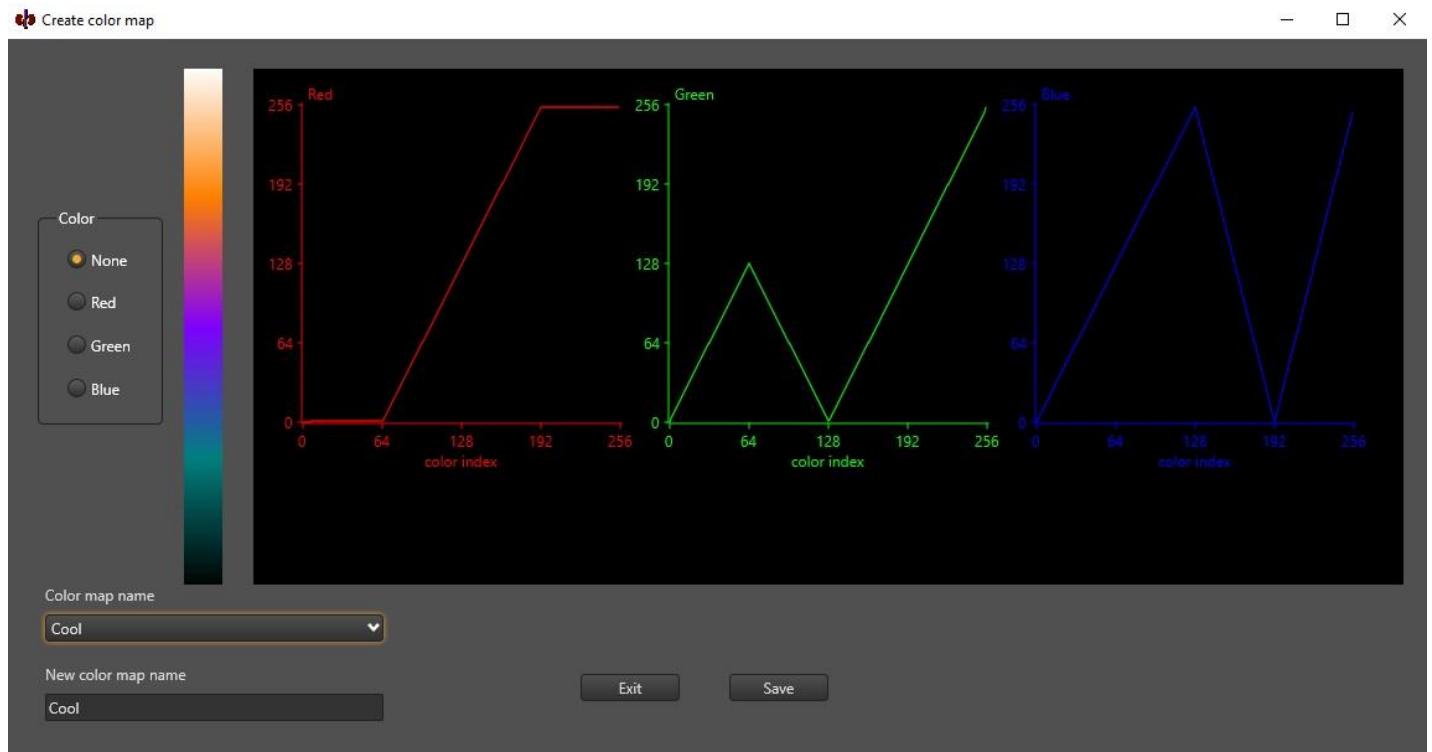


Fig.2.2

Select the color (red,green,blue) and the cursor turns into a cross on the selected colorpanel. Draw the color index/color intensity relation from index 0 to 255. To pin the line click the left mouse button. Finish with click of right mouse button.

## 2.2 Create predefined ROI

To create predefined ROIs (stored in the database for manipulation) select Maintenance->Create->Predefined->ROI and the dialog in fig.2.3 is shown.

The figure shows a dialog window titled 'Create predefined ROI'. It has two input fields: 'ROI dataset name:' containing 'roi1' and 'Predefined ROI name:' which is empty. At the bottom are two buttons: 'Ok' and 'Exit'.

fig.2.3

Select a ROI from the list of ROI datasets in the selected study and give it a unique name. Accept with Ok. Select another ROI from the list or exit with Exit.

## 2.3 Create study protocol relation

To create a relation between a study and up to 10 processing protocols select Maintenance->Create->Study protocol relation and the dialog in fig.2.4 is shown.

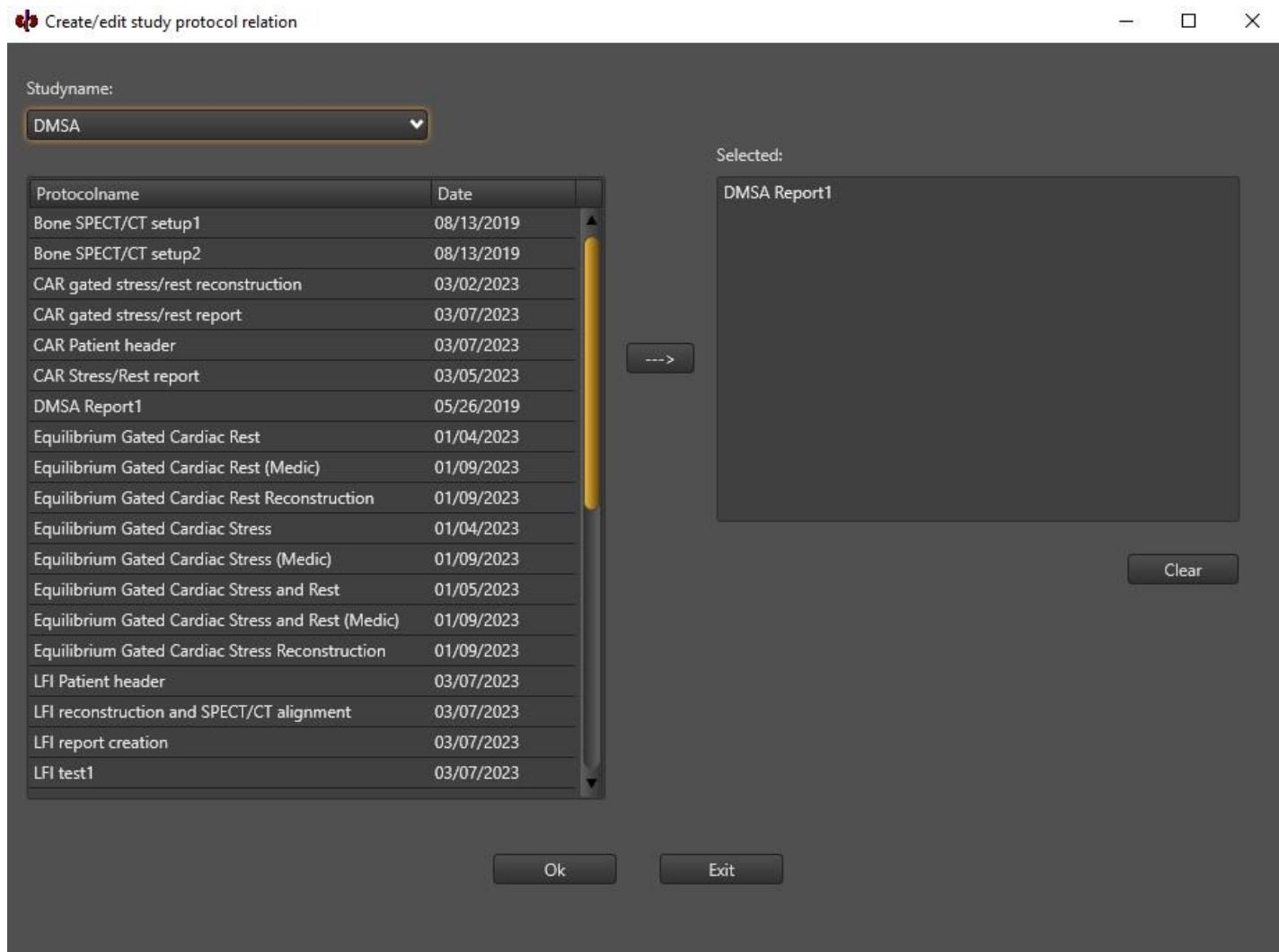


fig.2.4

Select the study you want the protocols to be related to from the “Studyname” drop-down box. Add the protocols from the processing protocols list to the “Selected” list (max 10 protocols) and press Ok. Select another study or pres Exit.

## 2.4 Delete studies

To delete studies from the database select Maintenance->Delete->Studies and the dialog in fig.2.5 is shown.

Study name	Study date	Study time	Patient name	Patient ID
<input type="checkbox"/> Bone SPECT/CT	24/02/2015	13:32	Bone SPECT/CT	006
<input type="checkbox"/> Bone Wholebody	01/01/1998	10:52	Bone Wholebody	001
<input type="checkbox"/> Cardiac Stress/Rest MPS	13/09/2017	12:51	Cardiac Stress/Rest	003
<input type="checkbox"/> DMSA scan	17/11/2015	12:49	DMSA scan	002
<input type="checkbox"/> Lung Ventilation-Perfusion	10/05/2017	10:39	Tc-99m/Kr-81 Lung SPECT/CT	005
<input type="checkbox"/> Parathyroid	01/12/2016	13:47	Tc-99m/I-123 Parathyroid scan	004
<input type="checkbox"/> Renography (DTPA)	03/02/1993	08:08	Tc-99m DTPA Renography normal	010160-0001
<input type="checkbox"/> Renography (MAG3)	09/03/2018	13:08	Tc-99m MAG3 Renography	010188-0000

Select all

Time interval  
01-01-1990 ▾ 14-03-2023 ▾ Update Delete Exit

Fig.2.5

Select the studies you want to delete in the selected time interval and press “Delete”. The studies and the associated datasets (including the datafiles) are deleted from the system.

## 2.5 Delete datasets

To delete dataset from a selected study select Maintenance->Delete->Datasets and the dialog in fig.7 is shown.

Delete datasets	
Dataset name	Dataset type
<input type="checkbox"/> Study header	Header
<input type="checkbox"/> RPO	Static
<input type="checkbox"/> LPO	Static
<input type="checkbox"/> POST	Static
<input type="checkbox"/> rightroi	ROI
<input type="checkbox"/> leftroi	ROI
<input type="checkbox"/> rightbkg	ROI
<input type="checkbox"/> leftbkg	ROI
<input type="checkbox"/> rightbkgroi	ROI
<input type="checkbox"/> leftbkgroi	ROI
<input type="checkbox"/> DMSA-report	Page

Delete Exit

fig.2.6

Select the datasets you want to delete and press “Delete” and the datasets (including the datafiles) are deleted from the system. NB! The “Study header” dataset can not be deleted.

## 2.6 Delete protocols

To delete processing protocols select Maintenance->Delete->Protocols and the dialog in fig.2.7 is shown.

Delete protocols	
Protocol name	Protocol date
<input type="checkbox"/> Bone SPECT/CT review	29/12/2021
<input type="checkbox"/> Bone Wholebody report1	29/12/2021
<input type="checkbox"/> Cardiac stress/rest report	09/12/2021
<input type="checkbox"/> DMSA processing	14/01/2022
<input type="checkbox"/> DMSA Report1	10/12/2021
<input type="checkbox"/> Lung Ventilation-Perfusion SPECT/CT report	09/12/2021
<input type="checkbox"/> Parathyroid preproces	09/12/2021
<input type="checkbox"/> Parathyroid preproces2	09/12/2021
<input type="checkbox"/> Parathyroid report1	10/12/2021
<input type="checkbox"/> Renography ( 99mTc-DTPA ) processing	10/12/2021
<input type="checkbox"/> Renography ( 99mTc-MAG3 ) processing	18/12/2021
<input type="checkbox"/> Renography (DTPA) report1	12/12/2021
<input type="checkbox"/> Renography (MAG3) report1	18/12/2021

fig.2.7

Select the protocols you want to delete and press “Delete” and the protocols are deleted from the system.

## 2.7 Delete colormaps

To delete colormaps used in the system select Maintenance->Delete->Colormaps and the dialog in fig.2.8 is shown.

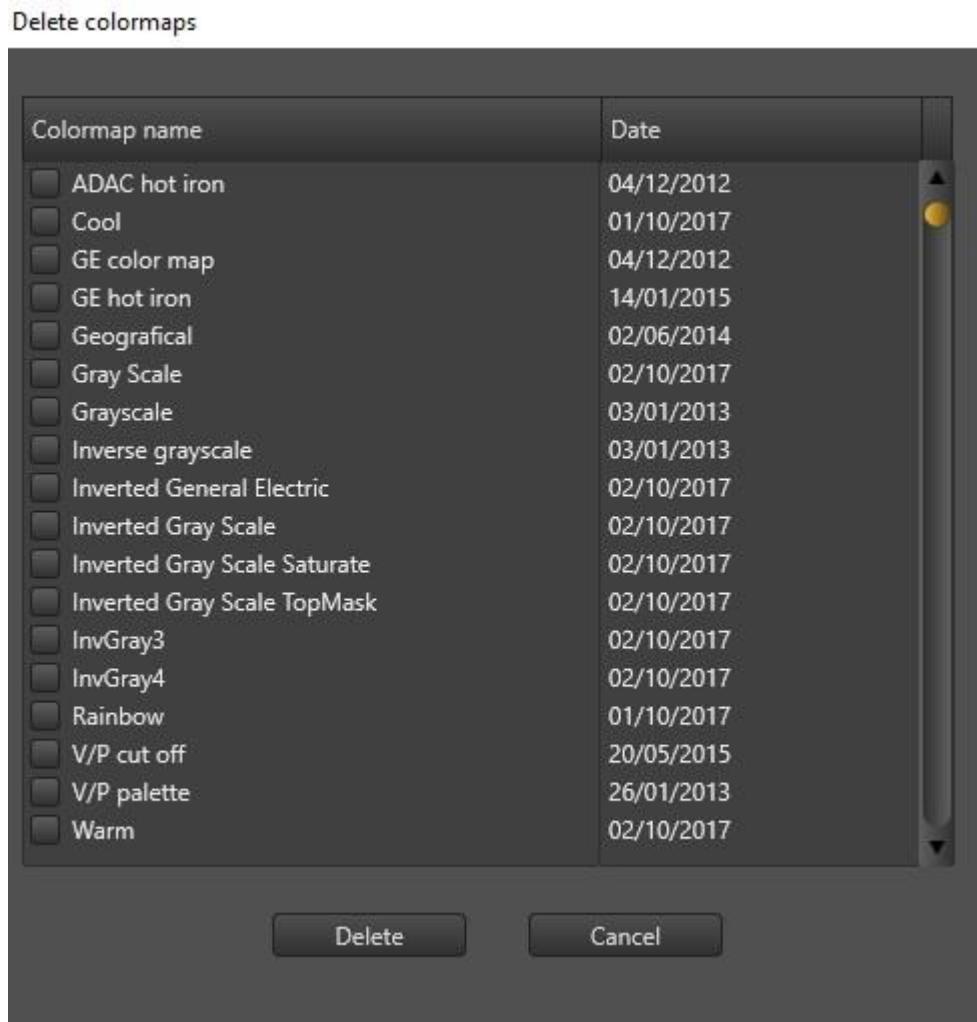


fig.2.8

Select the colormaps you want to delete from the system and press “Delete” and the colormaps are deleted from the system.

## 2.8 Delete predefined ROI

To delete predefined ROI's from the system select Maintenance->Delete->Predefined ROI and the dialog in fig.2.9 is shown.

Delete predefined ROI

Predefined ROI name	Predef. ROI date
<input type="checkbox"/> Left bkg	06/03/2013
<input type="checkbox"/> Left kidney	06/03/2013
<input type="checkbox"/> Left pelvis	06/03/2013
<input type="checkbox"/> Left ventricle	06/03/2013
<input type="checkbox"/> Right bkg	06/03/2013
<input type="checkbox"/> Right kidney	06/03/2013
<input type="checkbox"/> Right lower lung	06/03/2013
<input type="checkbox"/> Right pelvis	06/03/2013

fig.2.9

Select the predefined ROI's you want to delete from the system and press "Delete" and the predefined ROI's are deleted from the system.

## 2.9 Edit Patient/study data

To edit patient/study data in the system select Maintenance->Edit->Patient/study data and the dialog in fig.2.10 is shown.

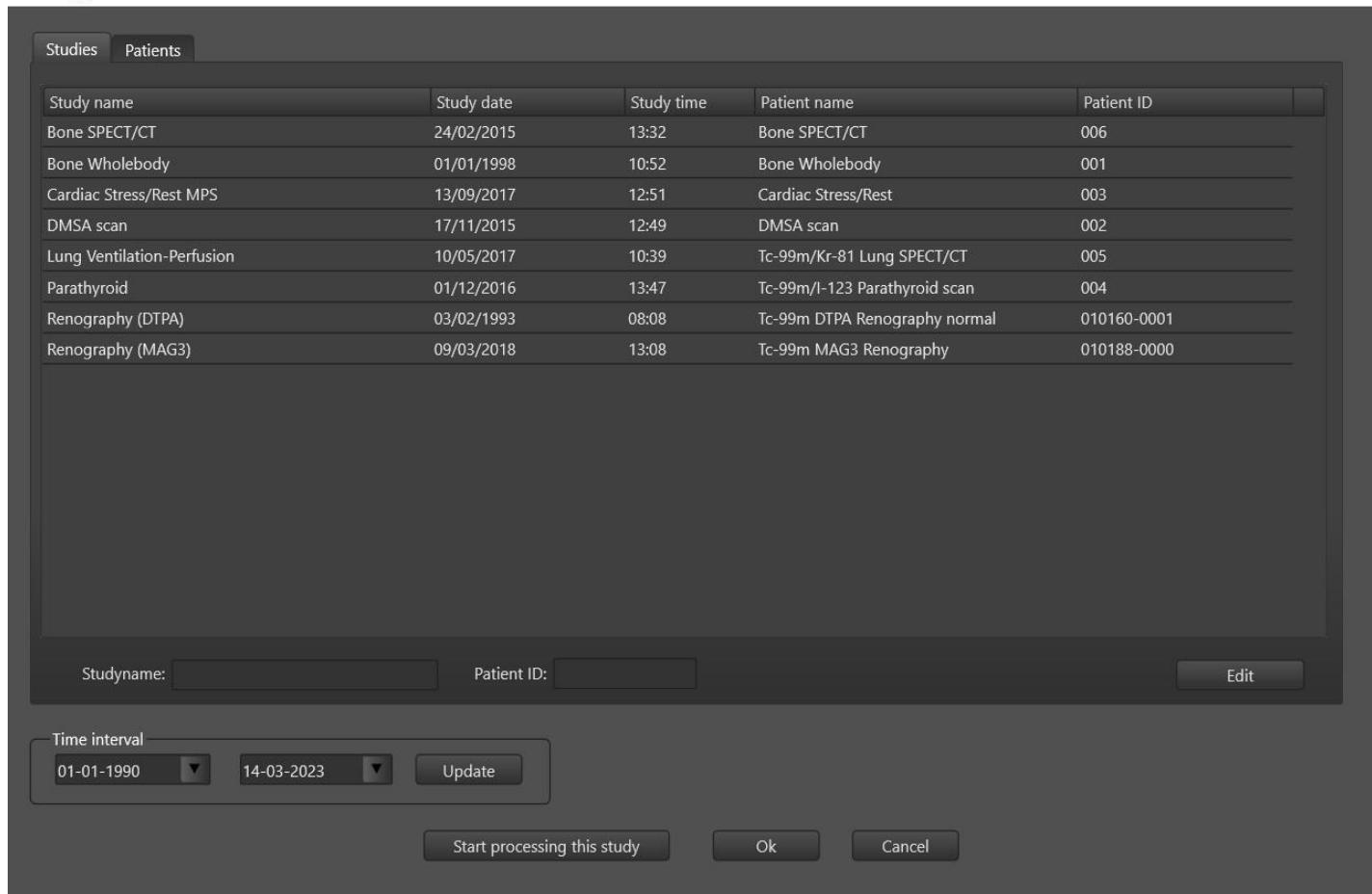


Fig.2.10

Select the study you want to edit and press “Edit” and the dialog in fig.2.11 is shown.

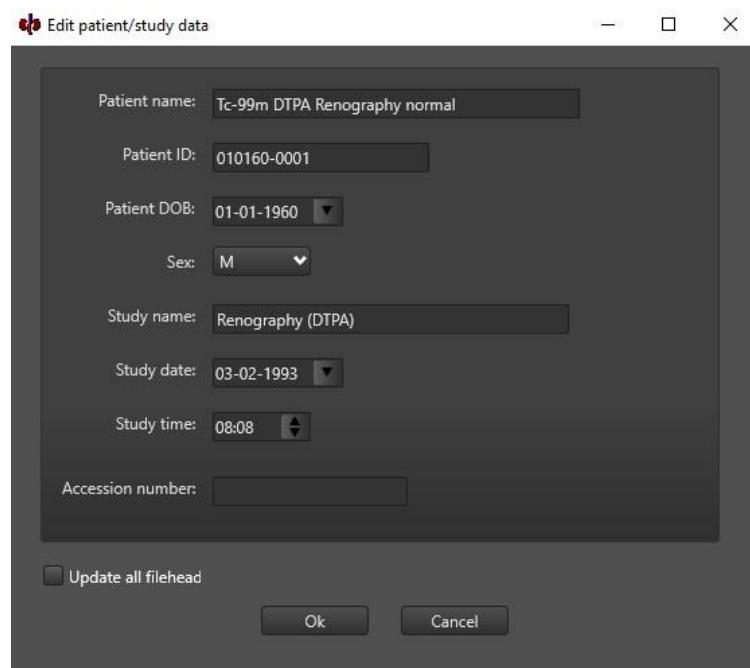


fig.2.11

Edit the data in the dialog. Check “Update all fileheaders” and press Ok.

## 2.10 Edit Study header

To edit the Study header of the selected study select Maintenance->Edit->Study header and the dialog in fig.2.12 is shown.

Edit study header

Patient name:	Tc-99m DTPA Renography normal
Patient ID:	010160-0001
Study name:	Renography (DTPA)
Study date:	03-02-1993 ▾
Study time:	08:08
Isotope:	99mTc-DTPA
Dose:	200 MBq
Department:	Dep
Height in cm:	180
Weight in kg:	75
Initials:	
Comments:	
Accessionnbr:	123456789

Ok Cancel

fig.2.12

Edit the data in the dialog and press Ok.

## 2.11 Edit dataset name

To edit the dataset name in a selected study select Maintenance->Edit->Dataset name and the dialog in fig.2.13 is shown.

Edit dataset name

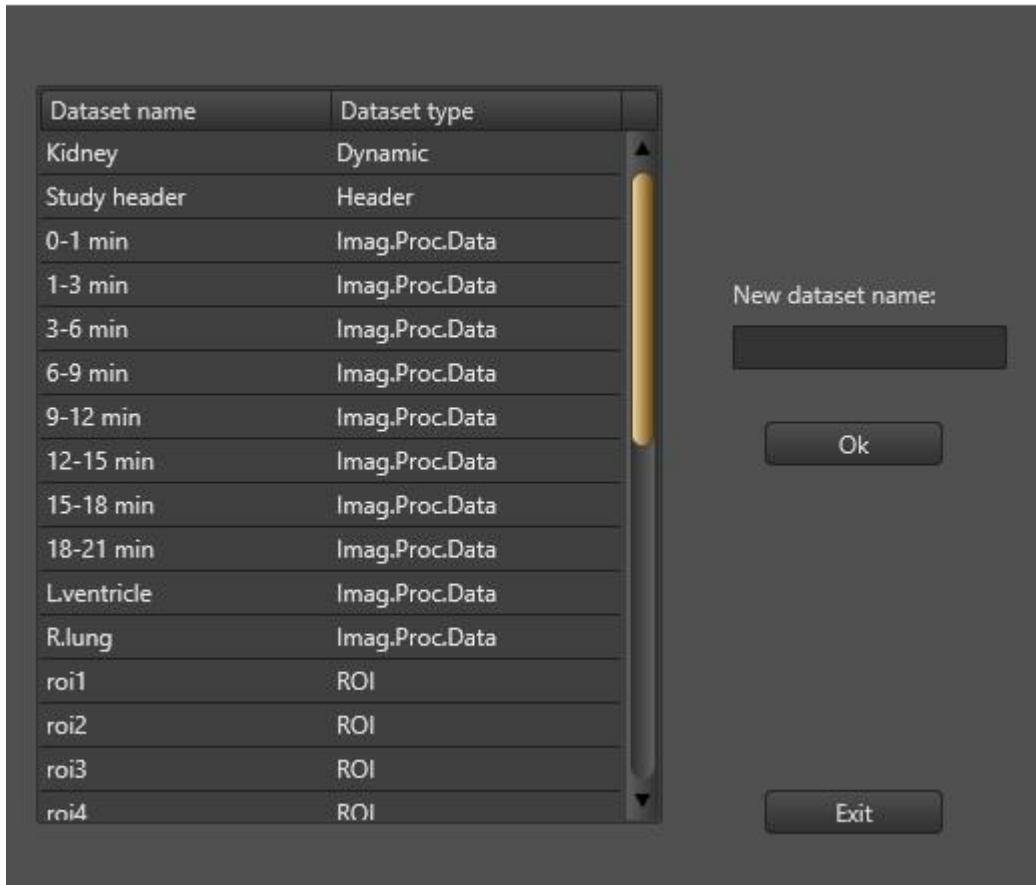


fig.2.13

Select a dataset from the list. Type a new name in the “New dataset name” edit-box (max 15 char) and press Ok.

## 2.12 Show dataset info

To show information about a selected dataset select the dataset from the list of datasets in the selected study select Maintenance->Edit->Show dataset info and the dialog in fig.2.14 is shown.

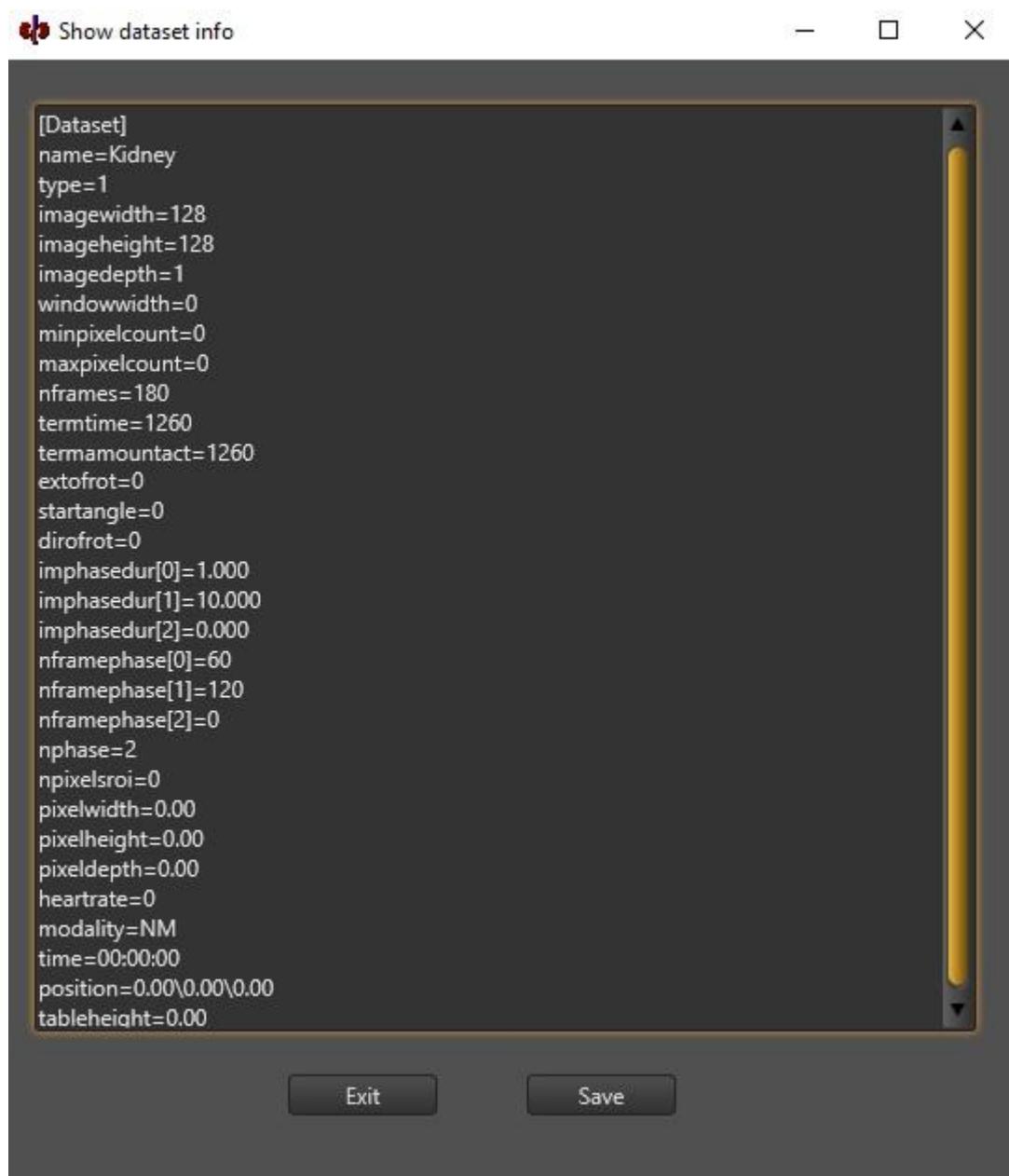


fig.2.14

## 2.13 Edit processing protocol

To edit a processing protocol (which is a simple textfile) select Maintenance->Edit->Processing protocol and the dialog in fig.2.15 is shown. The first line shows the protocol name after the ; char which is the comment char. An overview of the protocol functions can be shown from the Help->Medic prococol function overview.

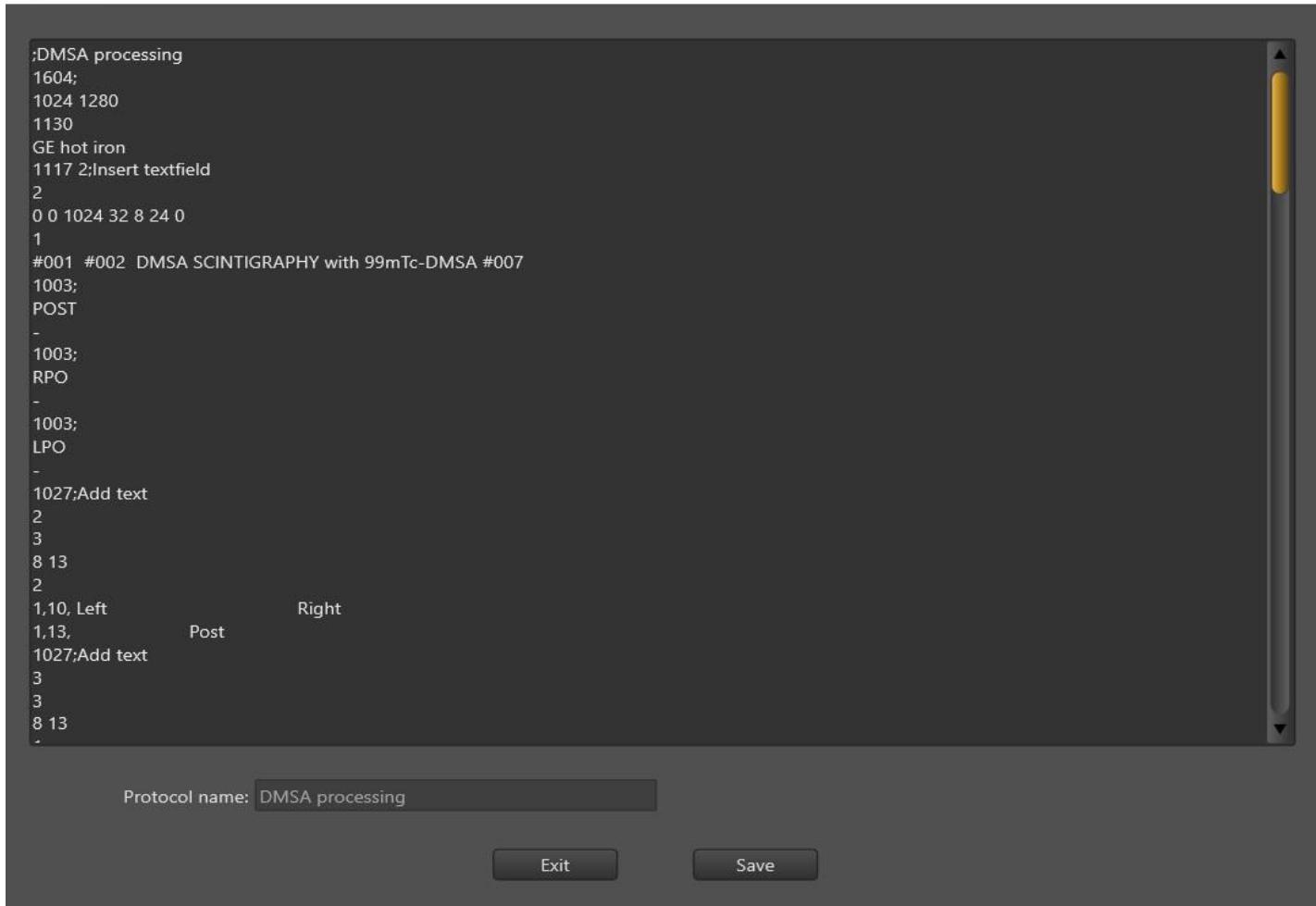


fig.2.15

Edit the protocol and press “Save”.

## 2.14 Edit study protocol relation

This is the same dialog as shown in fig.2.4.

## 2.15 Edit Medic setup

To edit the Medic configuration file select Maintenance->Edit->Medic setup. Windows Notepad will open and show the content of the .ini configuration file (default c:\medic\medic.ini). See fig 2.16. The details in this configuration file is explained in section 4.

The screenshot shows a Windows Notepad window titled '\*medic.ini - Notesblok'. The window contains the configuration file 'medic.ini' with the following content:

```
[medic]
textfile=c:\medic\medic.uk
|localdatabase=MEDICCONNECTION
workdir=c:\medic
applicationname=Medic
dicomserver=0
backgroundcolor=240,240,240
host=localhost
port=8090
autoimport=0
keepalivetimer=1
testdicom=0
uselocaldatabase=1
datasetidfile=c:\medic\medic.did
exportdir=c:\medic\export
dicomfileexportdir=c:\medic\dicomfiles
enableautologin=1
createPACSRGBdataset=1
medicfunctionsURL=file:///c:/medic/medicfunctions.htm
[study]
dateformat=dd/mm/yyyy
startdate=01/01/1990
newstudywarning=1
[dataset]
datadir=c:\medic\data
singledatadir=1
[palette]
datadir=c:\medic\palette
default=Inverse grayscale
[protocol]
datadir=c:\medic\protocol
```

fig.2.16

## 2.16 Import datasets

To import datasets (in Medic format) to the system select Maintenance->Import->Datasets and dialog in fig.2.17 is shown.

Import dataset

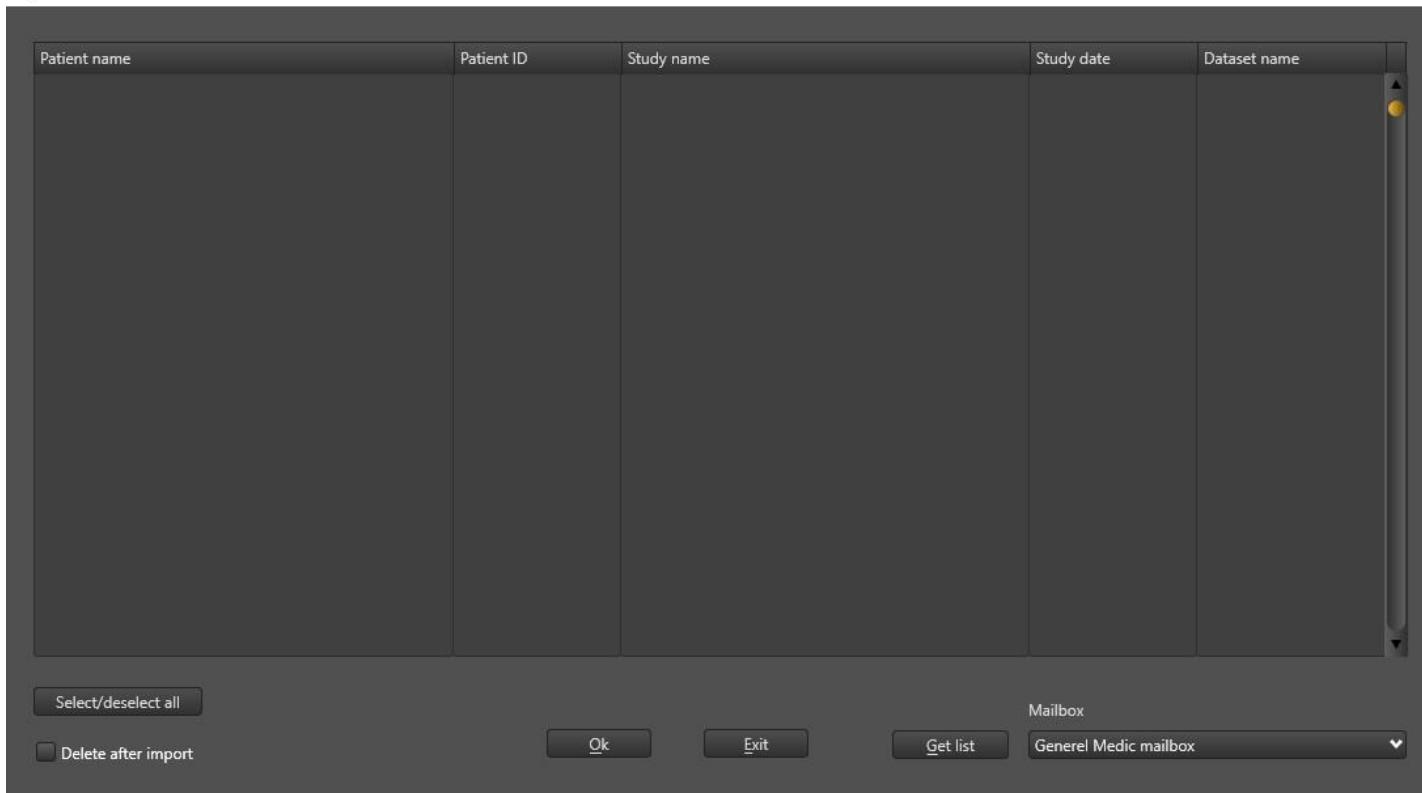


fig.2.17

Select the mailbox which contains the datasets to import from the “Mailbox” drop-down list (these mailboxes are defined in the Medic configuration file) and press Get list. Select the datasets you want to import and press Ok and the datasets will be imported in the system. If the system already contains the datasets these datasets will be overwritten with the imported datasets.

## 2.17 Import colormap from Medic file

To import a colormap (which is exported from another Medic system) select Maintenance->Import->Colormap from Medic file and a standard Windows “File open” dialog is shown. Select the file to import and press “Open”.

## 2.18 Import colormap fra bin file

To import a colormap (which is stored in 768 byte format R.....G.....B) select Maintenance->Import->Colormap from bin file and a standard Windows “File open” dialog is shown. Select the file to import and press “Open”. The colormap is given the name of the file without ext.

## 2.19 Import protocol

To import processing protocols (in Medic format) which have been exported from another Medic system select Maintenance->Import->protocol and a standard Windows “File open” dialog is shown. Select the protocol files you want to import and press “Open”.

## 2.19 Export processing protocols

To export processing protocols from the system select Maintenance->Export->Processing protocols and the dialog in fig.2.18 is shown.

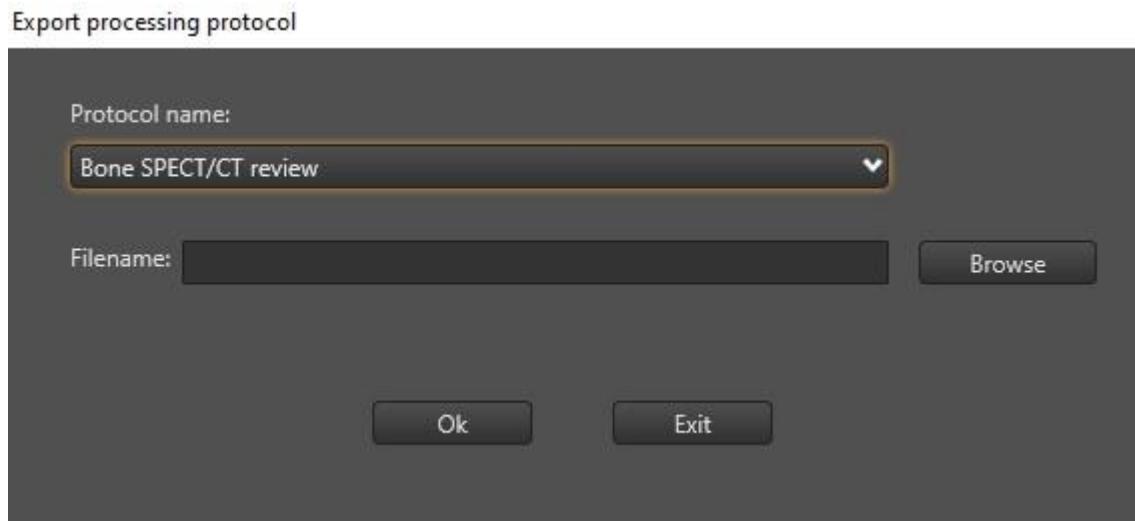


fig.2.18

Select the protocol you want to export from the “Protocol name” drop-down box. Write the full path in the “Filename” edit (directory must exist) and press Ok. A message will be shown on success.

## 2.20 Export Colormaps

To export colormaps from the system select Maintenance->Export->Colormaps and the dialog in fig.2.19 is shown.

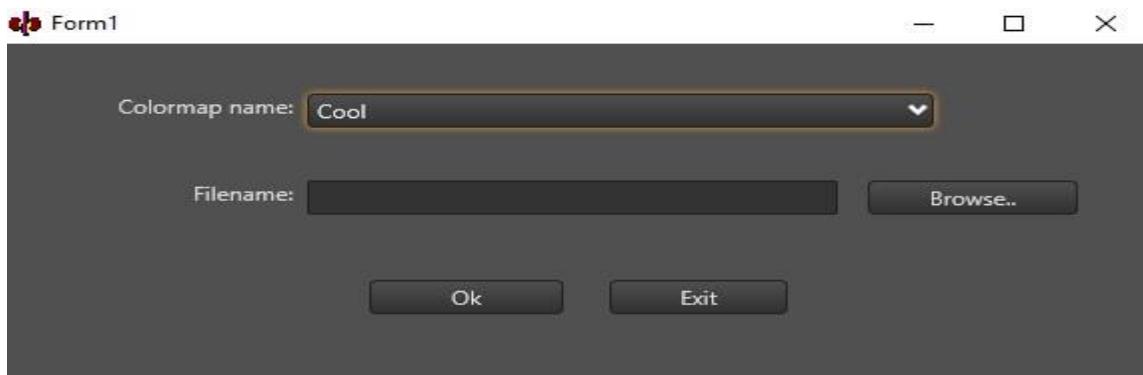


fig.2.19

Select the colormap you want to export from the “Colormap name” drop-down box. Write the full path in the “Filename” edit (directory must exist) and press Ok. A message will be shown on success.

## 2.21 Export Datasets

To export datasets from the system (in Medic format) select Maintenance->Export->Datasets and the dialog in fig.2.20 is shown.

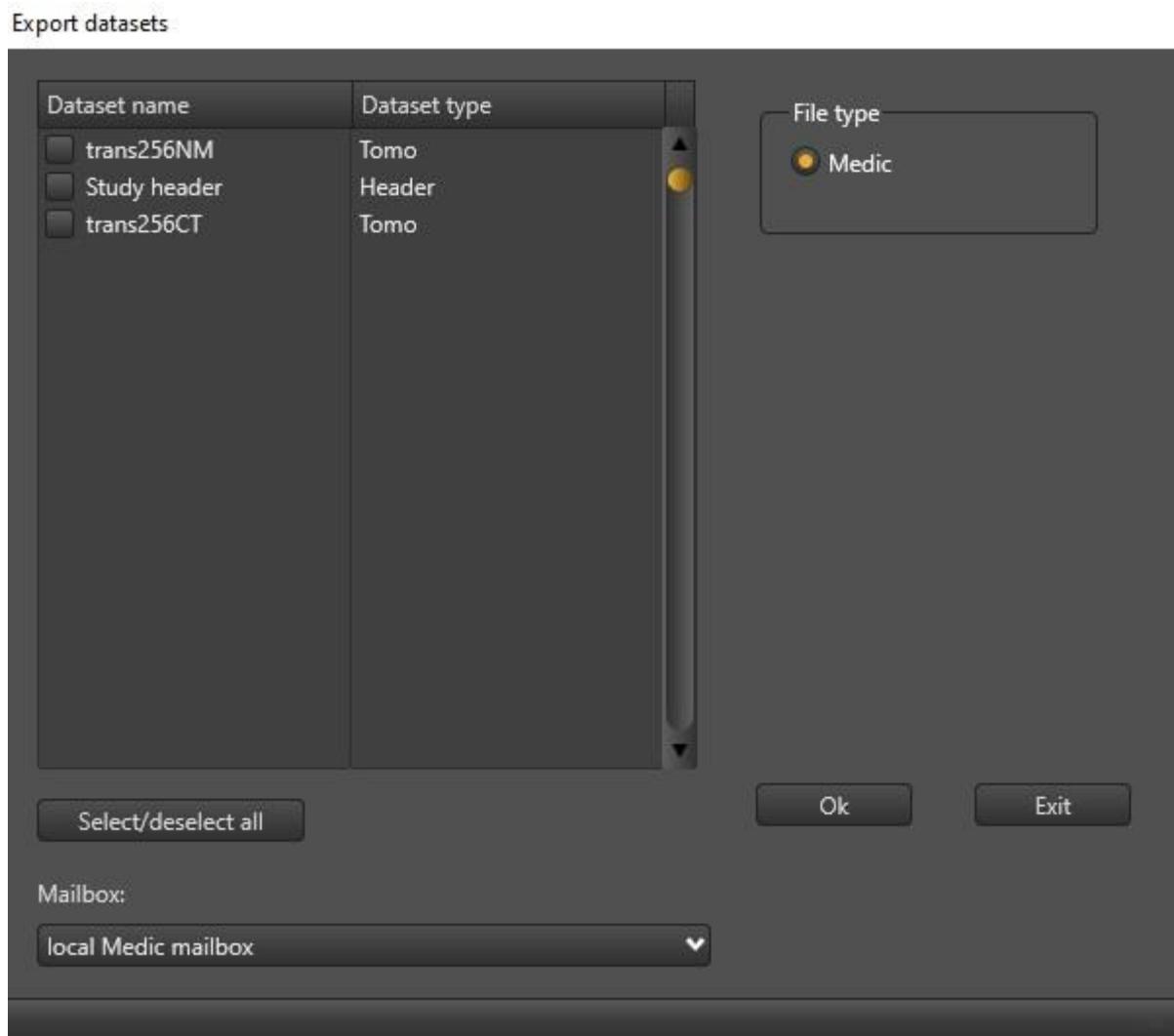


fig.2.20

Select the datasets you want to export and select the mailbox you want to export to from the “Mailbox” drop-down list (defined in the configuration file) and press Ok.

## 2.22 Export Dataset in DICOM format

To export datasets in DICOM format select Maintenance->Export->Datasets in DICOM format and the dialog in fig.2.21 is shown.

Export DICOM dataset

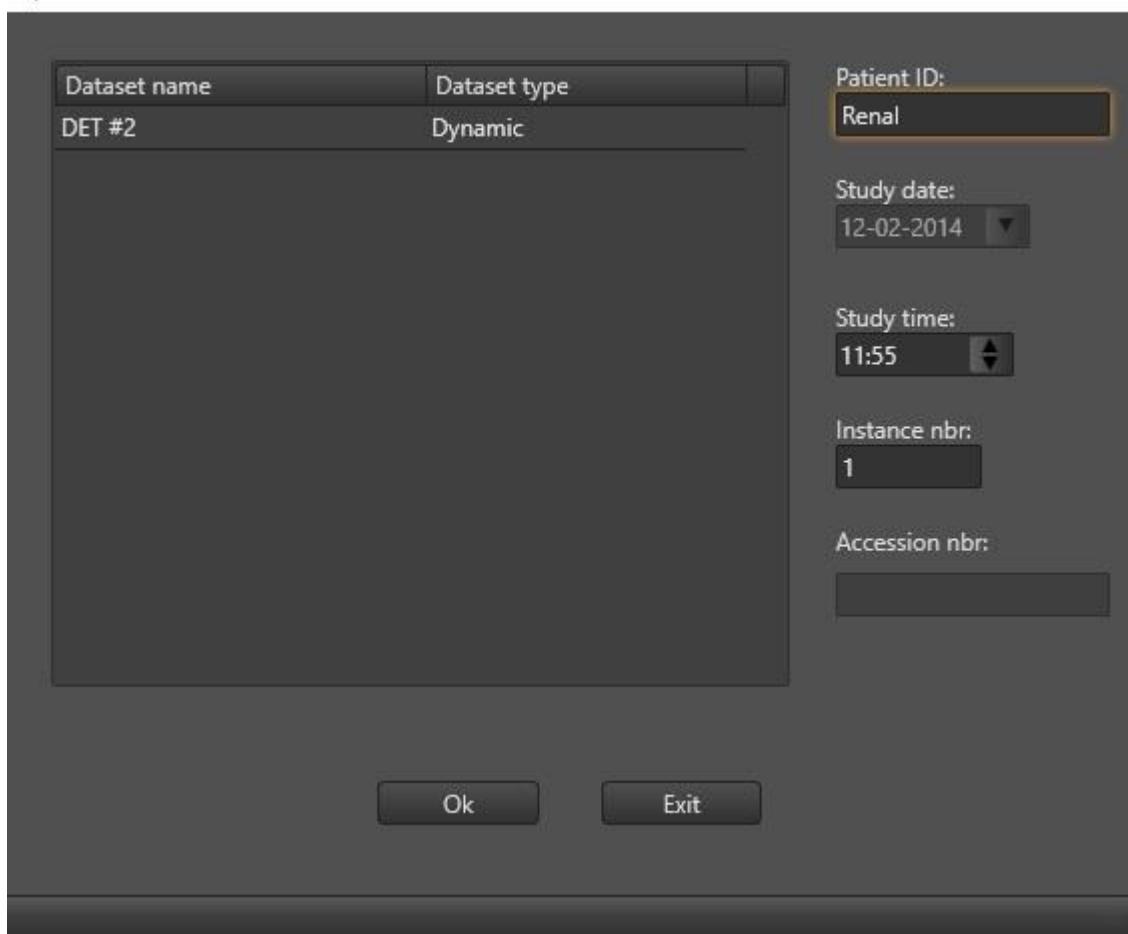


fig.2.21

Select the dataset from the list of datasets in the current study and press Ok. The dataset will be exported to a folder defined in the configuration file.

At the top of the window is the processing menu where you can handle images, registers, text, colormaps, reports, protocols, curves and profiles. All these functions including the functions from the pop-up menus are also available when you create a processing protocol.

### 3.0 Processing Window

The processing window opens when you select a study for processing from the main window. Either by double-clicking the study, or selecting a study and a related processing protocol and pressing “Start processing this study”. You can also double-click a dataset in the main window to show the content of this dataset in the processing window.

The processing window is shown in fig 3.1

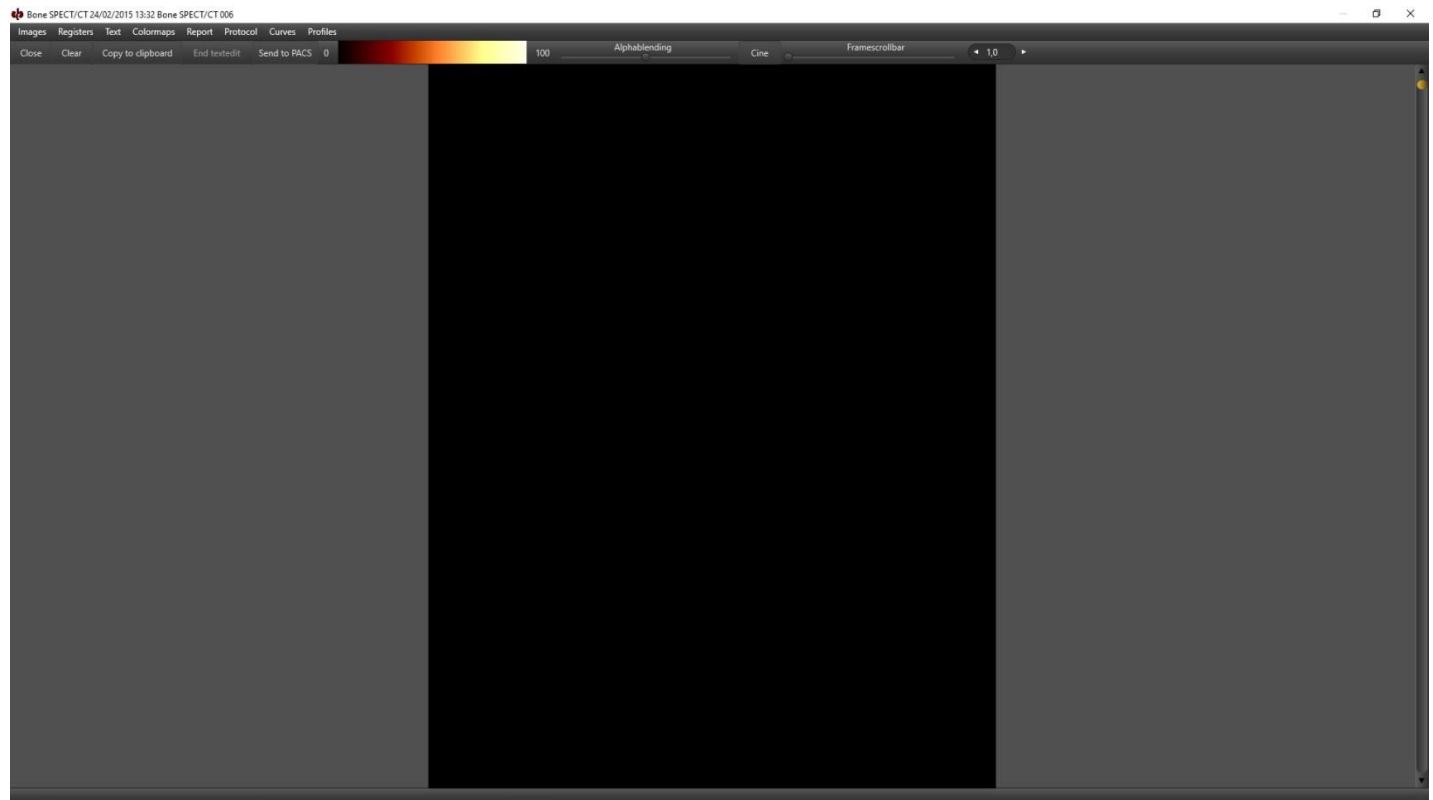


fig.3.1

In the middle of the processing window is the report area, which can be given the size you want. The report area can be scrolled if it exceeds the screen height. In the report area you can place objects as images, text panels, curve panels, profile panels and graphical object. These objects can be resized, zoomed (images), moved or deleted. Each object type has its own pop-up menu which can be activated by right-clicking the object. For image objects there are a special menu item “Selected” which means that the image reacts to changes in the controls at the top (colormap, alfablending, cine, framescrollbar and zoom). When an image is “selected” it is marked in the corners with small blue marks. This function can also be activated by middle button clicking the image. Middle button clicking again on the image removes the “selection”. The objects are placed with no overlapping. At the top of the window is the processing menu where you can handle images, registers, text, colormaps, reports, protocols, curves and profiles. All these functions including the functions from the pop-up menus are also available when you create a processing protocol. At the bottom of the window is a

statusbar where messages can be shown. In protocol processing mode messages from the protocol are shown in the titlebar at the top.

### 3.1 Insert static images

To insert static images on the report select Images->Static and choose between normal size, maximal size, interpolated to 256x256 or whole body 256x1024. A list of static images is shown in the Select datasets dialog in fig.3.2.

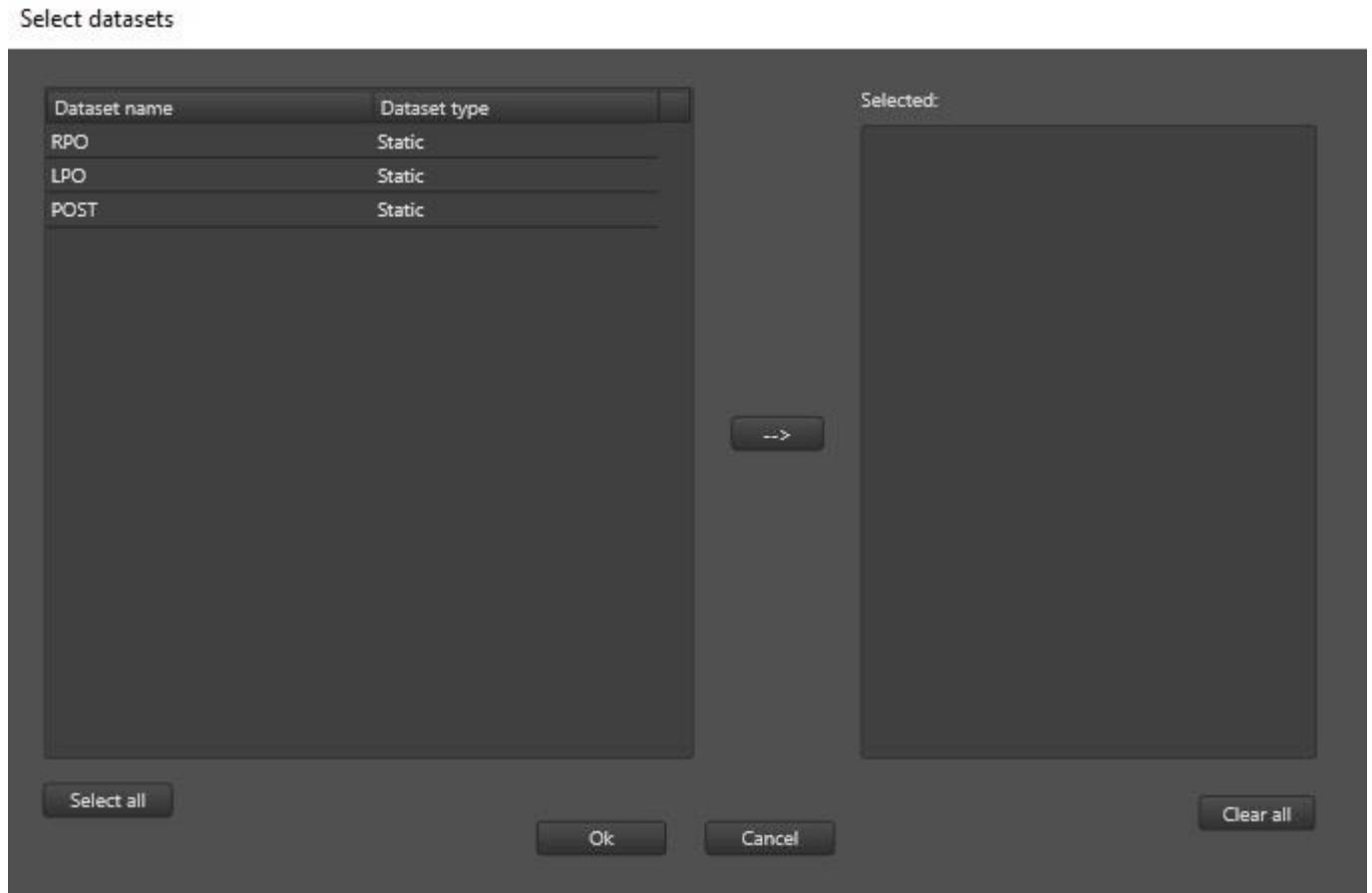


fig.3.2

Select the static images from the list of datasets in the order you want to place the images on the display either by double-clicking the image or selecting the image and press the → button. If there are no room for the image(s) in the report area, the image(s) will not be displayed. The minimum size for a image on the display is 128x128 so if the image is acquired in 64x64 it will be interpolated to 128x128 before it is displayed.

### 3.2 Insert dynamic images

Dynamic images can be single or multiple phase dynamic images, tomo or gated tomo acquired image and multigated images.

To insert dynamic images on the report select Images->Dynamic and choose between Cine, Cine 128x128, Cine 256x256 or Snake in different formats. The dialog to select the dynamic images is equal to the dialog in fig.3.2.

### 3.3 Insert 3D volume images

3D volume images are reconstructed tomo or gated tomo images, CT, PET or MR images. To insert 3D volume images on the report select Images->3D volume images and chose between volume image, volume image with MIP (maximum intensity projection), volume image 3x256x256, volume image 3x384x384, volume image 3x512x512, dual volume image, dual volume image with MIP, dual volume image 3x256x256 or dual volume image 3x384x384. For multiple dataset selection the dialog is the same as in fig.3.2. For single dataset selection the dialog is shown in fig.3.3 and for dual dataset selection the dialog is shown in fig.3.4.

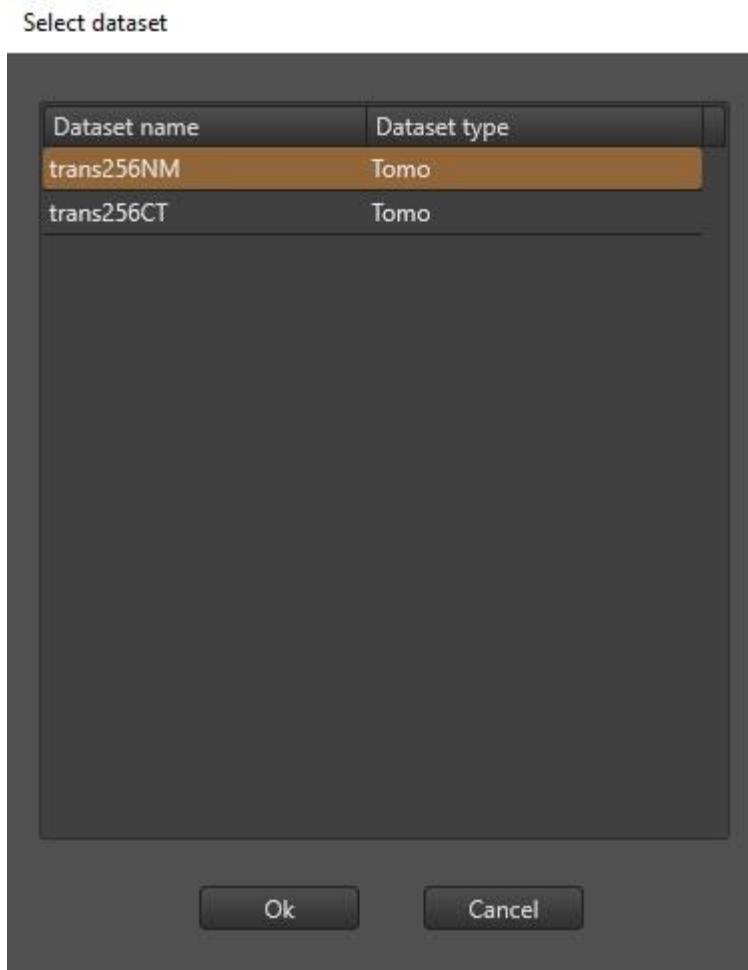


Fig.3.3

To select a single dataset select the dataset in the list of datasets and press Ok.

Select SPECT and then CT dataset

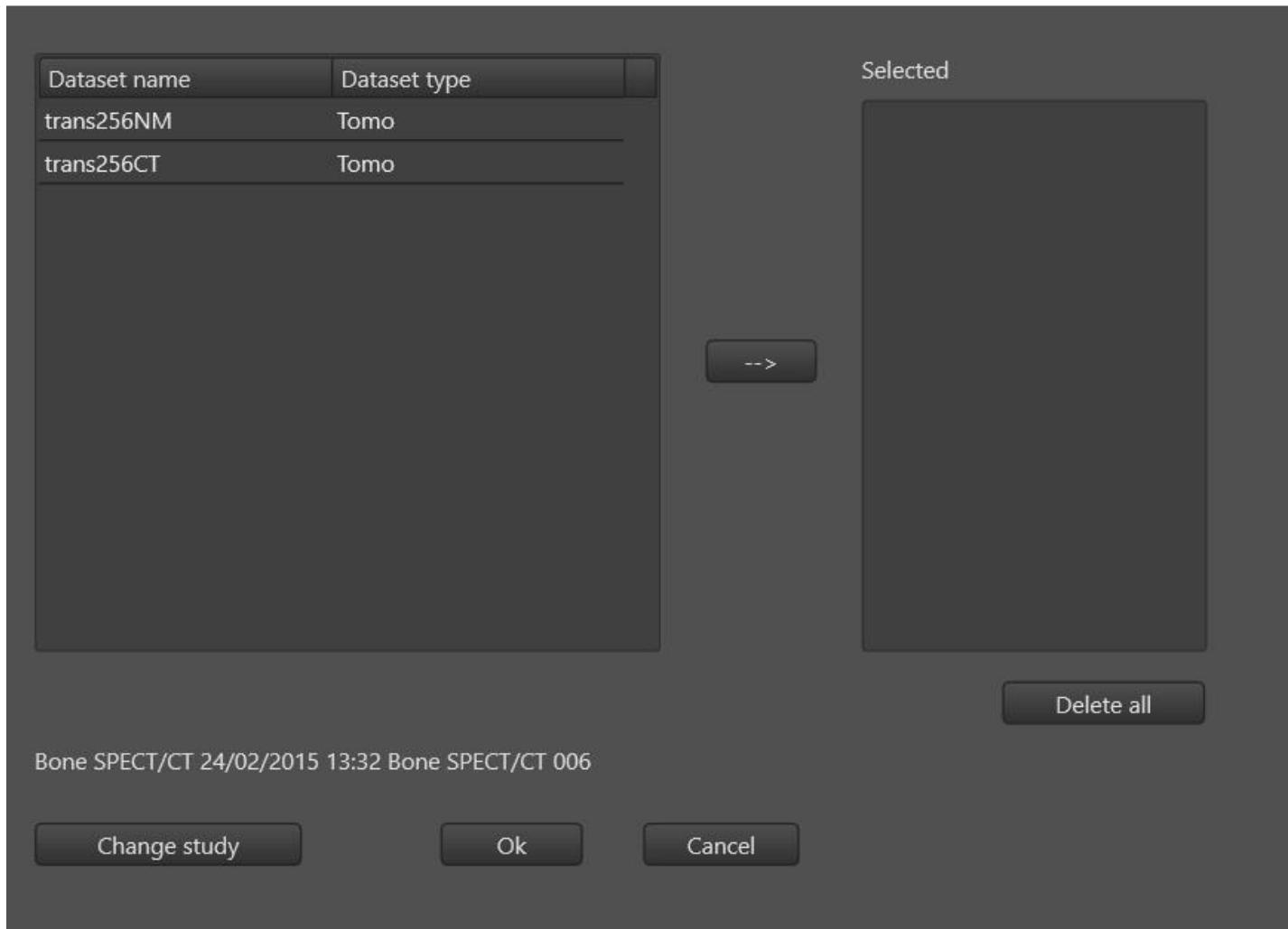


fig.3.4

To select dual datasets (SPECT and CT) select the first dataset from the list either by double-clicking the dataset or selecting the dataset and press the → button. If the second dataset is located in another study press “Change study” and a list of studies for the same patient is shown. After selecting the study a list of datasets in that study are shown. Select the second dataset and press Ok.

### 3.4 Insert RGB images

To insert RGB images (screen-dumps) on the report select Image->Insert RGB image and choose between normal, 75%, 50% or 33% size. The dialog to select the RGB images is equal to the dialog in fig.3.2. If there is no room for the image(s) in the report area, the image(s) will not be displayed.

### 3.5 Insert graphic image from file

To insert a graphic image from file (type: jpg, png or bmp) select Images->Insert graphic image from file and a standard Windows “File open” dialog is shown. Select the graphic file

to import and press “Open”. If there is no room for the graphic image in the report area, the graphic image will not be displayed.

## 3.6 Insert graphic image from clipboard

To insert a graphic image from windows clipboard Select Images->Insert graphic image from clipboard (a graphic image of type jpg, png or bmp must have been copied to the clipboard). If there is no room for the graphic image in the report area, the graphic image will not be displayed.

## 3.7 Image Reconstruction

To reconstruct tomo and gated tomo acquisitions select Images->Image Reconstruction and a select dataset dialog like fig.3.3 is shown. After selecting a dataset the dialog in fig.3.5 is shown.

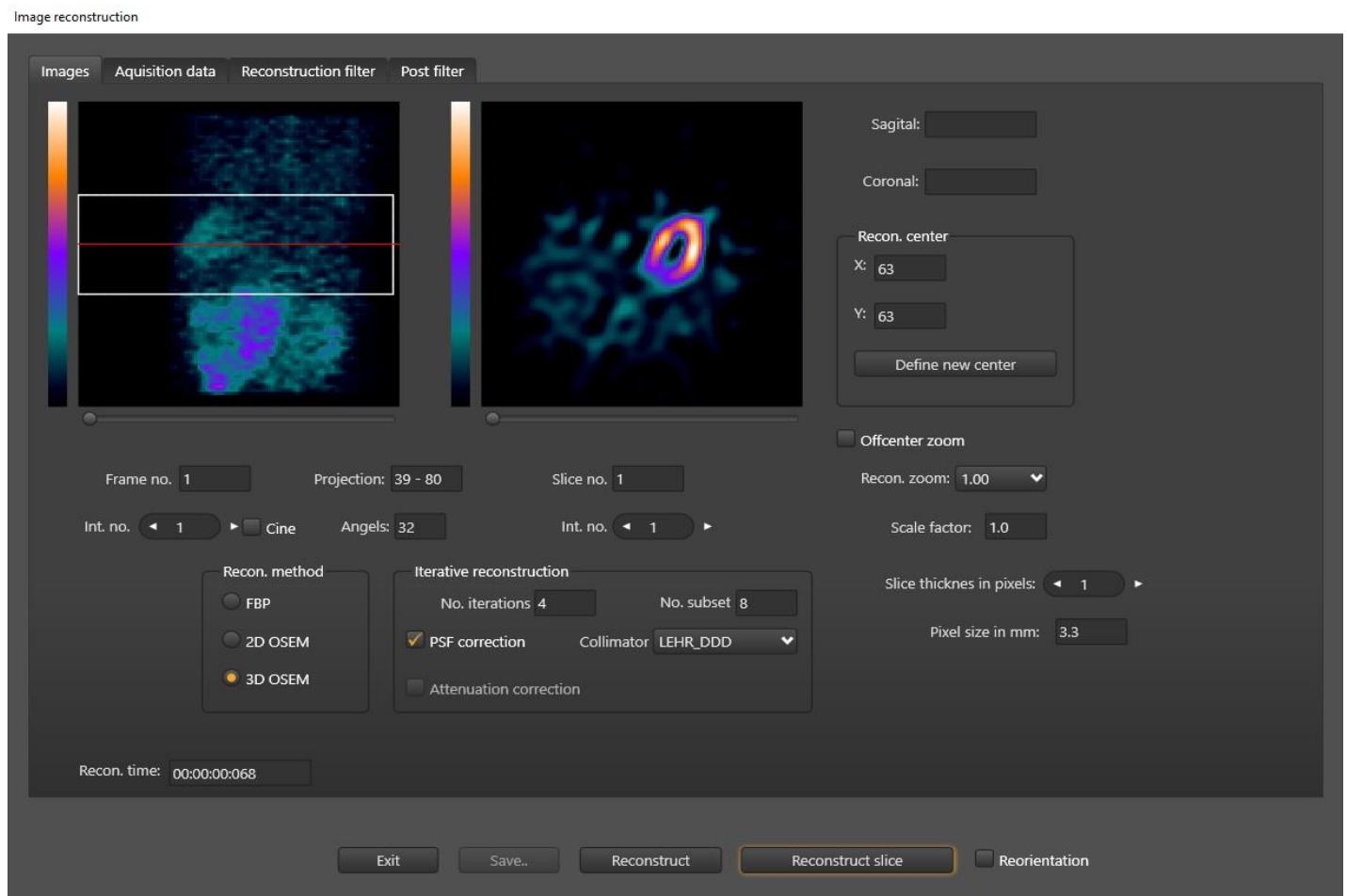


fig.3.5

In the left image panel are the acquired tomo (or gated tomo) images shown. Use the scroll-bar to see all the images. To define the part of the image to reconstruct set the white rectangle so it contains this part of the image. Select the reconstruction method (FBP (Filtered Back

Projection), 2D OSEM (Ordered Subset Expectation Maximum) or 3D OSEM (including PSF (Point Spread Function) correction). For the FBP method select the Reconstruction filter on the “Reconstruction filter” tab and the Post filter on the “Post filter” tab. For the OSEM methods select “No of iterations” and “No of subset” and for the 3D OSEM method select the collimator type from the “Collimator” drop-down list. Then select the Post filter on the “Post filter” tab. Go back to the “Images” tab and select “Reconstruct” (or “Reconstruct slice” to see the reconstructed slice corresponding to the red line in the left image panel). After the reconstruction you can see the result in the right image panel. If the reconstruction needs to be reoriented (cardiac and brain) check the “Reorientation” and the “Reorientation” tab is activated. This is shown in fig.3.6.

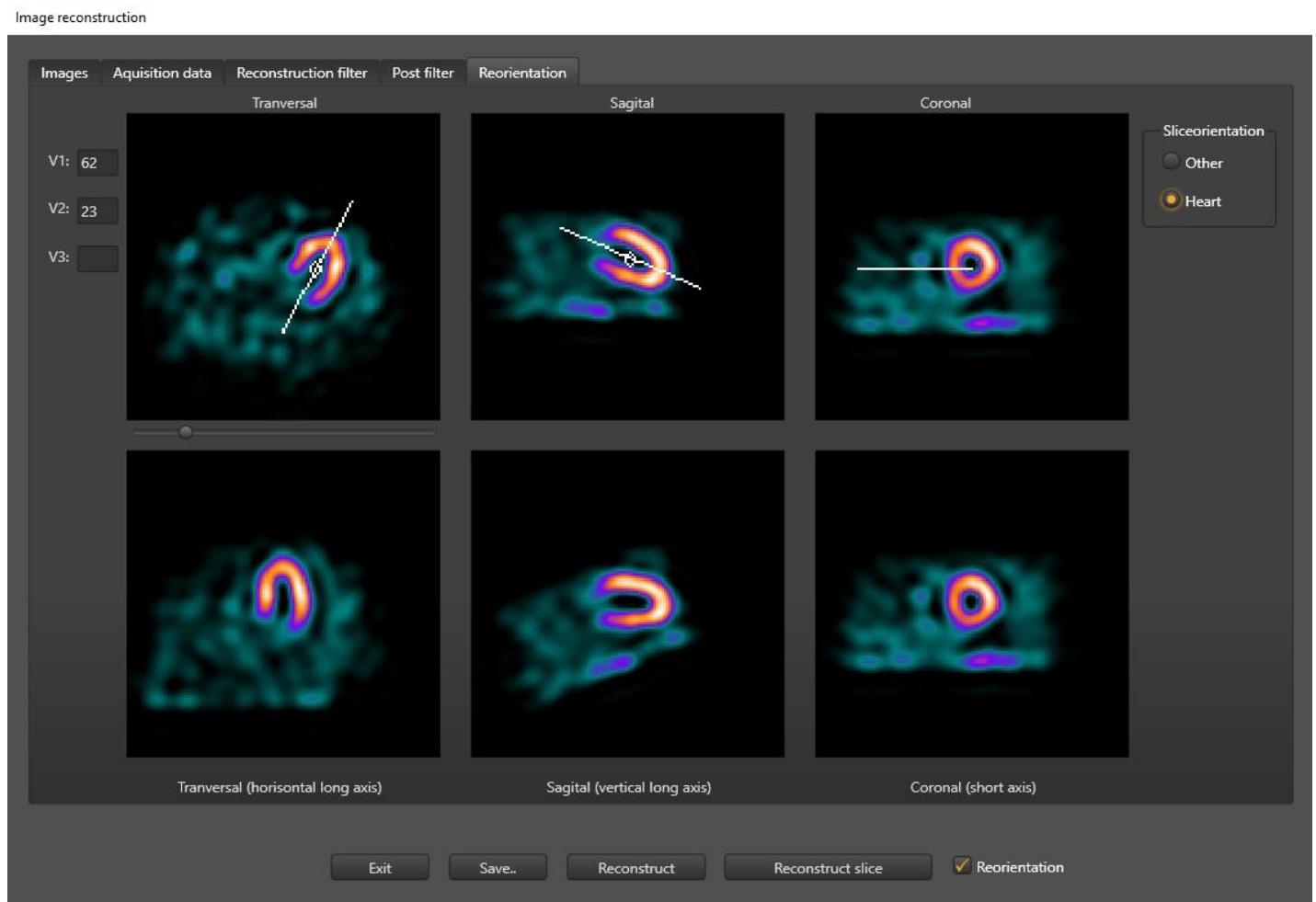


fig.3.6

Select sliceorientation either “Other” or “Heart” depending on study type. Move and rotate the line on the transverse image and sagital image to define new sagital (vertical long axis), coronal (short axis) and traversal (horizontal axis) images. Press “Save” to save the reconstructed (and reoriented) dataset and give it a unique name.

### 3.8 SPECT/CT image alignment

To align a SPECT and CT dataset select Images->3D volume images->SPECT/CT image alignment. Select a SPECT and a CT dataset from the Select SPECT and CT dataset dialog shown in fig.3.4 and the dialog in fig.3.7 is shown.

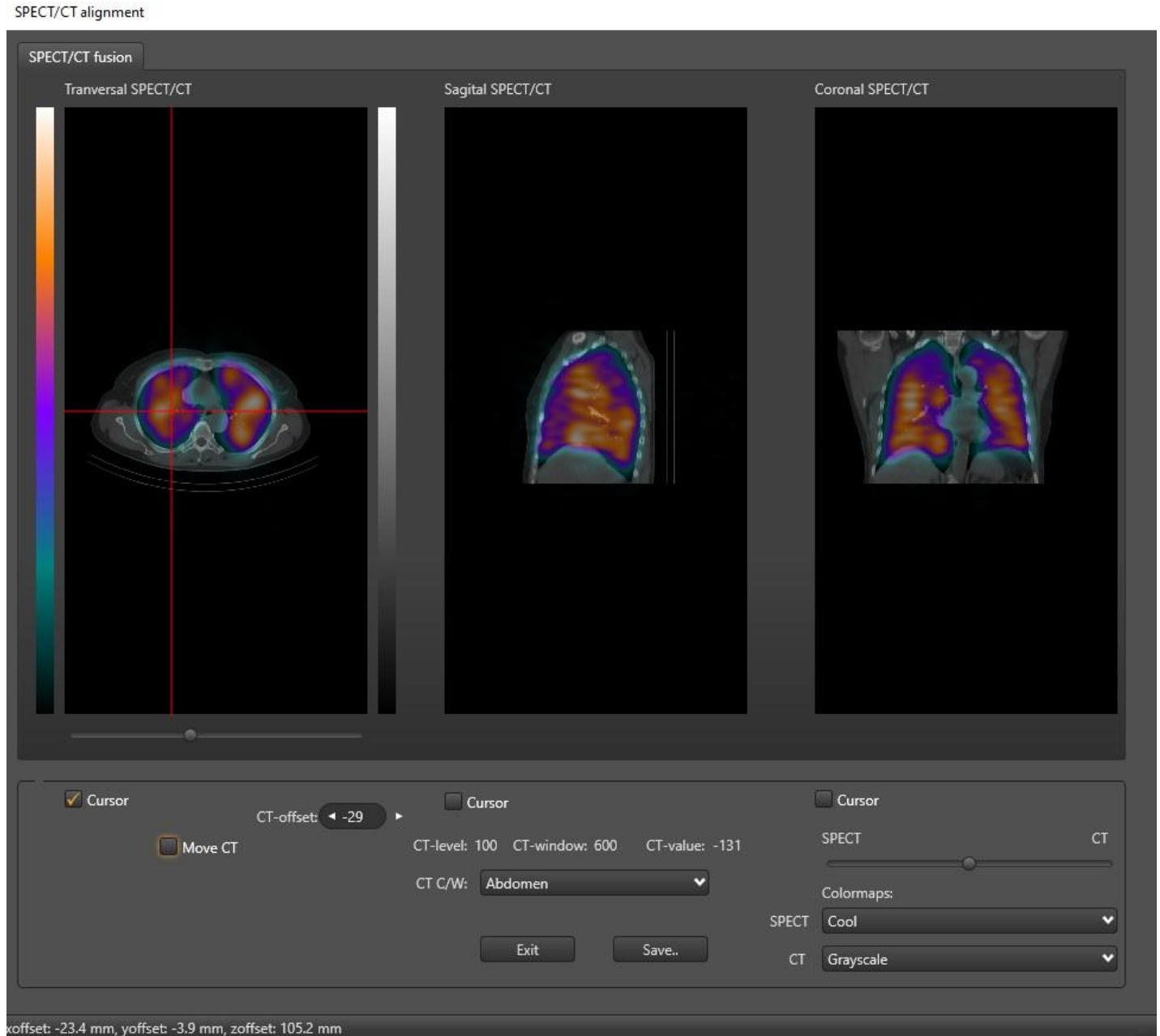


fig.3.7

Select the colormaps and CT C/W settings. Check the “Move CT” (which deactivates the cursor movement on the transvers image). Left mouse click in the direction you want to move the CT image. Change the CT-offset edit to align the images in the coronal direction. Press “Save” and give the dataset(s) a name (NM and CT is automatically added to this name to create the two datasets).

### 3.9 Add frames

To add frames in a dynamic study select Images->Add frames and choose between manually or automatic. For manual addition the dialog in fig.3.8 is shown.

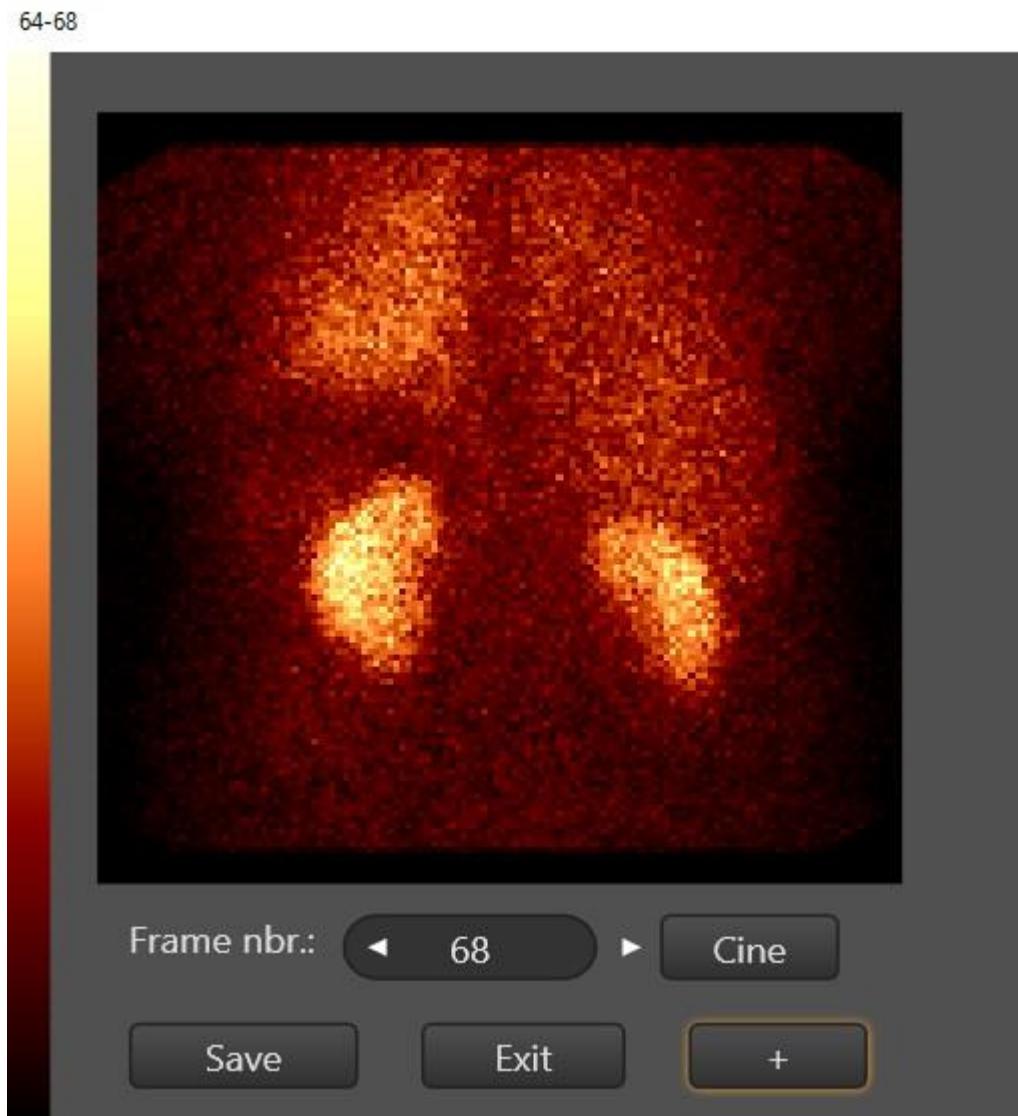


fig.3.8

Go to the image where you want to start the addition of frames with the “Frame nbr.” edit or the “Cine” button. Start adding with the “+” button. The frame numbers added are shown on the dialogs title bar. Press “Save” and give the dataset a unique name. If automatic is chosen the dialog in fig.3.9 is shown.

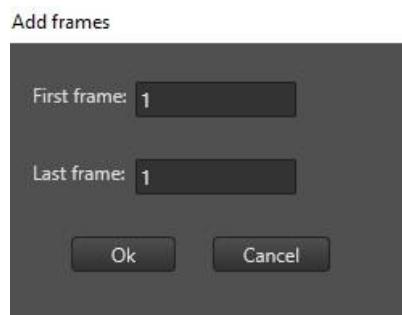


fig.3.9

Type in first frame and last frame to add and press “Ok”. Save the dataset with a unique name.

### 3.10 Image manipulation

To manipulate images select Images->Image manipulation and choose between Add/subtract, Multiply, Divide, Log, Exp, Minify, ROI include, ROI exclude, Rotate, Mirror around Y-axis, Motion correction, Geometric mean, Resample image, Convert gated to ungated and Image subtraction (with manually adjustable subtraction factor). Most of the functions are available from the dialog shown in fig.3.10.

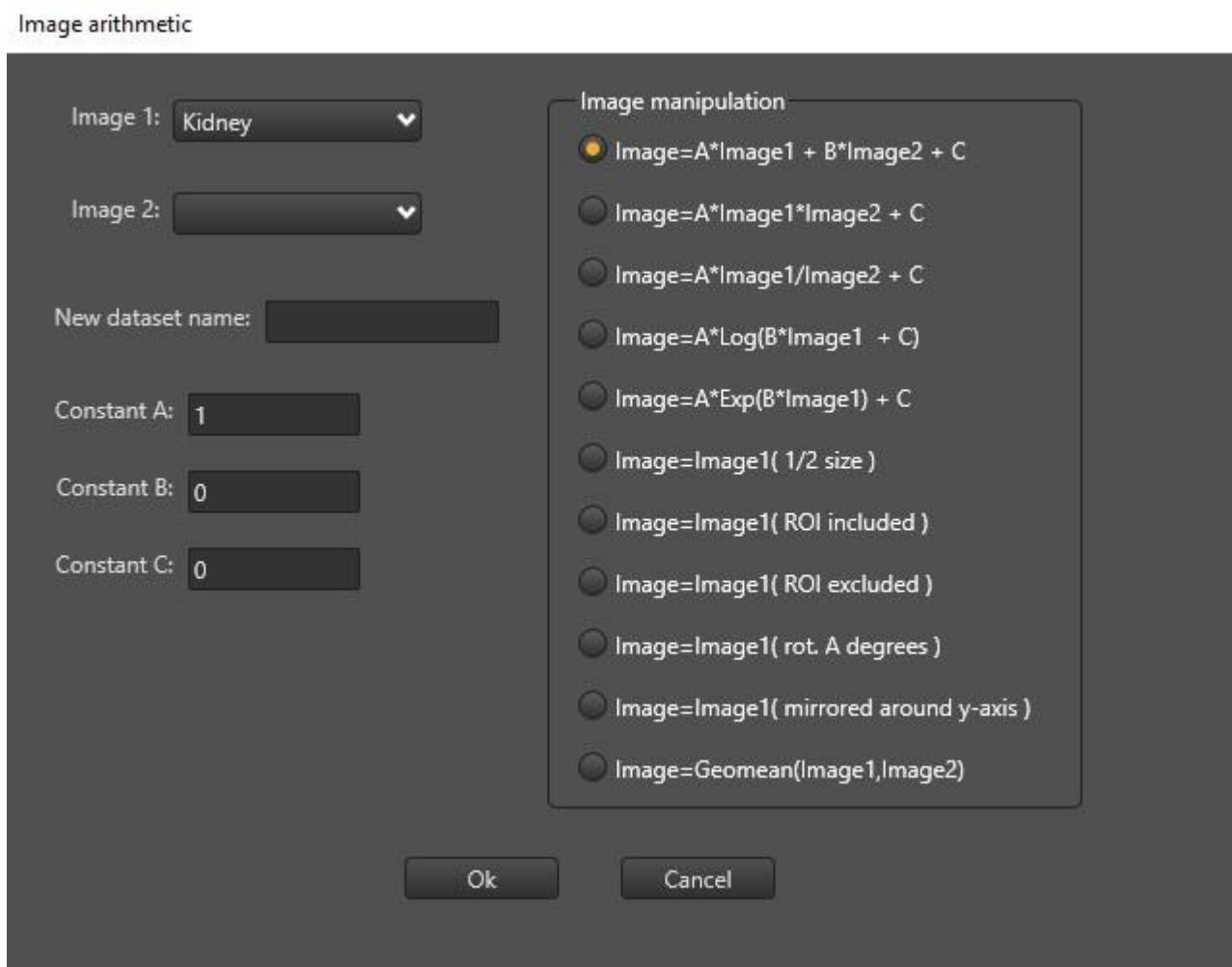


fig.3.10

Select the image(s) from the drop-down boxes. Give the new dataset a name. Type in the constants (or use data from registers e.g. #020) and press “Ok”.

### 3.10.1 Motion Correction

To motion correct dynamic or tomographic images select Images->Image manipulation->Motion correction. Select the dataset to be motion corrected (optional select a ROI if a region is earlier defined) and the dialog in fig. 3.10.1 is shown.

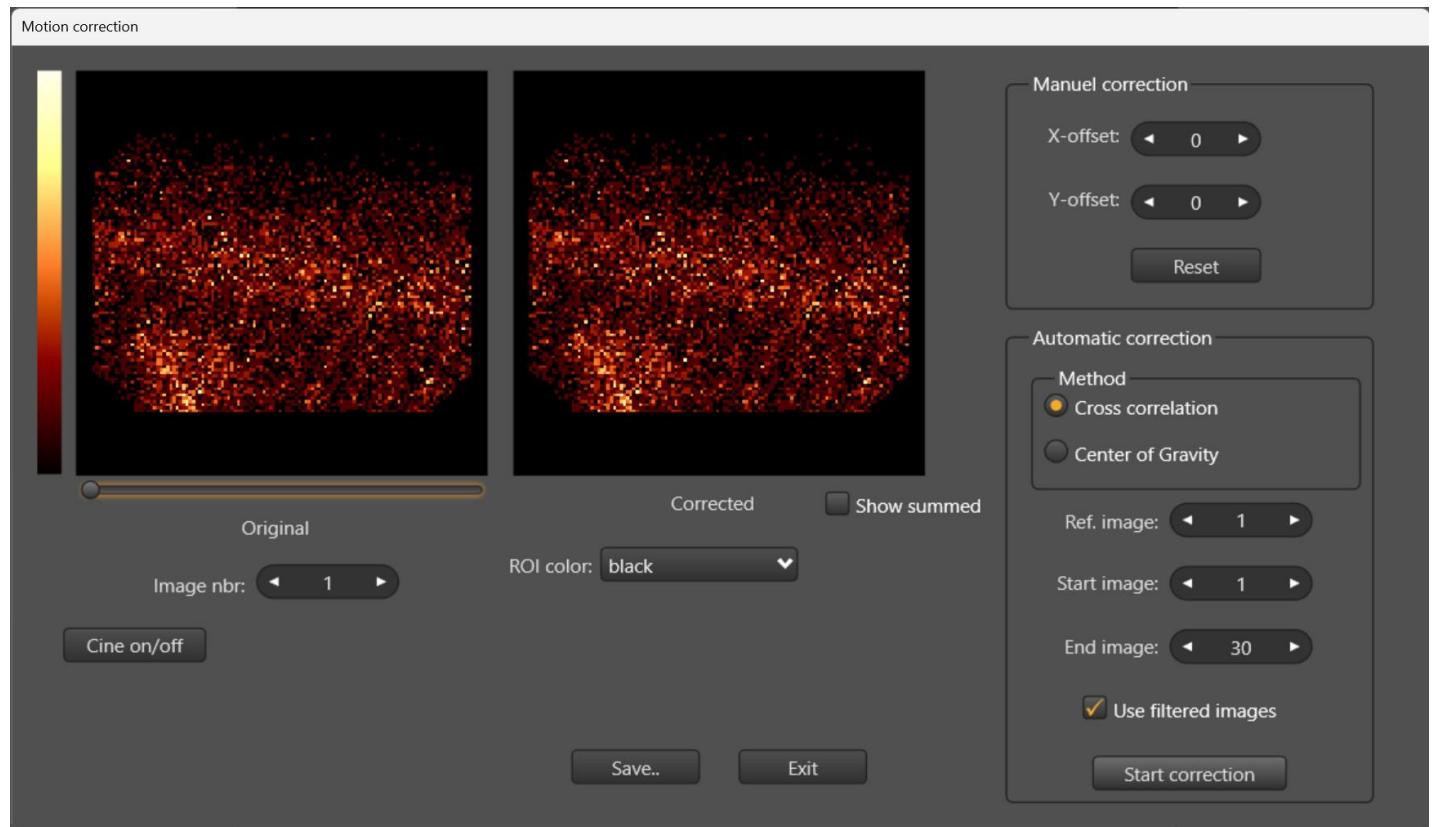


fig 3.10.1

If a dynamic dataset is selected choose the automatic correction method to be used: “Cross correlation” or “Center of Gravity” and press “Start correction”. Check “Show summed” to show the sum of the original and motion corrected dynamic images. Select “Save..” to save the summed result as static dataset. If “Show summed” is not checked you will only save the motion corrected dynamic dataset.

### 3.11 Image filtering

To filter an image (static, dynamic, tomo or gated tomo) select Images->Filtering and choose between Butterworth, Edge enhancement or Smoothing. If Butterworth or Edge enhancement is selected the dialog in fig 3.11 is shown.

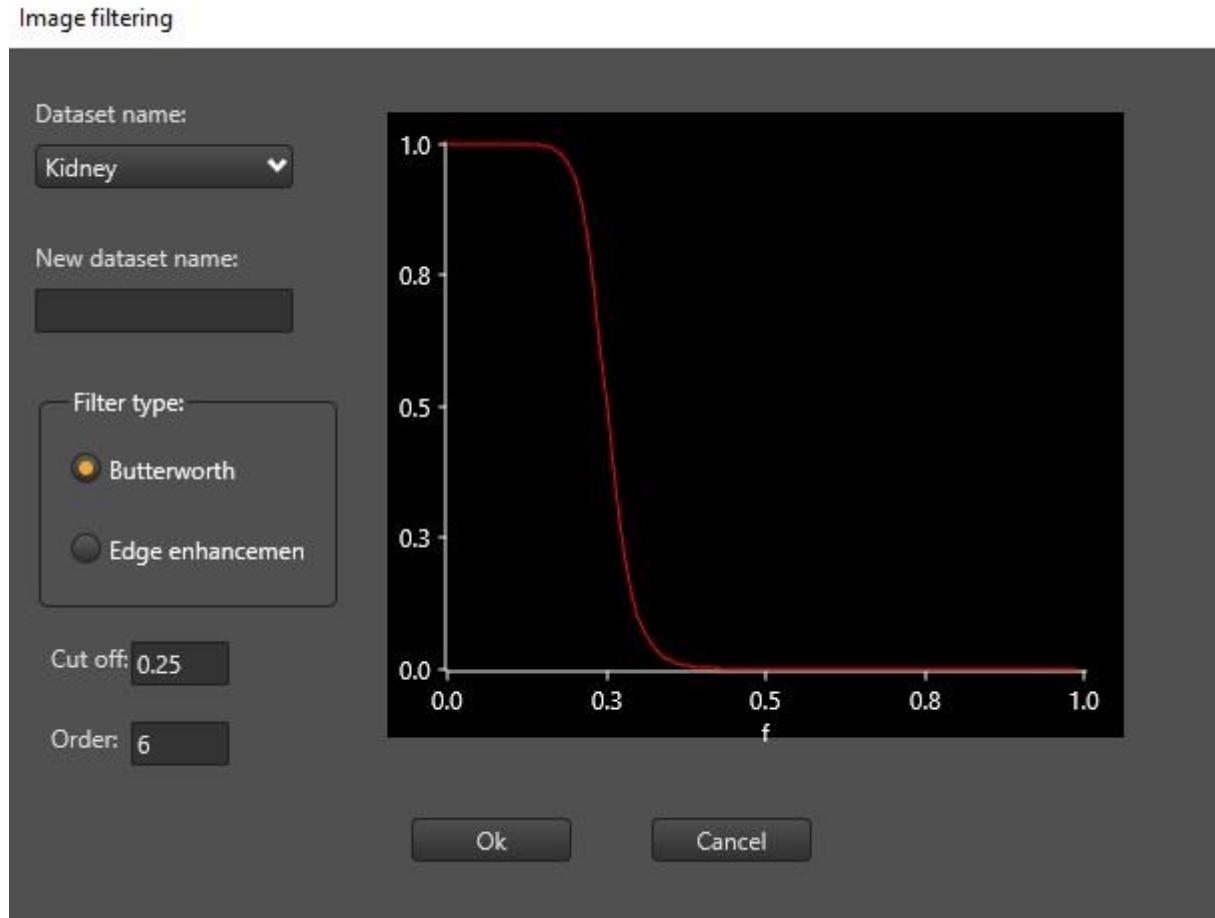


fig.3.11

Select Cut off. Frequency and filter order. Type in a new dataset name and press “Ok”. If Smoothing is selected the dialog in fig.3.12 is show.

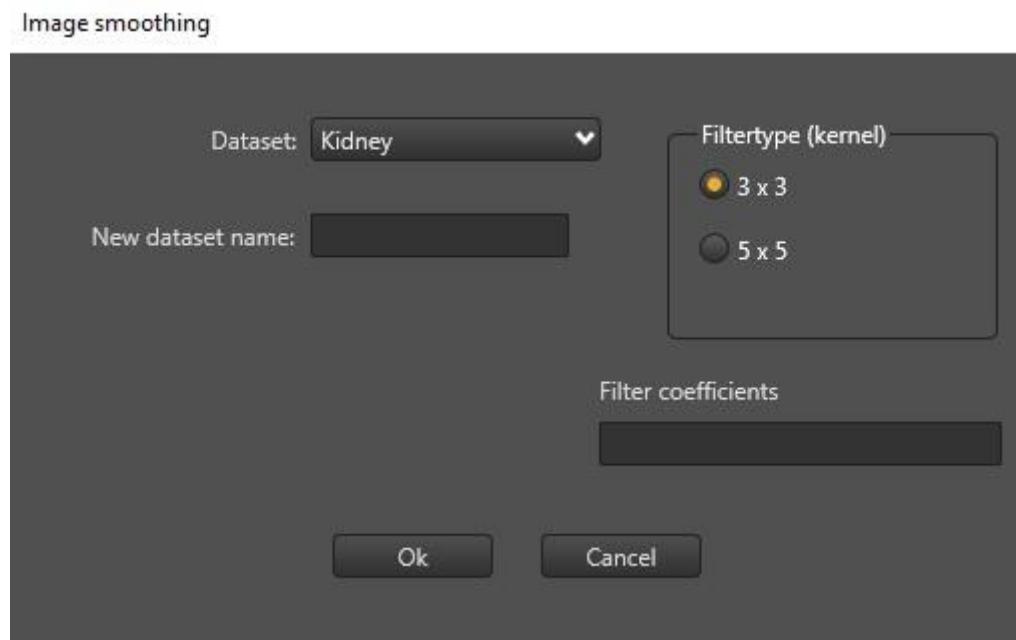


Fig.3.12

Select the Filtertype (kernel) 3x3 or 5x5 points and type in the filter coefficients in the Filter coefficients edit (row by row with , separation and . as decimal point. e.g. 0.7,1,0.7,1,2,1,0.7,1,0.7 for a 3x3 point filter).

### 3.12 Insert data in register

The Study header dataset (which is generated in each study) contains two hundred 40 character long registers which can be used to contain data from calculations or typed in data. The first 15 registers contain information about the patient/study. These data can be used in text fields or text on images by typing e.g. #020 which is then substituted with the content of the register. To insert data into a register select Registers->Insert data in register and the dialog in fig.3.13 is shown.

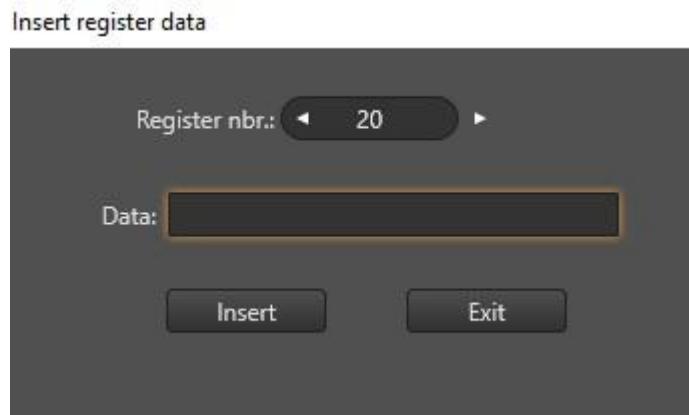


fig.3.13

Select the register number from the “Register nbr.” edit and type in the data in the “Data” edit and press “Insert”.

### 3.13 Edit register equation

To edit a register equation select Register->Edit register equation and the dialog in fig.3.14 is shown.

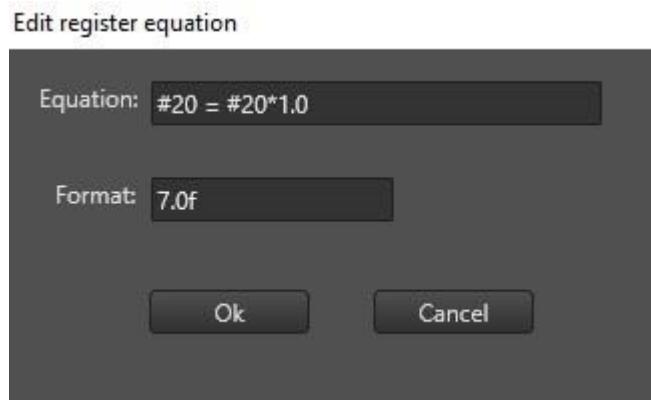


fig.3.14

Type in the equation in the “Equation” edit. The register at the left side of the equation will receive the result in a format specified in the “Format” edit (standard C format specification e.g. 7.0f means seven digits zero digits after the decimal point). In the equation you can use EXP, LOG, POW and SQR as exponential, logarithmic, power and square root functions.

### 3.14 Insert textfield

To insert a textfield on the report select Text->Insert textfield and the dialog in fig.3.15 is shown.



fig.3.15

Type in the size and position of the textfield and press “Ok”. If the position is not filled out you will get a dotted rectangle with the specified size. Place it on the report where you want it and click the left mouse button. Clicking the right mouse button cancels the operation. After the textfield is placed the textfield is active to receive keyboard input. From the Text menu it is possible to select font type, text color, text background color and line color (if the textfield is framed). End the text editing by pressing “End textedit”.

### 3.15 Insert study header

To insert a standard study header at the top of the report (size 768x128) select Text->Insert study header.

### 3.16 Edit study header

To edit the content of the study header dataset select Text->Edit study header and the dialog in fig.2.12 is shown. This is the same function as the Edit study header in the Main menu.

### 3.17 Selecting Colormaps

The report can operate with up to four simultaneous colormaps. To change between active colormap double-click the colorbar at the top.

To select a colormap (or up to four colormaps) select Colormaps-> and choose between one, two or four colormaps. The dialog in fig.3.16 is shown.

Select two color maps

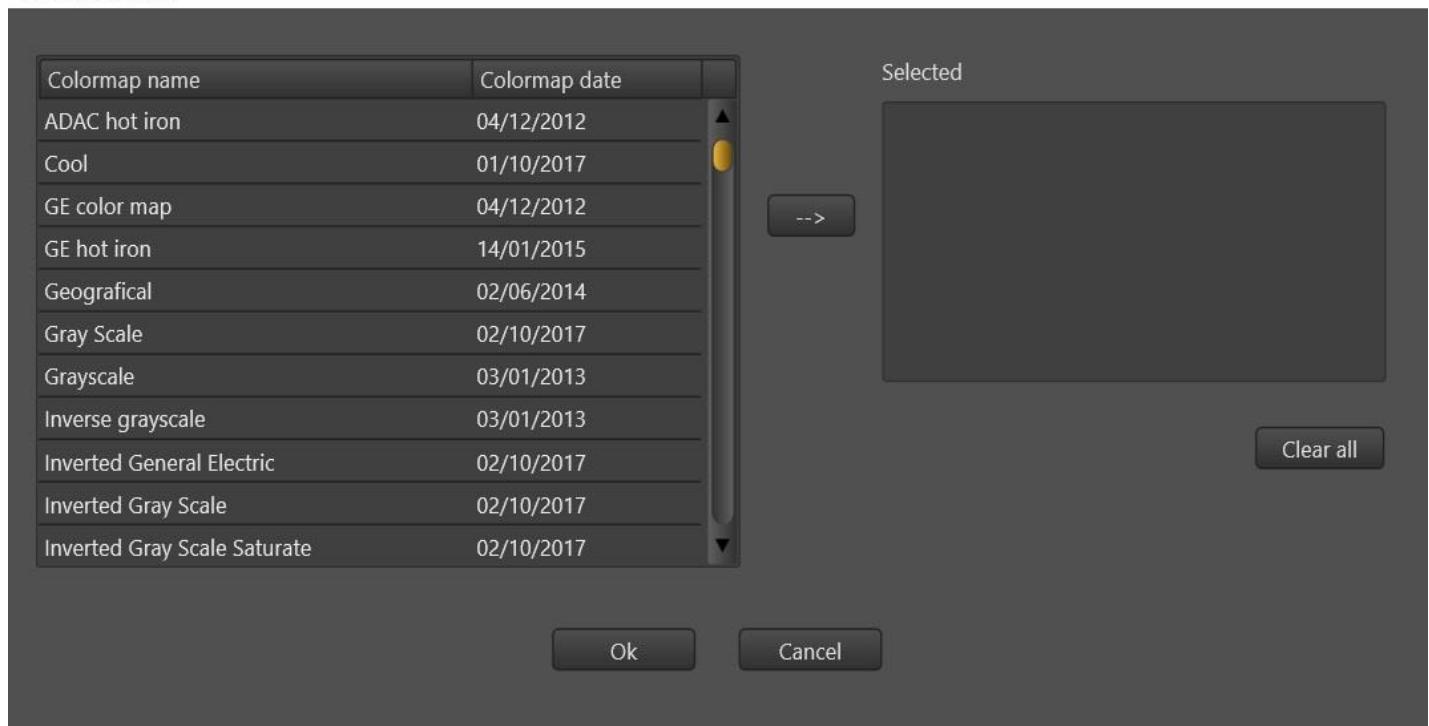


fig.3.16

Select the desired number of simultaneous colormaps by double clicking the colormap or selecting the colormap and press →. Accept with “Ok”.

### 3.18 Setting the report size

To set the report size select Report->Size and choose between manually, 768x1024, 768x1280, 1024x1024, 1024x1280, 1152x1152, 1152x1280, 1152x1536 or 1536x2048. If manually is selected the dialog in fig.3.17 is shown.

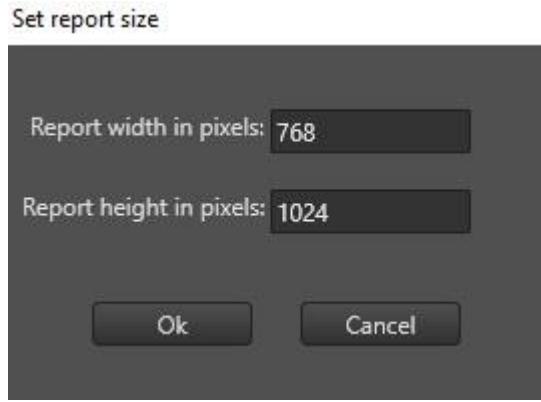


fig.3.17

Set the report size (in pixels (multiple of 4)) and press “Ok”.

### **3.19 Load report**

To load a report (type Page) select Report->Load and select the report from the list of report datasets.

### **3.20 Load RGB report**

To load a RGB report select Report->Load RGB report and select a RGB dataset from the list of RGB datasets.

### **3.21 Save report**

To save the current report select Report->Save. Type in a unique dataset name and press Ok.

### **3.22 Save report as RGB dataset**

To save the current report as a RGB dataset select Report->Save as->RBG dataset. Type in a unique dataset name and press Ok.

### **3.23 Save report as jpeg file**

To save the current report as a jpeg file select Report->Save as->JPEG file and the dialog in fig.3.18 is shown.

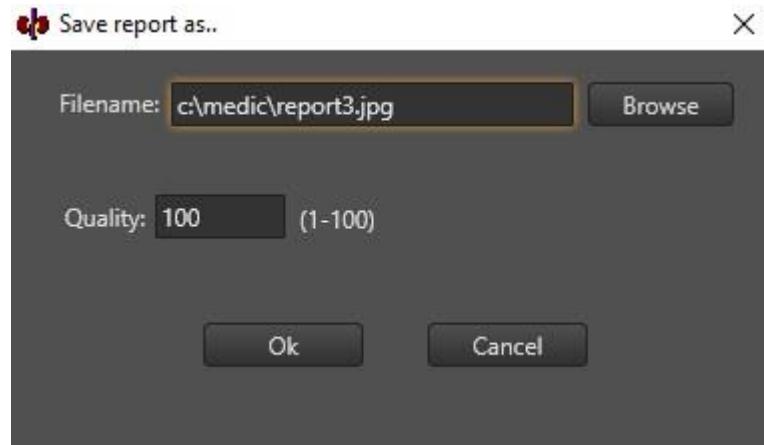


fig.3.18

Type in filename (directory must exist) and image quality and press Ok.

### **3.24 Copy report to clipboard**

To copy the current report to clipboard select Report->Copy to clipboard and the report are copied to the clipboard as a graphical image.

### **3.25 Send report to PACS system**

To send the current report to a PACS system select either Report->Send to PACS or press the “Send to PACS” button at the toolbar. The report are saved as a RGB dataset and send to a folder (defined in the configuration file) where the MedicImport application picks it up and sends it to a PACS system as a DICOM SECONDARY CAPTURE dataset.

### **3.26 Print report**

To print the current report on a connected windows printer select Report->Print and the dialog in fig.3.19 is shown.

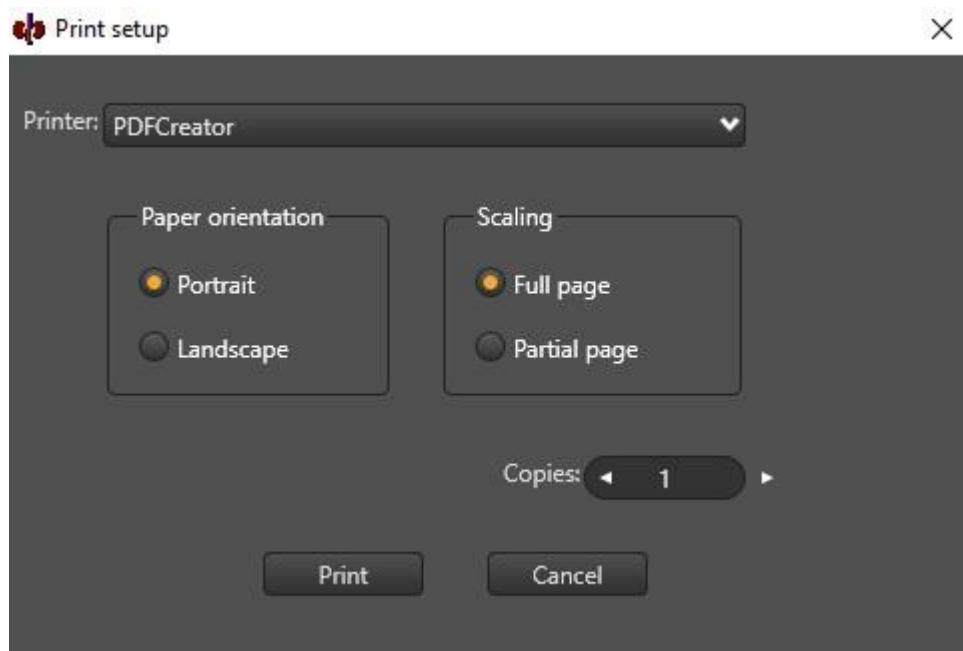


fig.3.19

Select the paper orientation, scaling and number of copies and press “Print”.

### 3.27 Select protocol

To select a processing protocol from the total list of processing protocols select Protocol->Select and the dialog in fig.3.20 is shown.

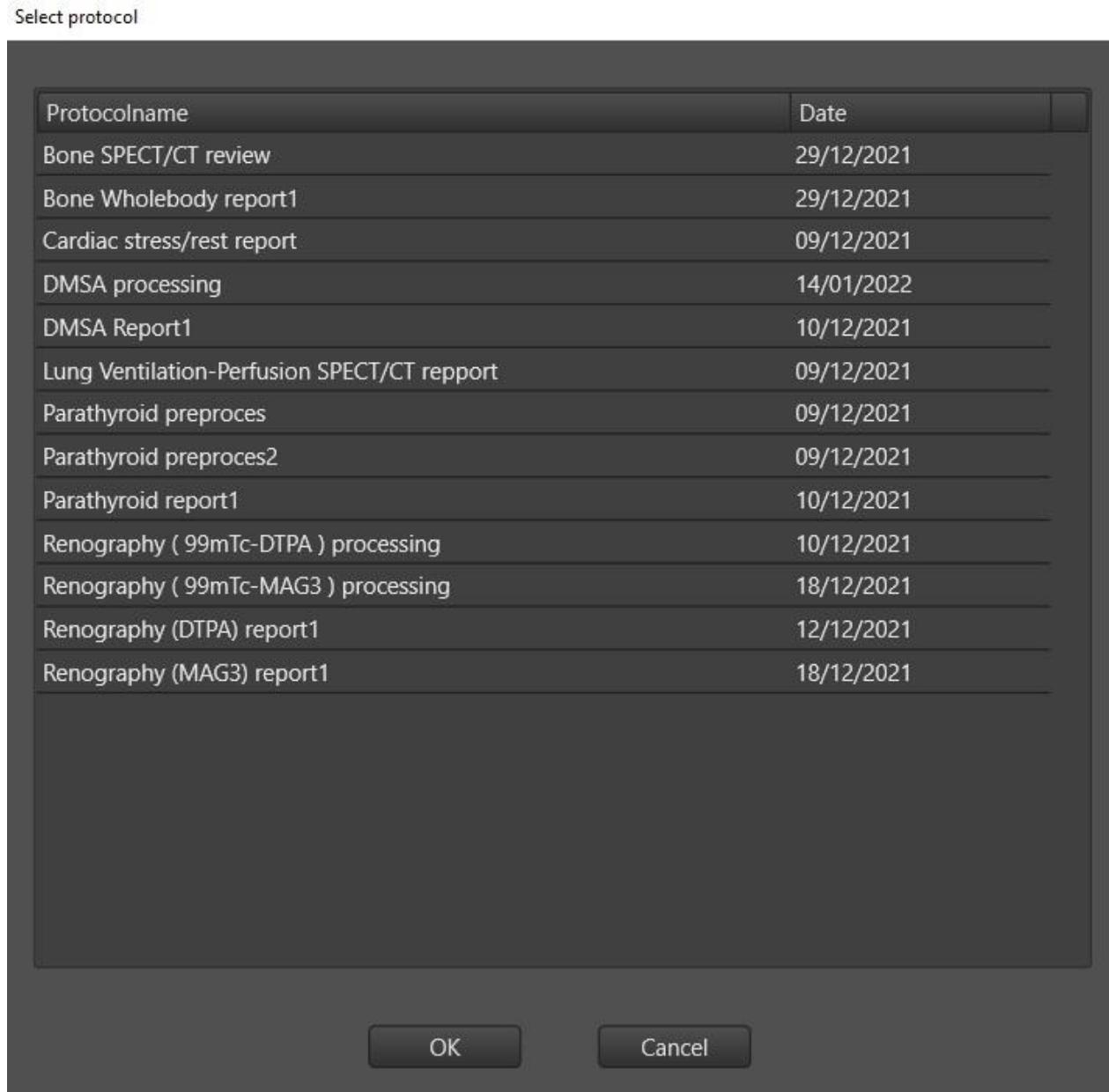


fig.3.20

Select the processing protocol either by double-clicking the protocol or selecting the protocol and pressing Ok. The processing will start immediately.

### 3.28 Run protocol

It is recommended to use the Run protocol function because in the run protocol you can only choose a protocol which is related to the current study. Select Run->Protocol->Protocol name and the protocol processing starts immediately.

### 3.29 Create Protocol

To create a processing protocol select Protocol->Create and the dialog in fig.3.21 is shown.

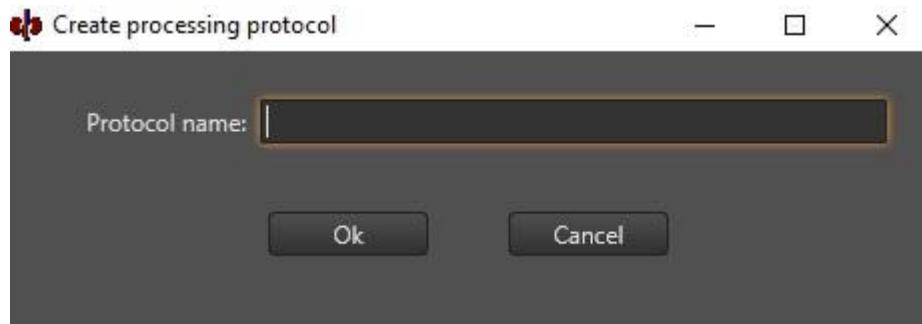


fig.3.21

Give the protocol a unique name and press “Ok”. Now the system is in recording mode so that all the selections and processing you are doing will be recorded in the processing protocol. The statusbar shows “Protocol-creation!”. It is recommended to start with selecting the report size and the colormap(s).

### 3.30 End Protocol

To terminate the protocol creation select Protocol->End and the protocol recording mode are terminated.

### 3.31 Test(singlestep) Protocol

To test a protocol where something is wrong select Protocol->Test(singlestep) and the dialog in fig.3.22 is shown.

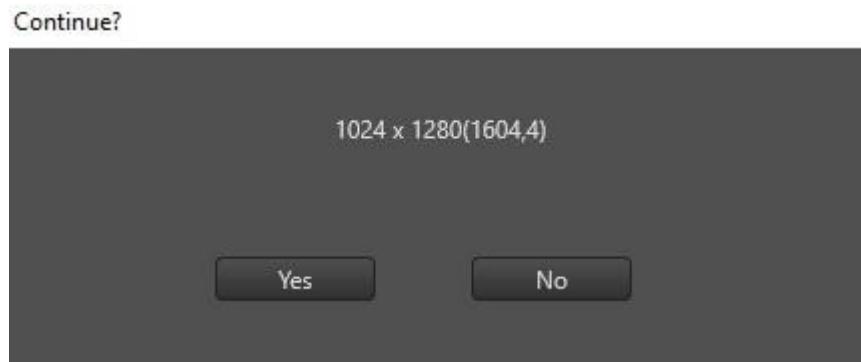


fig.3.22

The text shows the menu selection and the function number and subfunction number in the brackets. Click “Yes” to execute the function or “No” to terminate singlestep mode.

### 3.32 Clean Protocol

If something goes wrong in a protocol and protocol processing is terminated before the protocol is finished select Protocol->Clean to clean the protocol environment.

### 3.33 Show Protocol text

To show the text content of a protocol select Protocol->Show protocol text and the dialog in fig.3.23 is shown.

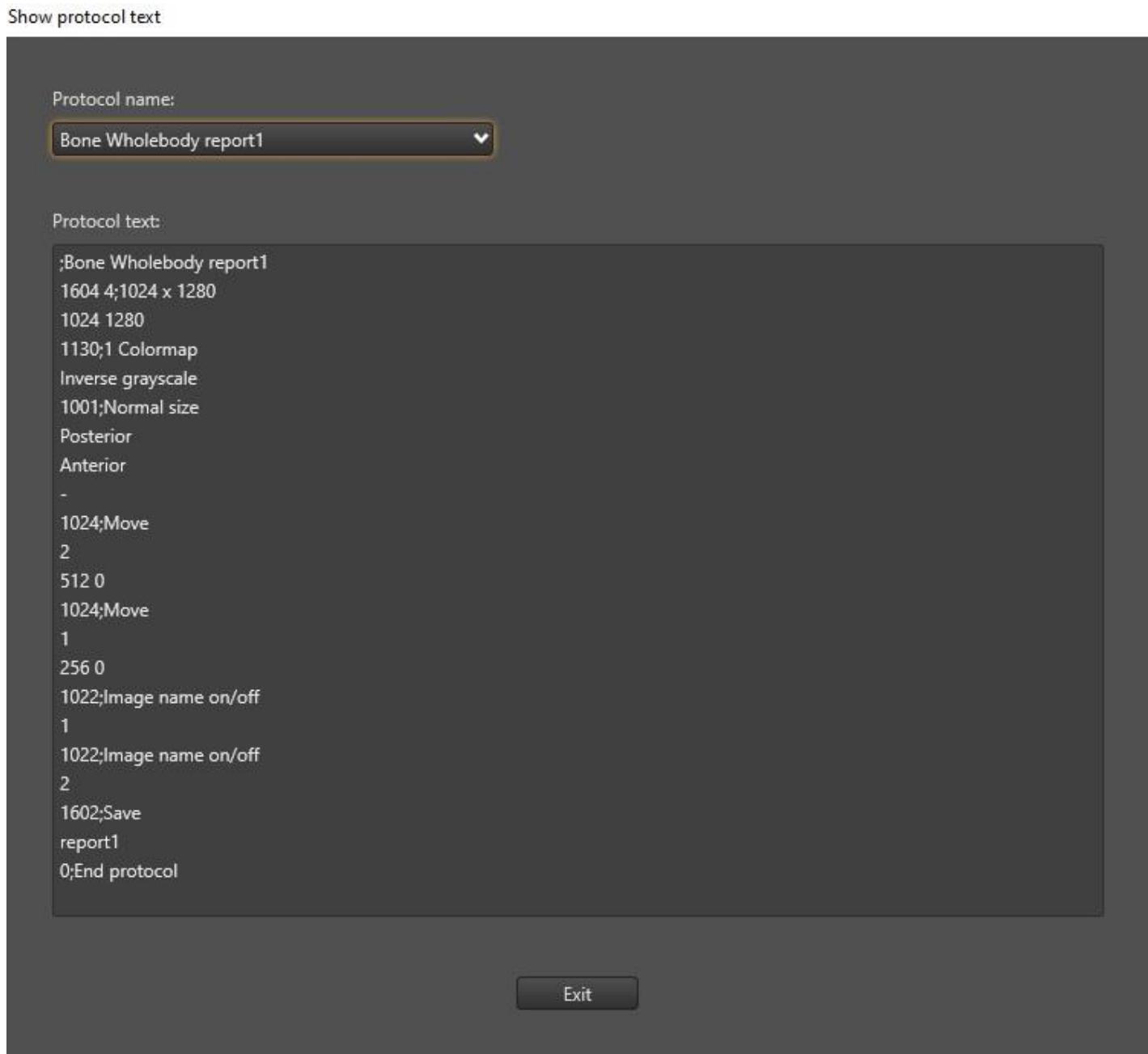


fig.3.23

Select the protocol from the “Protocol name” drop-down list and the text of that protocol are shown in the “Protocol text:” memo. The text after ; is comments. The line at the top of the protocol contains the name of the protocol after the ;

### 3.34 Create curves from ROI's

To create curves from ROI's select Curves->Create curves->Create curves from ROI's. Select the dynamic dataset from the Select dataset list and the ROI's from the Select datasets dialogs. After the curves are created give the created curve datasets unique names. Standard names are ROI name.c.

### 3.35 View Curves

To view curves select Curves->View curves and select the curves from the Select datasets list. The dialog in fig.3.24 is shown.

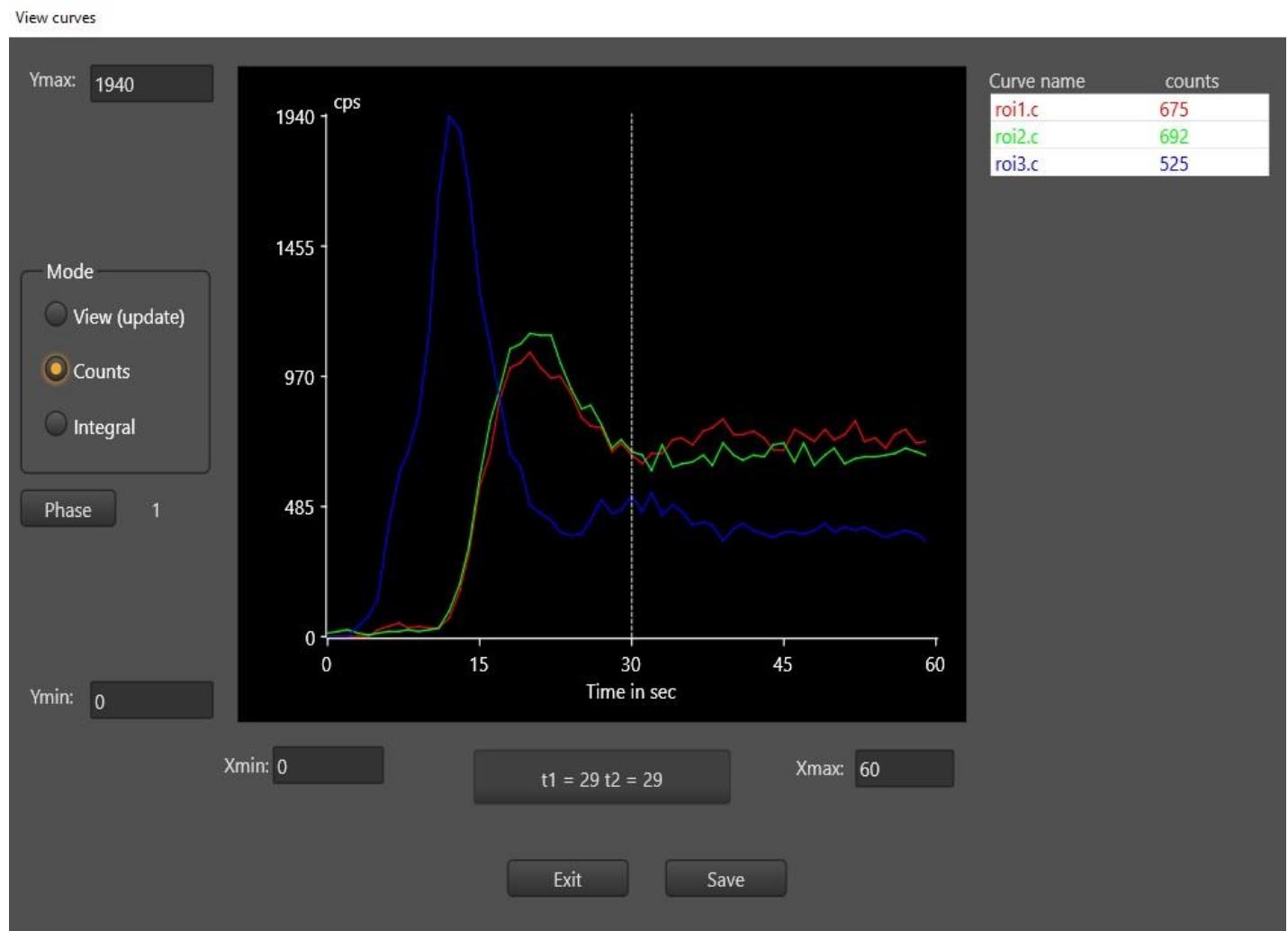


fig.3.24

In the View curves dialog you can get the counts at a given time defined by the dotted cursor or the integral counts in the selected time interval between the two dotted cursors. These informations can be saved in the registers starting with the register you select.

### 3.36 Insert curve panel

To insert a curve panel on the report select Curves->Insert curve panel and select the curve datasets to include in the curve panel. The curve panel can be resized, edited, moved or deleted.

### 3.37 Curve arithmetic

To do curve arithmetic select Curves->Curve arithmetic and choose between Add/subtract, Multiply, Divide, Log, Exp and Geometric mean and the dialog in fig.3.25 is shown.

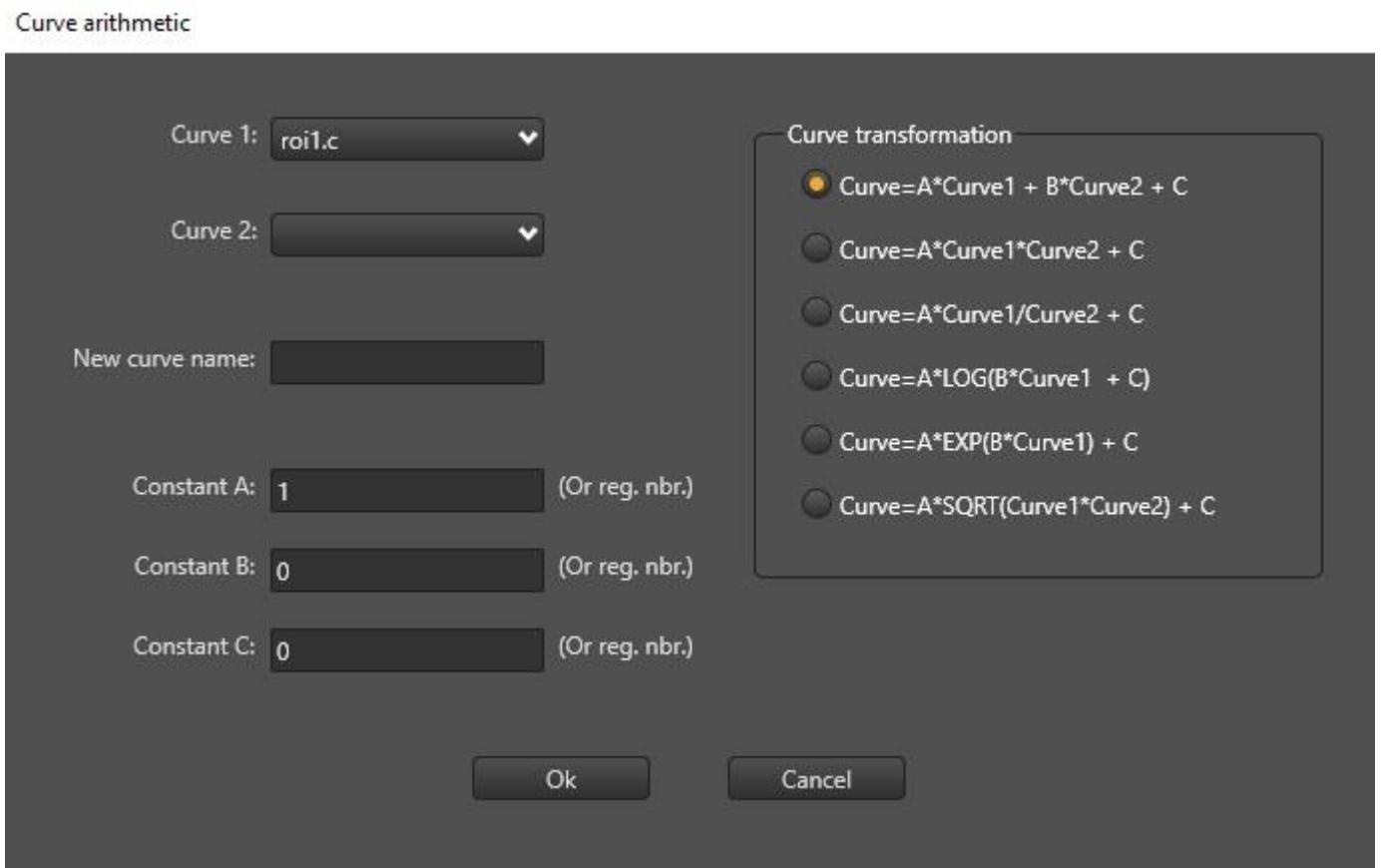


Fig.3.25

Select the curves(s) from the drop-down boxes. Give the new dataset a name. Type in the constants (or use data from registers e.g. #020) and press “Ok”.

### 3.38 Insert profile panel

To insert a profile panel on the report select Profiles->Insert profile panel and select the profile datasets to include in the profile panel. The profile panel can be resized, edited, moved or deleted.

### 3.39 View profiles

To view profiles select Profile->View profiles and select the profiles from the Select datasets list. The dialog in fig.3.26 is shown.

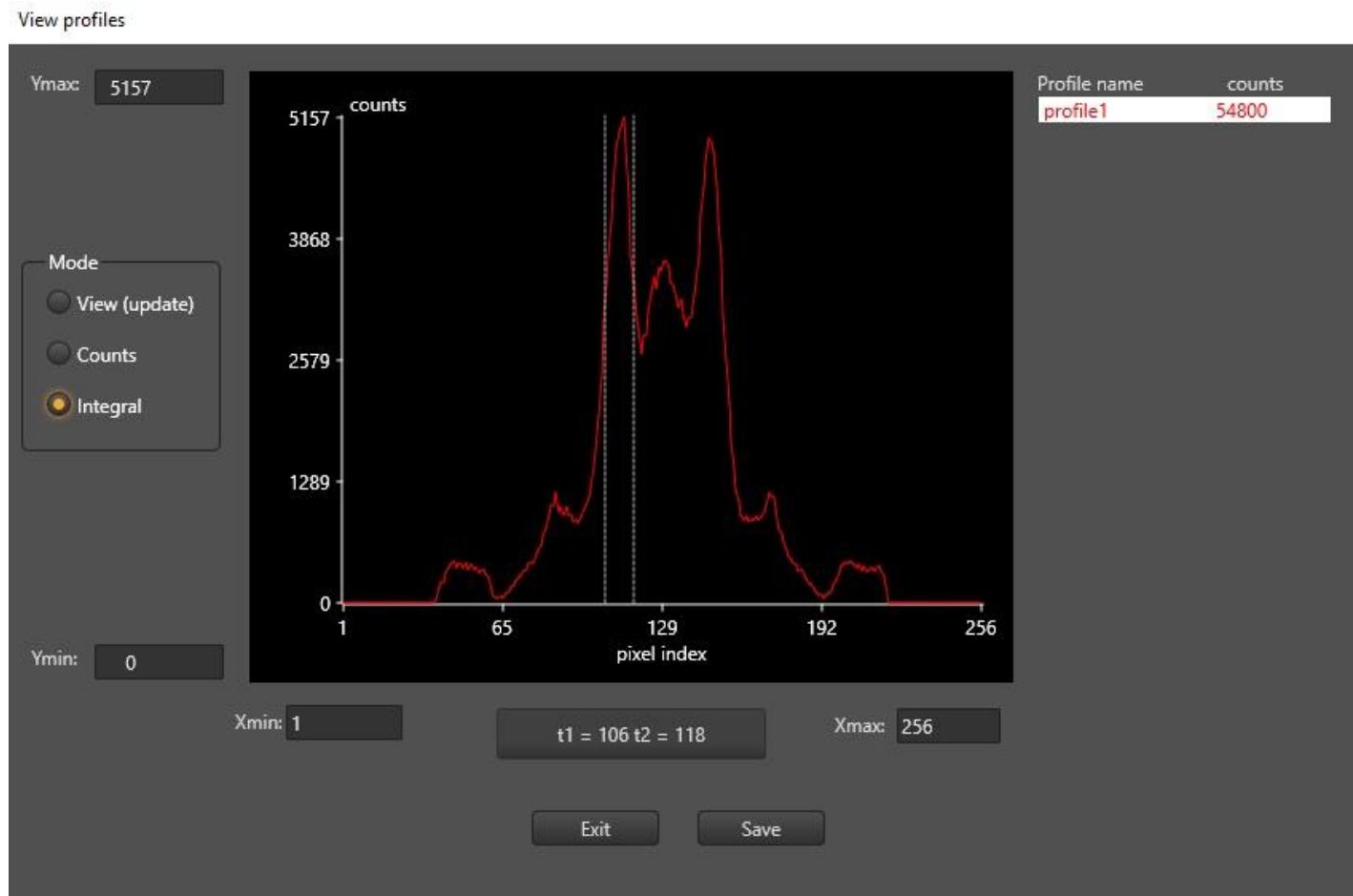


fig.3.26

In the View profiles dialog you can get the counts at a given pixel index defined by the dotted cursor or the integral counts in the selected pixels interval between the two dotted cursors. These informations can be saved in the registers starting with the register you select.

### 3.40 Renography

If the study selected is recognized as a Renography (configured in the configuration file in the [Renography] section) the “Renography” menu will be visible. Before starting the processing the renography curves must have been created. The processing expect that at least 3 curves are present (right kidney, left kidney and heart (left ventricle)). Up to 8 curves can be created (right kidney, left kidney, heart, right kidney background, right pelvis, left pelvis, lower part

of right lung and left kidney background). A special dataset is created which contains all the raw and processed curves together with all the calculated parameters. The renography reports gets their information from this dataset (DTPA reno/data or MAG3 reno/data).

### 3.4.1 First processing...

This starts a total (automatic) processing of the renography.

### 3.4.2 Review/reprocess all

This enables a total (manual) reviewing/reprocessing of the renography. The dialog in fig.3.4.1 is shown.

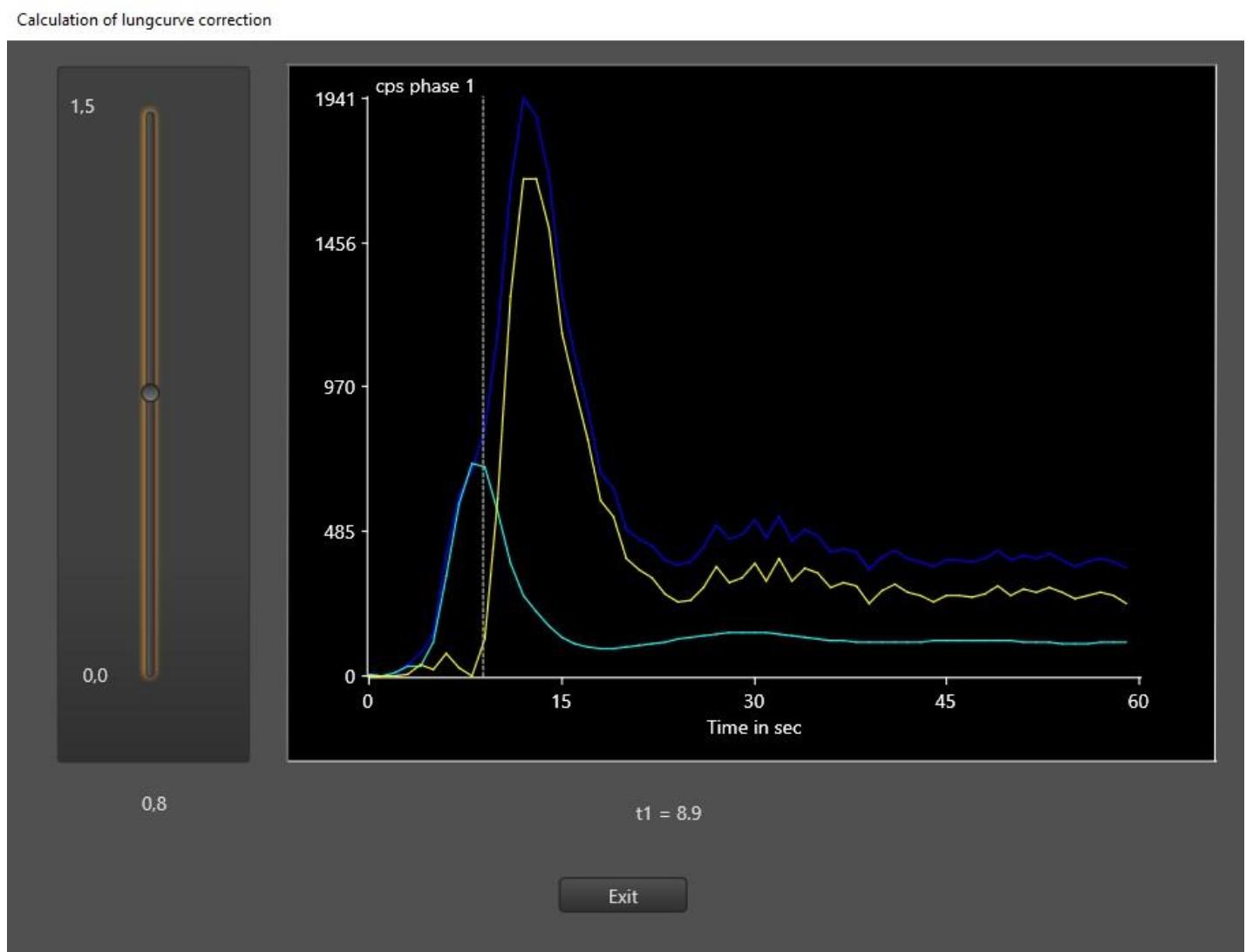


Fig.3.4.1

This dialog shows the correction of the curve measured over the left ventricle corrected for lung activity to get a more correct blood first pass curve. Use the slider to change the correction factor and the dotted cursor to change the appearance time of the lung curve.

In the following sections the rest of the processing is described.

### 3.4.3 Review/reprocess uptake function

From the dialog shown in fig.3.4.2 the function of the right and left kidney uptake function can be calculated.

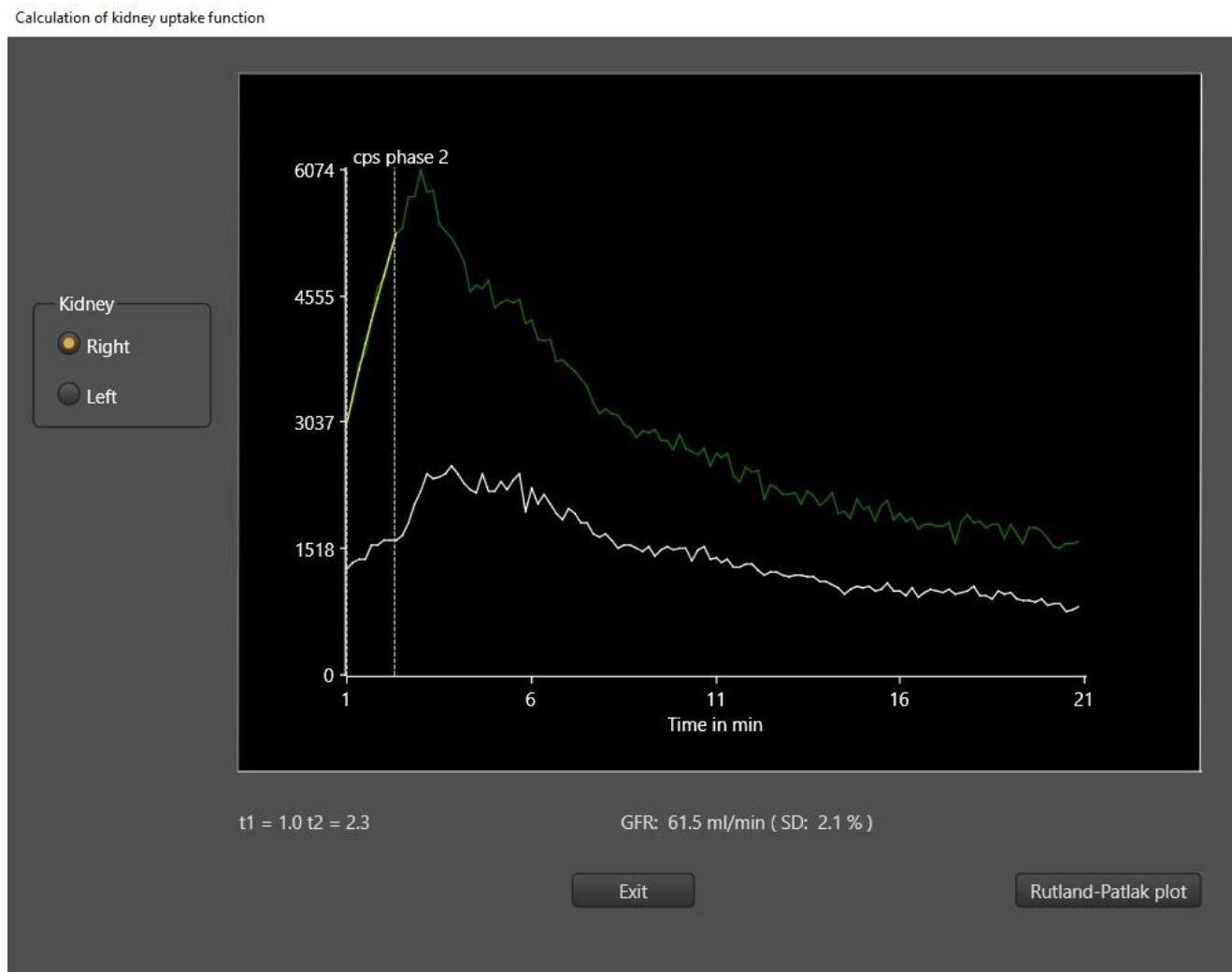


fig.3.4.2

Define the uptake phase by placing the two dotted cursors. Use the “Rutland-Patlak plot” to identify the linear part of the uptake phase.

### 3.4.4 Review/reprocess removal function

From the dialog shown in fig.3.4.3 the transit times of the parenchyma and pelvis can be determined (based upon a model for the fluid transport through the kidney).

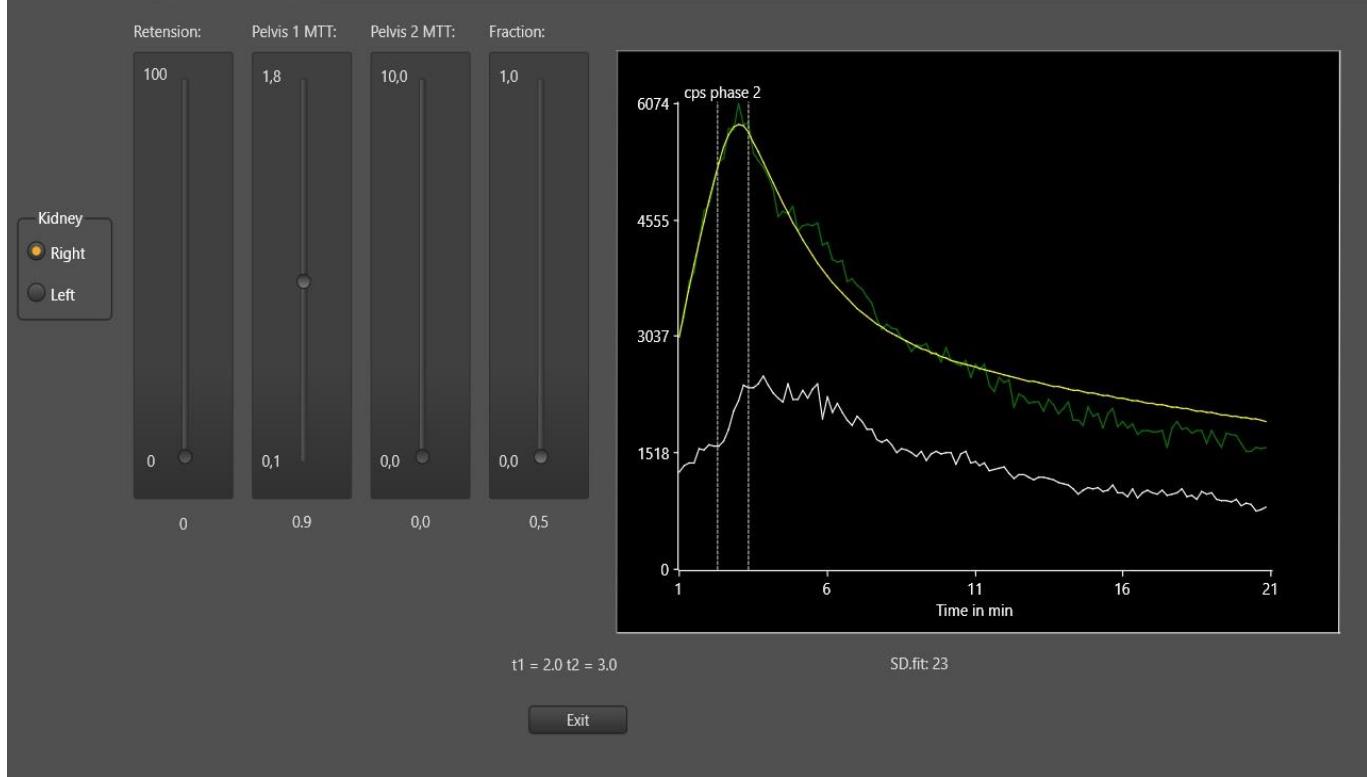


fig.3.4.3

Adjust the sliders and cursors to get an optimal fit of the recorded curves. Start with the dotted cursors which defines the minimum and maximum parenchymal transit times.

### 3.4.5 Review/reprocess vascular function

From the dialog shown in fig.3.4.4 the transit times through vascular system of the kidneys can be determined (based upon a model for the vascular system).

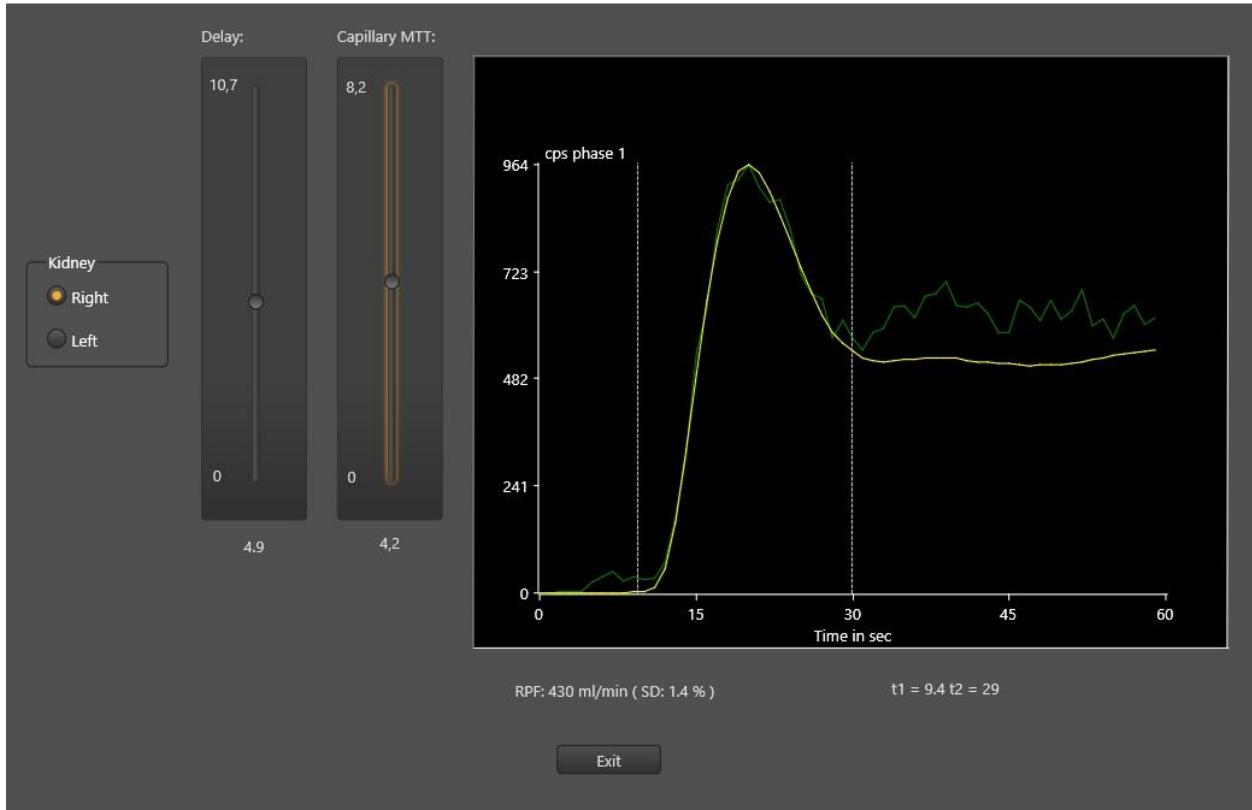


fig.3.4.4

Define the appearance time and recirculation time with the dotted cursors and adjust the sliders to get an optimal fit to the recorded curves.

### 3.4.6 Edit renography data

The renography data can be edited in the dialog shown in fig.3.4.5.

Edit renography data

This dialog box contains several sections for entering patient and study data, and selecting processing options.

- Patient data:**
  - Height: 179 cm
  - Weight: 70 kg
  - Volume voided: [redacted] ml
  - Time: [redacted] min
  - Diuresis: 5.0 ml/min
- Study data:**
  - Sign: mm | (text input field)
  - Last frame: 180
- Kidney present:**
  - Right
  - Left
- Right kidney:**
  - Relativ function
  - Absolute function
  - Parenchymal MTT
  - Pelvic MTT
- Left kidney:**
  - Relativ function
  - Absolute function
  - Parenchymal MTT
  - Pelvic MTT
- Processing:**
  - First phase background correction (right)
  - First phase background correction (left)
  - First phase lungactivity correction

At the bottom are 'Ok' and 'Cancel' buttons.

fig.3.4.5

In this dialog you can type in patient data and select processing options.

### **3.4.7 Update curves**

If new raw curves have been created use this function to update the curves in the renography dataset.

### **3.4.8 Report**

From this menu you can compose your final renography report. Choose between total report, parietal report, small curve panel, large curve panel, small result panel, large result panel, 6 images, 6 images (scaled), 8 images and 8 images (scaled).

## 4.0 Display objects inheritance tree

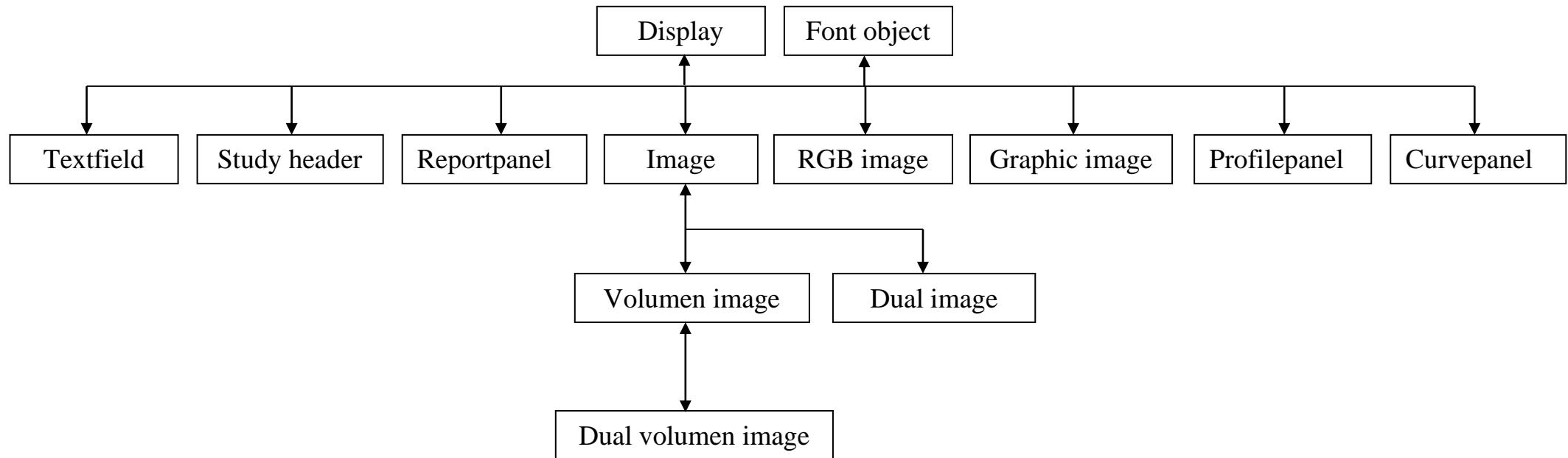


fig.4.1

Fig. 4.1 shows the display object inheritance tree. The display objects are the objects which can be placed on the report page. “Display” and “Font object” are the base classes of all display objects. Each display object has its own pop-up menu but functions as Resize, Move and Delete are common to all display objects. In section 5.0 the functions of the individual objects pop-up menu are described.

## 5.0 Object menus

### 5.1 Image

#### 5.1.1 Selected

Image selected means that the image receives commands from the controls at the toolbar. When an image is selected it is marked in the corners with small blue marks. This is a toggle function.

#### 5.1.2 Edit

If the edit function is selected the dialog in fig 5.1.1 is shown.

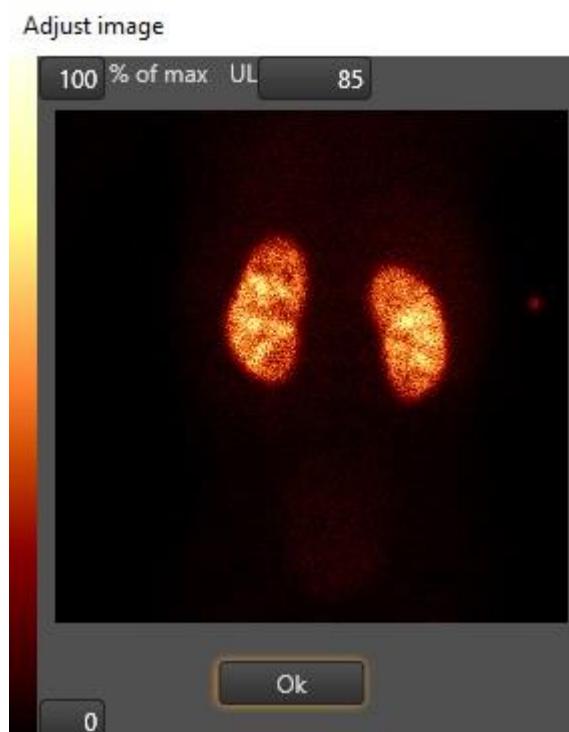


fig.5.1.1

To change the contrast in the image change the upper level and lower level numbers or draw in the colorbar with the mouse (upper half upper level lower half lower level).

#### 5.1.3 Clear overlay

This is used to clear text, ROI's or markers on the image.

#### 5.1.4 Image name on/off

Toggles the image name at the bottom of the image.

## **5.1.4 Image number on/off**

Toggles the image number text at the bottom of the image.

## **5.1.5 Add image text**

The image area turns into a semi transparent text field and you can select font type and color from the Text menu. End text editing with “End textedit”.

## **5.1.6 Frame number scrollbar on/off**

This activates/deactivates the “Framescrollbar” on this image. The image needs not to be selected. The framescrollbar function can only be active on one image at a time.

## **5.1.7 Zoom**

Sets the zoom factor for the image. Select between 100, 125, 150, 175, 200, 250 or 300 %.

## **5.1.8 Pan**

Enables the panning of a zoomed image. Use the mouse to pan the image. End this function by right-clicking the mouse.

## **5.1.9 Colormap**

If more colormaps are selected sets the colormap of the image.

## **5.1.10 Show XY cursor**

Toggles the XY cursor on this image. The cursors are only active when the image is selected.

## **5.1.11 Add ROI**

From a list of ROI's in the current study select the ROI's you want to place on this image. The colors of the ROI's are defined in the configuration file but can be changed in the Image->Set ROI overlay color order menu.

## **5.1.12 ROI statistics**

From a list of ROI's in the current study select the ROI's you want to calculate the statistics of and the dialog in fig.5.1.2 is shown.

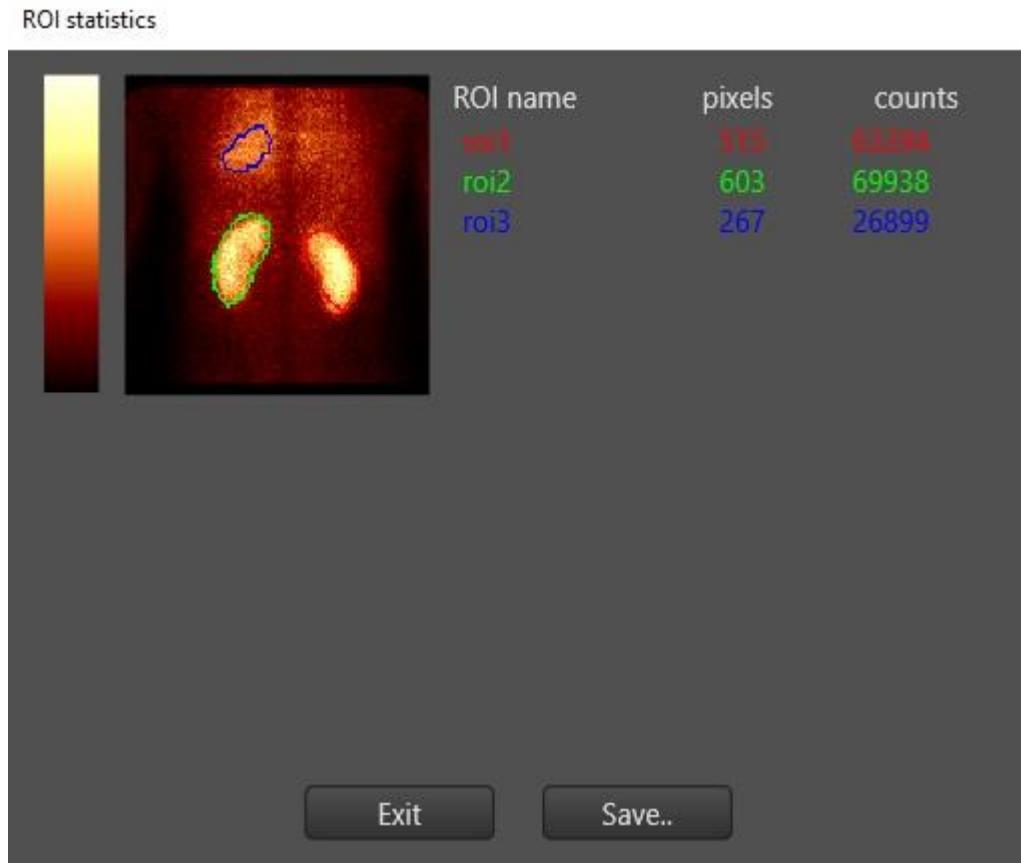


fig.5.1.2

To save the data in the registers (ROI name, number of pixels, number of counts) press “Save” and select the start register.

### 5.1.13 Create ROI

The dialog in fig.5.1.3 is shown.

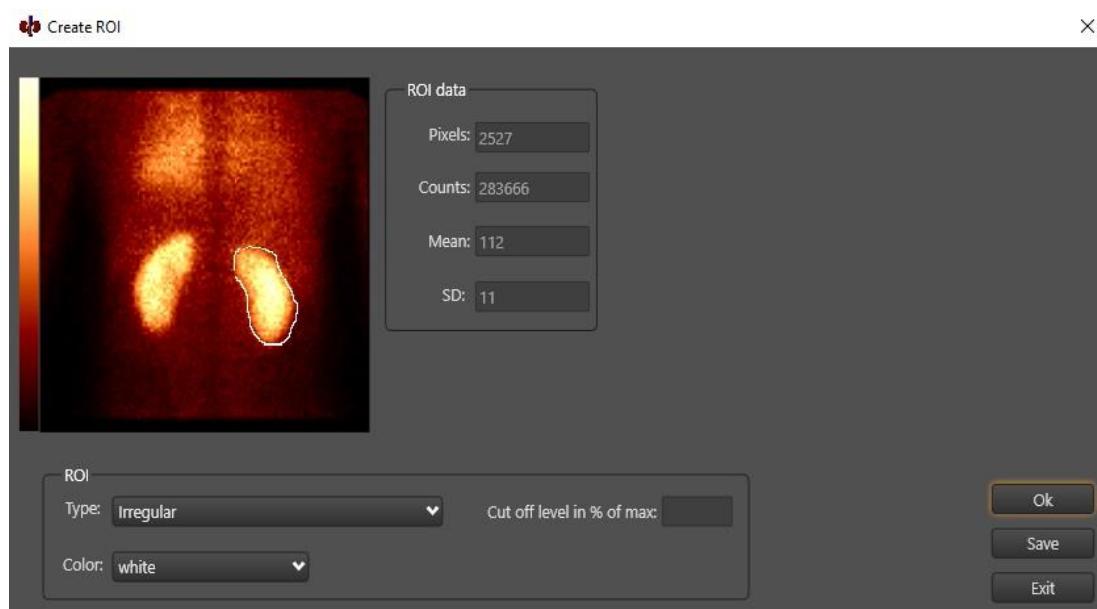


fig.5.1.3

Select the type of ROI you want to create. Use the mouse to draw or define the ROI or use the keyboard to manipulate earlier created ROI's or predefined ROI's.

### 5.1.14 Create profile

Select between horizontal or vertical profile and the dialog in fig.5.1.4 is shown.

y1 = 141 y2 = 159

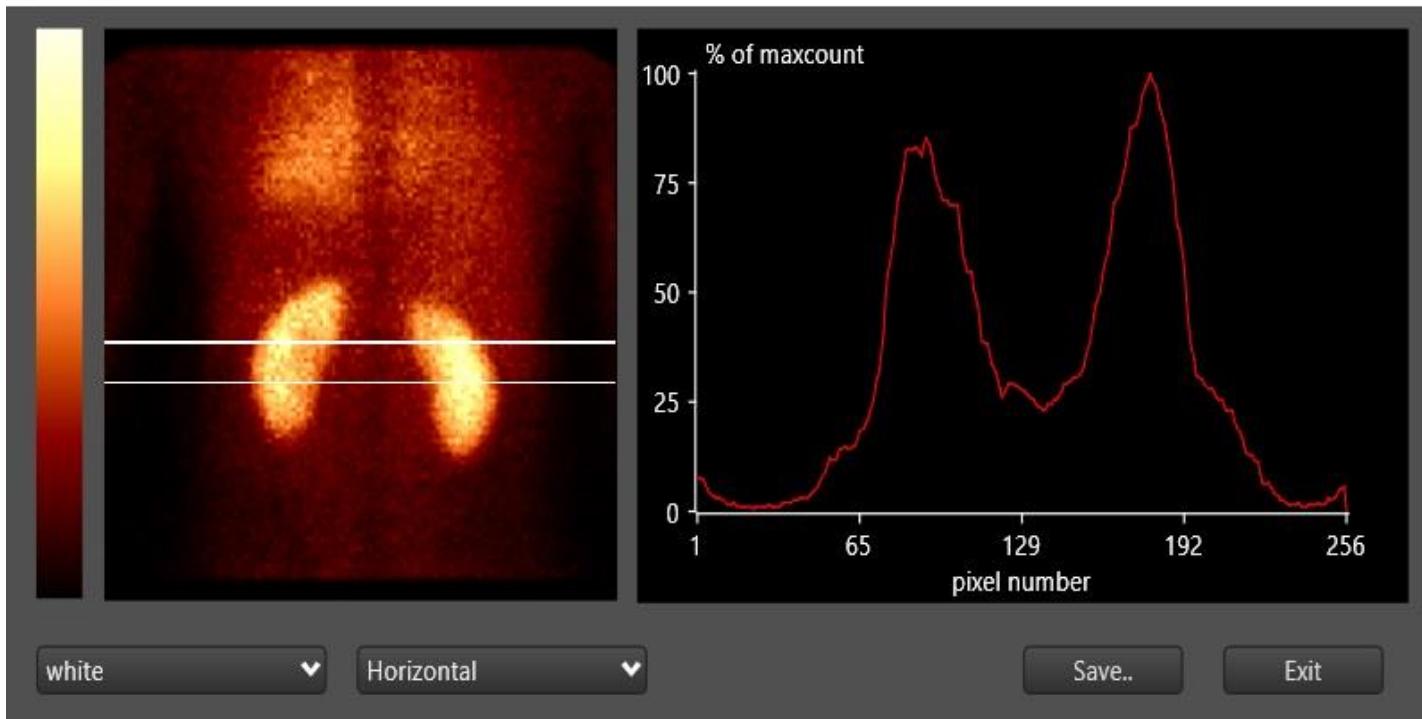


fig.5.1.4

Use the mouse to place the two cursors and press “Save” to save the profile with a unique name.

### 5.1.15 Image data

Choose between maximum, minimum, total counts, duration and acquisition time and place the result in a register.

### 5.1.16 Add markers

The dialog in fig.5.1.5 is shown.

x: 101 y: 252

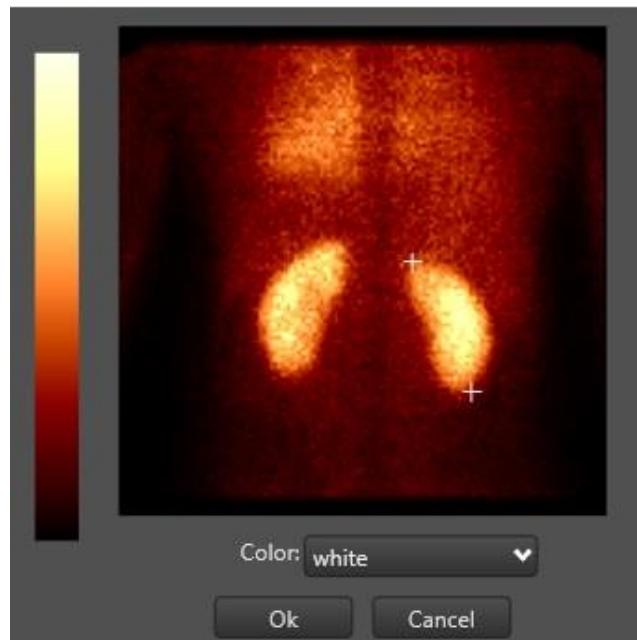


fig.5.1.5

Choose the color of the marker and use the mouse to place the markers. Press “Ok” and the markers are added to the image as overlay.

### 5.1.17 Measure distance

The dialog in fig.5.1.6 is shown.

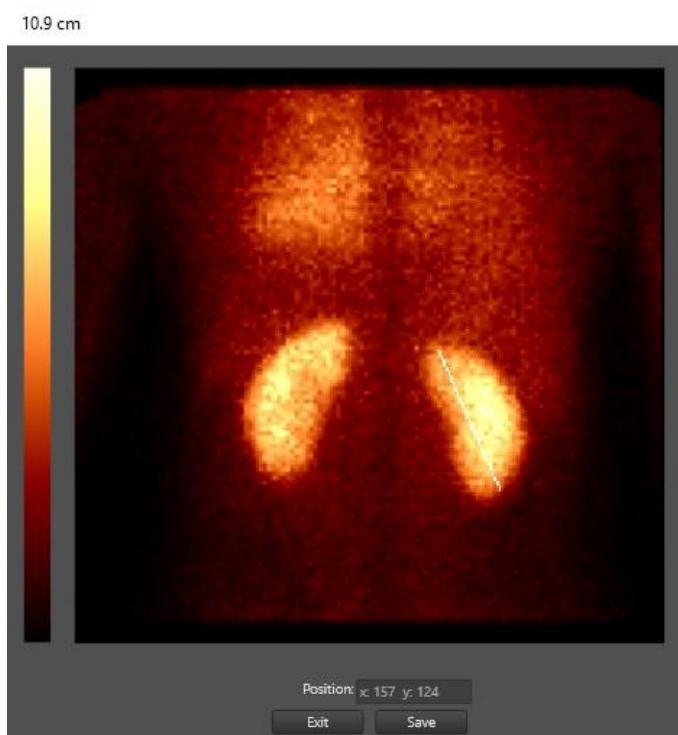


fig.5.1.6

Press the left mouse button to start the distance measurement. The distance is show on the title bar of the dialog. Fix the distance with left mouse click at the endpoint. Press “Save” to save the result in a register.

## 5.2 Volume image

The volume image object shares a lot of functions with the general image object so these functions will not be mentioned here.

### 5.2.1 Image info on/off

This function adds information of the slicewidth in mm, position in mm from the top of the dataset and C/W information if it is a CT image.

### 5.2.2 Set frame number

This enables the user to set the frame number of the dataset (in protocol create mode).

### 5.2.3 Cine on/off

This function starts a cine of the entire dataset.

### 5.2.4 Viewing mode

Select between Transversal, Sagital, Coronal or MIP.

### 5.2.5 CT windows

If the dataset is a CT image this function enables the user to select a C/W setting of HU to optimize the contrast information in the image. These settings are defined in the configuration file.

### 5.2.6 Show XY cursor

This is an enhanced version of the same function for the image object. If the volume image is selected and there are other selected volume image datasets on the report, these datasets will triangulate according to the position of the XY cursors.

### 5.2.7 Slice position on/off

This toggles the slice positions of the triangulated dataset.

## 5.3 Dual volume image

The dual volume image shares the most function with the volume image so these functions will not be mentioned here.

### 5.3.1 Colormap1

This is the colormap for the first image.

## 5.3.2 Colormap2

This is the colormap for the second image.

## 5.3.3 Alphablending value

Choose between 0, 0.25, 0.5, 0.75 or 1.0.

## 5.4 RGB image

The RGB image shares the basic functions from the image object: selected, move, delete, clear overlay, resize, image name on/off, image number on/off (multiframe RGB), add image text and frame number scrollbar on/off (multiframe RGB).

## 5.5 Graphic image

The graphic image object has only the basic functions: move, resize and delete.

## 5.6 Textfield

Besides the basic functions there are a few special functions of the textfield.

### 5.6.1 Edit

This function activates the text editing function of the textfield object.

### 5.6.2 Set textfield attributes

The dialog in fig.5.6.1 is shown.

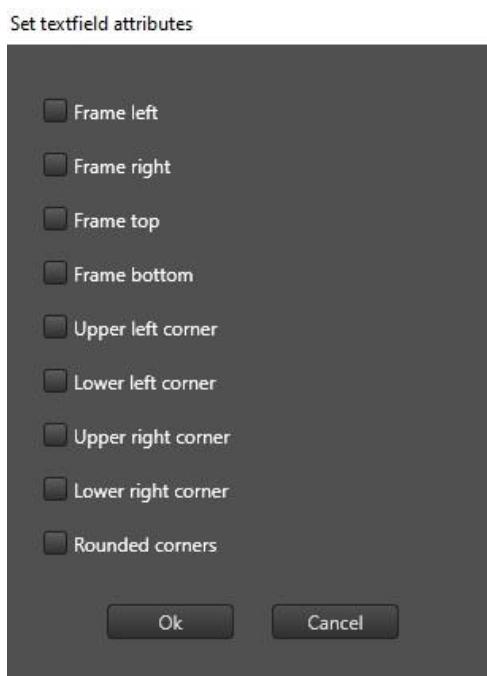


fig.5.6.1

The textfield can be framed left, right, top and bottom. In this dialog you can choose how the where the textfield are framed.

### 5.6.3 Background color

This sets the background color of the textfield.

### 5.6.4 Line color

This sets the color of the frame.

### 5.6.5 Text font

This sets the font type (family, size and stroke).

### 5.6.6 Text color

This sets the text color of the textfield.

## 5.7 Curvepanel

The curvepanel is the object that handles the display of curves generated from dynamic images. Besides the basic functions the curvepanel has only a single function.

### 5.7.1 Edit

This function activates the dialog in fig.5.7.1.

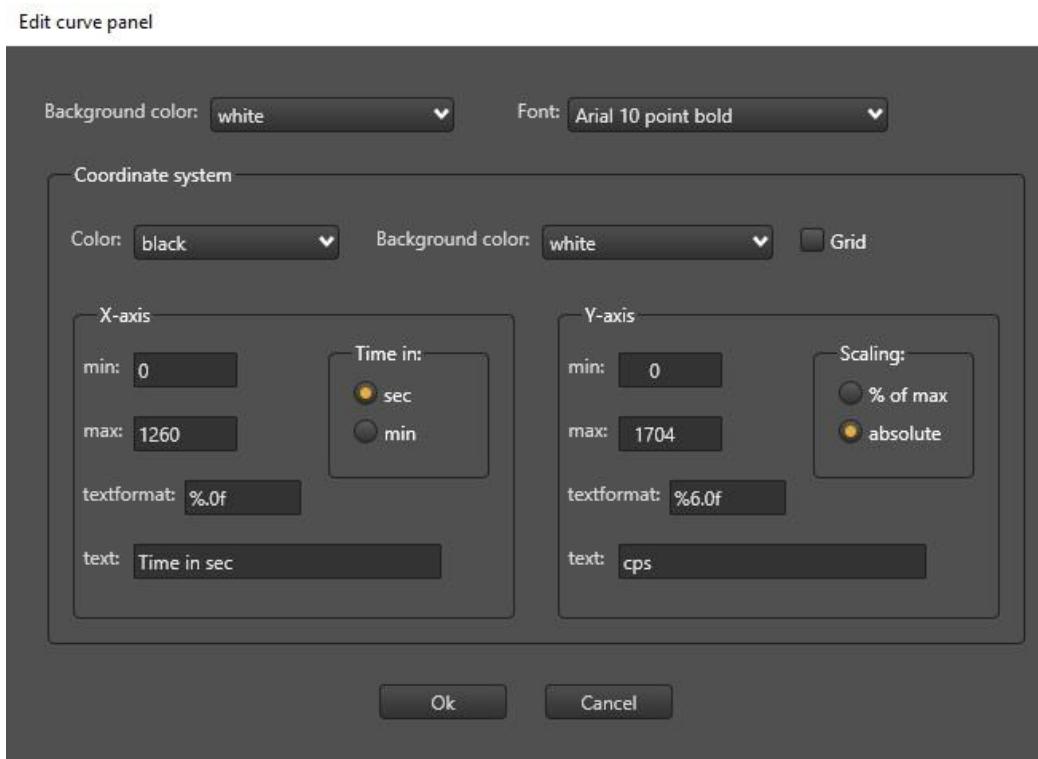


fig.5.7.1

In this dialog you can edit the different settings in the curvepanel. Like background color, font type and parameters defining the coordinate axes. (The textformat specification is standard C format specification).

## 5.8 Profilepanel

The profilepanel is the object that handles the display of profiles. Besides the basic functions the profilepanel has only a single function.

### 5.8.1 Edit

This function activates the dialog in fig.5.8.1.

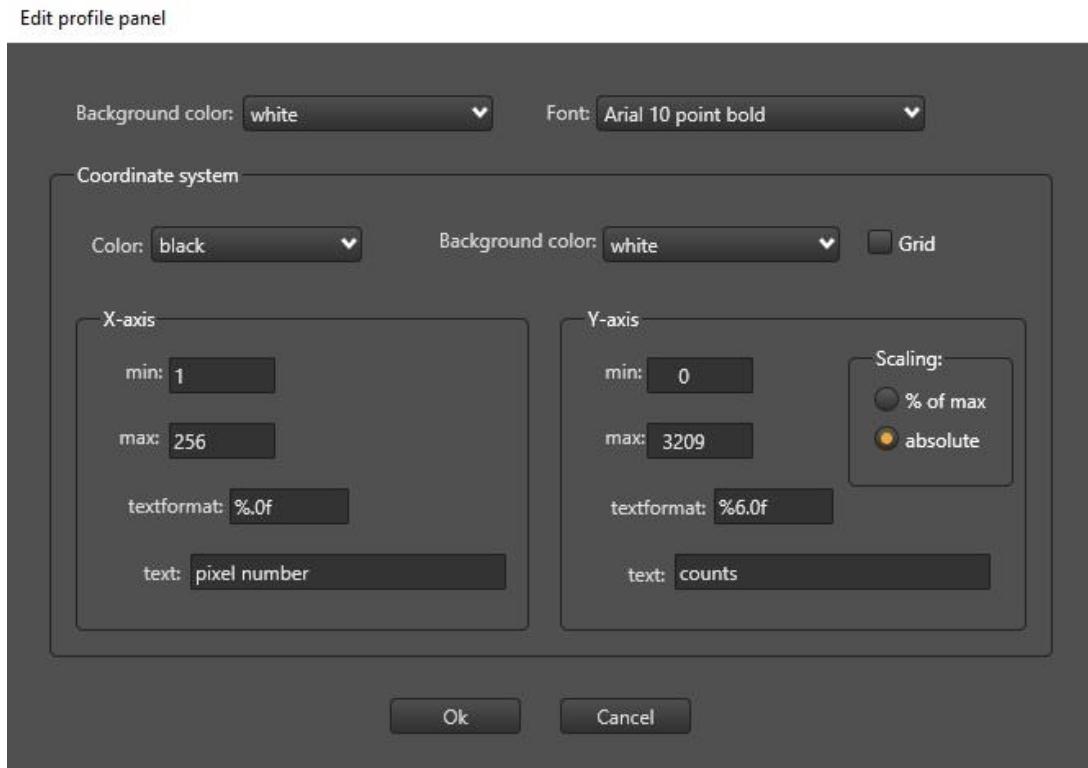


fig.5.8.1

In this dialog you can edit the different settings in the profilepanel. Like background color, font type and parameters defining the coordinate axes. (The textformat specification is standard C format specification).

# 6.0 Configuration file

As mentioned in the Introduction section the Medic system configuration is stored in a windows .ini file (default name medic.ini located in the c:\medic folder). If the Medic application is started from a short-cut the “Destination” line can be configured to contain a reference to a specific user configuration file:

(e.g. C:\medic\bin64\MedicClient64.exe /i:c:\medic\mymedic.ini )

where the information following the /i: contains the reference to the configuration file.

## 6.1 Content of the Medic configuration file

```
[medic]
textfield=c:\medic\medic.uk
;thetextfield contains name and file extension of dataset types and texts used in Renography
;processing
localdatabase=MEDICCONNECTION
;only used in Trial version
workdir=c:\medic
applicationname=Medic
backgroundcolor=240,240,240
host=localhost
;server name or IP address
port=8090
;port number of MedicServer on server
autoimport=0
keepalivetime=1
uselocaldatabase=1
;1 for Trial version, 0 for client/server full version
datasetidfile=c:\medic\medic.did
exportdir=c:\medic\export
dicomfileexportdir=c:\medic\dicomfiles
enableautologin=1
createPACSRGBdataset=1
loginname=user
medicfunctionsURL=file://c:/medic/medicfunctions.htm
[study]
dateformat=dd/mm/yyyy
startdate=01/01/1990
newstudywarning=1
[dataset]
datadir=c:\medic\data
[palette]
default=Inverse grayscale
```

```
[protocol]
protocoltimerinms=2
[predefroi]
datadir=c:\medic\prdefroi
[CTwindows]
;name and C/W of standard CT settings
Bone=500,1500
Bone2=400,1200
Abdomen=100,600
Lung=-600,1600
Lung2=-400,1200
Mediastinum=-50,400
[collimators]
;definition of collimators
;Structure
;Collimator name=FWHM at 0 cm, FWHW at 10 cm
LEHR_DDD=0.38,0.77
LEGP_GE=0.38,1.2
[mailbox]
local Medic mailbox=c:\medic\mailbox
Export to PACS=c:\medic\export
[autoimportmailboxes]
nboxes=2
box1=DICOMFILE,c:\medic\dicomin
box2=MEDIC,c:\mailbox
[mouse]
windowadjustbutton=2
[printer]
pagesize=768 1024
device=PDFCreator
[studyheader]
department=Hospital Name, Department Name
defaultfontID=12
[fonts]
;here are the definitions of fonts in the system.
;The structure are
;fontname in the system=fontID,fontsize,Font family name,stroke :0 normal 1 bold
Times New Roman 8 point=1,8,Times New Roman,0
Times New Roman 11 point=4,11,Times New Roman,0
Arial 9 point=8,9,Arial,0
Arial 11 point=12,12,Arial,0
Arial 10 point=13,13,Arial,0
Arial 10 point bold=16,12,Arial,1
Arial 11 point bold=17,14,Arial,1
```

Arial 12 point=22,20,Arial,0  
Arial 14 point=24,22,Arial,0  
Arial 16 point=26,27,Arial,0  
Times Roman 12 point=42,16,Times New Roman,0  
[fontid]  
1=Times New Roman 8 point  
4=Times New Roman 11 point  
8=Arial 9 point  
12=Arial 11 point  
13=Arial 10 point  
16=Arial 10 point bold  
17=Arial 11 point bold  
22=Arial 12 point  
24=Arial 14 point  
26=Arial 16 point  
42=Times Roman 12 point  
[textfield]  
defaultfontID=12  
[image]  
defaultfontID=8  
namefontID=13  
windowfontID=20  
defaulttextcolor=8  
[report]  
defaultfontID=17  
[curves]  
colororder=1,2,3,4,5,6,7,8,0,9,10,11,12,13,14,15  
defaultfontID=16  
[profiles]  
colororder=1,2,3,4,5,6,7,8,0,9,10,11,12,13,14,15  
defaultfontID=16  
[ROI]  
colororder=1,2,3,4,5,6,7,8,0,9,10,11,12,13,14,15  
overlaycolororder=1,2,3,4,5,6,7,8,0,9,10,11,12,13,14,15  
[colors]  
black=0  
red=1  
green=2  
blue=3  
yellow=4  
cyan=5  
magenta=6  
lightgray=7  
white=8

darkred=9  
darkgreen=10  
darkblue=11  
darkyellow=12  
darkcyan=13  
darkmagenta=14  
darkgray=15  
[Renography]  
kidneytransportcalmode=1  
studyname1=Renography (DTPA):0  
studyname2=Renography (MAG3):1  
;this defines the study names and type of Renographhy whish result in addition of the  
;“Renography” menu to the processing menu  
;0: DTPA, 1: MAG3  
[dialogsize]  
;Here are the users last used sizes of dialogboxes in the processing window which is sizeable  
CreateROI=1294,676  
CreateProfile=861,695  
ImageView=601,660  
Distance=674,686  
ROIStatistics=876,536  
SumFrames=512,536  
ViewCurves=991,692  
SelectOrderedDatasets=684,428  
SelectDataset=376,462  
CreateDataset=279,140  
ImageReconstruction=1265,868  
ViewSPECT\_CTFusion=1076,988

# 7.0 Overview of protocol processing functions in the Medic system

Funct.nbr	arg.	functionname	Description
0	-	<b>End protocol</b>	Terminates current protocol.
1000	1	<b>Edit image contrast</b> obj.nbr. 1 or 2 or 3 max min colormap nbr or Image nbr. max min colormap nbr.	Window/contrast adjustment of selected image.  manual adjustment fixed ( in counts ) fixed ( in % of max ) Static image  Dynamic image
1001	-	<b>Select static images</b> datasetname(s) -	Inserts selected static images on the display
1001	1	<b>Select static images with maximal size</b> datasetname(s) -	Inserts selected static images on the display with maximal size.
1001	5	<b>Select whole body images as 256 x 1024</b> datasetname(s) -	Inserts whole body images as 256 x 1024 on the display
1003	-	<b>Select interpolated static images</b> datasetname(s) -	Inserts selected interpolated ( 256 x 256 ) static images on the display.
1004	-	<b>ImageFusion</b> dataset name 1 dataset name 2 -	Inserts fused static images on the display.
1004	4	<b>Insert fused 3D volumen images</b> dataset name 1 dataset name 2 -	Inserts fused 3D volumen images on the display.
1004	5	<b>Insert fused 3D volumen images with MIP</b> dataset name 1 dataset name 2 -	Inserts fused 3D volumen images on the display including MIP images in memory.
1004	7	<b>Insert fused 3D volumen images in 256 x 256 format</b> dataset name 1 dataset name 2	Inserts 3 fused 3D volumen images on the display in 256 x 256 format.

		-	
1004	8	<b>Insert fused 3D volumen images in 384 x 384 format</b> dataset name 1 dataset name 2 -	Inserts 3 fused 3D volumen images on the display in 384 x 384 format.
1005	-	<b>Cine</b> datasetname(s) -	Inserts selected dynamic images on the display.
1005	1	<b>Cine 128 x 128</b> datasetname(s) -	Inserts selected dynamic images interpolated to 128 x 128 on the display.
1005	2	<b>Cine 256 x 256</b> datasetname(s) -	Inserts selected dynamic images interpolated to 256 x 256 on the display.
1006	-	<b>Insert 3D volumen image</b> datasetname(s) -	Inserts a 3D volumen image on the display.
1006	1	<b>Inserts a 3D volumen image with MIP</b> datasetname(s) -	Inserts a 3D volumen image on the display. Inkluding MIP images in memory.
1007	-	<b>Snake 24 128 x 128</b> datasetname	Shows the selected dynamic image sequence in "snake-mode" ( 24 images in 128 x 128 format ).
1007	1	<b>Snake 24 128 x 128</b> datasetname	As above but the images are interpolated to 128 x 128 ( 24 images ).
1007	2	<b>Snake 12 128 x 128</b> datasetname	As above but the images are interpolated to 128 x 128 ( 12 images ).
1007	3	<b>Snake 6 256 x 256</b> datasetname	As above but the images are interpolated to 256 x 256 ( 6 images ).
1007	4	<b>Snake 3 256 x 256</b> datasetname	As above but the images are interpolated to 256 x 256 ( 3 images ).
1007	5	<b>Snake 6 128 x 128</b> datasetname	As above but the images are interpolated to 128 x 128 ( 6 images ).
1007	6	<b>Snake 8 128 x 128</b> datasetname	As above but the images are interpolated to 128 x 128 ( 8 images ).
1007	7	<b>Snake 16 128 x 128</b> datasetname	As above but the images are interpolated to 128 x 128 ( 16 images ).
1007	8	<b>Snake 18 128 x 128</b> datasetname	As above but the images are interpolated to 128 x 128 ( 18 images ).
1007	9	<b>Snake 32 128 x 128</b> datasetname	As above but the images are interpolated to 128 x 128 ( 32 images ).
1007	10	<b>Snake 4 256 x 256</b> datasetname	As above but the images are interpolated to 256 x 256 ( 4 images ).
1007	11	<b>Snake 8 256 x 256</b> datasetname	As above but the images are interpolated to 256 x 256 ( 8 images ).
1007	12	<b>Snake 9 256 x 256</b> datasetname	As above but the images are interpolated to 256 x 256 ( 9 images ).
1007	13	<b>Snake 12 256 x 256</b>	As above but the images are interpolated to 256 x 256

		datasetname	256 ( 12 images ).
1007	14	<b>Snake 16 256 x 256</b> datasetname	As above but the images are interpolated to 256 x 256 ( 16 images ).
1009	-	<b>Manual image summation.</b> dataset name message new dataset name	Manual summation of images (in a dynamic image sequence).
1010	-	<b>Automatic image summation</b> dataset name start image nbr. end image nbr. new dataset name	Automatic summation of images.
1011	-	<b>Butterworth filtering of image(s)</b> dataset name new dataset name	Fast Fourier Transformation ( FFT ) filtering of image(s).  (old function with fixed cut.off and filter order ).
1011	1	<b>Butterworth filtering af billede(r)</b> dataset name new dataset name filtertype cutoff filterorder	Fast Fourier Transformation ( FFT ) filtering of image(s).  1: Butterworth cutoff ( 0-1.0 ) filterorder ( 1-20 )
1011	2	<b>Edgefiltrering of image(s)</b> dataset name new dataset name filtertype cutoff filterorder	Fast Fourier Transformation ( FFT ) filtering of image(s).  2: Edgefiltrering cutoff ( 0-1.0 ) filterorder ( 1-20 )
1011	10	<b>Smoothing of image(s)</b> dataset name new dataset name filtertype filtercoefficients	Smoothing of image(s).  filterkernel type 0: 3 x 3 , 1: 5x 5 filtercoefficients rowwise e.g.: 1,2,1,2,3,2,1,2,1
1012	-	<b>Add/subtract images</b> image nbr.1 name image nbr.2 name image nbr.3 name A ( const. or reg.nbr. ) B ( - do - ) C ( - do - )	Image arithmetic after equation: Image nbr.3 = A*image nbr.1 + B*image nbr.2 + C where A,B and C are constants ( fixed or from data-register ( # before the register number ) ).
1012	1	<b>Multiply images</b> image nbr.1 name image nbr.2 name image nbr.3 name A ( const. or reg.nbr. )	Image arithmetic after equation: Image nbr.3 = A*image nbr.1*image nbr.2 + C where A,B and C are constants ( fixed or from data-register ).

		B ( - do - ) C ( - do - )	
1012	2	<b>Divide images</b> image nbr.1 name image nbr.2 name image nbr.3 name A ( const. or reg.nbr. ) B ( - do - ) C ( - do - )	Image arithmetic after equation: Image nbr.3 = A * image nbr.1 / image nbr.2 + C where A,B and C are constants ( fixed or from data-register ).
1012	3	<b>Log(nat) image</b> image nbr.1 name image nbr.2 name image nbr.3 name A ( const. or reg.nbr. ) B ( - do - ) C ( - do - )	Image arithmetic after equation: Image nbr.3 = A * log <sub>nat</sub> (B * image nbr.1 + C) where A,B and C are constants ( fixed or from data-register ).
1012	4	<b>Exp image</b> image nbr.1 name image nbr.2 name image nbr.3 name A ( const. or reg.nbr. ) B ( - do - ) C ( - do - )	Image arithmetic after equation: Image nbr.3 = A * exp(B * image nbr.1) + C where A,B and C are constants ( fixed or from data-register ).
1012	5	<b>Minify image</b> image nbr.1 name image nbr.2 name image nbr.3 name A ( const. or reg.nbr. ) B ( - do - ) C ( - do - )	Minify image to half size. Image nbr.2. name are not used. The constants A,B and C are not used.
1012	6	<b>Reset image outside ROI</b> image nbr.1 name roi name image nbr.3 name A ( const. or reg.nbr. ) B ( - do - ) C ( - do - )	The image are reset (zeroed) outside the selected ROI: The constants A,B and C are not used.
1012	7	<b>Reset image inside ROI</b> image nbr.1 name roi name image nbr.3 me A ( const. or reg.nbr. ) B ( - do - ) C ( - do - )	The image are reset (zeroed) inside the selected ROI: The constants A,B and C are not used.
1012	8	<b>Rotate image</b> image nbr.1 name image nbr.2 name image nbr.3 name A ( const. or reg.nbr. )	The image are rotated A degrees (CCW).  B and C are not used.

		B ( - do - ) C ( - do - )	
1012	9	<b>Mirroring of image around the Y-axis</b> image nbr.1 name image nbr.2 name image nbr.3 name A ( const. or reg.nbr. ) B ( - do - ) C ( - do - )	Mirroring of image around the Y-axis  Dataset name  New dataset name A, B and C are not used.
1012	10	<b>Split dual isotope image</b> dataset name new dataset name 1 new dataset name 2	Splitting of dual isotope image in to separate datasets.  Isotop 1 dataset name Isotop 2 dataset name
1012	15	<b>Geometric mean of 2 images</b> image nbr.1 name image nbr.2 name image nbr.3 name A ( const. or reg.nbr. ) B ( - do - ) C ( - do - )	Dataset 1 Dataset 2 New dataset name A, B and C are not used.
1012	25	<b>Resample images</b> Dataset name New dataset name X Y Matrix size Slice direction Slice orientation	Resample tomographic image transversal, sagital or coronal in a given matrix size og given pixel size.  pixel size in 1/100 mm 0: 128 x 128, 1: 256 x 256, 2: 384 x 384, 3: 512 x 512 0: Top to bottom, 1: Bottom to top 0: Transversal, 1: Sagital, 2: Coronal
1012	50	<b>Manual image subtraction</b> datasetname1 datasetname2 new datasetname	Manual image subtraction of static, dynamic or 3D volume images.
1014	-	<b>Get max of selected image on display</b> obj. nbr. reg. nbr.	The selected image maximum counts are stored in the selected register.
1014	1	<b>Get total counts of selected image</b> obj. nbr. reg. nbr.	The selected image total counts are stored in the selected register.
1014	2	<b>Get image duration of selected image</b> obj. nbr. reg. nbr.	The selected image duration are stored in the selected register.
1014	3	<b>Get minimum counts of selected image</b> obj. nbr.	The selected image minimum counts are stored in the selected register.

		reg. nbr.	
1014	4	<b>Get acquisition time of selected image</b> obj. nbr. reg. nbr.	The selected image acquisition time are stored in the selected register.
1015	0	<b>Clip out image in 512 x 768 format</b> dataset name mode x y w h new dataset name	Clip part of image in (format 512 x 768)  1: automatic, 0: manual x-pos, y-pos, width, height of the clipped area
1015	1	<b>Clip out image in 256 x 768 format</b> dataset name mode x y w h new dataset name	Clip part of image (format 256 x 768)  1: automatic, 0: manual x-pos, y-pos, width, height of the clipped area.
1015	2	<b>Clip out image in 256 x 512 format</b> dataset navn mode x y w h new dataset name	Clip part of image (format 256 x 512)  1: automatic, 0: manual x-pos, y-pos, width, height of the clipped area.
1015	3	<b>Clip out image in 256 x 256 format</b> dataset name mode x y w h new dataset name	Clip part of image (format 256 x 256)  1: automatic, 0: manual x-pos, y-pos, width, height of the clipped area.
1015	4	<b>Clip out image in 128 x 128 format</b> dataset name mode x y w h new dataset name	Clip part of image (format 128 x 128)  1: automatic, 0: manual x-pos, y-pos, width, height of the clipped area.
1015	5	<b>Clip out image in 64 x 64 format</b> dataset name mode x y w h new dataset name	Clip part of image (format 64 x 64)  1: automatic, 0: manual x-pos, y-pos, width, height of the clipped area.
1015	6	<b>Clip out image in 512 x 512 format</b> dataset name mode x y w h new dataset name	Clip part of image (format 512 x 512)  1: automatic, 0: manual x-pos, y-pos, width, height of the clipped area.
1015	7	<b>Clip out image in 512 x 1024 format</b> dataset name mode	Clip part of image (format 512 x 1024)  1: automatic, 0: manual

		x y w h new dataset name	x-pos, y-pos, width, height of the clipped area.
1015	8	<b>Clip out image in 256 x 1024 format</b> dataset name mode x y w h new dataset name	Clip part of image (format 256 x 1024)  1: automatic, 0: manual x-pos, y-pos, width, height of the clipped area.
1015	10	<b>Manually clip out image</b> dataset name mode x y w h new dataset name	Clip part of image manually.  1: automatic, 0: manual x-pos, y-pos, width, height of the clipped area.
1015	30	<b>Clip out RGB image in 512 x 768 format</b> dataset name mode x y w h new dataset name	Clip part of RGB image (format 512 x 768)  1: automatic, 0: manual x-pos, y-pos, width, height of the clipped area
1015	31	<b>Clip out RGB image in 256 x 768 format</b> dataset name mode x y w h new dataset name	Clip part of RGB image (format 256 x 768)  1: automatic, 0: manual x-pos, y-pos, width, height of the clipped area
1015	32	<b>Clip out RGB image in 256 x 512 format</b> dataset name mode x y w h new dataset name	Clip part of RGB image (format 256 x 512)  1: automatic, 0: manual x-pos, y-pos, width, height of the clipped area
1015	33	<b>Clip out RGB image in 256 x 256 format</b> dataset name mode x y w h new dataset name	Clip part of RGB image (format 256 x 256)  1: automatic, 0: manual x-pos, y-pos, width, height of the clipped area
1015	34	<b>Clip out RGB image in 128 x 128 format</b> dataset name mode x y w h new dataset name	Clip part of RGB image (format 128 x 128)  1: automatic, 0: manual x-pos, y-pos, width, height of the clipped area
1015	35	<b>Clip out RGB image in 512 x 512 format</b> dataset name mode x y w h new dataset name	Clip part of RGB image (format 512 x 512)  1: automatic, 0: manual x-pos, y-pos, width, height of the clipped area
1015	36	<b>Clip out RGB image in</b>	Clip part of RGB image (format 256 x 1024)

		<b>256 x 1024 format</b> dataset name mode x y w h new dataset name	1: automatic, 0: manual x-pos, y-pos, width, height of the clipped area
1015	37	<b>Clip out RGB image in 512 x 1024 format</b> dataset name mode x y w h new dataset name	Clip part of RGB image (format 512 x 1024)  1: automatic, 0: manual x-pos, y-pos, width, height of the clipped area
1015	50	<b>Manually clips out RGB image</b> datasætnavn mode x y w h new dataset name	Clip part of RGB image manually.  1: automatic, 0: manual x-pos, y-pos, width, height of the clipped area
1017	-	<b>Motion correction</b> dataset name	Motion correction
1018	1	<b>Image zoom 100%</b> obj.nbr.	Image zoom 100%
1018	2	<b>Image zoom 125%</b> obj.nbr.	Image zoom 125%
1018	3	<b>Image zoom 150%</b> obj.nbr.	Image zoom 150%
1018	4	<b>Image zoom 175%</b> obj.nbr.	Image zoom 174%
1018	5	<b>Image zoom 200%</b> obj.nr.	Image zoom 200%
1018	6	<b>Image zoom 250%</b> obj.nbr.	Image zoom 250%
1018	7	<b>Image zoom 300%</b> obj.nbr.	Image zoom 300%
1018	10	<b>3D volumeimage zoom 100%</b> obj.nbr.	3D volumeimage zoom 100%
1018	11	<b>3D volumeimage zoom 150%</b> obj.nbr.	3D volumeimage zoom 150%
1018	12	<b>3D volumeimage zoom 200%</b> obj.nbr.	3D volumeimage zoom 200%
1018	13	<b>3D volumeimage zoom 250%</b> obj.nbr.	3D volumeimage zoom 250%
1018	14	<b>3D volumeimage zoom 300%</b> obj.nbr.	3D volumeimage zoom 300%
1018	20	<b>3D Fused volumeimage zoom 100%</b>	3D fused volumeimage zoom 100%

		obj.nbr.	
1018	21	<b>3D Fused volumeimage zoom 150%</b> obj.nbr.	3D fused volumeimage zoom 150%
1018	22	<b>3D Fused volumeimage zoom 200%</b> obj.nbr.	3D fused volumeimage zoom 200%
1018	23	<b>3D Fused volumeimage zoom 250%</b> obj.nbr.	3D fused volumeimage zoom 250%
1018	24	<b>3D Fused volumeimage zoom 300%</b> obj.nbr.	3D fused volumeimage zoom 300%
1019	-	<b>Image pan</b> obj.nbr. xpos ypos	Image pan
1019	1	<b>3D volumeimage pan</b> obj.nbr. xpos ypos	3D volumeimage pan
1019	2	<b>3Dfused volumelimage pan</b> obj.nbr. xpos ypos	3D fused volumeimage pan
1020	-	<b>Remove objekt</b> obj. nbr.	Remove object from the display.
1021	-	<b>Remove overlay on image</b> obj. nbr	Remove image overlay (ROI's, text and markers).
1021	2	<b>Remove overlay on RGB image</b> obj. nbr	Remove RGB image overlay (text).
1022	-	<b>Image name on/off</b> obj. nbr.	Image name on/off.
1022	1	<b>Image number on/off</b> obj. nbr.	Image number on/off.
1022	10	<b>RGB image name on/off</b> obj. nbr.	RGB image name on/off.
1022	11	<b>RGB image number on/off</b> obj. nbr.	RGB image number on/off.
1022	13	<b>3D volumen image number on/off</b> obj. nbr.	3D volumen image number (slice) on/off.
1022	14	<b>3D fused volumen image number (slice) on/off</b>	3D fused volumen image number (slice) on/off.

		obj. nbr.	
1024	-	<b>Move object</b> obj. nbr. xpos ypos	Move object.  New position (NB! multiple of 4 pixels).
1024	1	<b>Resize object</b> obj. nbr width height	Resize object  New size in screen pixels (multiple of 4)
1025	-	<b>Add marker on selected image</b> obj. nbr.	Add marker.
1027	-	<b>Add text on selected image</b> obj. nbr. 3 textcolor textfontID Nbr.of lines pos,linie,text .....	Add text (from protocol) on image.
1027	1	<b>Add text on fused image</b> obj. nbr. 3 textcolor textfontID Nbr.of lines pos,linie,text .....	Add text (from protocol) on fused image.
1027	2	<b>Add text on RGB image</b> obj. nbr. 3 textcolor textfontID Nbr.of lines pos,linie,text .....	Add text (from protocol) on RGB image.
1027	4	<b>Add text on 3D volumen image</b> obj. nbr. 3 textcolor textfontID Nbr.of lines pos,linie,text .....	Add text (from protocol) on 3D volumen image.
1027	5	<b>Add text on 3D fused volumen image</b> obj. nbr. 3 textcolor textfontID Nbr.of lines pos,linie,text .....	Add text (from protocol) on 3D fused volumen image.
1028	-	<b>Measure distance on</b>	Measure distance on image.

		<b>image</b> obj. nbr. pixelwidth pixelheight message reg. nbr.	( i 1/100 mm )
1029	1	<b>Resize image to 50%</b> Obj. nbr	Resize image to 50%
1029	2	<b>Resize image to 100%</b> Obj. nbr	Resize image to 100%
1029	3	<b>Resize image to 150%</b> Obj. nbr	Resize image to 150%
1029	4	<b>Resize image to 200%</b> Obj. nbr	Resize image to 200%
1029	5	<b>Resize image to 300%</b> Obj. nbr	Resize image to 300%
1029	6	<b>Resize image to 400%</b> Obj. nbr	Resize image to 400%
1029	7	<b>Resize image to 75%</b> Obj. nbr	Resize image to 75%
1029	10	<b>Resize fused image to 50%</b> Obj. nbr	Resize fused image to 50%
1029	11	<b>Resize fused image to 100%</b> Obj. nbr	Resize fused image to 100%
1029	12	<b>Resize fused image to 150%</b> Obj. nbr	Resize fused image to 150%
1029	13	<b>Resize fused image to 200%</b> Obj. nbr	Resize fused image to 200%
1029	14	<b>Resize fused image to 300%</b> Obj. nbr	Resize fused image to 300%
1029	15	<b>Resize fused image to 400%</b> Obj. nbr	Resize fused image to 400%
1029	20	<b>Resize RGB image to 50%</b> Obj. nbr	Resize RGB image to 50%
1029	21	<b>Resize RGB image to 100%</b> Obj. nbr	Resize RGB image to 100%
1029	22	<b>Resize RGB image to 150%</b> Obj. nbr	Resize RGB image to 150%
1029	23	<b>Resize RGB image to 200%</b> Obj. nbr	Resize RGB image to 200%
1029	31	<b>Resize volumen image to 50%</b>	Resize volumen image to 50%

		Obj. nbr	
1029	32	<b>Resize volumen image to 100%</b> Obj. nbr	Resize volumen image to 100%
1029	33	<b>Resize volumen image to 150%</b> Obj. nbr	Resize volumen image to 150%
1029	34	<b>Resize volumen image to 200%</b> Obj. nbr	Resize volumen image to 200%
1029	35	<b>Resize volumen image to 300%</b> Obj. nbr	Resize volumen image to 300%
1029	36	<b>Resize volumen image to 400%</b> Obj. nbr	Resize volumen image to 400%
1029	37	<b>Resize volumen image to 75%</b> Obj. nbr	Resize volumen image to 75%
1029	41	<b>Resize fused volumen image to 50%</b> Obj. nbr	Resize fused volumen image to 50%
1029	42	<b>Resize fused volumen image to 100%</b> Obj. nbr	Resize fused volumen image to 100%
1029	43	<b>Resize fused volumen image to 150%</b> Obj. nbr	Resize fused volumen image to 150%
1029	44	<b>Resize fused volumen image to 200%</b> Obj. nbr	Resize fused volumen image to 200%
1029	45	<b>Resize fused volumen image to 300%</b> Obj. nbr	Resize fused volumen image to 300%
1029	46	<b>Resize fused volumen image to 400%</b> Obj. nbr	Resize fused volumen image to 400%
1029	47	<b>Resize fused volumen image to 75%</b> Obj. nbr.	Resize fused volumen image to 75%
1030	1	<b>Select first colormap</b> Obj. nbr.	Select first colormap.
1030	2	<b>Select second colormap</b> Obj. nbr.	Select second colormap.
1030	3	<b>Select third colormap</b> Obj. nbr.	Select third colormap.
1030	4	<b>Select fourth colormap</b> Obj. nbr.	Select fourth colormap.
1031	1	<b>Select first colormap</b>	Select first colormap on image 1 (fused images)

		<b>on image 1</b> Obj. nbr.	
1031	2	<b>Select second colormap on image 1</b> Obj. nbr.	Select second colormap on image 1 (fused images).
1031	3	<b>Select third colormap on image 1</b> Obj. nbr.	Select third colormap on image 1 (fused images).
1031	4	<b>Select fourth colormap on image 1</b> Obj. nbr.	Select fourth colormap on image 1 (fused images).
1031	5	<b>Select first colormap on image 2</b> Obj. nbr.	Select first colormap on image 2 (fused images).
1031	6	<b>Select second colormap on image 2</b> Obj. nbr.	Select second colormap on image 2 (fused images).
1031	7	<b>Select third colormap on image 2</b> Obj. nbr.	Select third colormap on image 2 (fused images).
1031	8	<b>Select fourth colormap on image 2</b> Obj. nbr.	Select fourth colormap on image 2 (fused images).
1032	-	<b>Show interval number</b> obj. nbr.	Shows interval number on GATED TOMO image, when image nbr. are on.
1032	1	<b>Show slice number</b> obj. nbr.	Shows slice number on GATED TOMO image, when image nbr. are on.
1033	0	<b>Select image</b> Obj. nbr	Select image.
1033	10	<b>Select fused image</b> Obj. nbr	Select fused image.
1033	13	<b>Select volume image</b> Obj. nbr	Select volume image.
1033	14	<b>Select fused volume image</b> Obj. nbr	Select fused volume image.
1034	0	<b>Slice position cursors on/off</b> Obj. nbr Obj. nbr	Shows slice position cursors (only relevant on volumen images and fused volumen images).
1035	0	<b>Image nbr. scrollbar on/off</b> Obj. nbr. Obj. nbr.	Activated image nbr. scrollbar on image.
1036	0	<b>XY-cursor on/off</b> Obj. nbr. Obj. nbr.	Shows XY-cursors on image.
1036	10	<b>XY-cursor on/off</b> Obj. nbr. Obj. nbr.	Shows XY-cursors on fused image.

1036	13	<b>XY-cursor on/off</b> Obj. nbr. Obj. nbr.	Shows XY-cursors on volume image.
1036	14	<b>XY-cursor on/off</b> Obj. nbr. Obj. nbr.	Shows XY-cursors on fused volume image.
1037	-	<b>Set Frame Nbr</b> Obj. nbr. framenbr.	Set frame nbr. on selected image object.
1040	-	<b>Set CT image window/level</b> Obj.nbr level,window	Set CT image window/level settings.  level,window
1040	1	<b>Set fused image CT window/level</b> Obj.nbr level,window	Set fused image CT window/level settings.  level,window
1040	2	<b>Set volume image CT window/level</b> Obj.nbr level,window	Set volume image CT window/level settings.  level,window
1040	3	<b>Set fused volume image CT window/level</b> Obj.nbr level,window	Set fused volume image CT window/level settings.  level,window
1044	-	<b>Set volume image view transversal</b> Obj.nbr	Set volume image view transversal.
1044	1	<b>Set volume image view sagittal</b> Obj.nbr	Set volume image view sagittal.
1044	2	<b>Set volume image view coronal</b> Obj.nbr	Set volume image view coronal.
1044	3	<b>Set volume image view MIP</b> Obj.nbr	Set volume image view MIP.
1045	-	<b>Set fused volume image view transversal</b> Obj.nbr	Set fused volume image view transversal.
1045	1	<b>Set fused volume image view sagittal</b> Obj.nbr	Set fused volume image view sagittal.
1045	2	<b>Set fused volume image view coronal</b> Obj.nbr	Set fused volume image view coronal.
1045	3	<b>Set fused volume image view MIP</b> Obj.nbr	Set fused volume image view MIP.

1046	-	<b>Set fused volume image alpha value 0% Obj.nbr.</b>	Set fused volume image alpha value 0%
1046	1	<b>Set fused volume image alpha value 25% Obj.nbr.</b>	Set fused volume image alpha value 25%
1046	2	<b>Set fused volume image alpha value 50% Obj.nbr.</b>	Set fused volume image alpha value 50%
1046	3	<b>Set fused volume image alpha value 75% Obj.nbr.</b>	Set fused volume image alpha value 75%
1046	4	<b>Set fused volume image alpha value 100% Obj.nbr.</b>	Set fused volume image alpha value 100%
1047	-	<b>Set volume image slicewidth 1 pixel Obj.nbr.</b>	Set volume image slicewidth 1 pixel
1047	1	<b>Set volume image slicewidth 5 pixels Obj.nbr.</b>	Set volume image slicewidth 5 pixels
1047	2	<b>Set volume image slicewidth 10 pixels Obj.nbr.</b>	Set volume image slicewidth 10 pixels
1047	3	<b>Set volume image slicewidth 25 pixels Obj.nbr.</b>	Set volume image slicewidth 25 pixels
1047	4	<b>Set volume image slicewidth 50 pixels Obj.nbr.</b>	Set volume image slicewidth 50 pixels
1047	5	<b>Set volume image slicewidth 100 pixels Obj.nbr.</b>	Set volume image slicewidth 100 pixels
1048	-	<b>Set fused volume image slicewidth 1 pixel Obj.nbr.</b>	Set fused volume image slicewidth 1 pixel
1048	1	<b>Set fused volume image slicewidth 5 pixels Obj.nbr.</b>	Set fused volume image slicewidth 5 pixels
1048	2	<b>Set fused volume image slicewidth 10 pixels Obj.nbr.</b>	Set fused volume image slicewidth 10 pixels
1048	3	<b>Set fused volume image slicewidth 20 pixels Obj.nbr.</b>	Set fused volume image slicewidth 20 pixels

		<b>pixels</b> Obj.nbr.	
1050	-	<b>Set volume image info on/off</b> Obj.nbr.	Set volume image info on/off
1050	1	<b>Set fused volume image info on/off</b> Obj.nbr.	Set fused volume image info on/off
1070	-	<b>Insert RGB image</b> dataset name	Insert RGB image on the display.
1070	1	<b>Insert RGB image in 75% size</b> dataset name	Inserts RGB image in 75% size on the display.
1070	2	<b>Insert RGB image in 50% size</b> dataset name	Inserts RGB image in 50% size on the display.
1070	3	<b>Insert RGB image in 33% size</b> dataset name	Inserts RGB image in 33% size on the display.
1072	-	<b>Create a MIP ( Maximum Intensity Projection) dataset from a volume image dataset</b> dataset name New dataset name Cut off, angel incr.	Creates a MIP dataset from a volume image dataset.  lowerlevel cutoff, angel incr. in degrees.
1073	-	<b>Create CT image from BrightView CT dataset</b> dataset name new dataset name	Create a CT image dataset from a BrightView CT dataset.
1080	-	<b>Insert graphic image from file</b> filename	Insert a graphic image (.bmp, .jpg or .png file) on the display.
1100	-	<b>Clear display</b>	Clear display.
1105	-	<b>Set report panel attributes</b> obj. nbr. 2 attrib. flags	Set report attributes (frame, rounded corners).  frame, rounded corners ( 0:not set, 1:set )
1110	-	<b>Edit displayed study header</b> obj. nbr.	Edit selected study header.  obs! old function.
1110	2	<b>Edit displayed study header</b> obj. nbr. fontID	Edit selected study header.  -
1110	1	<b>Set study header attributes</b> obj. nbr. 3 attrib. flags	Sætter undersøgelses-hoved attributter ( frame, shadow, rounded corners ).  Attributes:

			frame, shadow, rounded corners ( 0:not set, 1: set)
1111	-	<b>Edit Study Header dataset</b>	Edit Study Header dataset.
1112	-	<b>Insert study header</b>	Insert study header on display.
1117	-	<b>Insert textfield</b> 1 or 2 x y width height textcolorID nbr. of textlines text.... .... ....	Insert textfield on display. (old function) Text from keyboard Fixed text from protocol  If 2 (text from protocol)
1117	1	<b>Insert textfield</b> 2 x y width height textcolorID fontID nbr. of textlines text ... .... ....	Insert textfield on display. (old function) Fixed text from protocol
1117	2	<b>Insert textfield</b> 2 x y width height ttextcolorID fontID backgroundcolorID Nbr. of textlines text ... .... ....	Insert textfield on display. (New function) including backgroundcolor of textfield. Fixed text from protocol.
1118	-	<b>Edit textfield</b> obj. nbr.	Edit textfield.
1119	-	<b>Set textfield attributes</b> obj. nbr. 11 attrib. flags	Set textfield attributes. attributes: frame left, frame right, frame top, frame bottom, shadow right, shadow bottom, upper left corner, lower left corner, upper right corner, lower right corner, rounded corners (0:not set, 1: set)
1120	-	<b>Edit register equation</b> equation format	Edit register equation. E.g. #20 = #21 + 100 ( # register number ) E.g. 7.2f (7 digits 2 digits after decimal point).
1121	-	<b>Insert data in register</b> usermessage reg. nbr.	Insert data in register.
1121	1	<b>Insert data in register from protocol</b> reg. nbr.	Insert data in register from protocol.
1130	-	<b>Select 1 colormap</b>	Select 1 colormap.

		Colormap name	
1131	-	<b>Select 2 colormaps</b> colormap nbr.1 name colormap nbr.2 name	Select 2 colormaps.
1132	-	<b>Select 4 colormaps</b> colormap nbr.1 name colormap nbr.2 name colormap nbr.3 name colormap nbr.4 name	Select 4 colormaps.
1133	-	<b>Select 4 colormaps</b> colormap nbr.1 name colormap nbr.2 name colormap nbr.3 name colormap nbr.4 name	Select 4 colormaps.
1200	-	<b>Draw irregular ROI</b> image obj. nbr. usermessage new ROI-dataset name	Draw irregular ROI.
1200	1	<b>Draw irregular ROI</b> image obj. nbr. usermessage ROIcolorID new ROI-dataset name	Draw irregular ROI. (new function including ROI color).
1201	-	<b>Draw polygon ROI</b> image obj. nbr. usermessage new dataset name	Draw polygon ROI.
1201	1	<b>Draw polygon ROI</b> image obj. nbr. usermessage ROIcolorID new dataset name	Draw polygon ROI. (new function including ROI color).
1203	-	<b>Draw circular ROI</b> image obj. nbr. usermessage new ROI-dataset navn	Draw circular ROI.
1203	1	<b>Draw circular ROI</b> image obj. nbr. usermessage ROIcolorID new ROI-dataset navn	Draw circular ROI. (new function including ROI color).
1204	-	<b>Draw elliptically ROI</b> image obj. nbr. usermessage new ROI-dataset name	Draw elliptically ROI.
1204	1	<b>Draw elliptically ROI</b> image obj. nbr. usermessage ROIcolorID new ROI-dataset name	Draw elliptically ROI. (new function including ROI color).
1205	-	<b>Manipulate ROI</b>	Manipulate ROI.

		ROI-dataset name image obj. nr. Usermessage new ROI-dataset name	
1205	1	<b>Manipulate ROI</b> ROI-dataset name image obj. nr. Usermessage ROIcolorID new ROI-dataset name	Manipulate ROI. (new function including ROI color).
1206	-	<b>Manipulate predefined ROI</b> ROI-dataset name image obj. nbr. usermessage new ROI-dataset name	Manipulate predefined ROI.
1206	1	<b>Manipulate predefined ROI</b> ROI-dataset name image obj. nbr. usermessage ROIcolorID new ROI-dataset name	Manipulate predefined ROI. (new function including ROI color).
1207	-	<b>Calculate ROI statistics on this image</b> image obj. nbr. ROI-dataset name(s) - Start register nbr.	Calculates ROI-statistics for the selected ROI'(s) on this image and saves the data in the registers.
1208	-	<b>Create curves from ROI'(s)</b> image-dataset name ROI-dataset name(s) -	Creates curves from the selected dynamic image from the selected ROI'(s).
1209	-	<b>Insert curvepanel</b> kurve-datasetname(s) -	Insert the selected curves in a curve panel on the display.
1209	5	<b>Edit curvepanel</b> obj. nbr. Coordiantesystype panelbgcolor color coordsysbkgcolor fontID grid scaling xmin xmax xtext xformat ymin ymax ytext	Edit curve panel.  0: Cartesian  grid: 0 off 1 on, scaling: 0 absolute 1 procent of max  “C” floating point formatspecifikation e.g. %6.3f shown as 6 digits with 3 digits after decimalpoint.

		<b>yformat</b>	
1210	-	<b>Show curves</b> curve-dataset name(s) - usermessage startregister nbr.	Shows the selected curves in a dialog box. Possibility to save counts from single point or interval and time in the registers.( Se function 1210 10 og 1210 11 ).
1210	1	<b>Copy curves to clipboard</b> curve-dataset name(s) -	Copies the selected curves to clipboard.. Format: Number of curves Curve 1 name Number of points curve 1 x-value tab y-value etc.
1210	10	<b>Show curves</b> curve-dataset name(s) - usermessage startregister nbr.	Shows the selected curves in a dialog box. Curve name, counts and time are saved in the registers.
1210	11	<b>Show curves</b> curve-dataset name(s) - usermessage startregister nbr.	Shows the selected curves in a dialog box. Curvename,integral counts, starttime and endtime of integral are saved in the registers.
1210	12	<b>Show curves</b> curve-dataset name(s) - usermessage t1 t2 startregister nbr.	Shows the selected curves in a dialog box. The cursors are placed with the initial values t1 and t2. Curvename,integral counts, starttime and endtime of integral are saved in the registers.
1211	-	<b>Add ROIs to imageoverlay</b> ROI-dataset name(s) - image obj. nbr.	Shows the selected ROI's on the selected image.
1212	-	<b>Create diastole/systole images</b> image-dataset name cvedataset name Diastole image dataset name Systole image dataset name	Creates a diastole and systole image from a dynamic image dataset and a curve from the relevant heart ventricle.
1213	-	<b>Create first harmonic images</b> Multigateddataset name amplitude image name phase image name	Creates amplitude and phase images from a multigated dataset.
1213	5	<b>Imagereconstruction ( FBP )</b>	Shows imagereconstruction dialog box (old function).

		Tomo dataset name Zoom Trans. dataset name Sagittal dataset name Coronal dataset name	
1213	6	<b>Imagereconstruction ( FBP )</b> Tomo dataset name zoom,scaling,slicewidth reconfilter type $\text{filter}_{\text{cutoff}}$ if reconfilter 0,else $\text{filter}_{\text{cutoff}}$ filterorder postfilter type If 0: no parameters If 1: $\text{filter}_{\text{cutoff}}$ filterorder gain If 2: Gain Startangel rotationondirection rotationangle Reconstructions type If 0: no parameters If 1: Nbr. of iterations If 2: Nbr. of subset nbr.of iterations x1 y1 x2 y2 x3 y3 x4 y4 Trans. dataset name Sagittal dataset name Coronal dataset name	Automatic imagereconstruction.  Reconstructionfilter type 0: Rampe + square, 1: rampe + butterworth  Postfilter type 0: none, 1: Butterworth + res. enh, 2: Resolution enh.  Startangel, rotationondirection 0: CW, 1: CCW, rotationangle Reconstructions type 0: FBP, 1: ML-EM, 2: OS-EM  Reconstructions box Sliceplanes limits box
1213	7	<b>Imagereconstruction ( FBP )</b> Tomo dataset name zoom,scaling,slicewidth reconfilter type $\text{filter}_{\text{cutoff}}$ if reconfilter 0,else $\text{filter}_{\text{cutoff}}$ filterorder postfilter type If 0: no parameters If 1: $\text{filter}_{\text{cutoff}}$ filterorder gain If 2: Gain Startangel rotationondirection rotationangle Reconstructions type	Automatic imagereconstruction.  Reconstructionfilter type 0: Rampe + square, 1: rampe + butterworth  Postfilter type 0: none, 1: Butterworth + res. enh, 2: Resolution enh.  Startangel, rotationondirection 0: CW, 1: CCW, rotationangle

		If 0: no parameters If 1: Nbr. of iterations If 2: Nbr. of subset nbr.of iterations x1 y1 x2 y2 x3 y3 x4 y4 Trans. dataset name Sagittal dataset name Coronal dataset name	Reconstructions type 0: FBP, 1: ML-EM, 2: OS-EM  Reconstructions box Sliceplanes limits box
1214	18	<b>Show reconstructed SPECT/CT with fusion</b> x-offset y-offset CT-window name CT colormap SPECT colormap SPECT fusion colormap cursorcolorID cursor type savemode dataset1name ..(dependent of the value of savemode)	Show reconstructed SPECT/CT with fusion (new function replaces 1214 8). X-offset og y-offset in 1/10 mm of CT system  (Only if imagesize < 512)  cursor type : 0 savemode 0: Save as RGB dataset, 1: Save only transversal dataset, 2: Save only sagittal dataset, 3: Save only coronal dataset, 4: Save transversal, sagittal and coronal dataset.
1216	1	<b>Calculation of V/P ratio dataset from transversal ventilation/perfusion dataset with CT</b> Vent.datasetname Perf.datasetname CT datasetname New dataset name Cut-off level in % Absolute maximum Normalisation method	Calculation of V/P ratio dataset from transversal ventilation/perfusion dataset.  0
1217	-	<b>Set ROI color order</b> 1,3,2...16(orderlist)	Set ROI color order (color index from configuration file).
1230	-	<b>Add/subtract curves</b> curve nbr.1 name curve nbr.2 name curve nbr.3 name A ( const. or reg.nbr. ) B ( - do - ) C ( - do - )	Curve arithmetic after the equation: Curve nbr.3 = A*curve nbr.1 + B*curve nbr.2 + C Where A,B and C are constants ( fixed or from dataregisters (# infront of register number )).
1230	1	<b>Multiply curves</b> curve nbr.1 name curve nbr.2 name curve nbr.3 name	Curve arithmetic after the equation: Curve nbr.3 = A*curve nbr.1*curve nbr.2 + C where A,B og C are constants ( fixed or from data-registers (# infront of register number )).

		A ( const. or reg.nbr. ) B ( - do - ) C ( - do - )	
1230	2	<b>Divide curves</b> curve nbr.1 name curve nbr.2 name curve nbr.3 name A ( const. or reg.nbr. ) B ( - do - ) C ( - do - )	Curve arithmetic after the equation: Curve nbr.3 = A*curve nbr.1/curve nbr.2 + C where A,B and C are constants ( fixed or from data-registers (# infront of register number )).
1230	3	<b>Log curve</b> curve nbr.1 name curve nbr.2 name curve nbr.3 name A ( const. or reg.nbr. ) B ( - do - ) C ( - do - )	Curve arithmetic after the equation: Curve nbr.3 = A*log <sub>nat</sub> (B*curve nbr.1 + C) where A,B and C are constants ( fixed or from data-registers (# infront of register number )).
1230	4	<b>Exp curve</b> curve nbr.1 name curve nbr.2 name curve nbr.3 name A ( const. or reg.nbr. ) B ( - do - ) C ( - do - )	Curve arithmetic after the equation: Curve nbr.3 = A*exp(B*curve nbr.1) + C where A,B and C are constants ( fixed or from data-registers (# infront of register number )).
1230	5	<b>Geometric mean of 2 curves</b> curve nbr.1 name curve nbr.2 name curve nbr.3 name A ( const. or reg.nbr. ) B ( - do - ) C ( - do - )	Curve arithmetic after the equation: Curve nbr.3 = A*sqrt(curve1*curve2) + C where A,B and C are constants ( fixed or from data-registers (# infront of register number )).
1240	-	<b>Smoothing of curve</b> Curve-datasetname new dataset name filtertype filtercoefficients	Smoothing of curve  filter type 0: 3-point , 1: 5-point filtercoefficients e.g: 1,2,1
1300	-	<b>Create horisontal profile on this image</b> obj. nbr. message new dataset name	Create a horisontal image profile.
1301	-	<b>Create vertical profile on this image</b> obj. nbr. message new dataset name	Create a vertical image profile.
1302	-	<b>Insert profile panel on display</b> Profile-datasetname(s) -	Insert selected profiles on the display.

1302	5	<b>Edit profile panel</b> obj. nbr. Coordinatsystype panelbkgcolor coordsyscolor color fontID grid scaling xmin xmax xtext xformat ymin ymax ytext yformat	Edit profile panel. New function. 0: Cartesisk  grid: 0 off 1 on, scalingg: 0 absolut 1 procent of max  “C” floating point formatspecification e.g. %6.3f shown as 6 digit total 3 digits after decimalpoint.
1303	-	<b>Show profiles</b> Profiel-datasetname(s) - message startreg. nbr.	Shows the selected profiles in a window. Possibility to save counts from single points or interval in the registers.
1602	-	<b>Save page</b> datasetname	Saves the report page.
1603	-	<b>Load page</b> datasetname	Load a saved report page.
1604	-	<b>Set report size in pixels</b> width,height	Set report size. Width( in pixels),height( in pixels ). NB! all values a multiple of 4.
1604	1	<b>Set report to 768 x 1024</b>	Set report size to 768 x 1024
1604	2	<b>Set report to 768 x 1280</b>	Set report size to 768 x 1280
1604	3	<b>Set report to 1024 x 1024</b>	Set report size to 1024 x 1024
1604	4	<b>Set report to 1024 x 1280</b>	Set report size to 1024 x 1280
1604	5	<b>Set report to 1152 x 1152</b>	Set report size to 1152 x 1152
1604	6	<b>Set report to 1152 x 1280</b>	Set report size to 1152 x 1280
1604	7	<b>Set report to 1152 x 1536</b>	Set report size to 1152 x 1536
1604	8	<b>Set report to 1536 x 2048</b>	Set report size to 1536 x 2048
1605	3	<b>Save report as a JPEG image</b> filename compressionquality	Save the report as a JPEG image with the selected compression quality.  NB! Larger number = better image quality
1605	4	<b>Save page as a RGB dataset</b> datasetname	Save page as a RGB dataset ( can be exported as a DICOM secondary capture )
1605	5	<b>Send report to PACS</b>	Send report to PACS (as a DICOM secondary capture).
1606	-	<b>Copy page to</b>	Copy page to Windows clipboard.

		<b>clipboard</b>	
1608	0	<b>Save report as a JPEG image</b> filename compressionquality	Save the report as a JPEG image with the selected compression quality.  NB! Larger number = better image quality
1608	1	<b>Save report as a JPEG image</b> filename compressionquality	Save the report as a JPEG image with the selected compression quality.  NB! Larger number = better image quality
2000	-	<b>Select new study</b> Usermessage	Select new study.
2001	-	<b>Run protocol</b> protocol-name nbr. of obj.	Run a processing protocol.  Number of objects on the page when the protocol starts.
2003	-	<b>End protocol</b> 0	End protocol-processing.
5000	-	<b>Renography first processing</b>	First processing of renography ( DTPA or MAG3 )
5001	-	<b>Show/reproces all renography calculations</b>	Reproces/show total renography calculations.
5002	-	<b>Show/reproces uptake function</b>	Reproces/show renography uptake function.
5003	-	<b>Show/reproces transport and removal function</b>	Reproces/show renography transport and removal function.
5004	-	<b>Show/reproces vascular function</b>	Reproces/show renography flowphase.
5005	-	<b>Edit renography studydata</b>	Create/edit patient/study data ( diuresis, height, weight ).
5006	-	<b>Edit renography study data</b>	Do
5007	-	<b>Updates curves in the renography-dataset</b>	Updates the curves in the renography-dataset (NB! After a new curve generation)
5010	-	<b>Insert 6 renography images</b>	Insert 6 128 x 128 images on the display.
5010	1	<b>Insert 6 scaled renography images</b>	Insert 6 scaled 128 x 128 image on the display. Scaled relative to the 1-3 min image.
5011	-	<b>Insert 8 renography images</b>	Insert 8 128 x 128 images on the display.
5011	1	<b>insert 8 scaled renography</b>	Insert 8 128 x 128 scaled images on the display. Scaled relative to the 1-3 min image.
5012	-	<b>Insert partial renography report</b>	Insert small renography-report on the display.
5013	-	<b>Insert total renography report</b>	Insert total renography-report on the display.
5014	-	<b>Insert small curvepanel</b>	Insert small renography-curvepanel on the display.
5015	-	<b>Insert large curvepanel</b>	Insert large renography-curvepanel on the display.

5016	-	<b>Insert small resultspanel</b>	Insert small renography-resultspanel on the display.
5017	-	<b>Insert large resultspanel</b>	Insert large renography-resultspanel on the display.
5030	-	<b>Set renography kidney parameters</b> r1 r2 r3 r4 l1 l2 l3 l4	Set renography kidney parameters.  right1 right2 right3 right4 left1 left2 left3 left4

## 8.0 Overview of keyboard short-cuts in the Medic system

Keyboard short-cut	Function	Comment
Ctrl + S	Select all images	Mark all images on the display
Ctrl + D	Deselect all images	
Ctrl + U	Change study	Change current study
Ctrl + A	Exit	Close processing window
Ctrl + N	Static->Normal size	
Ctrl + M	Static->Maximal size	
Ctrl + I	Static->Interpolated to 256 x 256	
Ctrl + C	Dynamic->Cine	
Ctrl + H	Text->Edit study header	
Ctrl + Alt + S	Stop processing protocol	

# **9.0 Overview of predefined register content**

## **9.1 Study related content**

Reg.nr	parameter	comments
1		patient name
2		patient ID.
3		birthdate
4		height ( in cm )
5		weight ( in kg )
6		study name
7		study date
8		study time
9		isotope
10		dose
11		department
12		comment ( first 39 characters of STUDY HEADER commentfield )
13		comment ( resterende characters of commentfield )

## **9.2 Renography (DTPA/MAG3) related content**

Reg.nr	parameter	comments
40	Tmax	time to maximum, right kidney
41	A20	Residual fraction, right kidney
42	Tmax	time to maximum, left kidney
43	A20	Residual fraction, left kidney
44		Relativ function (%), right kidney
45		Relativ function (%), left kidney

46		diuresis (ml/min)
49		heart curve normalization factor (ROI size 32 cm <sup>2</sup> )
50	UI	uptake index (1/min), right kidney
51	UI	uptake index (1/min), left kidney
52	FI	flow index (1/min), right kidney
53	FI	flow index (1/min), left kidney
54	f0	total retention, right kidney
55	f0	total retention, left kidney
56	t1	minimum parenchymal transittid (min), right kidney
57	t1	minimum parenchymal transittid (min), left kidney
58	t2	maximum parenchymal transittid (min), right kidney
59	t2	maximum parenchymal transittid (min), left kidney
60	tpe	pelvis mean transittid (min), right kidney
61	tpe	pelvis mean transittid (min), left kidney
62	ta	appearance time (bolus phase) (sec), right kidney
63	ta	appearance time (bolus phase) (sec), left kidney
64	td	"delay" time (bolus phase) (sec), right kidney
65	td	"delay" time (bolus phase) (sec), left kidney
66	tc	"capillary" time (bolus phase) (sec), right kidney
67	tc	"capillary" time (bolus phase) (sec), left kidney
68	VSF	vascular subtractions factor, right kidney
69	VSF	vascular subtractions factor, left kidney
70	ESF	extra-vascular subtractions factor, right kidney
71	ESF	extra-vascular subtractions factor, left kidney

72	VLSF	vascular lung subtractions factor
73	ELSF	extra-vascular lung subtractions factor
74	HCF	heart curve correction factor (after lung curve subtraction)
75		time shift of lung curve (sec)
78	R20	Removed fraction, right kidney
79	R20	Removed fraction, left kidney