**Medic**

USER’S MANUAL

This manual describes how to use the Medic processing and documentation software.

Ver 1.0

Table of content

[1.0 Introduction 4](#_Toc129968694)

[1.1 Configuration 4](#_Toc129968695)

[2.0 Main Window 5](#_Toc129968696)

[2.1 Creating new colormaps 6](#_Toc129968697)

[2.2 Create predefined ROI 6](#_Toc129968698)

[2.3 Create study protocol relation 7](#_Toc129968699)

[2.4 Delete studies 7](#_Toc129968700)

[2.5 Delete datasets 8](#_Toc129968701)

[2.6 Delete protocols 9](#_Toc129968702)

[2.7 Delete colormaps 9](#_Toc129968703)

[2.8 Delete predefined ROI 10](#_Toc129968704)

[2.9 Edit Patient/study data 11](#_Toc129968705)

[2.10 Edit Study header 13](#_Toc129968706)

[2.11 Edit dataset name 13](#_Toc129968707)

[2.12 Show dataset info 14](#_Toc129968708)

[2.13 Edit processing protocol 15](#_Toc129968709)

[2.14 Edit study protocol relation 16](#_Toc129968710)

[2.15 Edit Medic setup 16](#_Toc129968711)

[2.16 Import datasets 17](#_Toc129968712)

[2.17 Import colormap from Medic file 18](#_Toc129968713)

[2.18 Import colormap fra bin file 18](#_Toc129968714)

[2.19 Import protocol 18](#_Toc129968715)

[2.19 Export processing protocols 19](#_Toc129968716)

[2.20 Export Colormaps 19](#_Toc129968717)

[2.21 Export Datasets 20](#_Toc129968718)

[2.22 Export Dataset in DICOM format 20](#_Toc129968719)

# 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.

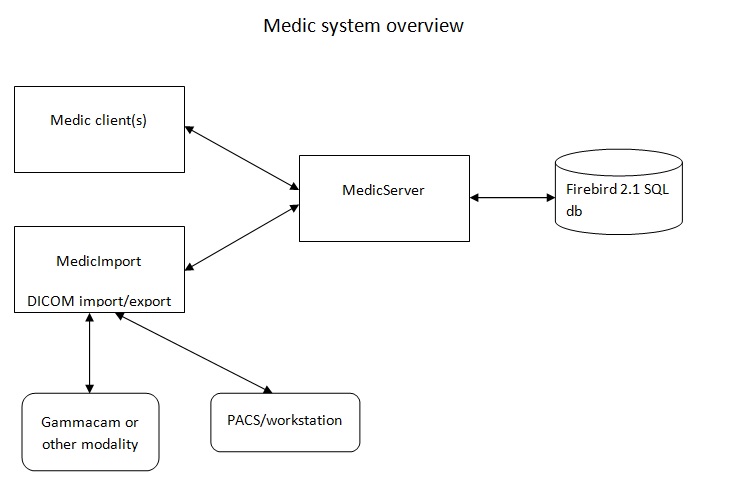


Fig. 1.1

## 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 XX.X.

# 2.0 Main Window

The main window is show in fig. 2.1

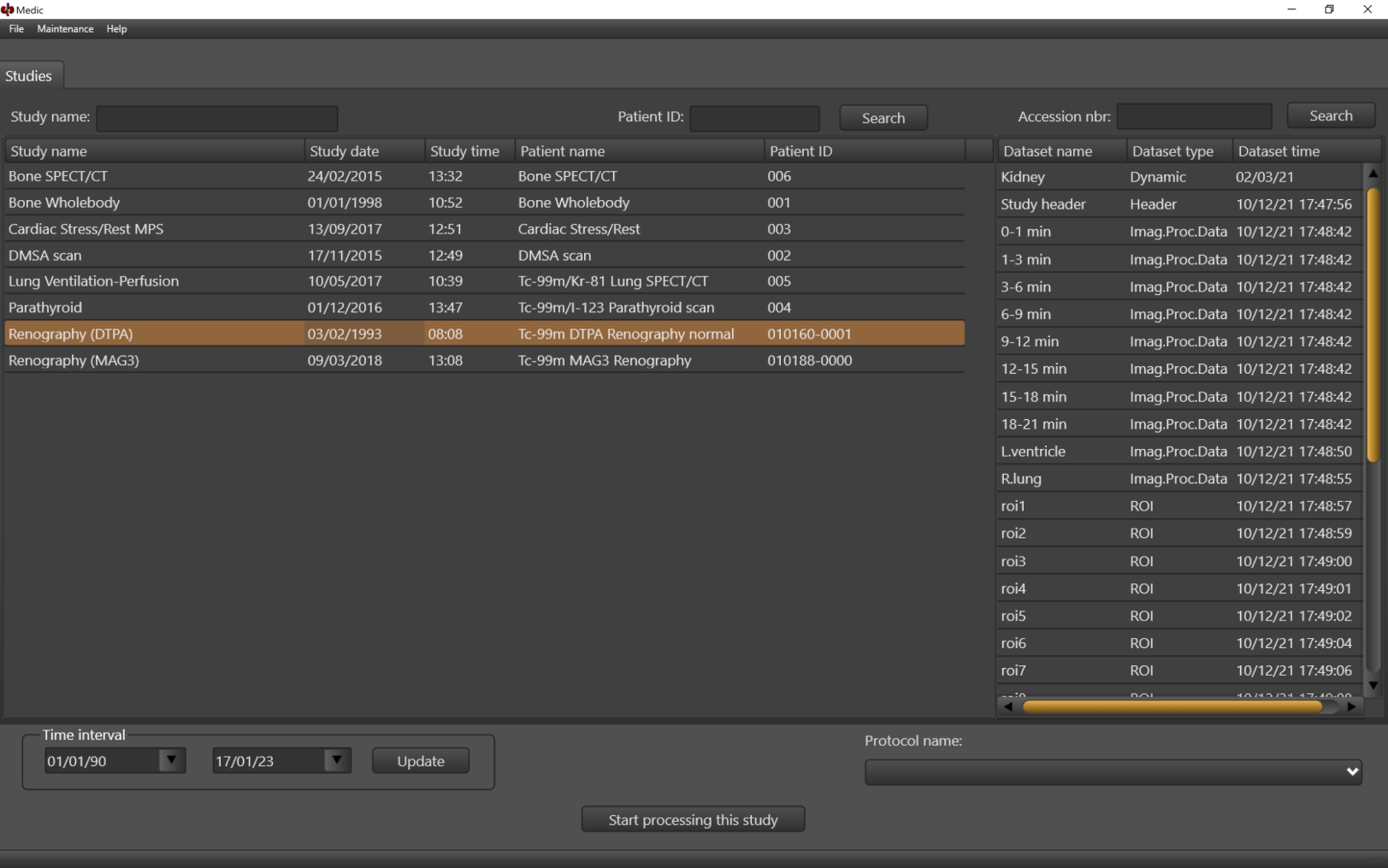


Fig. 2.1

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 releations, 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.

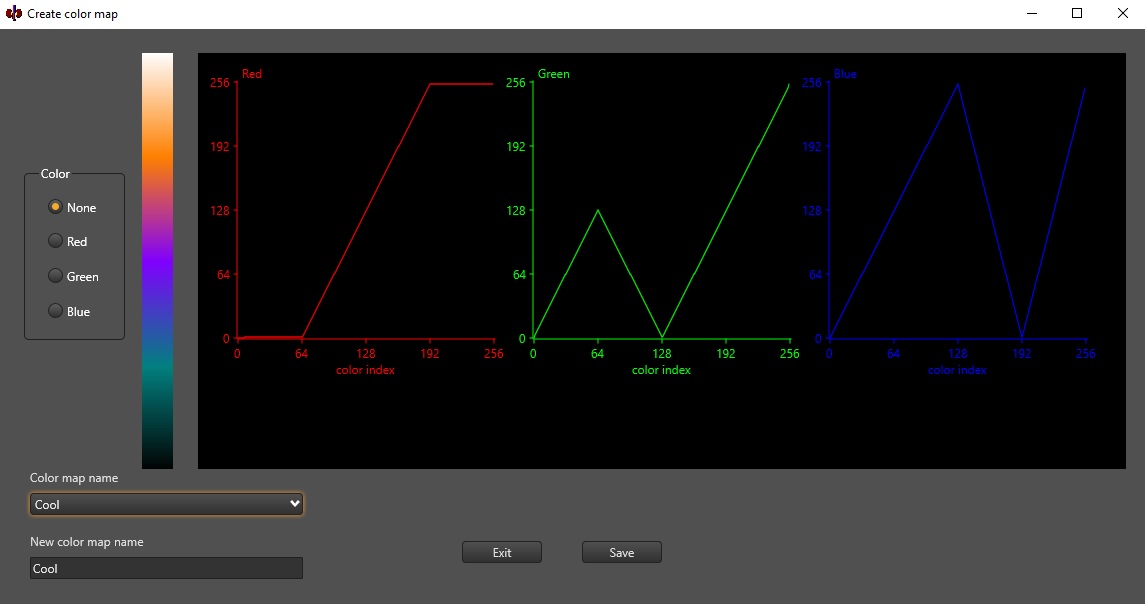


Fig.2.2

Select the color (red,green,blue) and the cursor turns into a cross on the selected colorpanel. Draw the color index/color intensity releation 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.

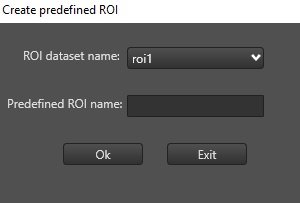


fig.2.3

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.

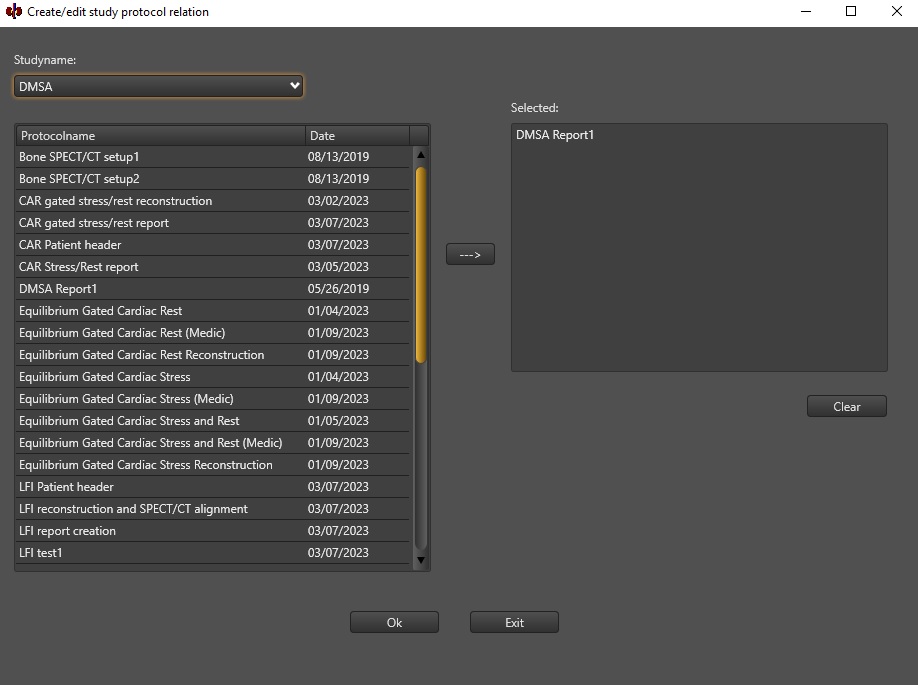


fig.2.4

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.

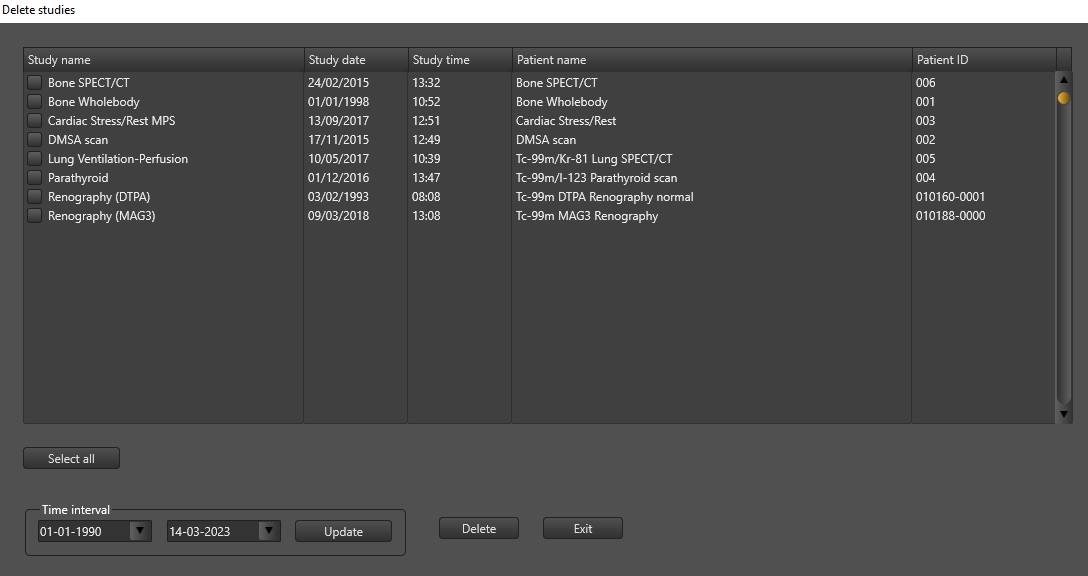


Fig.2.5

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

## 2.5 Delete datasets

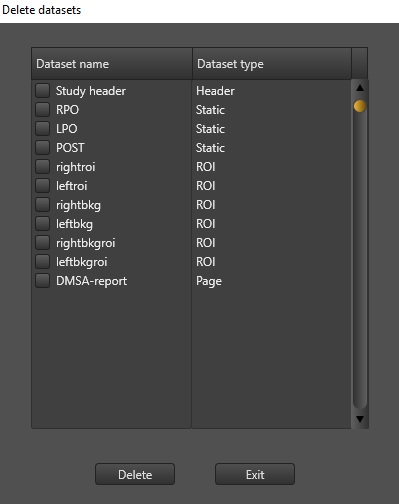
To delete dataset from a selected study select Maintenance->Delete->Datasets and the dialog in fig.7 is shown.

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.

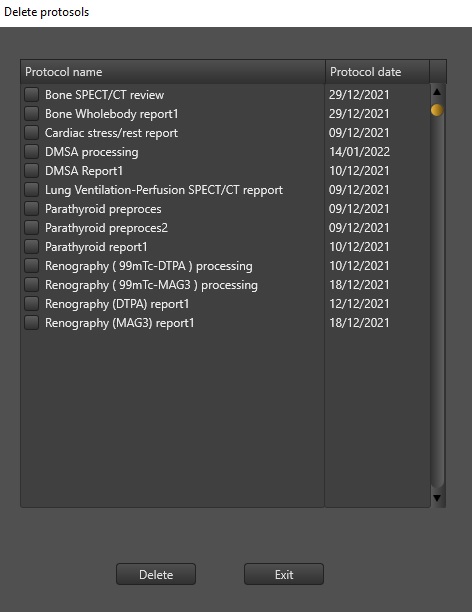


fig.2.7

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

## 2.7 Delete colormaps

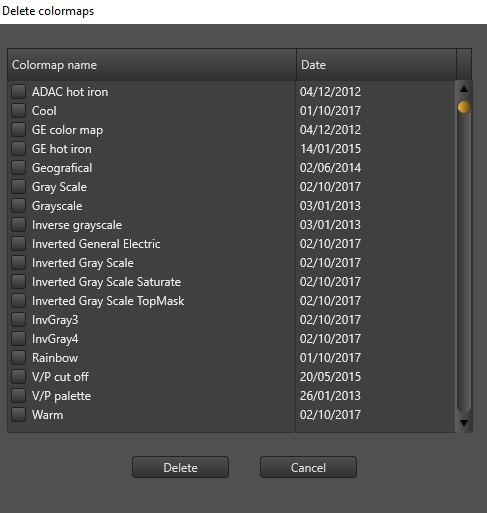
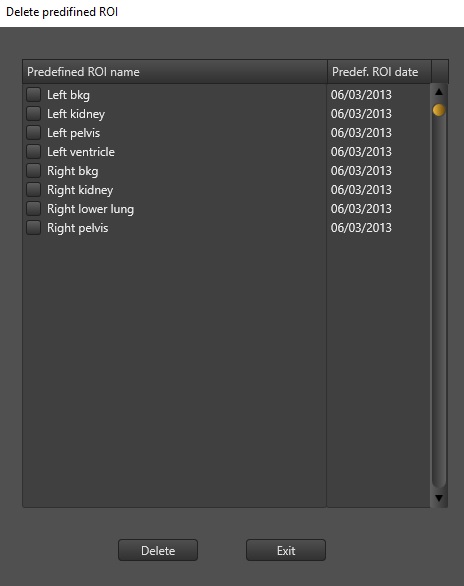
To delete colormaps used in the system select Maintenance->Delete->Colormaps and the dialog in fig.2.8 is shown.

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.

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.

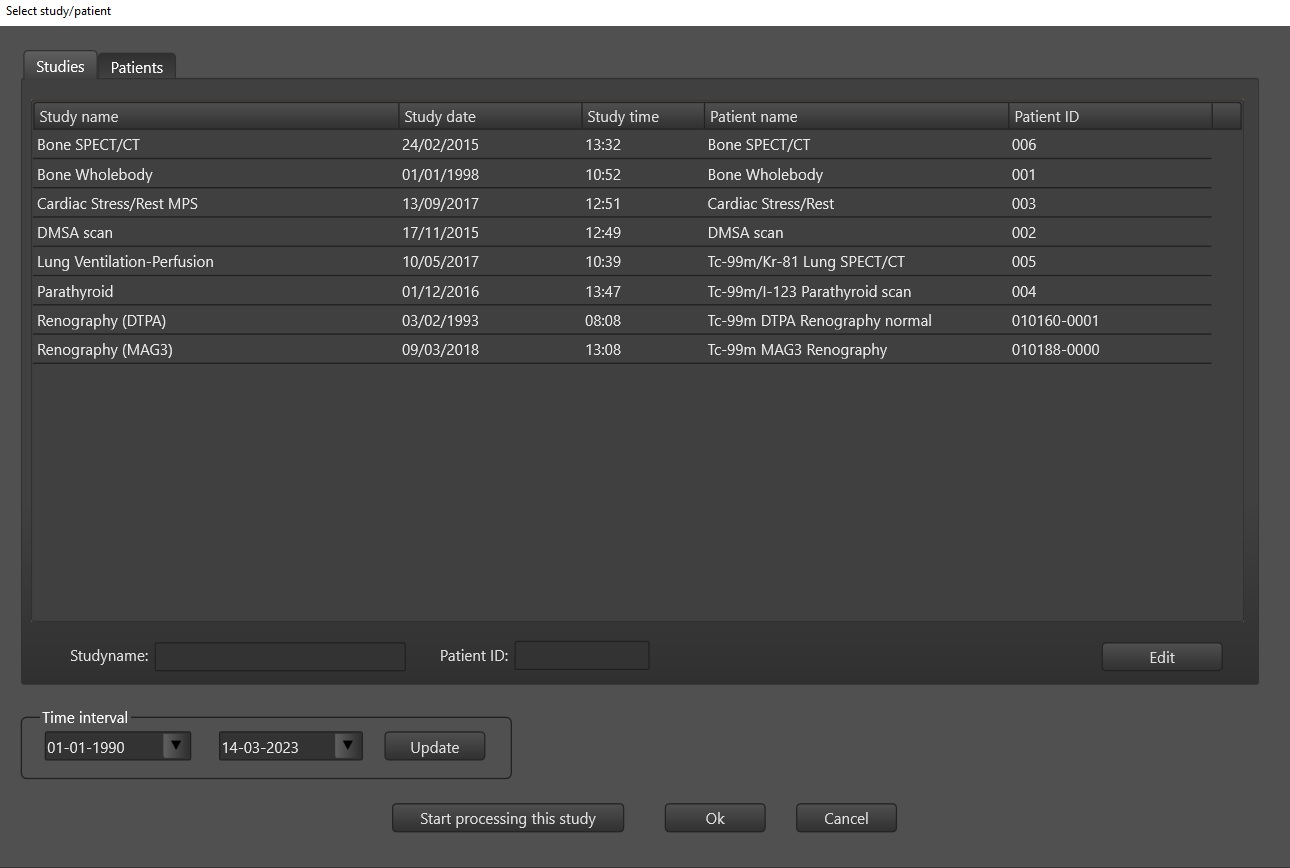
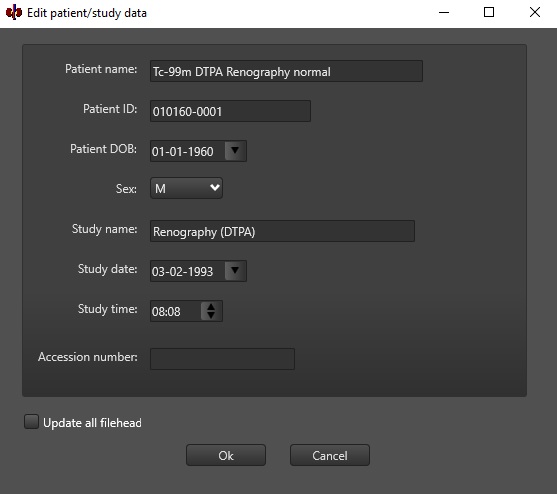


Fig.2.10

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.

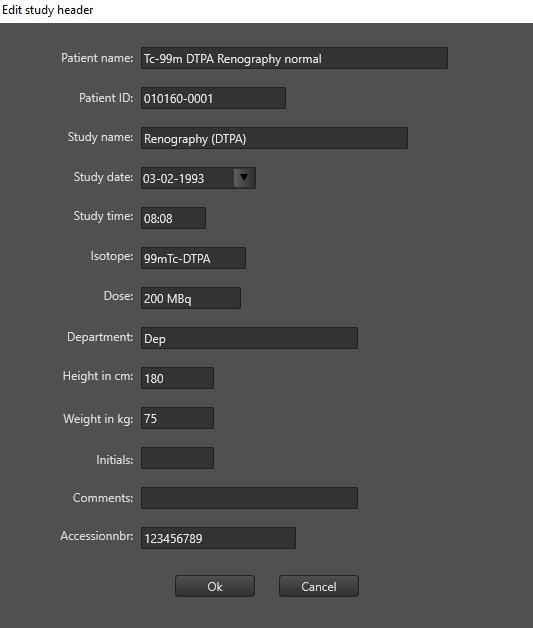
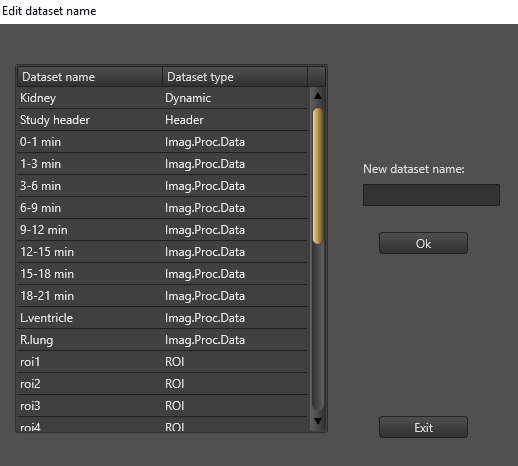


fig.2.12

Edit the data in the dialog and press Ok.

## 2.11 Edit dataset name

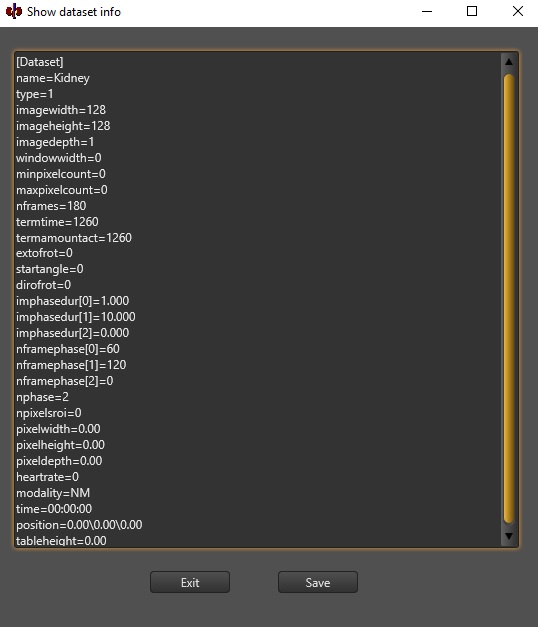
To edit the dataset name in a selected study select Maintenance->Edit->Dataset name and the dialog in fig.2.13 is shown.

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.

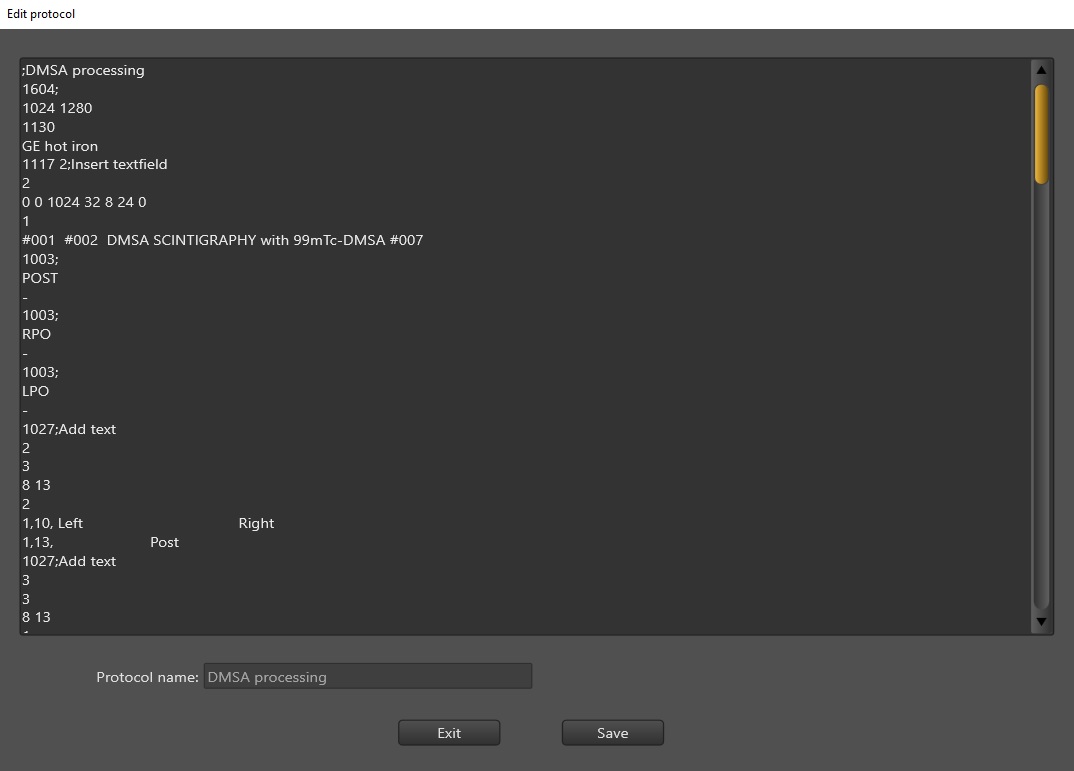


fig.2.15

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.

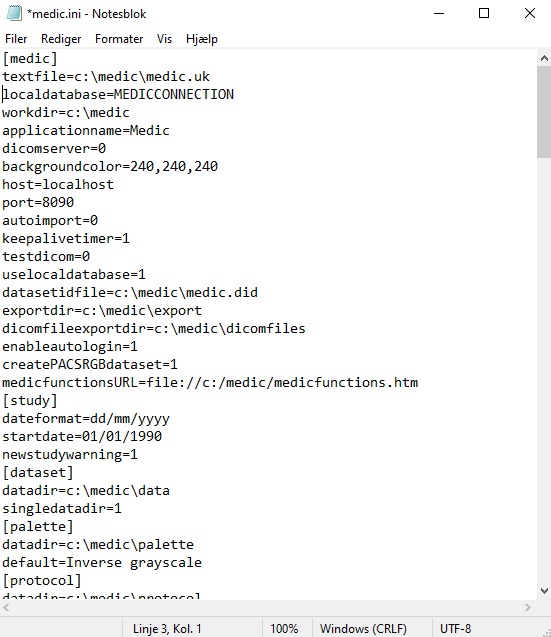


fig.2.16

## 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.

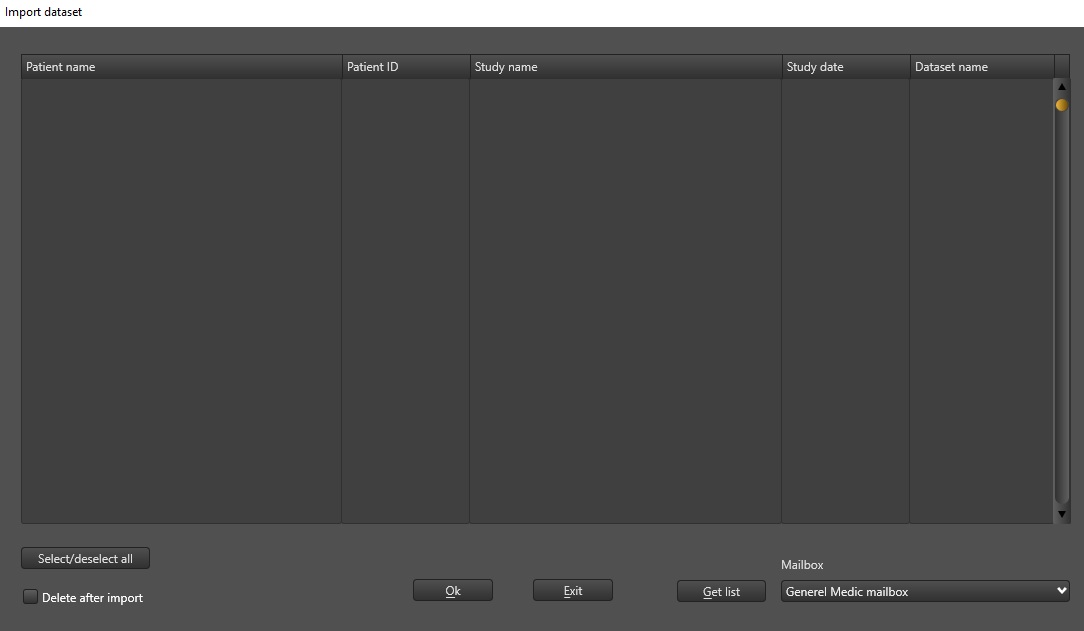


fig.2.17

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

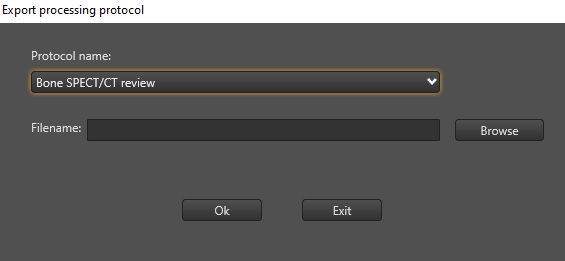
To export processing protocols from the system select Maintenance->Export->Processing protocols and the dialog in fig.2.18 is shown.

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

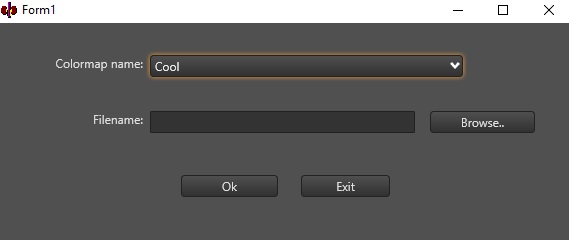
To export colormaps from the system select Maintenance->Export->Colormaps and the dialog in fig.2.19 is shown.

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

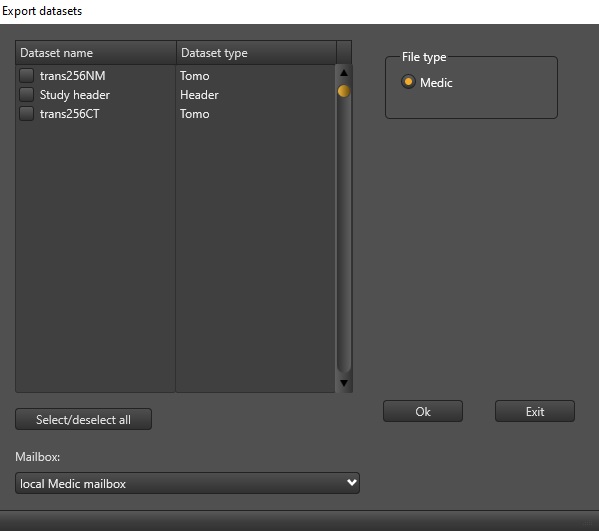
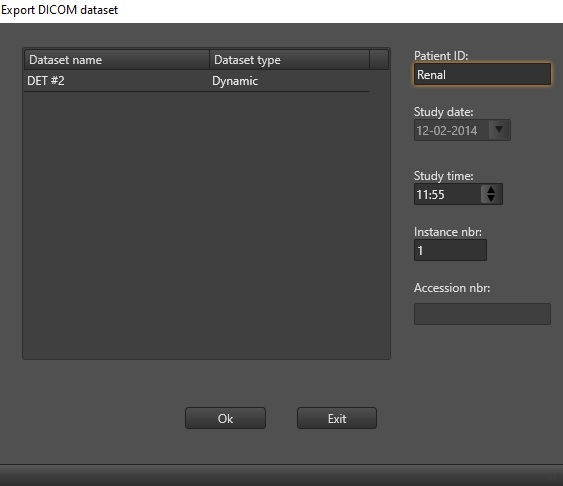
To export datasets from the system (in Medic format) select Maintenance->Export->Datasets and the dialog in fig.2.20 is shown.

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.

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.

# 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

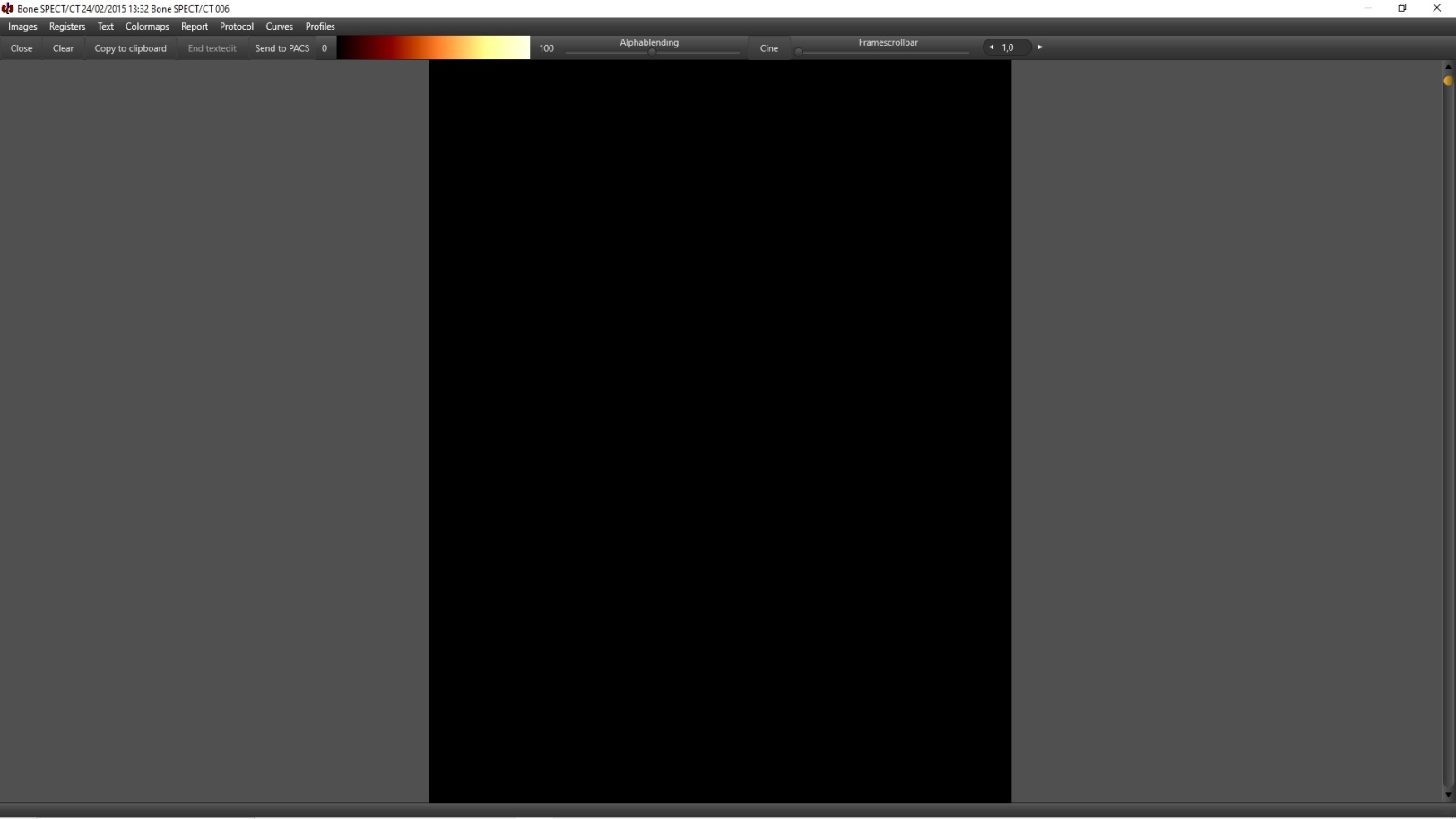


fig.3.1

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. Middel 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.

## 3.1 Insert static images

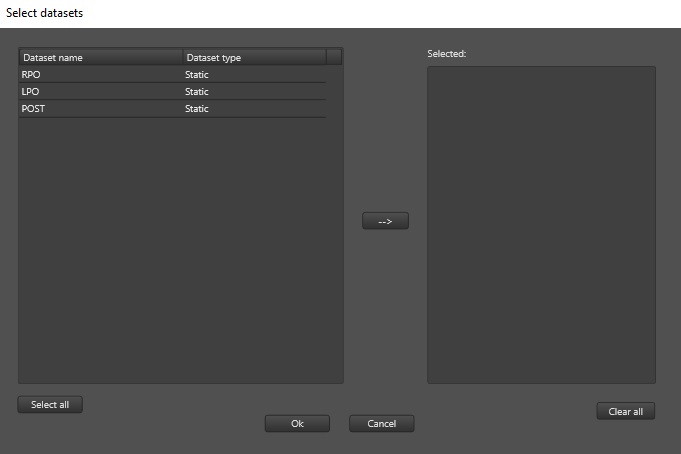
To insert static images on the report select Images->Static and choose between normal size, maximal size, interpolated to 256x256 or whole body 256x1024. A list of static images is shown in the Select datasets dialog in fig.3.2.

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

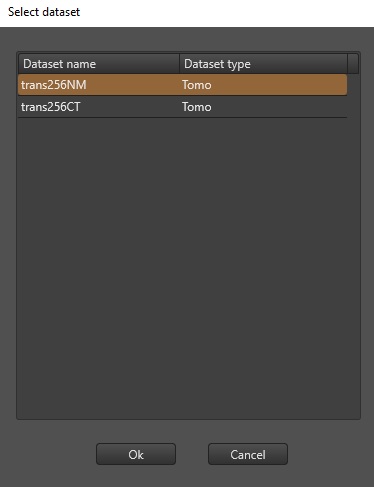
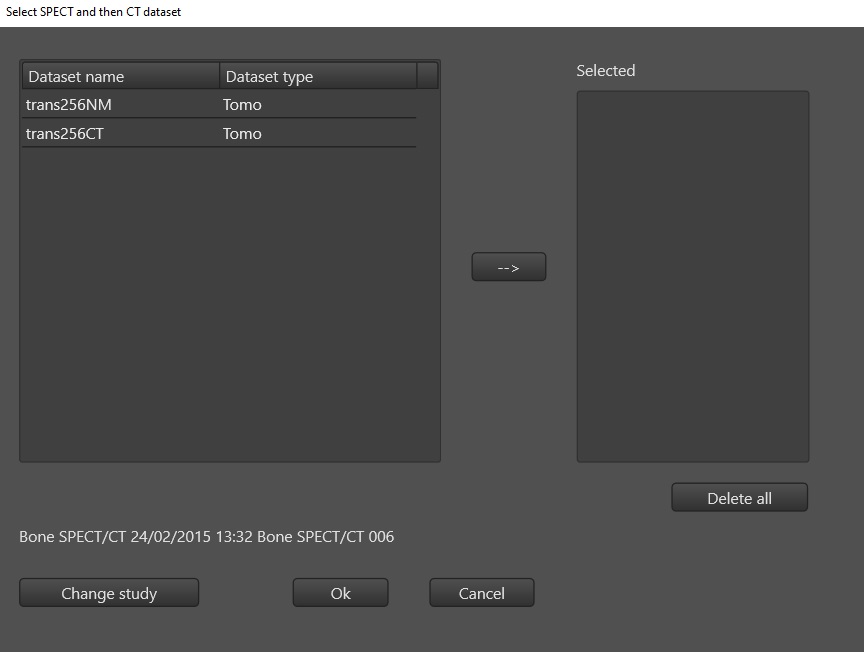
3D volume images are reconstructed tomo or gated tomo images, CT, PET or MR images. To insert 3D volume images on the report select Images->3D volume images and chose between volume image, volume image with MIP (maximum intensity projection), volume image 3x256x256, volume image 3x384x384, volume image 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.

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.

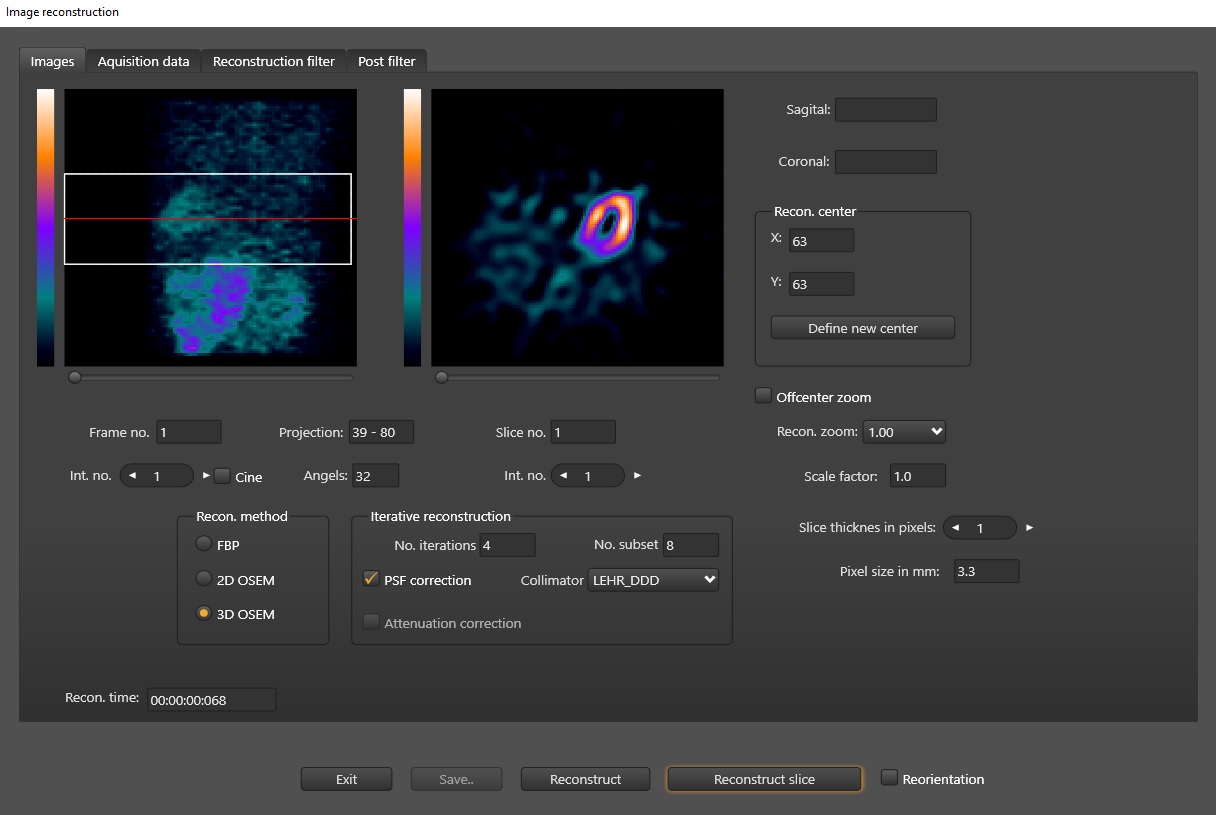


fig.3.5

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.

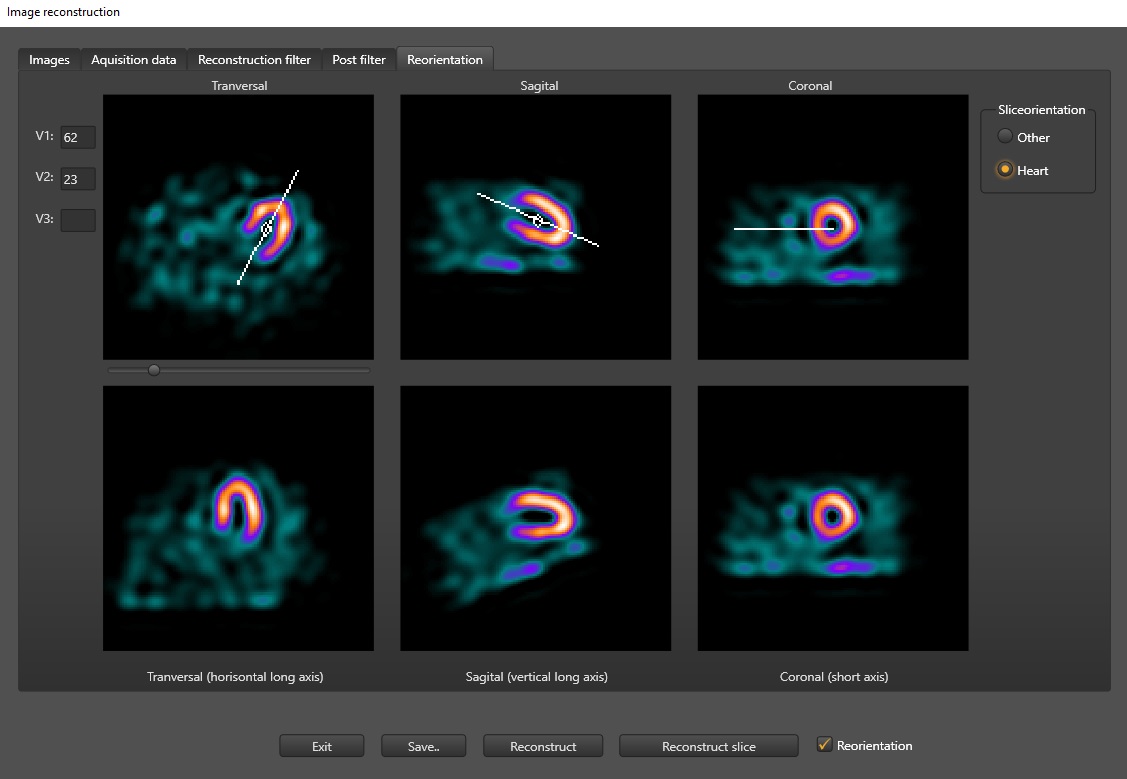


fig.3.6

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.

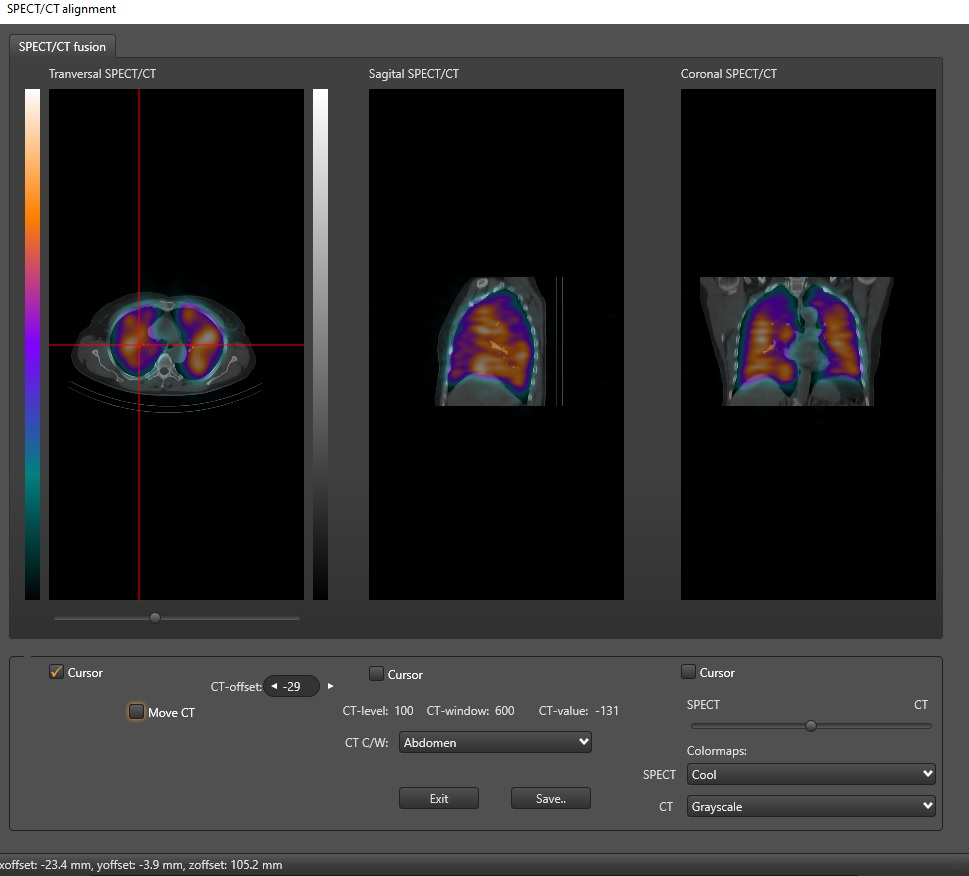


fig.3.7

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 to datasets).

## 3.9 Add frames

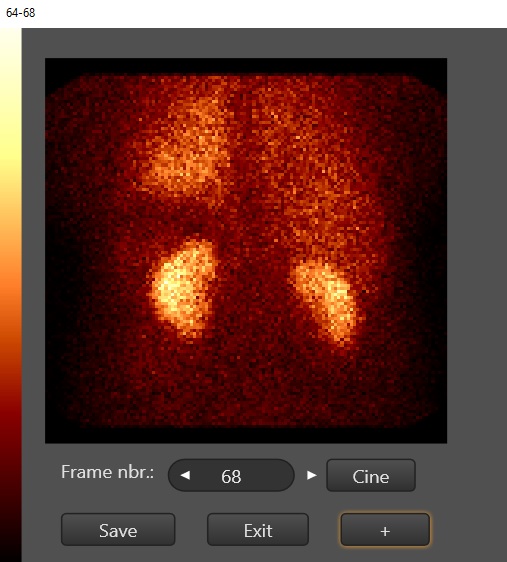
To add frames in a dynamic study select Images->Add frames and choose between manually or automatic. For manual addition the dialog in fig.3.8 is shown.

fig.3.8

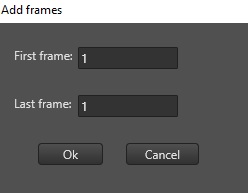
Go to the image where you want to start the addition of frames with the “Frame nbr.” edit or the “Cine” button. Start adding with the “+” button. The frame numbers added are shown on the dialogs title bar. Press “Save” and give the dataset a unique name. If automatic is chosen the dialog in fig.3.9 is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

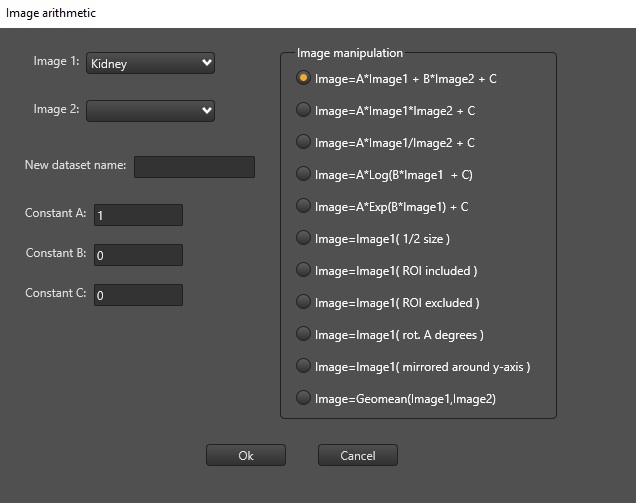
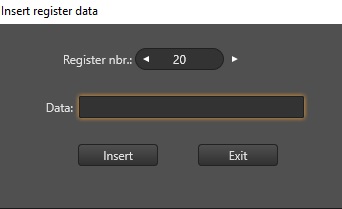
To manipulate images select Images->Image manipulation and choose between Add/subtract, Multiply, Divide, Log, Exp, Minify, ROI include, ROI exclude, Rotate, Mirror around Y-axis, Motion correction, Geometric mean, Resample image, Convert gated to ungated and Image subtraction (with manually adjustable 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”.

## 3.11 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 contains 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.3.11 is shown.

fig.3.11

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

## 3.12 Edit register equation

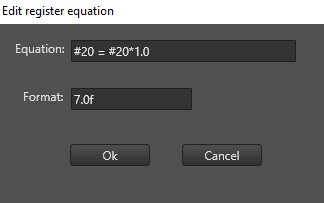
To edit a register equation select Register->Edit register equation and the dialog in fig.3.12 is shown.

fig.3.12

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.

## 3.13 Insert textfield

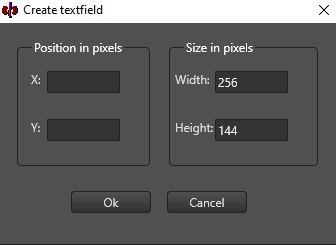
To insert a textfield on the report select Text->Insert textfield and the dialog in fig.3.13 is shown.

fig.3.13

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”.

## 3.14 Insert study header

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

## 3.15 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.

## 3.16 Selecting Colormaps

The report can opereate 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.3.14 is shown.

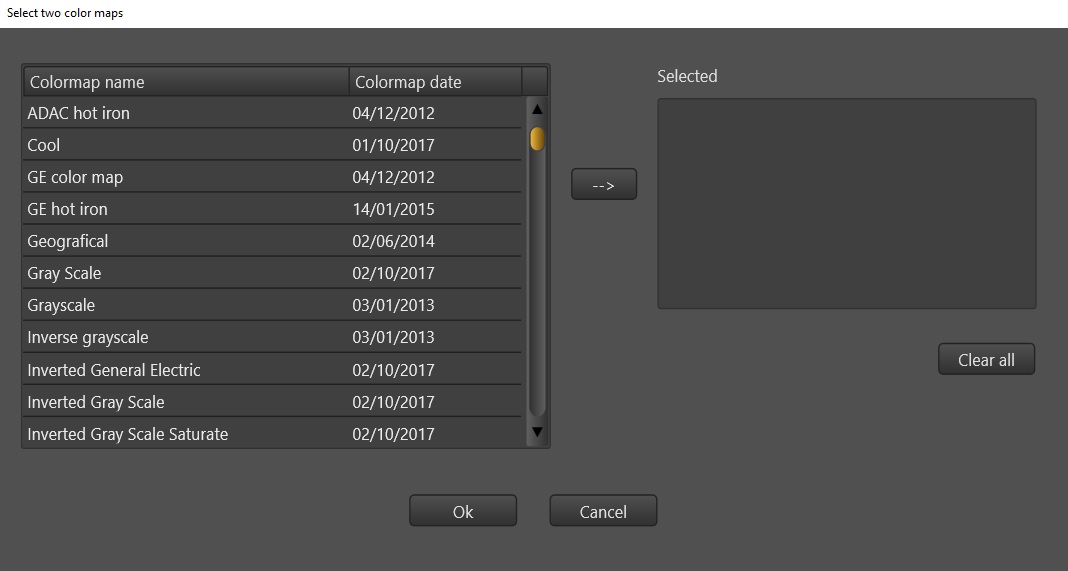


fig.3.14

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

## 3.17 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.3.15 is shown.

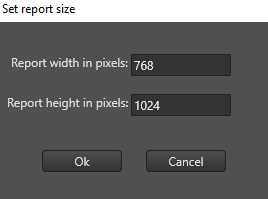


fig.3.15

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

## 3.18 Load report

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

## 3.19 Load RGB report

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

## 3.20 Save report

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

## 3.21 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.

## 3.22 Save report as jpeg file

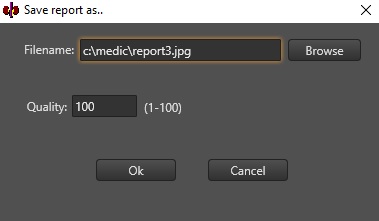
To save the current report as a jpeg file select Report->Save as->JPEG file and the dialog in fig.3.16 is shown.

fig.3.16

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

## 3.22 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.

## 3.23 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.

## 3.24 Print report

To print the current report on a connected windows printer select Report->Print and the dialog in fig.3.17 is shown.

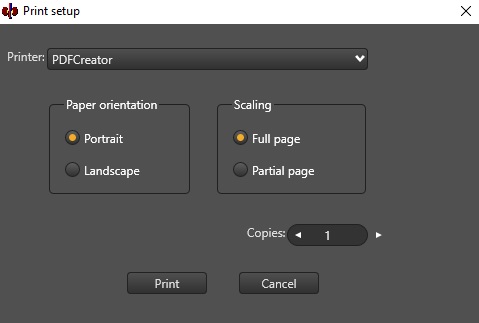


fig.3.17

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