Virtual Magnetic Resonance Scanner

User Manual

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Version 3.2.3, April 12, 2006

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Preface

The idea of this project is based on the wish to give future medical students a good access to the complexity of the magnetic resonance imaging. As not every medical student gets access to a clinical magnetic resonance scanner during his/her studies, the aim of this project was to simulate features and functions of such an scanner by a computer system.

In order to open the simulation to a large number of users, the project has been put under the control of the GPL license.

After a planning phase of more than one year the first concrete realization was made within the thesis of Christian Schalla and Andreas Trümper. Without the support of Professor Reusch, head of the institute of computer science I at the University of Dortmund, the project, certainly, would not have been realized.

The current version is a further development of the above mentioned thesis. Didactic aspects as well as a reduction and reorganization of the source code have played a central role so that other developers can also collaborate on the project later on.

Solingen, in November 2002

Contents

1 Installation

1.1 Hardware and software requirements

The *Virtual Magnetic Resonance Scanner* is programmed in pure Java. Therefore, the program runs on every computer a Java virtual machine or Java Runtime Environment (JRE), version 1.2 or higher, are installed on.

To perform the extensive calculations of the simulation within an acceptable time a Pentium II processor with a processor clock speed of 400 MHz and a random access memory (RAM) of 128 MB has to be available under Windows and Linux i386 at least. The system excellently runs on a Pentium II processor with 500 MHz and 256 MB. For a better performance a large amount of RAM is more important than a faster processor.

For the hard disk space is 1 MB sufficient.

If you want to install the virtual MR from a CD you have to connect the CD-ROM drive to the computer. If you want directly to start the program from the CD the CD-ROM drive has to be able to read the CD with speed 20X at least.

1.2 Windows

First make sure, that Java 1.4 or higher is installed on your PC. To test type in the Command-Window:

```
java -version
```

If Java is installed, a message stating the version is displayed. If Java is not installed you can download the current version from:

http://java.sun.com/j2se

Next download the *Virtual MR Scanner* from Sourceforge

http://sourceforge.net/projects/vmri

To run the simulation the "bin" Version is sufficient. The "full" version includes the "bin" version as well as the source files and the complete Netbeans project folder to compile the source files.

After decompressing the ZIP archive a folder containing all necessary files is available. By double clicking the file

```
vmrt_xx.bat
```

the *Virtual MR Scanner* is started using the current language settings defined in Windows. By clicking

```
vmrt_de.bat
```

```
vmrt_en.bat
```

```
vmrt_ee.bat
```

the simulation is started with the German, English or Estonian language settings.

1.3 Macintosh OS X

Download the *Virtual MR Scanner* from Sourceforge

http://sourceforge.net/projects/vmri

To run the simulation the "bin" Version is sufficient. The "full" version includes the "bin" version as well as the source files and the complete Netbeans project folder to compile the source files.

After decompressing the ZIP archive a folder containing all necessary files is available. By double clicking the file

```
vmrt_xx_mac
```

the *Virtual MR Scanner* is started using the current language settings.

1.4 Macintosh OS 9

Not tested. Could be problematic because Java 1.4.x was not available for OS 9 as a standard option.

1.5 Linux

Not tested. Should be done similar to the Windows installation. The downloadable files of the Virtual MR are pure Java and not operating system specific.

2 Generating the first image

In this chapter the functional principle of the virtual magnetic resonance scanner (virtual MR) will be illustrated with a simple example:

> The installed data set of a reference phantom is to be measured with an inversion recovery pulse sequence. The inversion time has to be set in this way that either the cystic fluid or the fat give no signal.

On a Windows system the program is started with a double click on the batch-file *vmrt.bat*. First a splash screen is displayed with references to the version number and to the GLP license.
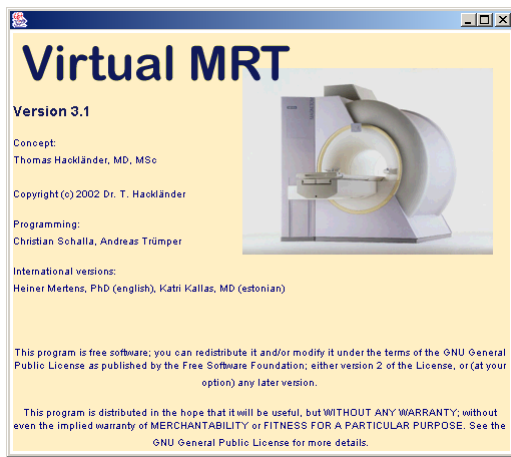
Then, the main window of the virtual MR is opened. It is divided into an image area on the left and a control area on the right.
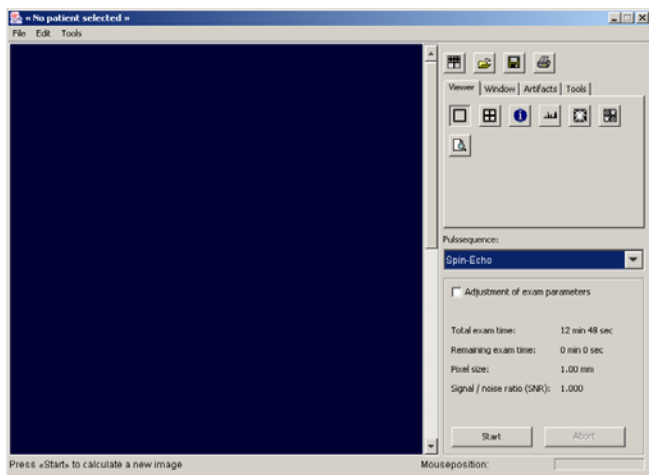
The title bar *No patient selected* indicates that there is still no object on the scanner for measuring.

By clicking on the left icon in the uppermost part of the control panel the data set of a reference phantom is loaded. The title bar is changed to *Information about the patient: Reference Phantom* and a window with the description of the data set is opened.
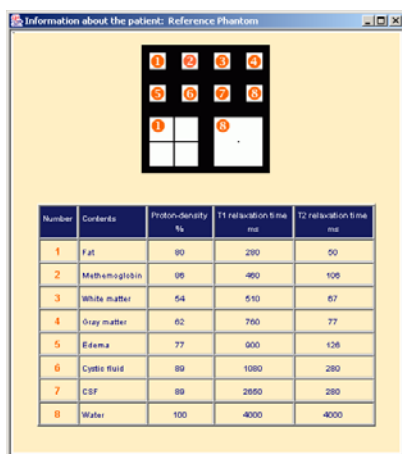
The window shows the arrangement of objects in the phantom in the upper part and a table of values in the lower part. In the phantom 8 smaller objects of the same size and 2 larger objects of the same size are arranged. The objects are composed of different substances. The substances are numbered and listed in the table. In the table the proton density as well as T1- and T2 relaxation time are given for each substance. In the phantom the cystic fluid is in the second row in the second column, the fat in the first row in the first column.

For imaging the phantom the pop-up menu *pulse sequence* in the middle of the control area has to be opened and *Inversion-Recovery* has to be selected.
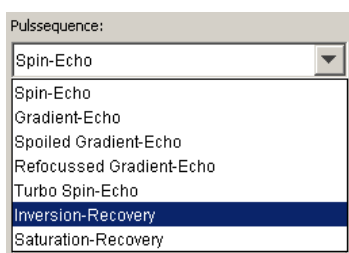
By selecting the check box *Adjustment of exam parameters* on the lowest panel of the control area a panel is opened in the lower half of the image area. The activation is indicated by a check mark. Via this panel the parameters of the pulse sequence can be determined:
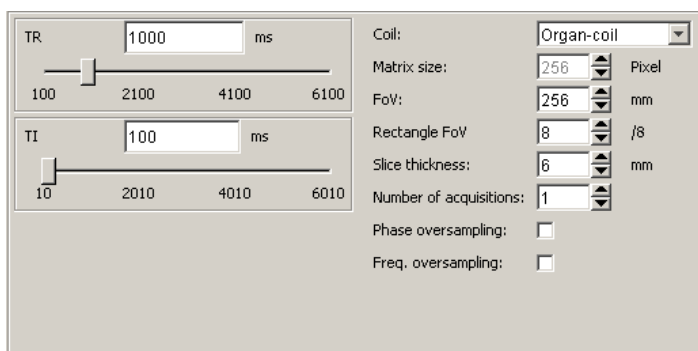
First the value of 5000 is entered for the TR (repetition time). For the TI (inversion time) the value of 749 is entered[1]. After entering all values the panel has to have the following appearance:

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[1] Calculation of the inversion time: The signal intensity I of the inversion recovery pulse sequence is defined by the formula: $I = k * PD (1 - 2 *e\text{-}TI/T1)$. In case of a given T1 value of a substance the equation can be solved

Now the parameter panel has to be deactivated by deselecting *Adjustment of exam parameters*.

By clicking on the *Start* button the calculation of the image is started. A few seconds later the result is shown in the image area of the virtual MR. As expected the image of the cystic fluid (in the second row in the second column) is black because the signal intensity is zero.
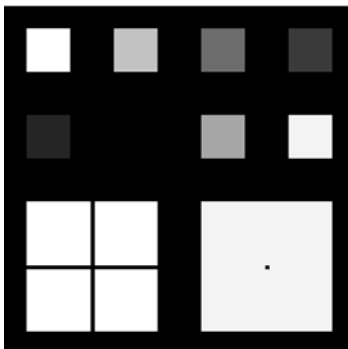
Now a value of 194 is entered for TI as described above. Subsequently, the calculation of the image is started again. The image of the fat is black i.e. no signal intensity (in the first row in the first column). Using this parameter setting the image of the cystic fluid has an intermediate signal intensity.

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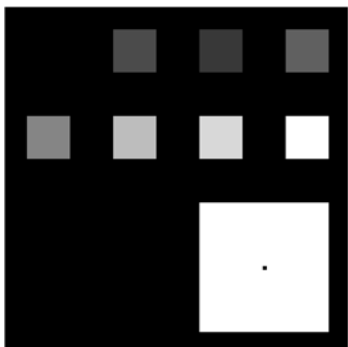
for TI; that is the point the signal intensity is zero: TI = -T1 * ln(1/2). For the cystic fluid with a T1 = 1080 ms TI is equal to 749 ms. For fat with a T1 = 280 ms TI is equal to 194 ms.

3 Operating the virtual magnetic resonance scanner

Essentially the main window of the virtual magnetic resonance scanner (virtual MR) is divided into an image area ❶ on the left and a control area on the right.

The control area is subdivided into three control panels numbered ❷, ❸ and ❹:

The uppermost part ❷ contains the commands *Load reference phantom*, *Select a new patient, Save the currently selected* image and *Print the currently selected image*.

On the tabbed pane ❸ functions are thematically grouped. The functions refer to the currently selected image.

From the control panel ❹ the pulse sequences can be selected and the parameters of the selected pulse sequence can be determined. Additionally, informations about the examination are displayed. Furthermore, this part contains the buttons to start or to abort the pulse sequence.

At the bottom the main window there is an information bar ❺ divided into status bar and *mouse position*. On the status bar informations about the processing are given to the user. The *mouse position* displays the current position of the mouse pointer on an image.

On the top of the main window there is the menu bar. Most of the entries can be also activated with the buttons of the control area. Only the command *Exit* as well as informations about the author and the version of the program are available by means of the menus.
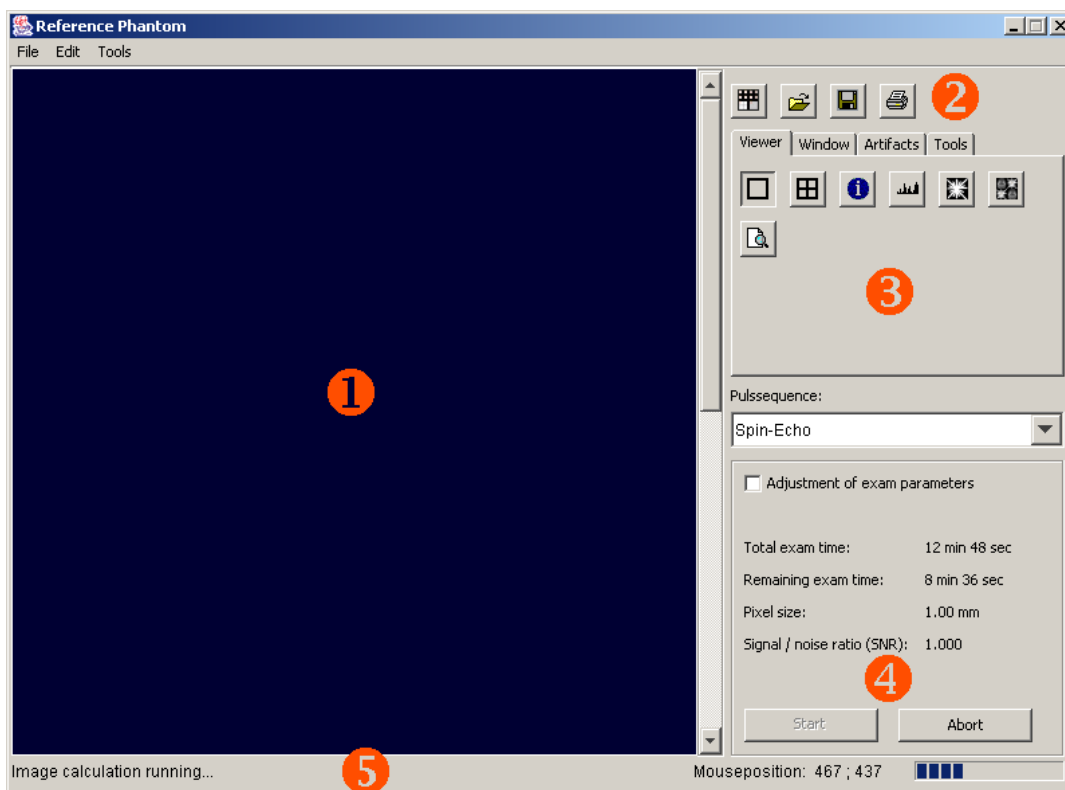
3.1 General functions

General functions of the virtual magnetic resonance scanner (virtual MR) can be selected by means of the operating elements of the control panel ❷.

⊞ Load reference phantom

With this button the installed data set of a reference phantom is loaded. This data set can be also applied if there are no parameter images availa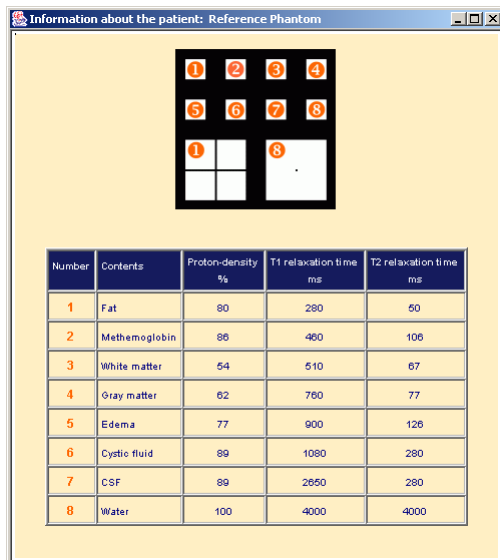ble. The arrangement of the objects in the phantom is displayed in the upper part of the figure shown below. These objects are composed of different physiological substances: fat ❶, methemoglobin ❷, white matter ❸, grey matter ❹, edema ❺, cystic fluid ❻ and CSF ❼ as well as water ❽. For each substance the proton density as well as the T1 and T2 relaxation time are shown in the table of the figure. Please note that these values depend on the magnetic field strength. The listed values are for 1.5T. The percentage of the proton density is referred to pure water and the T1 and T2 relaxation time are given in milliseconds. The larger fat object ❶ in the phantom contains a proton free cross. The larger water object ❽ in the phantom has a small proton free square in the middle.

Information about the patient: Reference Phantom

Number	Contents	Proton-density %	T1 relaxation time ms	T2 relaxation time ms
1	Fat	80	280	50
2	Methemoglobin	86	460	106
3	White matter	54	510	67
4	Gray matter	62	760	77
5	Edema	77	900	126
6	Cystic fluid	89	1080	280
7	CSF	89	2650	280
8	Water	100	4000	4000

◉ Load sample case

As a sample case a brain examination without pathology is loaded.

🗁 Select a new patient

Before the virtual MR can be used to simulate a magnetic resonance scanner it is necessary to load a data set of parameter images. These raw data sets are composed of 5 DICOM formatted parameter files. They optionally have a HTML page with in formations about the particular case. All these files are integrated in an index file with the extension *.idx*.
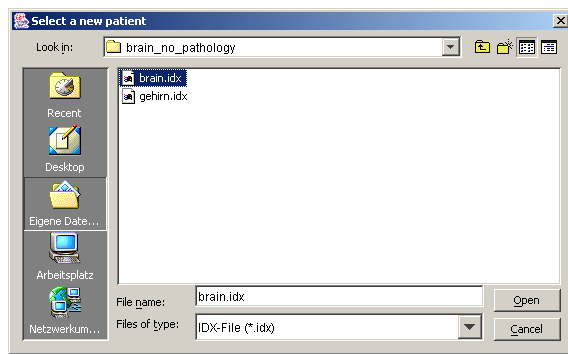
For loading a data set of parameter images the 📂 button is to be clicked on. Thereafter, an operating system specific dialog box for the file selection is opened. By means of this dialog the user can navigate through the directory structure of the file system. Furthermore, the raw data set that is be loaded can be selected by the index file. If a HTML page with informations about this case exists this page will be automatically displayed.

💾 Save the currently selected image

As soon as an image is generated and displayed on the screen this image can be selected. Subsequently, the image can be saved. After clicking on the 💾 button dialog window for the file selection appears to save the image. The target directory can be selected and the target file or the name of the file that is to be created can be entered. After clicking on the 💾 button the generated image is saved as a *DICOM-Secondary Capture* image. It can be loaded with any program that is DICOM compliant.
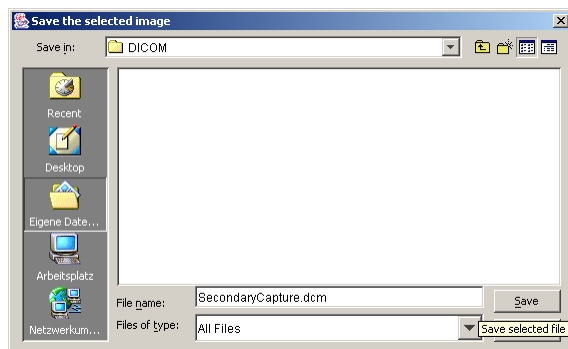
🖨 Print the currently selected image

The currently selected image can be printed as a hard copy on a printer installed on the system. For this purpose the 🖨 button has to be clicked on. The figure shows the dialog window for Windows operating system. Now the printer can be selected. After selecting the printer the print job is started by clicking on the *OK* button.
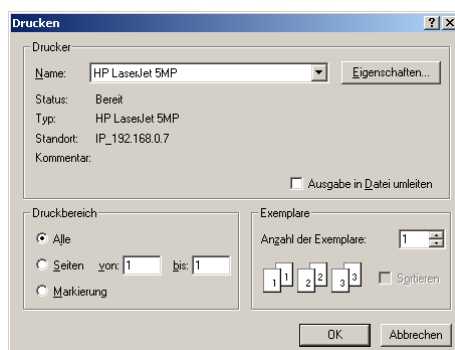
Navigating through the image stack and selecting an image

If more than one image has been generated it can be navigated through the image stack by means of the vertical scroll bar slider on the right margin of the image area. An image can be selected by a simple click on the image. This status is shown to the user by a red frame. Functions as *Save the currently selected image* and *Print the currently selected image* always refer to the currently selected image.
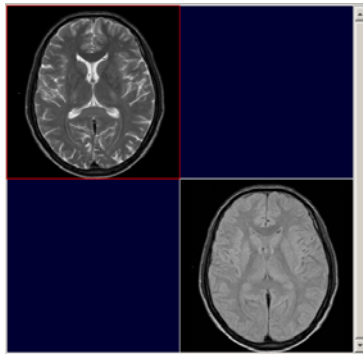
3.2   *Viewer* Tab

The functions under the tab *Viewer* enable the switching between the display of a single image and the display of 4 images, the display of the image labels, histograms and the display of k-space.
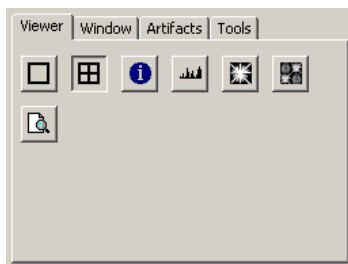
☐ Show 1 image
⊞ Show 4 images

As standard one image is displayed with a spatial resolution of 512*512 pixels. The images generated by the virtual magnetic resonance scanner (virtual MR) always have a spatial resolution of 256*256 pixels. Therefore, the images are displayed with a magnification of 2. By clicking on the ⊞ button four images can be displayed simultaneously. Then, every image is displayed at its original size that is a spatial resolution of 256*256 pixels. The frequency encoding axis is oriented horizontally, the phase encoding axis vertically.
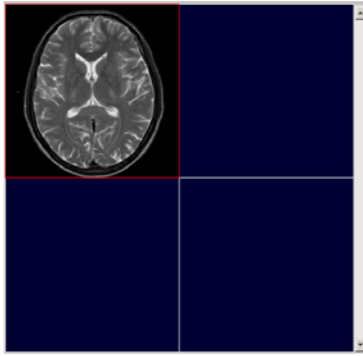
ⓘ Show/Hide image labels

The image labels beside an image can be faded in or faded out with this function. In the top left-hand corner parameters that specify the pulse sequence are shown: type of the pulse sequence (Sequence), repetition time (TR), echo time (TE), flip angle (FA) and echo train length (ETL). In the top right-hand corner the examination date (Examdate), the patient name (Name), birth date (Birthdate) and sex (Sex) are shown. In the bottom left-hand corner the slide position (SP) which is irrelevant to the virtual MR and the current value of the center (C) and window (W) are shown.
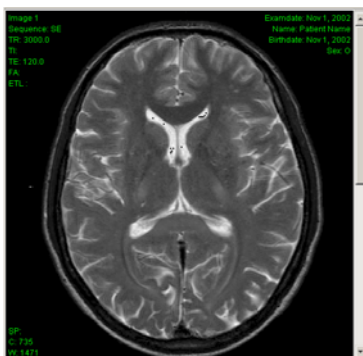
🔍 Display information about the patient

With this function a dialog window is displayed with textural and/or graphical informations about the current raw data set. Please note that such an information does not need to be available for each row data set.

⚊ Histogram of the currently selected image

By clicking on this button a histogram is displayed in a new window. This histogram shows the signal intensity of all voxels of the currently selected image. The shades of grey range from 0 to 255. The height of each bar represents the number of the voxels with the same shade of grey.
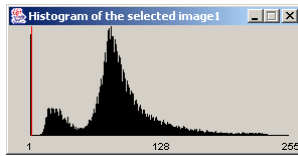
For a better graduation of the histogram the shades of grey that are very numerous are shown by red bars. These red bars do not have their full height because otherwise the other bars are hardly perceptible.

It is possible to open as many histogram windows as you like. The images have to be closed manually by clicking on the *Exit* button of the window frame.

⊞ k-space transform of the currently selected image

The k-space of the currently selected image is displayed in an own window. Here, the frequency encoding axis is oriented horizontally, the phase encoding axis vertically. By clicking on the buttons at the bottom of the window it can be switched between the magnitude and the phase image as well as between the real and imaginary part of the Fourier transform.

Please note that the shades of grey of the magnitude image correspond to logarithmic signal values. It is possible to open as many k-space windows as you like. The images have to be closed manually by clicking on the *Exit* button of the window frame.
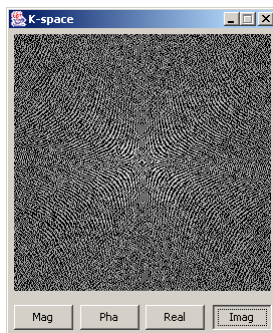
⊞ k-space manipulator for the currently selected image

The k-space manipulator offers the possibilities to alter the data in k-space and to assess the effects in the image space. In the top left-hand corner of the image area the image that was selected while opening of k-space manipulator is displayed. In the top right-hand corner the magnitude image of the Fourier transformed original image is shown. This magnitude image corresponds to k-space. In the bottom left-hand corner the original k-space is displayed initially. This original k-space can be manipulated with the operating elements of the control area.

In the bottom right-hand corner that image that was reverse transformed is displayed. Because the reverse transform requires time this reverse transform is not performed parallel to the manipulation of k-space but it has to be started by clicking on the *Reverse transform* button. As soon as a reverse transform is completed the window width and center of the reverse transformed

image can be adjusted by the mouse as described under the *Window Tab*. Besides, the image can be transferred on the virtual MR by clicking on the *Transfer to Viewer* button. The image is stored as a new image on the virtual MR corresponding to the settings of the *Tools Tab*.
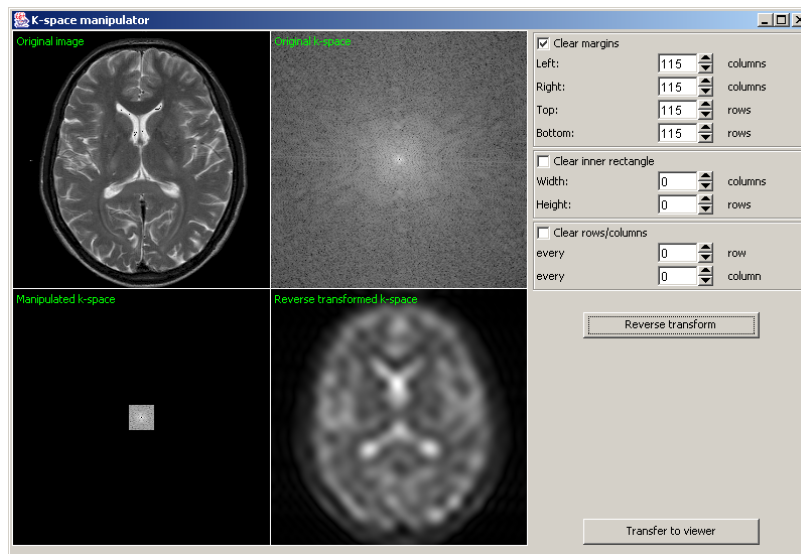
At the moment there are three operators of manipulation: *Clear margins*, *Clear inner rectangle*, *Clear row/column*. The operators are displayed in the control area of the main window. The operating elements of each operator are grouped into frames. An operator can be turned on/off. Its activation is indicated by a check mark next to the feature. As soon as the operator is turned on the settings of the operating elements of this operator have their effects on the manipulated k-space.

The manipulator *Clear margins* allows to clear the data from some rows or columns of the left-hand, right-hand, upper or lower margin separately i.e. the signal intensity of these rows or columns is set to zero. This manipulation has the effect that the detail-information in the image space get smaller.

The manipulator *Clear inner rectangle* allows to clear the data of the rectangle that is located in the centre of k-space. The height and the width of the rectangle can be determined before clearing the rectangle. If this rectangle becomes larger the contrast in image space will be lower and the edges of the image will be sharper.

The manipulator *Clear row/column* allows to clear the data from every nth rows or every nth columns. This manipulation has the effect that the higher order images get closer to the central image and are made visible in the reverse transformed (central) image. This can be seen as a wraparound artifact by the user.

3.3   *Window* Tab

The signal intensities of each voxel can be from 0 (pure black) to 4096 (pure white). But only 256 shades of grey can be visually distinguished. Therefore, the user has to determine the intensity range that is to be presented in these shades of grey. This operation is designated as *windowing*.

For that the width and the center of the window have to be determined for the signal intensities. Example: The width is 100 and the center is 200. Then, all signal intensities between 150 and

250 are converted to 256 shades of grey. All intensities from 0 to 149 are black, from 251 to 4096 are white.
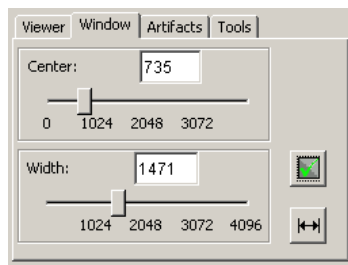
Manual windowing

The control panel has a scroll bar for the window center and for the window width as well as a text box for center and width. The values of the center and width can be directly entered into the text box or can be set by moving the scroll bar slider with the mouse while keeping the left mouse button pressed. With these options the windowing of the selected image can be done manually.

For windowing the image on the canvas the windowing function is activated as follows: The mouse pointer is positioned on the canvas, and the left mouse button is kept pressed while dragging. The activated function is displayed by altered mouse pointer. The up/down movement of the mouse changes the window center, the left/right movement the window width.

⊢⊣ Maximal window

With this function the windowing of the selected image is set to the maximum values, i.e. is set to the center 2048 and width 4096. With this setting all possible 12 bit values are presented in shades of grey. Usually, the image contrast is very poor.

☑ Optimal window

With this function the optimal window of the selected image is obtained. First of all, the smallest shade of grey-scale *min* and the largest shade of grey *max* is determined. The width is set to *max-min* and the center is set to *min+(max-min)/2*. In this way the image contrast is optimized.

Example

In the figure shown below one and the same image is displayed with four different window settings: In the top row the optimal window and maximal window are displayed. In the bottom row two manually selected window settings are shown.
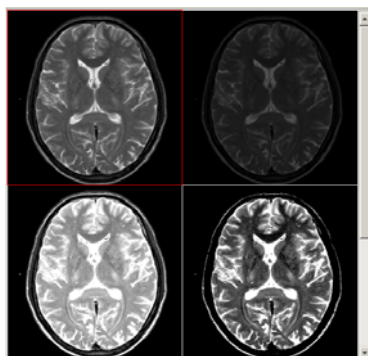
3.4   *Artifacts* Tab

Here the user can simulate the influence of different types of motion on the images. It is distinguished between a simple translational motion and a periodic motion.

Via a pop-up menu the user can select the types of artifact for the simulation. Depending on the selection additional setting options are visible on the panel.

Translational motion

Translational motion can be simulated along the x-axis and/or the y-axis. This corresponds to the situation when the body or part of the body move along the x-axis with constant velocity (horizontal velocity) and/or along the y-axis with constant velocity (vertical velocity). The x-axis corresponds to the frequency encoding axis, the y-axis to the phases encoding axis.
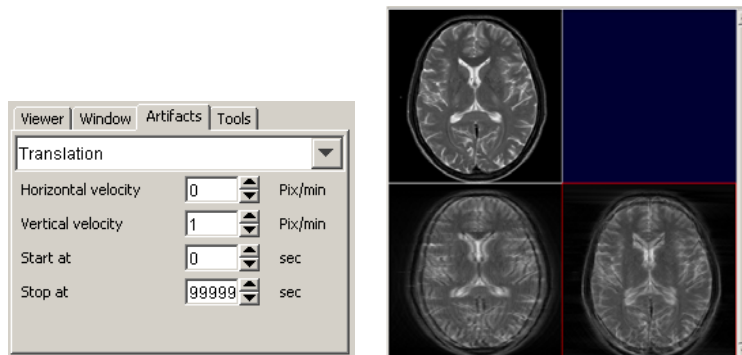
Via the panel the horizontal and/or vertical velocity can be determined. The velocity is given in pixel/minute. Furthermore, the start and the end time of the body movement can be determined. The start of the movement is delayed by 0 to 99999 seconds in comparison to the start of the examination.

Example: If the start is fixed at 30 seconds then more or less lines of k-space will be taken without artifacts depending on the pulse sequence selected.

In the top left-hand corner of the image area an image without artifacts is shown. In the bottom left-hand corner one artifact has been generated by superposition of a motion artifact along the frequency encoding axis (x-axis). In the bottom right-hand corner another one has been generated by superposition of a motion artifact along phase encoding axis (y-axis).

Periodic motion

Periodic motion e.g. respiratory motion can be simulated along the x-axis and/or along the y-axis. The x-axis corresponds to the frequency encoding axis, the y-axis to the phase encoding axis.

In addition to the maximum amplitude of the motion given in pixel the frequency of the motion given in 1/minute has to be also entered by means of the panel. Furthermore, the start and the end of the body movement can be determined. The start of the movement is delayed by 0 to 99999 seconds in comparison to the start of the examination.

Example: If the start is fixed at 30 seconds then more or less lines of k-space will be taken without artifacts depending on the pulse sequence selected.

In the top left-hand corner of the image area an image without artifact is shown. In the bottom left-hand corner one artifact has been generated by superposition of a motion artifact along the frequency encoding axis (x-axis). In the bottom right-hand corner another one has been generated by superposition of a motion artifact along phase encoding axis (y-axis).
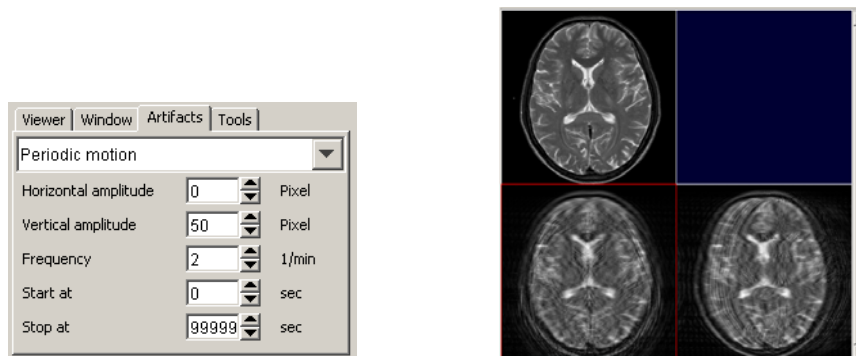
3.5   *Tools* Tab

Via this panel the next image can be positioned and the relative duration of the simulation can be determined.
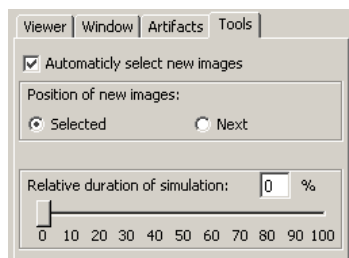
Position of a new image

With the function *Position of a next image* the user can determine the position the next calculated image is to be displayed on: The option *Selected* pastes the calculated image on the currently selected position. An image on this position will be overwritten. The option *Next* pastes a new image on the next free position within the image batch. The standard setting is the option *Next*.

Relative duration of simulation

The setting *Relative duration of simulation* gives the user an idea of the real examination time of a pulse sequence. The setting determines the duration of the simulation. The relative duration of the simulation refers to the percentage of the real examination time.

Example: If the relative duration is fixed at 50% the simulation will take 50% of the real examination time. If the relative duration is fixed at 0% the image will calculated as fast as possible. The image generation only needs the pure calculation time.

Especially for the fast pulse sequences the simulation time can be longer than the real examination time. Particularly the simulation of the Turbo-Spin-Echo may takes longer than the real examination time. This is because of several Fourier transforms which have to be done for the simulation.

The optional simulation of artifacts needs extra calculation time.

Activating a new image

If the check-box is selected a new calculated image is automatically selected.

3.6 Selection of the pulse sequence and setting the measuring parameters

From the pop-up menu *Pulse sequence* the type of pulse sequence can be determined.
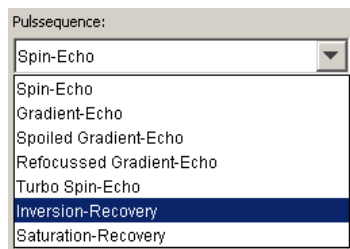
By selecting the check-box *Adjustment of exam parameters* a new control panel is opened in which the settings regarding the pulse sequence can be done. If all settings has been done the control panel can be deactivated by deselecting the check-box *Adjustment of exam parameters*. The settings are kept fixed until another type of pulse sequence is selected.

The control panel is divided into two parts: the right part is the same for all types of pulse sequence, the left part depends on the type of pulse sequence.
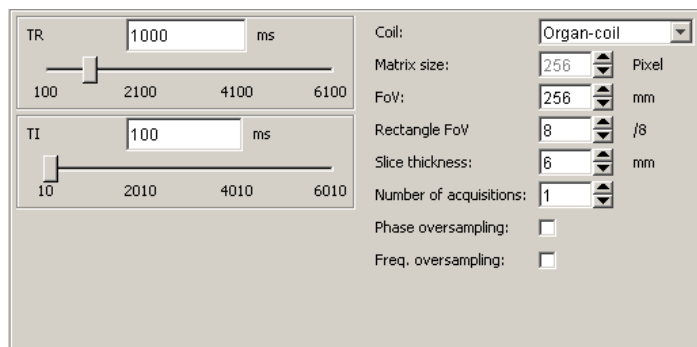
General parameters of a pulse sequence

- **Coil:** Body coil or organ coil can be selected. If the body coil is selected the noise will be stronger as on a real magnetic resonance scanner.

- **Image matrix:** The simulation uses a fixed image size of 256*256 pixels. This value is only informative and can not be changed.

- **FoV:** The field of view is given in millimeter (mm). The FoV determines the dimensions of the part of the body that is to be examined. The FoV is divided into 256 rows and 256 columns. In this way the pixel size is determined indirectly.

- **Rectangle:** The number of the phase encoding steps oriented along y-axis can be reduced. Example: The rectangle is 6/8. Then, for a single image the phase encoding step is repeated 192 times ([6/8]*256) instead of 256 times ([8/8]*256).

- **Slice thickness:** The slice thickness can be determined. A thinner thickness results in a lower signal-to-noise ratio and thus the image quality is reduced.

- **Number of acquisitions:** The number of acquisitions or excitations (NEX) determines how often a measurement is performed. An increase in the number of acquisitions prolongs the examination time by a factor of NEX.

- **Phase-OS:** With phase oversampling performed along the y axis the number of phase encoding steps are doubled resulting in doubling the examination time. Turning off the phase oversampling can lead to wraparound artifacts.

- **Frequency-OS:** With frequency oversampling performed along the x axis the sampling rate is doubled. There is no effect on examination time but turning off the frequency oversampling can lead to wraparound artifacts.

The values can be directly enter into the text box or can be determined by clicking on the ▾ button or the ▴ button.

Please note that the settings carried out for the general parameters of a pulse sequence can have an effect on the examination time, the pixel size and the signal to noise ratio.

Specific parameters of a pulse sequence

The specific parameters of a pulse sequence can be determined with the operating elements in the left part of the panel. For the inversion recovery pulse sequence shown in the above figure these are the repetition time *TR* and the inversion time *TI*. These value can be changed by moving the scroll bar slider with the mouse or these values can be directly entered into the text box.

The following specific parameters of a pulse sequence can be determined for each pulse sequence:

- **Spin echo pulse sequence:** repetition time (TR), echo time (TE)

- **Gradient echo pulse sequence:** repetition time (TR), echo time (TE), flip angle

- **Spoiled gradient echo pulse sequence:** repetition time (TR), echo time (TE), flip angle

- **Refocussed gradient echo pulse sequence:** repetition time (TR), echo time (TE), flip angle

- **Turbo spin echo:** repetition time (TR), echo spacing (ESP), effective echo time (TEeff), echo train length (ETL)

- **Inversion recovery pulse sequence:** repetition time (TR), inversion time (TI)

- **Saturation recovery pulse sequence:** repetition time (TR)

3.7 Image calculations

Informations about the examination are shown on the bottom panel of the control area. The simulation can be started by activating the *Start* button. As long as the calculation is carried out the *Abort* button can be selected. The calculation can be stopped with the *Abort* button at any time.
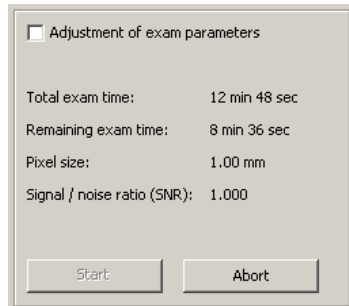
Furthermore, the following informations about the pulse sequence and the progression of the calculation are shown here:

- **Total exam time:** the time needed to perform the examination on a real magnetic resonance scanner using the selected pulse sequence

- **Remaining exam time:** the remaining time needed for a real examination

- **Pixel size:** the size of each pixel in the image

- **Signal / noise ration (SNR):** the signal to noise ratio

- The progression of the calculation is graphically shown by a horizontal progress bar.

3.8 Menus

In the current version of the virtual magnetic resonance scanner (virtual MR) there are functions that are not yet available via menus. The following entries have a function so far:

Menu *File*
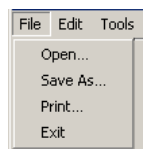
Open...
A new data set of parameter images is loaded. This entry corresponds to the 📂 button.

Save as...
The currently selected image is saved as DICOM file. This entry corresponds to the 💾 button.

Print…

The currently selected image is printed. This entry corresponds to the 🖶 button.

Exit

The program is terminated.

Menu *Edit*

File	Edit	Tools
	Delete Selected Image	
	Delete All Images	
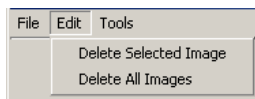
Delete selected image

The currently selected (red framed) image of the image area is deleted. Deleting the image has to be confirmed in a dialogue box. But it is still possible to abort the process.

Delete all image

All images of the image area are deleted. Deleting all images has to be confirmed in a dialog box. But it is still possible to abort the process.

Menu *Tools*

File	Edit	Tools
		About Virtual MRT…
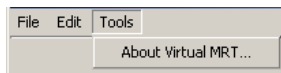
About Virtual MRT

The splash screen is displayed with references to the version of the program and to the GLP license.

Appendix A: Mathematics of the simulation

Abbreviation

α   Flip angle

ΔB   Magnetic field inhomogeneity

etl   Echo train length

ESP   Echo Spacing

γ   Gyromagnetic ratio of the proton = 42,6 MHz/T

k   Dimensionless constant varying for each measurement (current scanner setting)

PD   Proton density referred to pure water [%]

T1   T1 relaxation time [ms]

T2   T2 relaxation time [ms]

T2*   Effective T2 relaxation time [ms]

TE   Echo time [ms]

TE_{eff} Effective Echo time [ms]

TI   Inversion time [ms]

TR   Repetition time [ms]

Spin echo pulse sequence

$$I = k \cdot PD \cdot e^{-TE/T2} \cdot \left(1 - e^{-TR/T1}\right)$$

Inversion recovery pulse sequence

$$I = k \cdot PD \cdot \left(1 - 2 \cdot e^{-TI/T1}\right) + e^{-TR/T1}$$

Saturation recovery pulse sequence

$$I = k \cdot PD \cdot \left(1 - e^{-TR/T1}\right)$$

Turbo spin echo pulse sequence

$$I = k \cdot PD \cdot e^{-TE_{eff}/T2} \cdot \left(1 - e^{-TR/T1}\right)$$

The rows of k-space are filled with echos of different echo times.

$$TE_{eff} = TE - \left(\frac{etl - 1}{2} - n \right) \cdot ESP; \quad n = 0 \dots etl - 1$$

The effective echo time (TE_{eff}) is the echo time of those echos that are selected for the central portion of k-space.

Gradient echo pulse sequence

Instead of the T2 relaxation time the effective T2 relaxation time (T2*) has to be used. T2* depends on the T2 relaxation as well as on the relaxation caused by the magnetic field inhomogenity (ΔB). T2* is defined by the formula:

$$T2^* = \frac{1}{\frac{1}{T2} + \gamma \cdot \Delta B}$$

In case of the magnetic field inhomogenity[2] the virtual magnetic resonance scanner (virtual MR) simulates a 1.0 T scanner. This scanner has a magnetic field inhomogenity of 5 ppm applying a field of view (FoV) which is 50 cm in diameter. Using a FoV of 50 cm and a spatial resolution of 256*256 pixels (picture elements) the magnetic field inhomogenity over each pixel (ΔB) is equal to $19.5 * 10^{-9}$ T.

With the following substitutions

$$a = e^{-TR/T1}$$

$$b = e^{-TR/T2^*}$$

$$c = e^{-TE/T2^*}$$

the signal intensity of the different gradient echo pulse sequences is given by the following equations:

$$I = k \cdot PD \cdot \frac{c \cdot (1 - a) \cdot \sin \alpha}{(1 - a \cdot \cos \alpha) + b \cdot (\cos \alpha - a)}$$

Spoiled gradient echo pulse sequence

$$I = k \cdot PD \cdot \frac{c \cdot (1 - a) \cdot \sin \alpha}{1 - a \cdot \cos \alpha}$$

Refocused gradient echo pulse sequence

$$I = k \cdot PD \cdot \frac{\sin \alpha}{1 + \frac{T1}{T2^*} - \left(\frac{T1}{T2^*} - 1 \right) \cdot \cos \alpha}$$

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[2] Hashemi R: MRI the basics. Williams, Baltimore, 1997. Page 48.

Appendix B: Using the Jar bundler under Macintosh OS X

First download the developer tools from the Apple Support site.

Run the Jar bundler

`Developer/Applications/Java Tools/Jar Bundler`

Use the following information to fill the dialog box:

Card: `Build Information`

    `Choose…`

        `Select dist/vmri.jar File`

        `Select virtual.mrt.VMRT as "Main Class"`

    `Anti-alias Text`

    `Anti-alias Graphics`

    `JVM Version: 1.4*`

Card: `Classpath and Files`

    `Add…`

        `Select dist/lib/dcmlib.jar`

        `Select dist/lib/dicomie.jar`

        `Select dist/lib/jai_imagei.jar.jar`

Card: `Build Information`

    `Create Application…`

        `vmrt_xx_mac`

Appendix C: GPL License

GNU General Public License

Version 2, June 1991

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Updated: 3 Jan 2000 rms