

Table of content    Introduction	<ul> <li>Creating new images</li> <li>Delineating volumes of interest (VOIs)</li> <li>Annotating images with text</li> <li>Calculating VOI statistics</li> <li>Generating graphs</li> <li>Capturing the image region</li> <li>Shortcut editor</li> <li>Viewing and editing image attributes</li> <li>Image Attributes Dialog Box</li> <li>Tutorial</li> </ul>
<b>2</b>	

The presentation consists of two parts – the first contains 22 slides providing rough introduction of the MIPAV software - showing the main options and general interface. The second part is the tutorial - which shows how to deal with specific images to obtain desired results.

# Introduction Medical Image Processing, Analysis and Visualization — MIPAV Image processing, analysis and visualization software, used to extract quantitative information from various medical images It can run on virtually any platform, including (Windows, Solaris, Mac OS, Linux) — platform independent JAVA written software Extensible: works with JAVA written plugins Image browser for medical file types e.g. \*.dcm (DICOM¹)

This is a short characteristic of MIPAV - the most important about this software is that you can use it for free (non-commerce distribution), that it runs virtually on any platform, it is extensible for java language and supports the most important medical format - DICOM.

MIPAV is written in java, so you have to make sure that you have java virtual machine installed on your PC, otherwise you will need to download and install it from Sun Corporation web site.

## Downloading MIPAV Download link: http://mipav.cit.nih.gov/clickwrap.php Read the license and accept terms of use Fill the form (only name and e-mail required) Choose between beta and stable version Choose your operating system: Support for 32-bit and 64-bit systems Any Java-enabled platform Start the download of 115 MB installMIPAV.exe file

It is important to choose a proper operating system (32/64 bits) to obtain the best results. We recommend to download stable version for ordinary work – beta version is rather for developers and people who are already familiar with MIPAV and can recognize any bugs. Another vital issue is a license – this topic is covered on the next slide.

## License

The software is a freeware software, an acceptance to the agreement needed

### Main points of the agreement:

- It is not allowed to use the software for treating or diagnosing of human subjects
- No distribution or licensing is allowed
- Use of software just at recipients institution or location
- Neither services nor improvements are provided
- ▶ The use of the software is "on users own risk"
- Extending and modifying of software aren't allowed unless consulted with the provider
- It's not allowed to reverse engineer, decompile, or disassemble the software

**5** 

# Installing MIPAV □ To launch MIPAV on Windows you need to install Java Virtual Machine for Windows systems (Sun's Java website - http://www.oracle.com/technetwork/java/index.html). □ Run installMIPAV.exe and follow instructions: □ Choose directory for the application □ Agree with the terms of use □ Go to Start Menu/MIPAV/mipav.bat □ Specify the allocation of the memory (do not exceed the computer's physical RAM; you can change it later: Menu Help/Memory Allocation). □ 6

Since MIPAV is written in Java, you can choose how much of RAM will be used by it for image processing. You specify it at the first launch, but you can change it later in Help Menu. We recommend you to allocate about 200mb for ordinary work and as much as possible for 3D processing.

```
Supported formats

MIPAV supports three categories of graphic file formats:

• vector (i.e., volume of interest,)

• bitmap (i.e., 2D to 5D grayscale or RGB images)

• 3D images

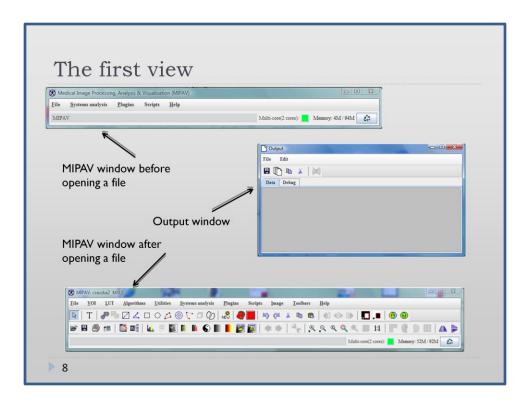
Among them:

• Medical (*.dcm, *.xml, *.ima, *.img, *.mnc, *.sig, *.head, *.nii, *.rec, *.frec, *.nrrd, *.gz, *.bz2); DICOM

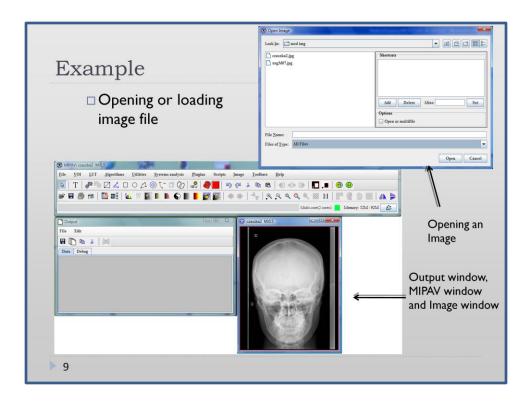
• Microscopy (*.avi, *.ics, *.liff, *.lsm, *.pic, *.stk, *.tif, *.tiff, *.xml)

Images from CT, MRI, PET, Confocal Microscopy
```

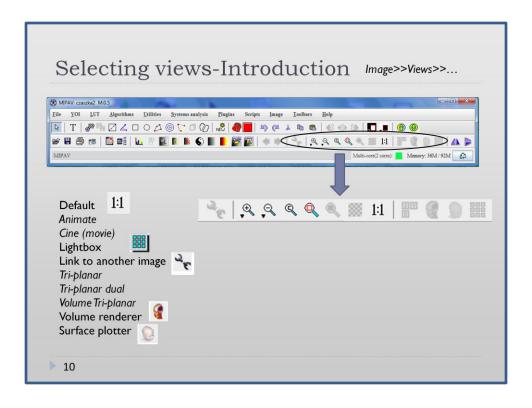
DICOM (e.g. \*.dcm files) is a vital file format for medical data (DICOM states for Digital Imaging and Communications in Medicine). It is a standard used commonly over a whole globe, therefore people can easily exchange medical data and work using it. This format is characterized e.g. by embedded details of a patient. Some other important medical formats are \*.img, \*.ima and some compressed ones: \*.gz.



After starting the programme 2 windows open: Output window in which appear results of calculations and Main MIPAV window. Before opening any file the MIPAV window is very simple and consists of very limited menu. After opening the file the MIPAV window is getting bigger and richer with various icons.



This is a first view after opening an image (File Menu/Open image from disk). We will cover this topic in details in the Tutorial part of the presentation.



Light box- this icon makes it possible to put several pictures into one window.

Cine view- MIPAV advances one frame a time. As a result sth like a film appears.

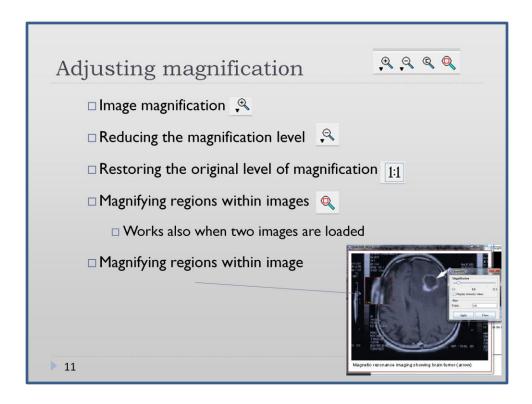
Animate view is a similar option to Cine wiev. Here however it is possible to determine the speed in which the pictures are advanced, direction (forward/reverse). It is also possible to pause or stop which wasn't possible in the cine view option.

Tri-planar view-makes it possible to see orthogonal planes of 3D or 4D datasets

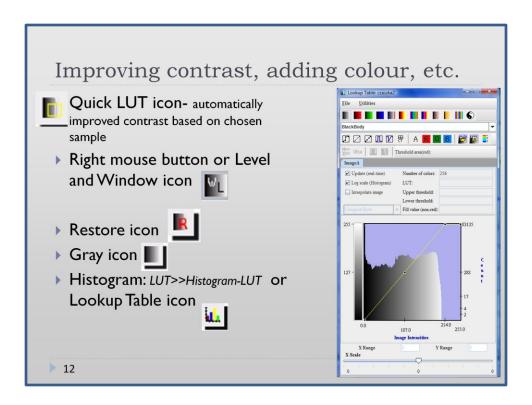
Tri-planar dual- orthogonal planes of 2 images and their blended version

Surface plotter- the 3D picture out of 2D picture is made: the intensities in 2D pic. are represented by height in the 3D pic.

Link to another image-connects two sets of slices so that slices change in both pictures simulaneously.



There are many options for dealing with magnifications - the most interesting is probably the option for magnifying regions within the image (imitating magnifying glass). An example is showed on the slide.



Some definitions to start with:

**look-up table (LUT)**—Indicates the intensity of each voxel in the image and, in MIPAV, allows you to remap the original intensities to other intensities.

**transfer function**—Reflects the relationship between the original image intensity values and how they are mapped into the LUT. The line in the histogram represents the transfer function.

LUT — Look-up Table. The LUT allows to remap the original intensities in other intensities. The user may remap the intensities by the predefined, offered by MIPAV color LUTs or change the transfer function manually. There are severeal ways to use the LUTs functions.

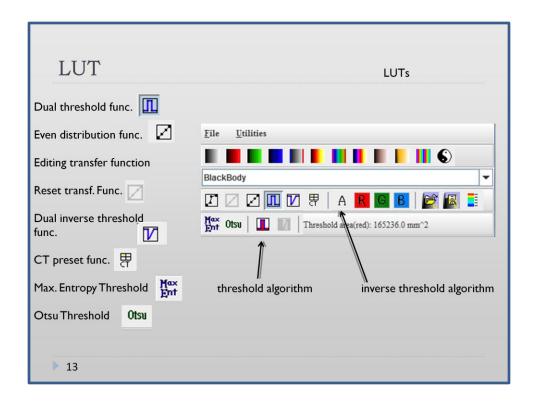
- 1. Lookup Table icon or Quick LUT icon
- 2. In the MIPAV window click LUT>>Histogram-LUT. If VOI was defined before that, its possible to choose wether the histogram should be applied just to VOI or to whole image. Then the Look-up Window appears.

Level and Window icon is an easy tool to manipulate transfer function

Restore icon- coming back to original settings

Gray icon- changing LUT back to grayscale

Look-up window contains of the Histogram (possibility to change from log scale to decimal scale, interpolate image) menu-bar and toolbar.

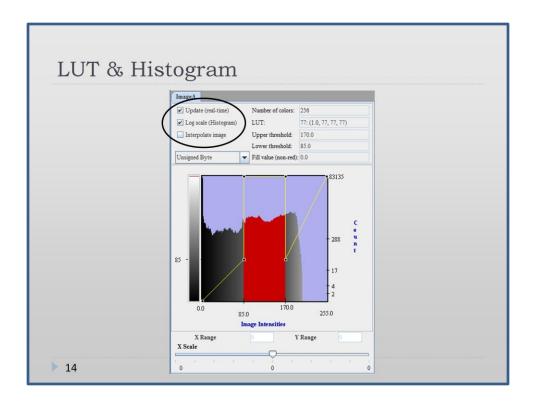


Menubar gives possibilities to save the created LUT, open saved LUT or open/save threshold.

Toolbar presents defined LUTs. A LUT may be chosen by clicking the appriopriate icon or by choosing a LUT from more extensive list. Below the list of LUT there's a series of icons for transfer function change and reset as well as for dual (inverse) transfer function. There are also icons for editing red, green, blue LUT function which allow to edit particular components of LUT. Also open/save/generate LUT icon should be mentioned. Another functions are maximum entrophy threshold, Otsu threshold, Running threshold algorithm and running the inverse threshold algorithm (details appear in outpt window).

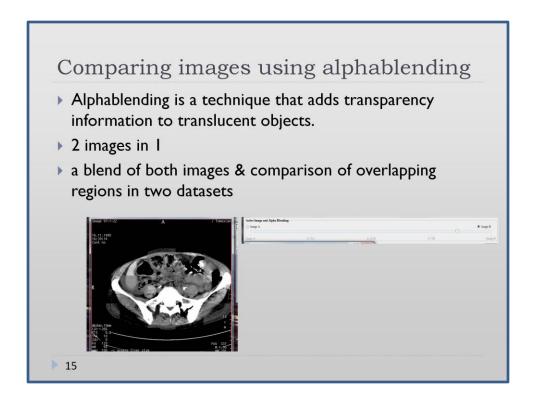
CT icon- choosing the LUT adequate for the body part presented in the picture.

Otsu Threshold- reduction of graylevel image to binary image- as a result the image contais two classes of pixels.



The lower part of the "LUT window" contains histogram. It is possible to change from decimal to logarythmic scale.

Ticking off the "Update" option causes that the changes made by pulling the transfer function are seen on the picture after the actual change is done.



Alphablending is a very useful technique, especially, when we would like to compare two images of the same region of a body, but taken at different time, e.g. before treatment and after it. I could be also used for the comparison of the same regions of the body, but of different patients. One can control the level of transparency of each image or display images using checkerboard pattern.

## Creating new images

A) The image file is not open

File>>Open Image(A)>>Create Blank Image

B) The image file is open

File>>Load Image(B)>>Create Blank Image

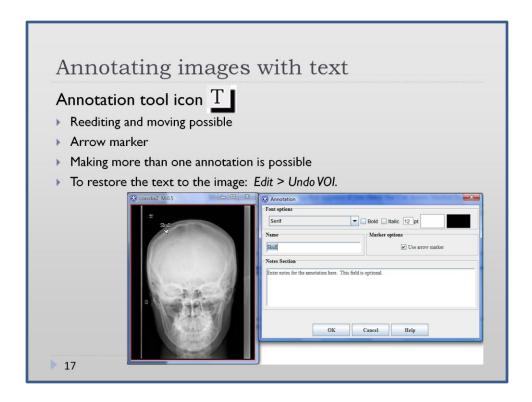
Then:

Select the image type, units of measure for each dimension, enter the header offset and byte ordering information.

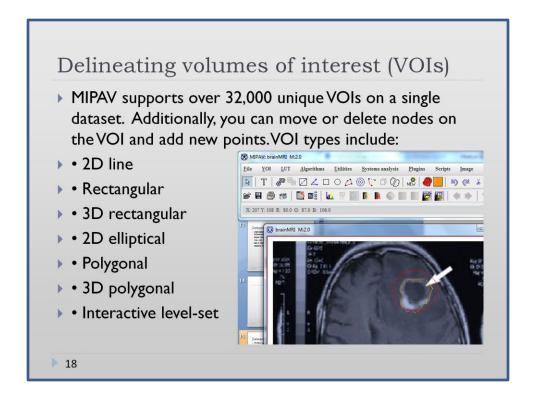
VOI and paint tools for creation the image.

**1**6

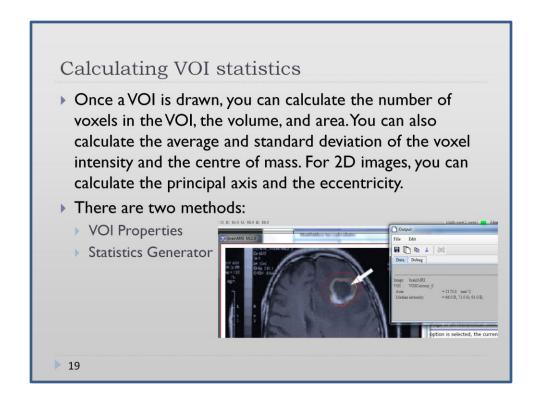
You can open a blank image and create your own graphics using simple paint tools. Painting tools may be specially usefull for marking and highlighting wished areas or points.



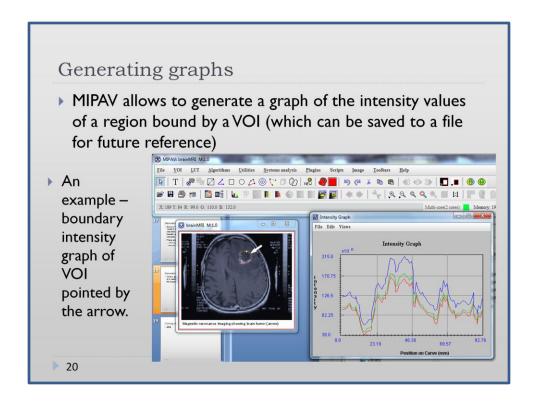
After clicking the annotation tool icon the window appears where typing the annotation is possible. You can also change the characteristics of the text: font, color etc.



Volume of Interest (or Region of Interest - ROI) is a region of the image that we are the most interested in. It might be a region of some morphological changes, or tissue damages etc. The advantage of MIPAV is that we are not limited as far as the shapes of the VOI are concerned - we have mane pre-defined shapes, and we can draw our own using mouse. Moreover, there are some tools with active contour properties, so we can select desired shaped even more accurately. Circular (red) and user-shaped (using mouse and active contour) (orange) VOIs are showed on the slide.



VOI Properties and Statistics Generator are two very important options in MIPAV. They are both used for calculating different properties of VOI, e.g. median intensity, area, perimeter, min and max intensity, Std Dev intensity, geometric centre, centre of mass, principal axis and others. To obtain these data we can go to the properties of a given VOI - then tick desired properties and click Calculate – as a result we obtain the answers in output window - we can save it to a file. Or - we can use Menu/VOI/Statistics Generator – to do it.

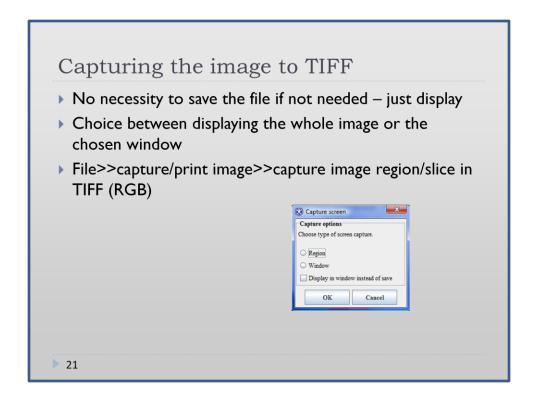


Beside saving data to a file we can display and save them in a form of graphs. To generate a graph:

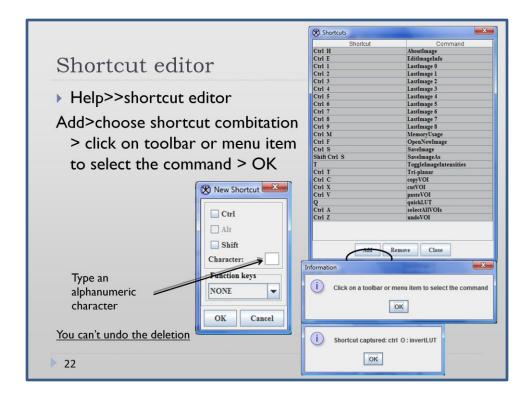
Select a VOI in an image window, then use the right mouse button to call the context menu, then select one of the following:

- Graph > Boundary Intensity
- Graph > Total Intensity
- Graph > Average Intensity
- Graph > Total Intensity with Threshold
- Graph > Average Intensity with Threshold

The chosen Intensity Graph window appears. You can close the graph by either selecting File > Close graph or pressing CTRL+X.



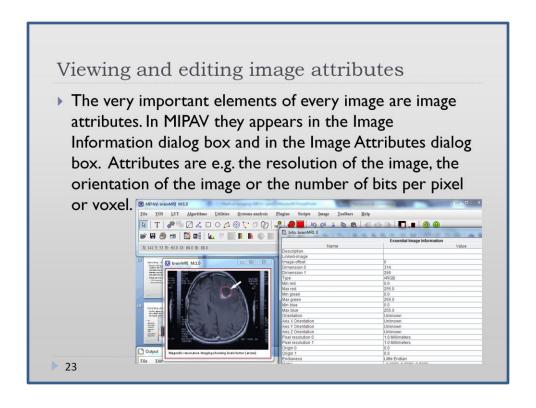
Tagged Image File Format (abbreviated TIFF)



In order to add or edit existing shortcuts you have to go to Menu Help, then shortcut editor. The list of existing shortcuts appears where on the bottom three buttons are seen: add, remove, close.

After clicking "add" button another window appears where the combination for the shortcut has to be specified. Then you will be asked to click on a toolbar or menu item in order to select the command.

You should be careful because it is not possible to undo the deletion.



You can access image attributes from Menu/Image/Attributes/View header. A header is a very interesting source of information about an image, especially in a case of DICOM images, where there are more attributes then in other formats. You can easily edit many attributes of an image. To do so, you have to go to the Menu/Image/Attributes/Edit header.

## Image Attributes Dialog Box

► Image>>Attributes>>Edit Attributes – an Image Attributes Dialog Box opens

General: image modality, image edian order (big/little)

**Resolutions:** resolutions for separate dimentions, slice thickness, definition of unit of measure

**Orientations/Origin:** image orientation definition, orientation of x-,y-,z-axis orientation in the picture, definition of their origin

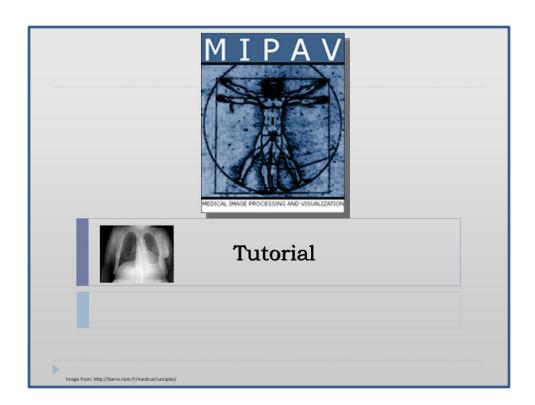
**Transform matrix:** adding, saving, inverting, (...) transformation matrix

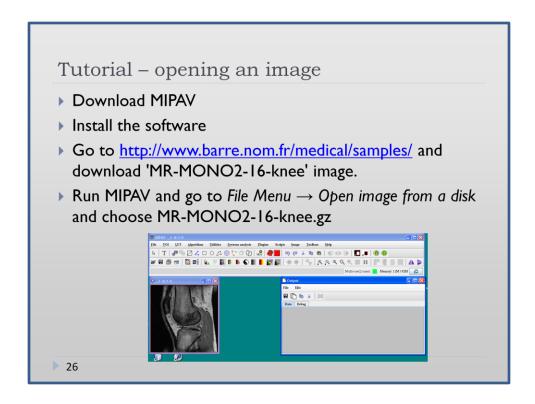
**Talairach:** loading and saving talairach tarnsformation matrix

**24** 

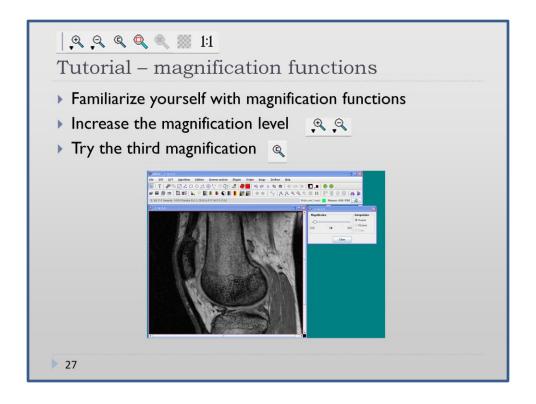
Modality- choice between: Unknown Modality, Biomagnetic Imaging, Color Flow Doppler, Computed Radiography, Computed Tomography, Diaphanography, Digital Radiography, Duplex Doppler, Endoscopy, External Camera Photography, FA, General Microscopy, Hardcody, ICG, Intraoral Radiography, Laser Surface Scan, Magnetic Resonance Angiography, Mammography, Magnetic Resonance, Nuclear Medicine, Other, Positron Emission Tomography, Panoramic X-ray, Radio Fluoroscophy, Radiographic Imaging, Radiotherapy Dose, Radiotherapy Image, Radiotherapy Plane, Radiotherapy Record, Radiotherapy Structure Set, Red Free, Slide Microscopy, Single Photon Emission Computer Tomography, Thermography, Ultrasound, and X-ray Angiography

Information regarding Endiannes: In computing, endianness is the ordering of individually addressable sub-units (words, bytes, or even bits) within a longer data word stored in *external memory*. The most typical cases are the ordering of bytes within a 16-, 32-, or 64-bit word, where endianness is often simply referred to as byte order. The usual contrast is between *most* versus *least* significant byte first, called bigendian and little-endian respectively. Mixed forms are also possible; the ordering of bytes within a 16-bit word may be different from the ordering of 16-bit words within a 32-bit word, for instance; although fairly rare, such cases exist, and may sometimes be referred to as mixed-endian or middle-endian.

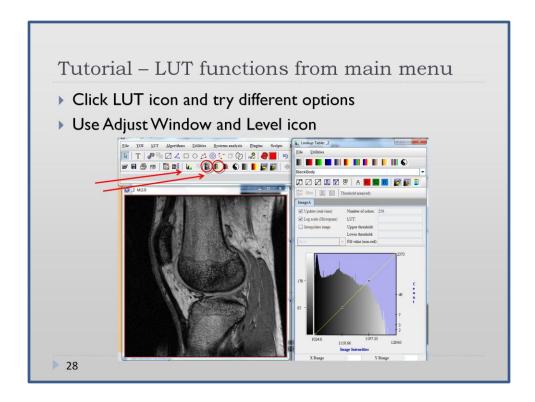




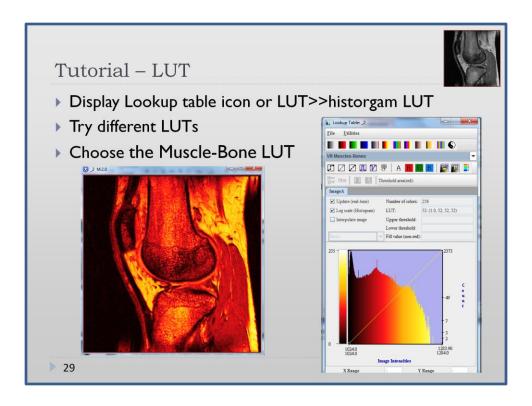
- Download MIPAV from: mipav.cit.nih.gov
   (for details see the introduction of that presentation)
- Install the software
- Go to <a href="http://www.barre.nom.fr/medical/samples/">http://www.barre.nom.fr/medical/samples/</a> and download 'MR-MONO2-16-knee' image.
- Run MIPAV (remember to allocate a proper amount of RAM memory) and go to File
  Menu → Open image from a disk and choose MR-MONO2-16-knee.gz
- You should see three main windows the main window, the image window and the output window.



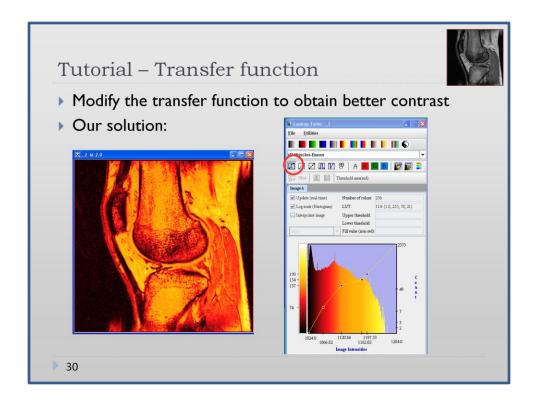
- First of all try to increase the magnification level by using a mouse scroll adjust the level for your convenience or use the first or the second icon from magnification toolbar
- ► The third icon opens magnification options you can choose an interpolation method here.



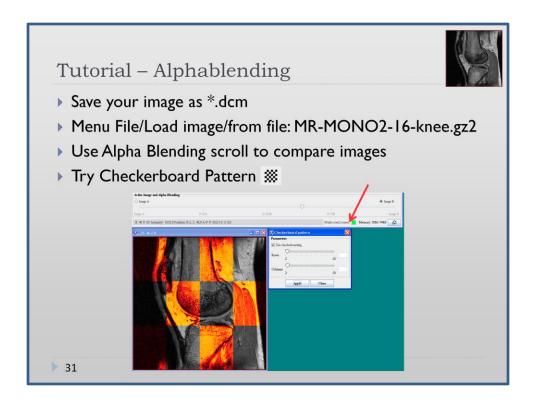
- ▶ Use quick LUT icon. Try out different VOI and finally select the one you are the most interested in. You can use Reset LUT function to reset the applied changes.
- Use Adjust Window and Level icon to make the border between the bone and soft tissue better visible.



- Display Lookup table icon or LUT>>histogram LUT
- > Try different LUTs, finally choose from the LUT list the Muscle-Bone LUT

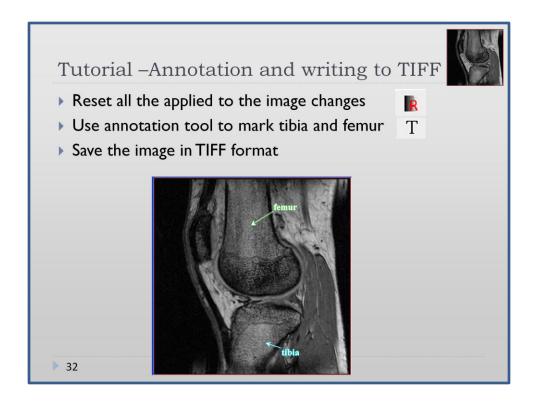


- Transfer function can be modified by choosing different threshold icons or choosing the first one (the one that is circled) and shape it manually by dragging points.
- Go to File Menu and save your LUT and Transfer Function (so you can reopen it later)
- Another way of modifying the transfer function is by using Level and Window Tools (mentioned previously on slide 28). Therefore, changing parameters of transfer function using LUTs we discard any changes made using Level and Window Tool.

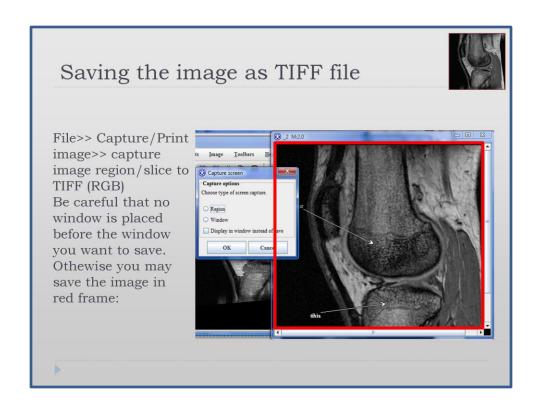


Alphablending is a very useful technique, especially, when we would like to compare two images of the same region of a body, but taken at other time, e.g. before treatment and after it. I could be also used for the comparison of the same regions of the body, but taken from different patients. One can control the level of transparency of each image, or display images using checkerboard pattern.

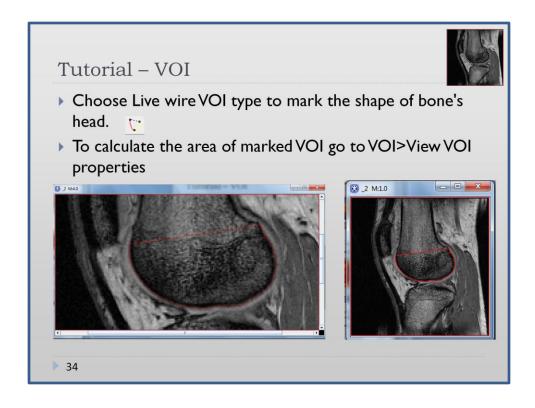
In our case we are comparing the image before and after processing to evaluate usefulness of our transforms.



Set different colours so the notations are better visible. You can use "bold" and enlarge the letters for better visibility of the notation. Original position of the notation may be changed. You can move both notation and arrow as well as make just the arrow longer (in order to do that you have to go with the mouse on the tip of the arrow so that a cross is visible)

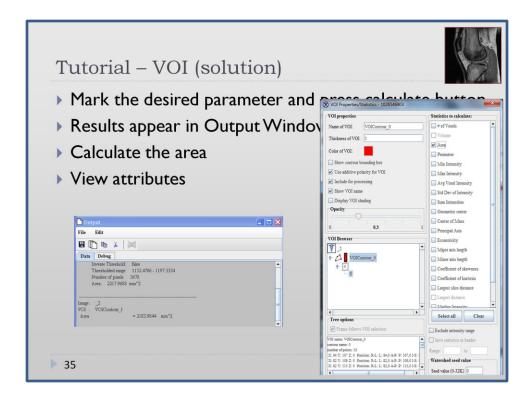


When you choose "capture image region/slice to TIFF (RGB)" option from the menu, a window appears where you have to decide if you want to save just a region or a window or you don't want to save it at all and you want to have the image just displayed. If you want to select just a region then you have to mark the region by drawing a rectangle and press ok. If you want to save the whole window you have to click the wanted window. Make sure that the wanted window is not covered by any others. It may happen that you will save the image of wanted image together with part of the other window which was covering the first one.

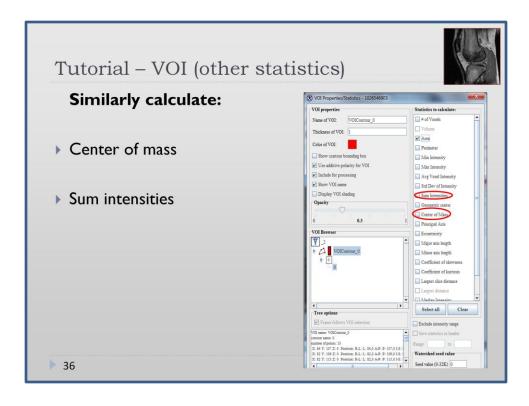


From now, we will use some options with Volumes Of Interest. The first option is Live wire – it enables to choose more complicated shapes of VOI. VOIs can be used to make some calculations.

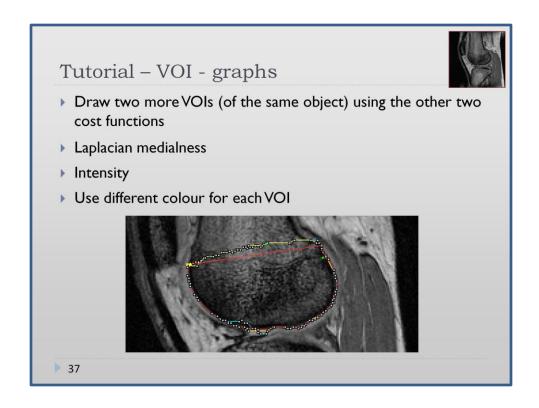
If you didn't manage to obtain closed shape you can use the Close VOI (Polyline->polygon) from contextual menu.



The result is in that case presented in unit mm<sup>2</sup>. This results from the attributes from header of the image saying about pixels-real dimension relation. View attributes to see correlation between pixels and real dimensions in the picture.



Put tick on the list next to two parameters which are to be calculated: Center of mass and Sum intensities. Then click calculate button on the bottom of the window. The results of the calculations are seen in the output window.

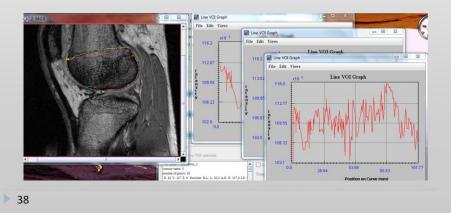


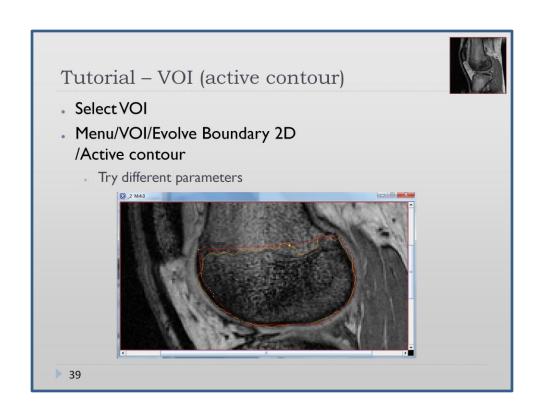
If you didn't manage to obtain closed shape you can use the Close VOI (Polyline->polygon) from contextual menu.

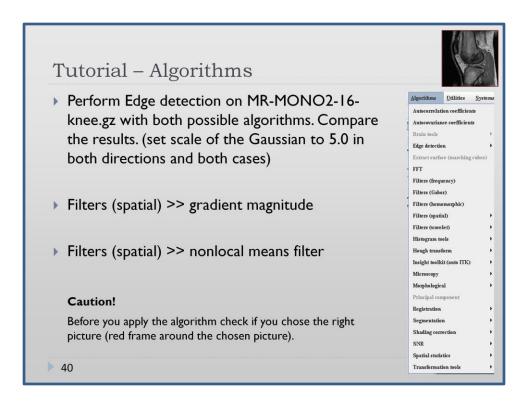
# Tutorial – VOI - graphs



- Choose the VOIs from previous example -> Graph -> Boundary Intensity for each type of live wire
- ▶ Compare three graphs







The option Algorithms in Menu of MIPAV window gives many possibilities for easy and fast enhancement of images. After clicking "Algorithms" on menu we see the list of algorithms we can apply.

#### Be careful which picture is chosen (red frame appears on it)

#### Autocorrelation coefficients

Autocovariance coefficients- help to provide a description of the texture or a nature of the noise structure.

#### Edge detection

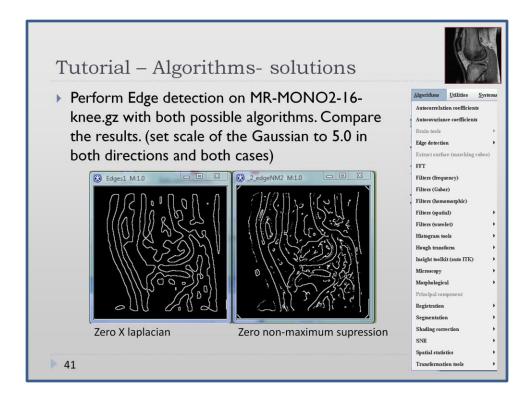
- Zero X laplacian- The algorithm finds edges that form a closed contour, which completely bound an object
- Zero X non-maximum suppression-The method produces an edge map of the zero-crossings of the non-maximum suppression

Filters (frequency)- application of different types of filters (highpass, bandpass, lowpass or bandstop)

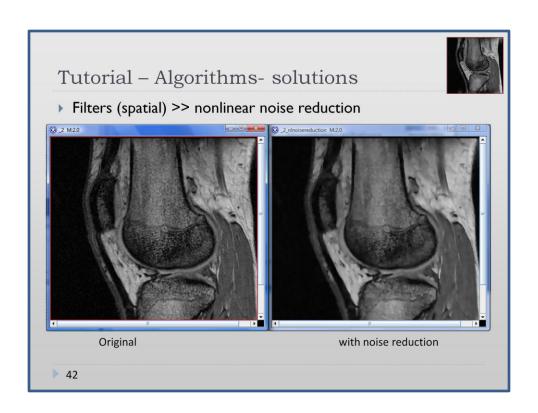
Filters(Gabor) –linear filter for edge detection

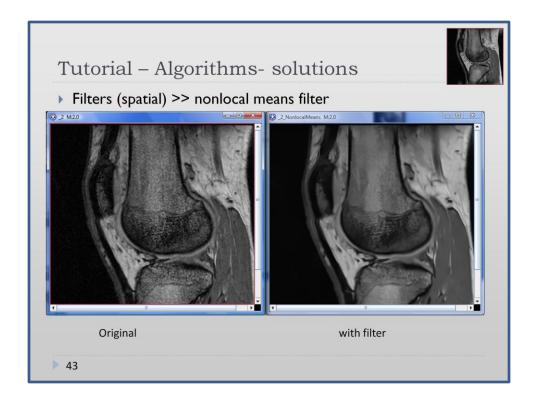
Filters (spatial)- a set of filters reducing noise, blurring or edge detection)

Filters (wavelet) – de-noising BLS GSM and thresholding

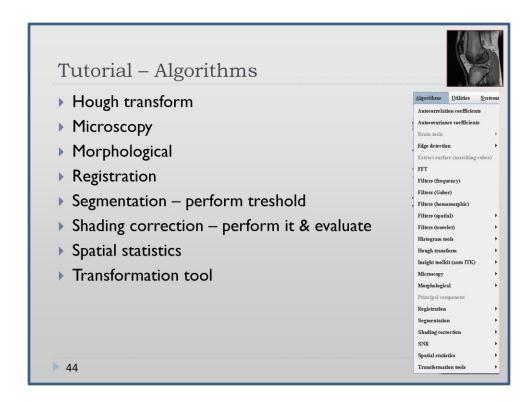


Perform Edge detection on MR-MONO2-16-knee.gz with both possible algorithms. Compare the results. (set scale of the Gaussian to 5.0 in both directions and both cases).

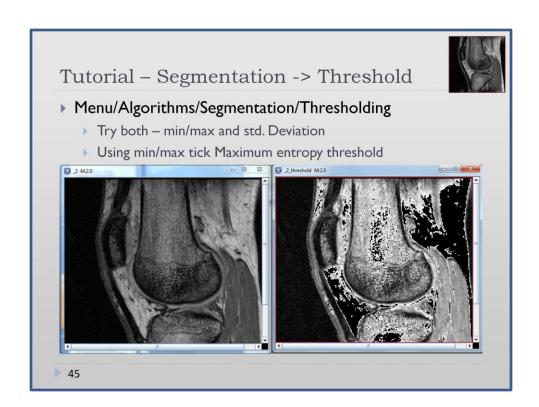




One should notice that the second algorithm gives better results as far as an edge of the image are concerned.



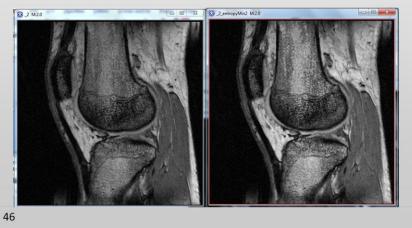
- Hough transform The Hough transform is a technique which is used to determine and isolate features of a particular shape within an image (To use this algorithm you have to have binary image – you can use gradient magnitude and tresholding to obtain such a picture)
- Microscopy series of transformations used with images obtained from confocal microscopy (including fluorescent images)
- Morphological a lot of algorithms connected with morphology of an image, e.g. closing of given region, holes filling, edge detection and other
- Registration: Landmark-TPSpline The Landmark-TPSpline algorithm allows align two or more images along a corresponding VOI that is delineated in all of the images
- Different types of segmentation, e.g.:
  - Watershed an interactive algorithm that allows automatically segment the image regions of interest using the topographical approach
  - Treshold the algorithm replaces the image pixel values with the fill values specified by a user. The pixel values change or remain unchanged depending on whether the original color value is within the threshold range
  - Fuzzy C means: Multispectral and single channel algorithms performs both hard and soft segmentation on multiple images
- Shading correction corrects for shading artefacts often seen in MRI
- Transformation tool changes shape of VOI

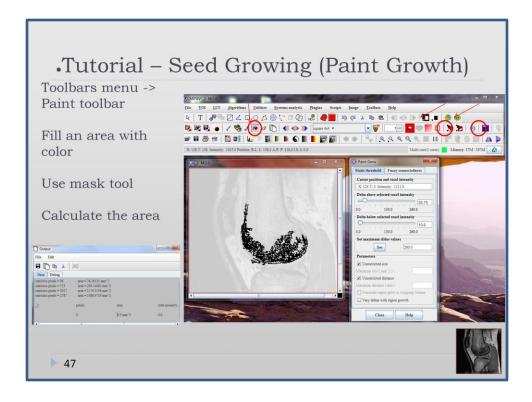


### Tutorial – Shading correction

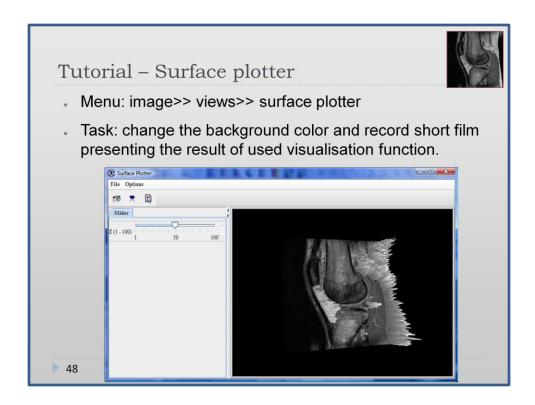


- ▶ Menu/Algorithms/Shading correction/Entropy min.
  - Try this correction with different value. Try to use thresholding at the same time

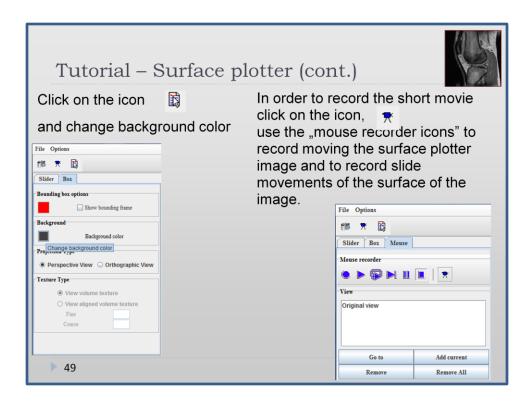




- Fill an Area with Desired Color
- •Click the Fill an Area with Desired Color icon. The Paint Grow dialog box appears.
- •Select the seed point, which is used as a starting point for the paint grow operation. To do this, move the pointer to the image. As you move the cursor, the location and intensity of the voxel under the pointer tip appears in the Cursor position and voxel intensity text box. Click the voxel you want to designate as the seed point.
- •Adjust the delta values and parameters.
- •Use the mask button to make selected region more visible
- •Calculate the area of that region



Surface plotter serves as a visualisation of intensity levels using height of the image surface. Higher intensities are peaks and lower are valleys. The image itself may be slided up and down with the use of slider on the left hand side. If LUT was applied to the image then the surface plotter is presented in the same LUT as well. It is possible to record the movements done on the 3D image which is a result of surface plotting.

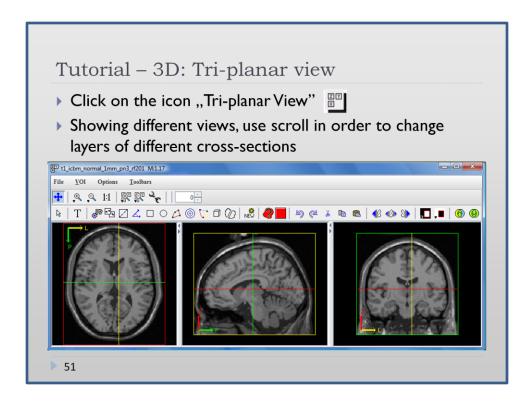


How to record the movie: click on the record icon. Since that moment the movement of the picture are recorded (rotating, translating and zooming). Move the micture by clicking with left mouse button and moving the mouse. Then change to "slider" tab and change the position of picture surface. Then go back to the "Mouse" tab and finish recording by clicking the "stop" icon. If you want to pause recording then click on the pause icon. Replay the just recorded movie by clicking the "replay" icon.

#### Tutorial - 3D

- Go to <a href="http://mouldy.bic.mni.mcgill.ca/cgi/brainwebl">http://mouldy.bic.mni.mcgill.ca/cgi/brainwebl</a>
- Leave default settings and press "start download!"
   and then "start download!" once again
- Save the file on your disc and open it with MIPAV
- Use any option to enhance the image
- Open the original image in other window
- Connect the both images using "Link to the other image" icon then use scroll.
- By cklicking the same icon disconnect the images
- Close one of them

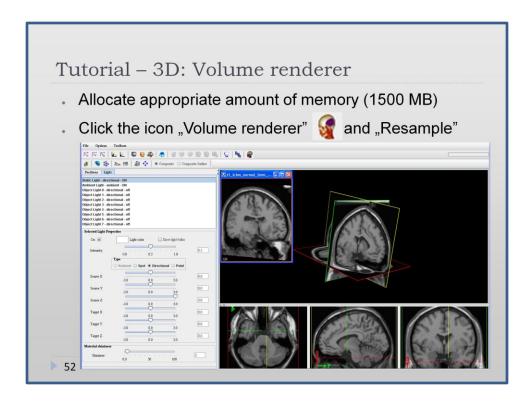
The icon link to the other image causes that two sets of images are connected so that going to slice number X of one picture means that the same slice of the other image is shown as well. It helps by comparing two sets of images.



Go with the mouse pointer to the first view, use scroll: the transverse cross-sections are changing.

Go with the mouse pointer to the second view, use scroll: the saggital cross-sections are changing.

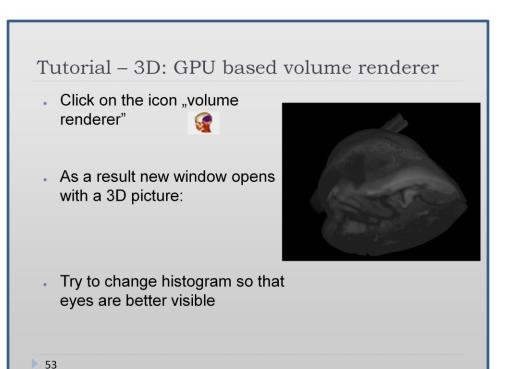
Go with the mouse pointer to the third view, use scroll: the coronal cross-sections are changing.



What you obtain is the window where in lower part you have the Tri-planar view like previously but also you can see how those three planes are positioned with respect to each other.

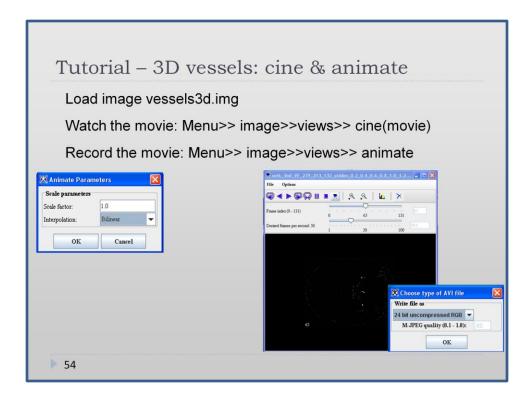
Because of the fact that the documentation of the programme is still under construction and information concerning Volume renderer option are not available better description of the possible options was difficult.

However, clicking the icon "Extract rotated image" causes opening of the other window with a view, which represents cast of the three planes on the screen plane. The casts are then combined into one image.

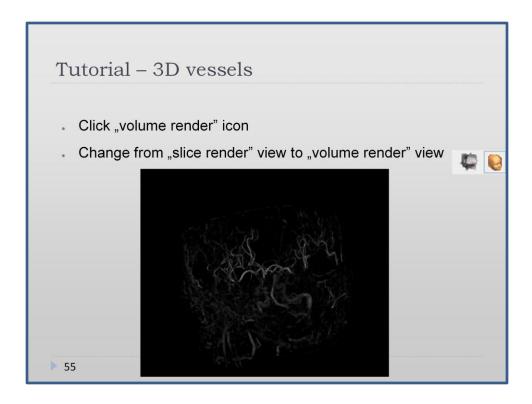


There are two ways to render an image – using CPU or GPU processor. We recommend to use the first algorithm unless you have some dedicated graphic card.

The obtained 3D picture represents the view "from the outside", in this case the upper part of the head and at the botom little "insight" into the body. It is not possible to get deeper into image, which means, to select just the part of the slices for creation the 3d object.



Another visualization method in MIPAV is to playback slices from 3D MRI image and save them as a movie (avi). For quick preview use cine (movie) option from Image>>Views and for more options go to Animate tool. Using Animate Tool you can choose different properties for movie playback and you can save it to avi file.



#### Load image bloodVessels

The image is a processed 3D picture of CT scan. Looking at the single slides we see just white spots but after volume render, a net of blood vessels may be seen.

### Summary - What is MIPAV

- MIPAV (Medical Image Processing, Analysis and Visualization)
- Java based freeware software for Image processing, analysis and visualization, used to extract quantitative information from various medical images
- For 2D and 3D pictures from PET, MRI, CT or microscopy





> 56

## Summary Main (presented) options



Advantages	Disadvantages
•Freeware software	•Requires some enhancements:
•Platform independent	• Increase of stability
•Documentation (support)	•Reorganisation of options available from
<ul> <li>Powerful tool for medical images</li> </ul>	menu and toolbars
processing, analysis and visualization	•It is not allowed to use the software for
•Compatible with various image formats	treating or diagnosing of human subjects
(incl. *.dcm, *.gz2, 3D formats etc)	•Documentation is incomplete (for more
•Copes with images from many modalities	advanced options)
(CT, MRI, PET, Confocal Microscopy)	
•User determines max RAM allocation	
Possibility to access DICOM database	
through TCP/IP connection and browse	
DICOM images	
57	

# Summary: What more can be done with MIPAV

- Expandable with scripts
- Processing of images from confocal microscopy
- Insight Toolkit and other algorithms for processing, analysis and visualization



**58** 

The Insight Toolkit (ITK) is an open-source software toolkit for performing registration and segmentation.

