

USER GUIDE FOR VELOMAP-TOOL

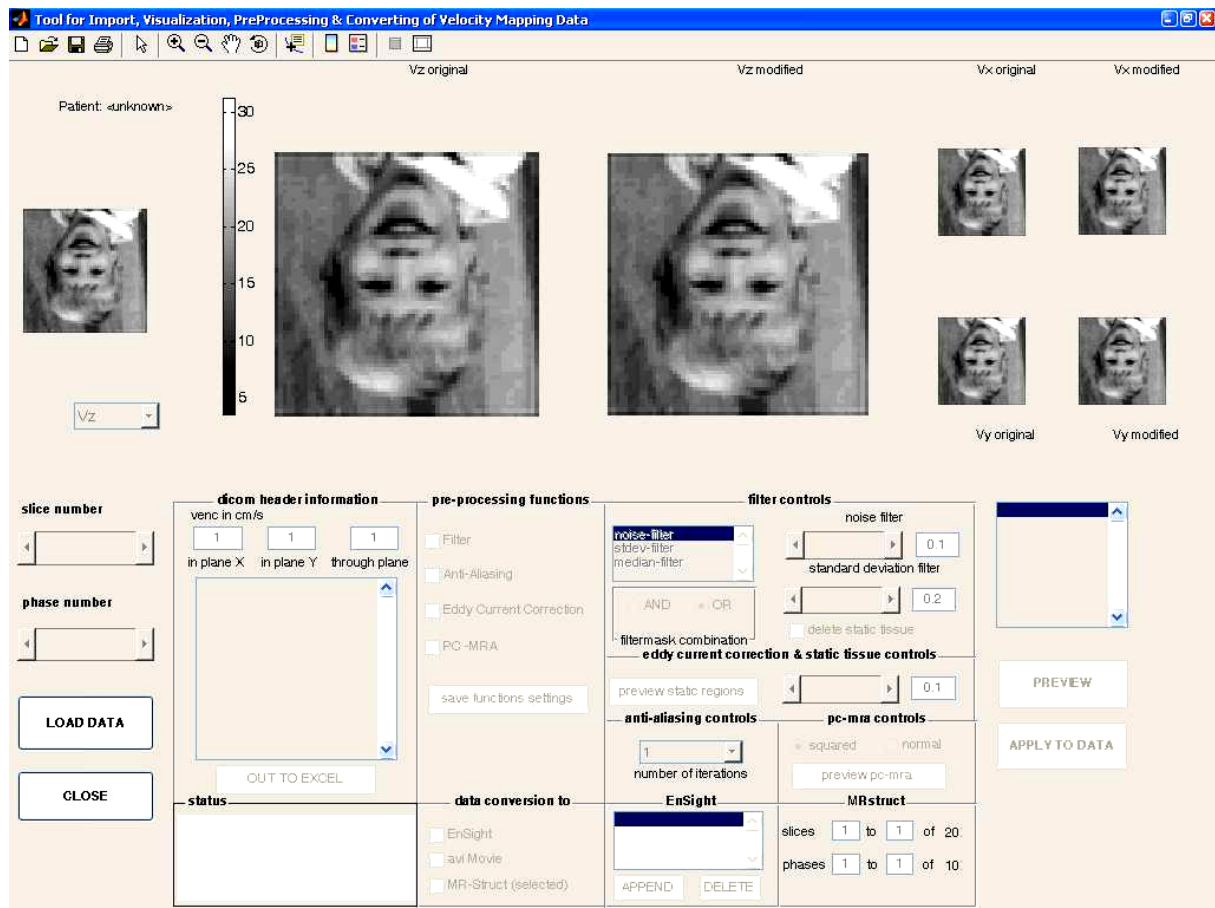
BEFORE STARTING:

- Make sure that you have the new version of *dicom_read_singlefile* ! (checkout module *matlab_new* in CVS)
- You MUST note that your magnitude data folder and velocity data folder are to be in the same directory and the folder's name is 'flow' for velocity data and 'mag' for magnitude data. Data must be (at the moment) in DICOM- file format.

START VELOMAP TOOL:

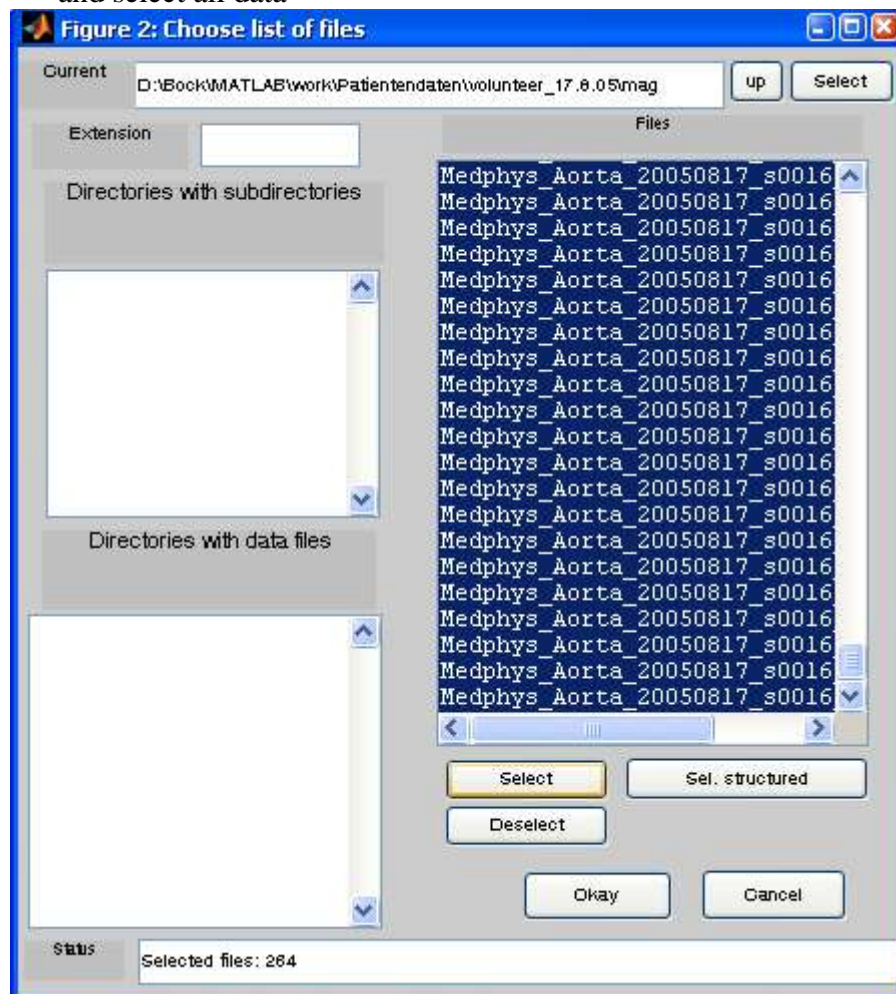
- from command window in Matlab → *velomap_tool*
- if you want mrstructs with flow and magnitude data as return values then you should call *velomap_tool* with command line
[magstruct flowstruct] = velomap_tool('returnstruct')

→ The following graphical user interface should appear



LOAD DATA

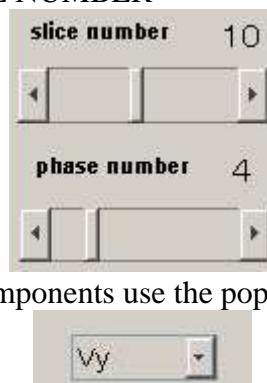
- to load data press button *LOAD DATA*
- *file_chooser_tool* should appear, choose folder ('mag') with your magnitude images and select all data



- flow data will be chosen automatically from folder ‘flow’

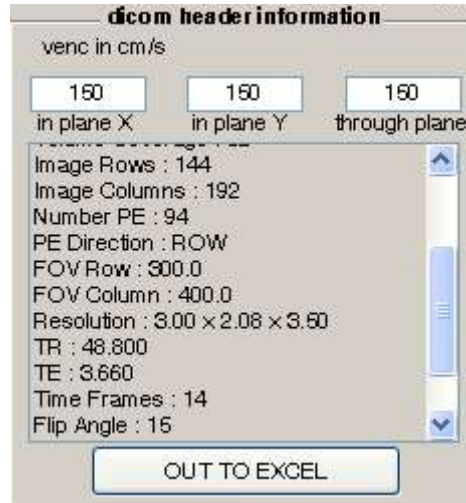
DATA VISUALIZATION

- a magnitude image and up to 3 velocity images will be appeared on the interface
- to visualize data from different slices and phases use two sliders
SLICE NUMBER and PHASE NUMBER



- to switch between velocity components use the pop-up

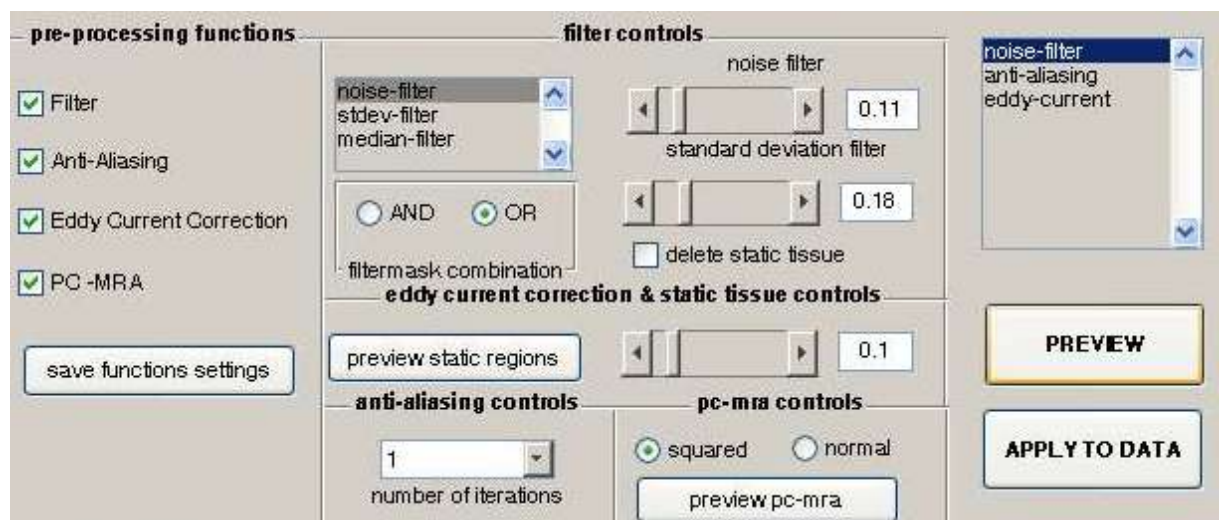
- Additionally the information from DICOM-header is read out and displayed



- The user has the possibility to save the information in an excel-file by pressing the button *OUT TO EXCEL*
- The encoding velocity *venc* could also be changed manually (press ENTER after change)

PREPROCESSING FUNCTIONS

- Different preprocessing functions could be selected, the selected function will appeared in the 'protocol window'



→ FILTER : there are 3 functions (*noise*, *stdev*, *median*) to filter noise from velocity data, for *noise* and *stdev* –functions user can set thresholds and combined these two function with *AND/OR*, additionally user can delete static tissue (for description see *EDDY CURRENT CORRECTION*)

→ ANTI-ALIASING: phase unwrap function, number of iterations can be set by user

→ EDDY CURRENT CORRECTION: threshold for separating static tissue from flow and noise can be set, to preview the

static tissue press the button
PREVIEW STATIC REGIONS

→ PC-MRA: calculate phase contrast MR-angiography
squared : for all time phases
normal: for each time phase
press the button *PREVIEW PC-MRA* to get a preview of the calculated angiography

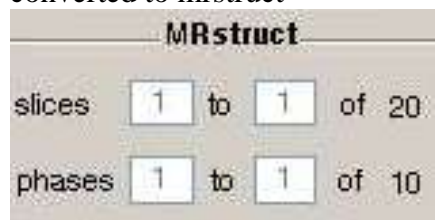
- The actual functions' settings could be saved as an excel-file by pressing the button *SAVE FUNCTIONS SETTING*
- Press the button *PREVIEW* to get a preview of data modified according to the actual functions' settings

CONVERT DATA

- Choose all file formats you want data to be converted to (EnSight, avi-movie, mrstruct)
- EnSight: user can append additional data like angiography (should also be DICOM format)

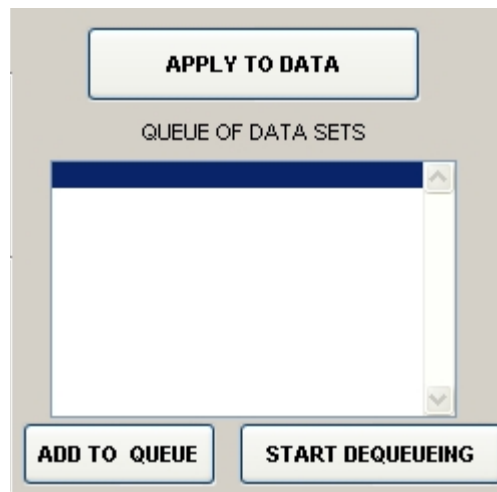


→ MRSTRUCT: user can select which slices and time phases should be converted to mrstruct



- To start the conversion of data press *APPLY TO DATA*

ADD DATA SETS TO QUEUE



- load data and
- choose preprocessing functions and conversion format(s) as described above
- instead of pressing the button “apply to data” press the button “add to queue”
- the actual data set will be added to the queue
- go on as described above for the further data sets
- when all data sets which should be processed are in the queue press the button “start dequeueing”
- you will be requested to choose a directory where the status report will be saved in



- dequeueing process is started