

USER GUIDE FOR VELOMAP-TOOL v2.0

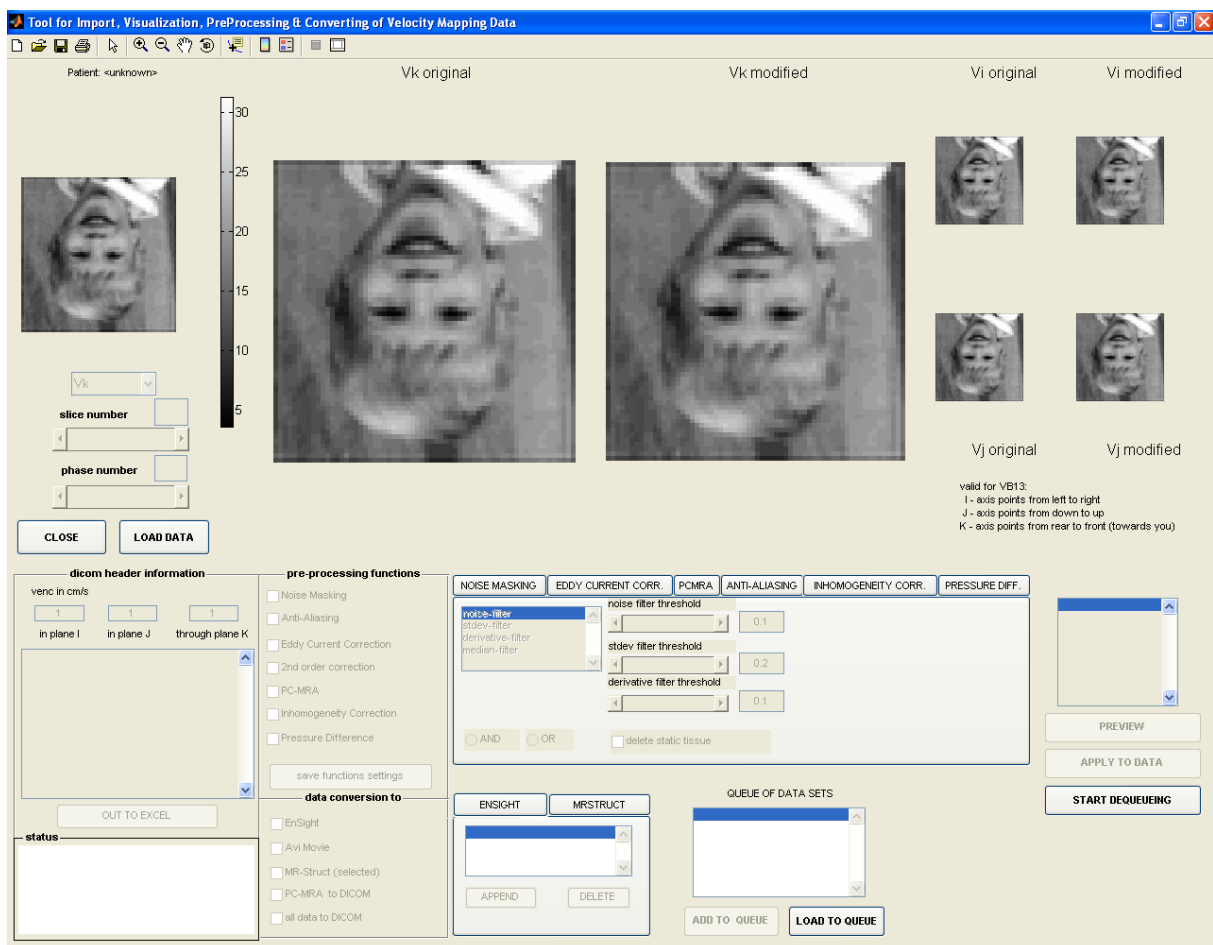
BEFORE STARTING:

- Magnitude data folder and velocity data folder are to be in the same directory
- 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:

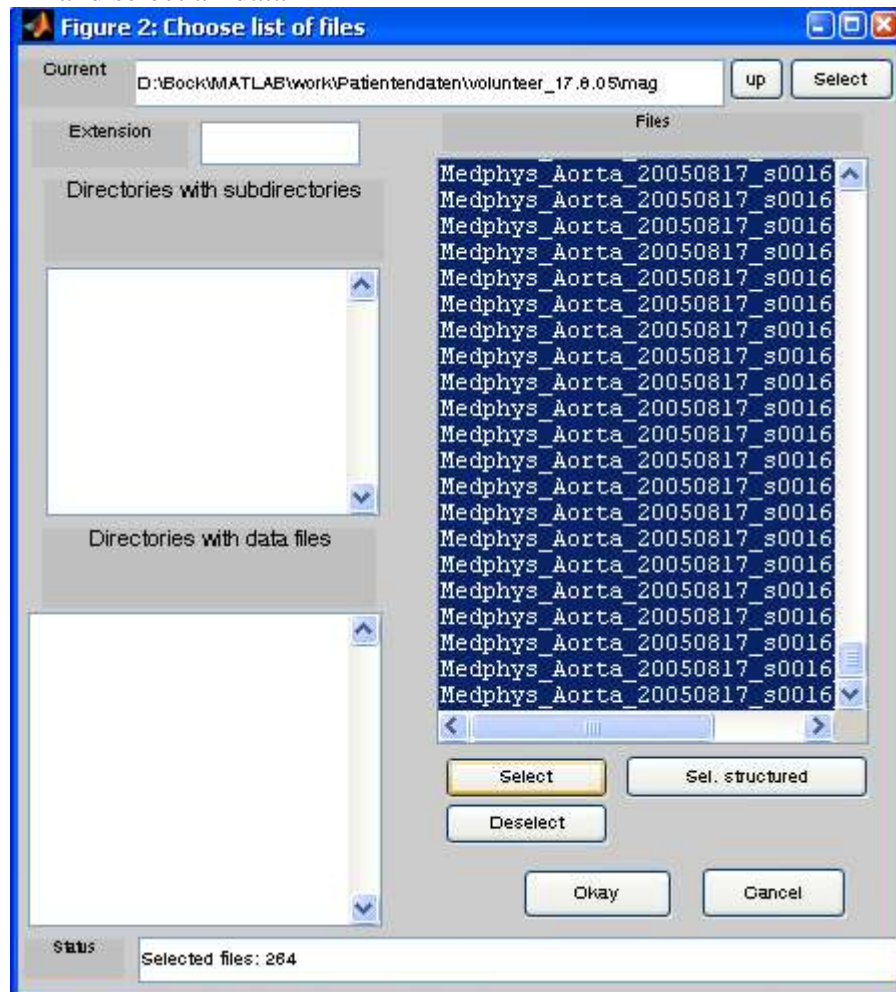
- from command window in Matlab → *velomap_tool*
- or start the Velomap_tool exe with double click

→ The following graphical user interface should appear



LOAD DATA

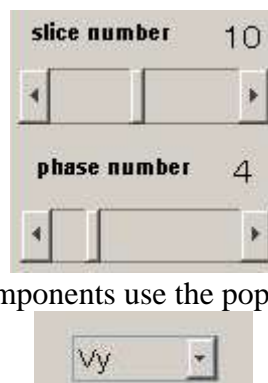
- to load data press button *LOAD DATA*
- *file_chooser_tool* should appear, choose folder ('mag') with your magnitude images and select all data



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

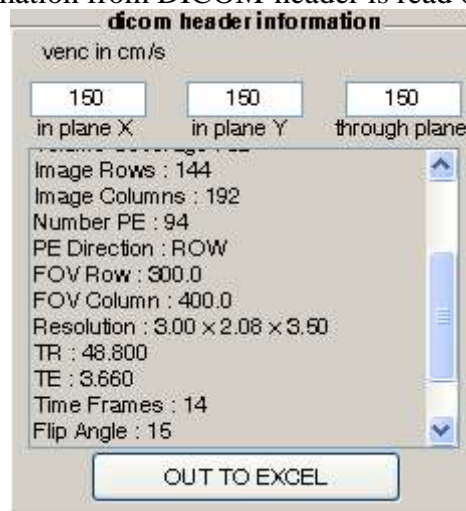
DATA VISUALIZATION

- a magnitude image and up to 3 velocity images will appear on the interface
- to visualize data from different slices and phases use two sliders
SLICE NUMBER and PHASE NUMBER or just enter slice/phase number in the boxes above



- to switch between velocity components use the pop-up

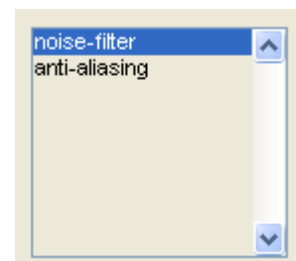
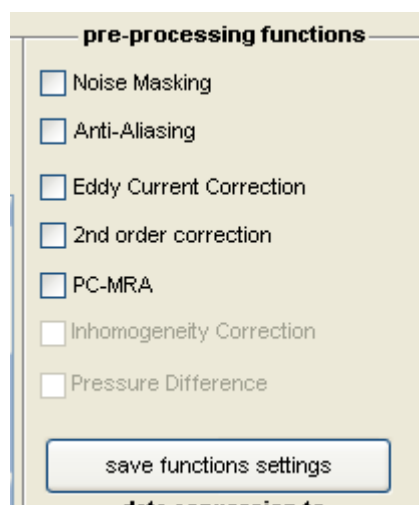
- Additionally the information from DICOM-header is read out and displayed



- 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 pre-processing functions could be selected, the selected function will appeared in the 'protocol window'



→ FILTER :

there are 4 functions (*noise*, *stdev*, *derivative*, *median*) to filter noise from velocity data, for *noise*, *stdev*, *derivative* –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 or you can unwrap manually

→ 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 with 3 different algorithms

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

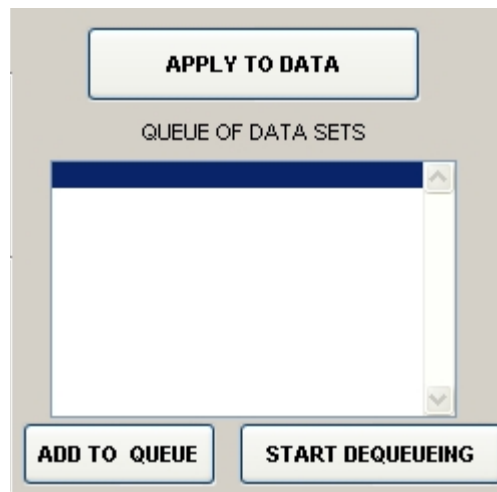
CONVERT DATA

- 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