Kinetics and Modelling with particular emphasis on imaging MR-exercise

Deconvolution of MR dynamic susceptibility contrast perfusion measurements

The aim of this exercise is to demonstrate the process of analysing a dataset of MR images acquired during the passage of a bolus of dynamic susceptibility contrast agent.

Part 1: Viewing a dataset.
- Start matlab
- Type `mr_ex`
- Select one of the files:
  ```
  d10805perf_dr2.sfh
  d10832perf_dr2.sfh
  d12046perf_dr2.sfh
  ```
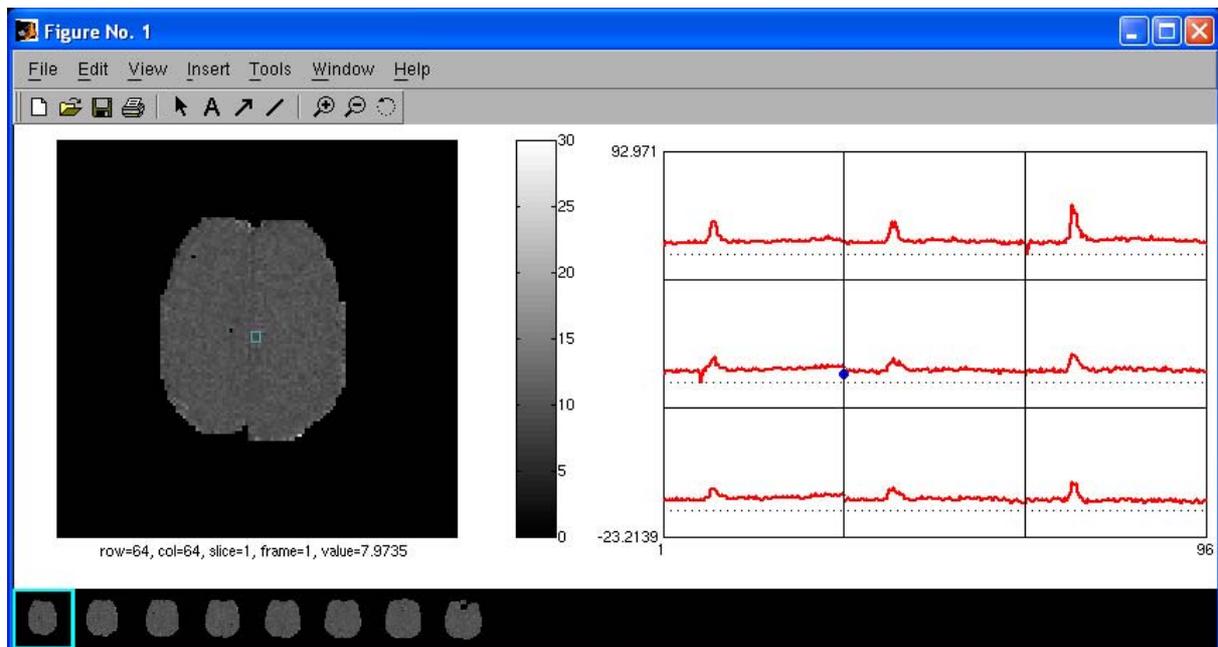- The following window should open (figure 1)

Figure 1

- The window shows the concentration of contrast agent in a section of 3x3 voxels from a brain volume as a function of time.
- See the textbox below for instructions to navigate through the dataset. See an example in figure 2.
- Look at the concentration curves and try to locate an artery which is suitable as the arterial input function (AIF).

```
        An interactive window is opened with an image and a series of
        timeseries plots. If the data contain multiple slices, a panel
        showing slice selection is shown at the bottom of the figure.
        - Clicking anywhere in the image moves the active
          region to that point, and the timeseries are updated.
        - Clicking on any image on the lower panel chanes to that slice.
        - Clicking anywhere in the central plot changes the displayed
          frame.
        - Clicking in the other plots moves the active region to be
          centered around that pixel.
        - Further functionality is available using the keyboard:
           '<' or left arrow: decreases the frame nr.
           '>' or right arrow: increases the frame nr.
           's' or up arrow: decreases the slice nr.
           'S' or down arrow: increases the slice nr.
           'M' : displays more plots
           'm' : displays fewer plots
           '+' : zooms in on plots
           '-' : zooms out on plots
           't' : tight zoom in on plots
           'a' : toggles displaying average curve of viewed timeseries
           'q' : quits and closes the window
```
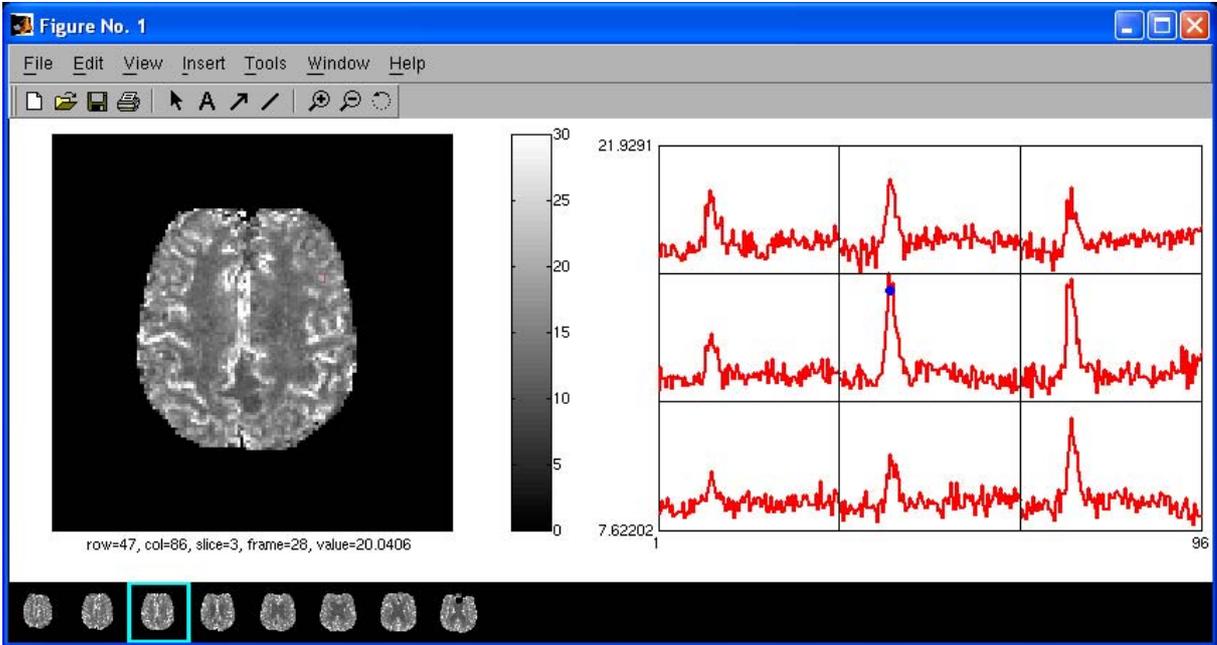

Figure 2

Part 2: Calculating perfusion
- Start matlab (if it isn't started already).
- Type voxelfinder
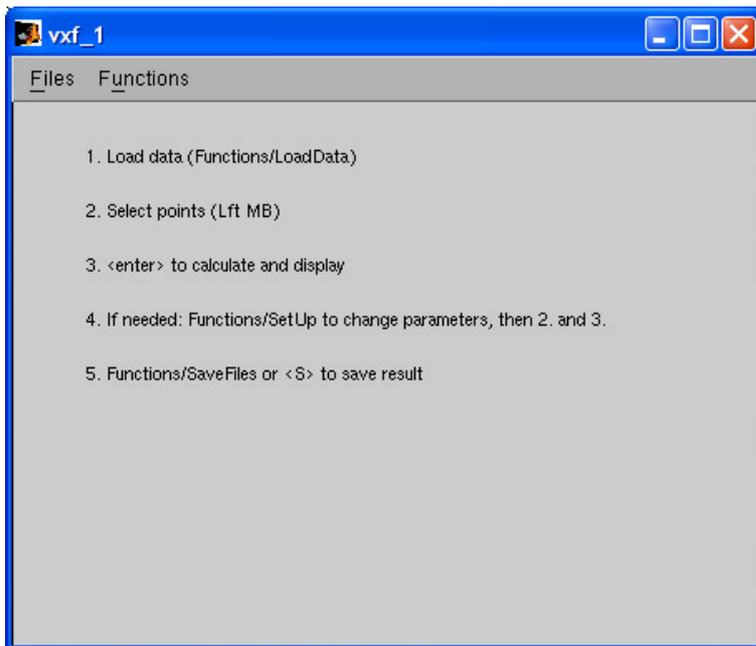- A window with instructions will open (figure 3).

Figure 3

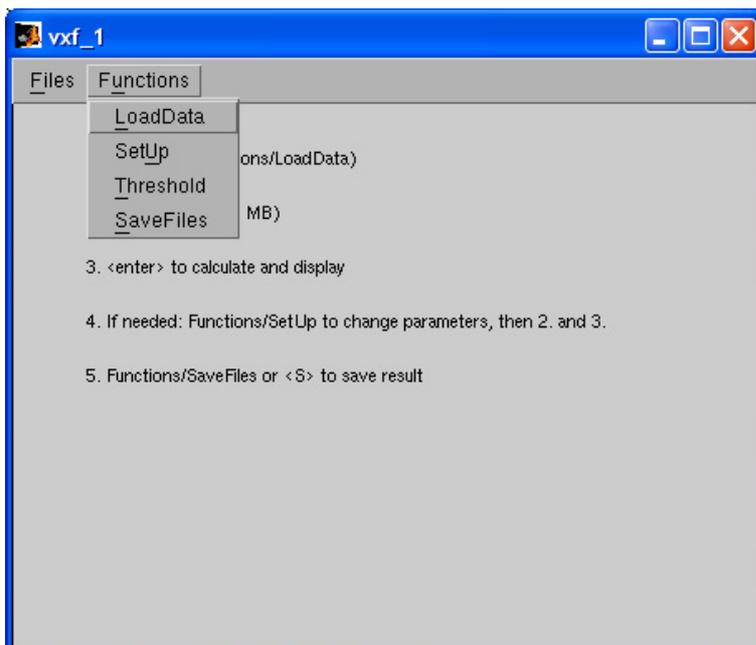- Select Functions/LoadData (figure 4)

Figure 4

- Select one of the datasets listed in part 1 above.
- After some calculations, two windows will open. The first is simply a mask of where the brain is in the images. The second is the mean tissue concentration curve (see figure 5).
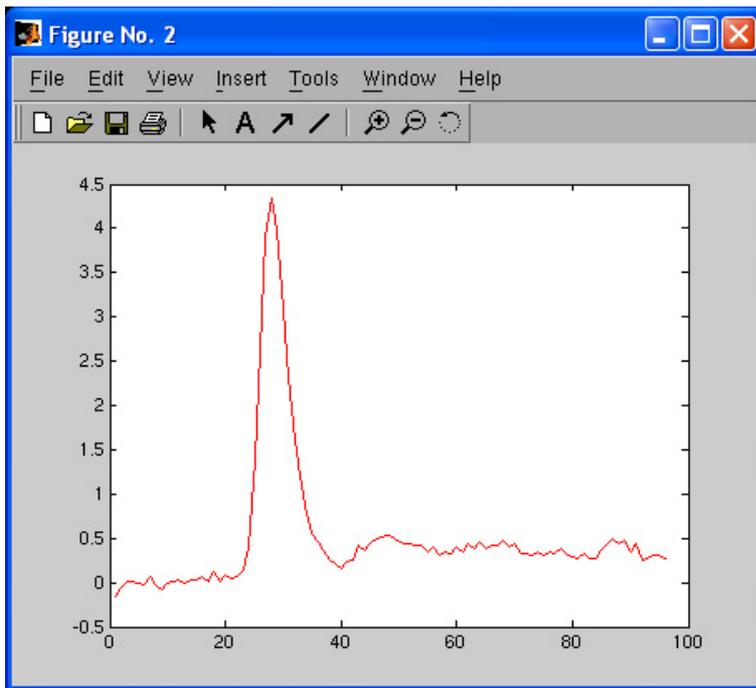
Figure 5

- The original will now look like figure 6. The program finds the 50 voxels that are most likely to be arteries and ranks them. Each row in figure 6 shows the timecourse of one of these voxels. The concentration is then depicted by colour as a function of time (which is along the x-axis).
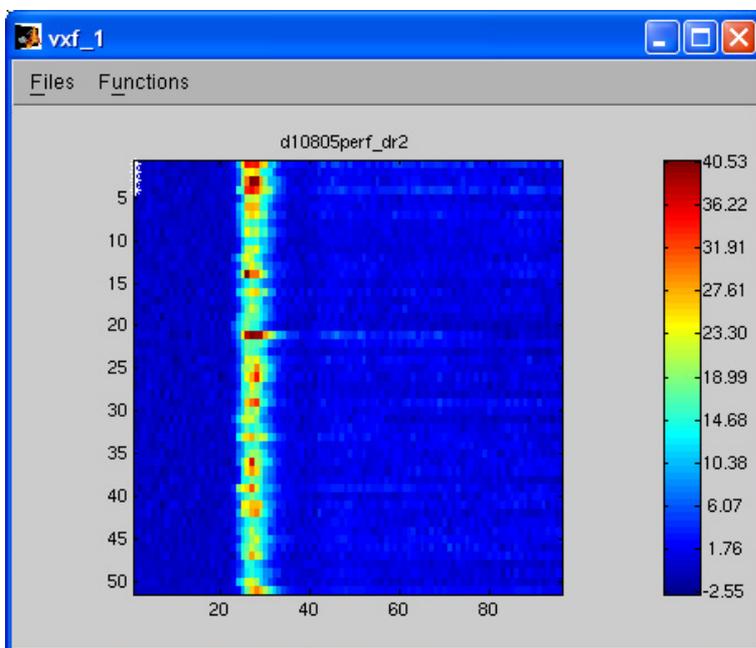

Figure 6

- Note that there are five white markers in the upper left corner of figure 6. These indicate that the five top rows and thereby the first five voxels are selected. You select/deselect any row by clicking on it.
- When you press Enter the AIF is set to the average of the concentration timecourse in the selected voxels and three more windows will open (figures 7 – 9).
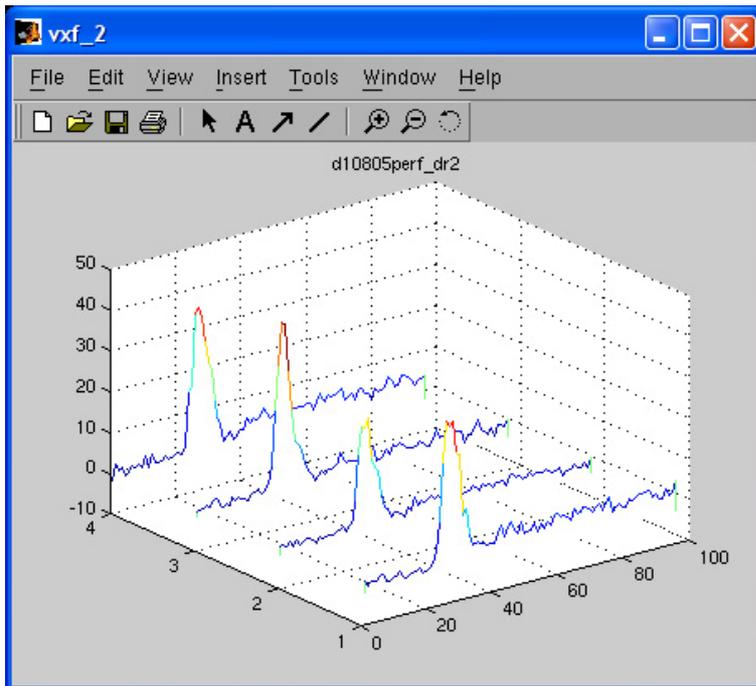
Figure 7

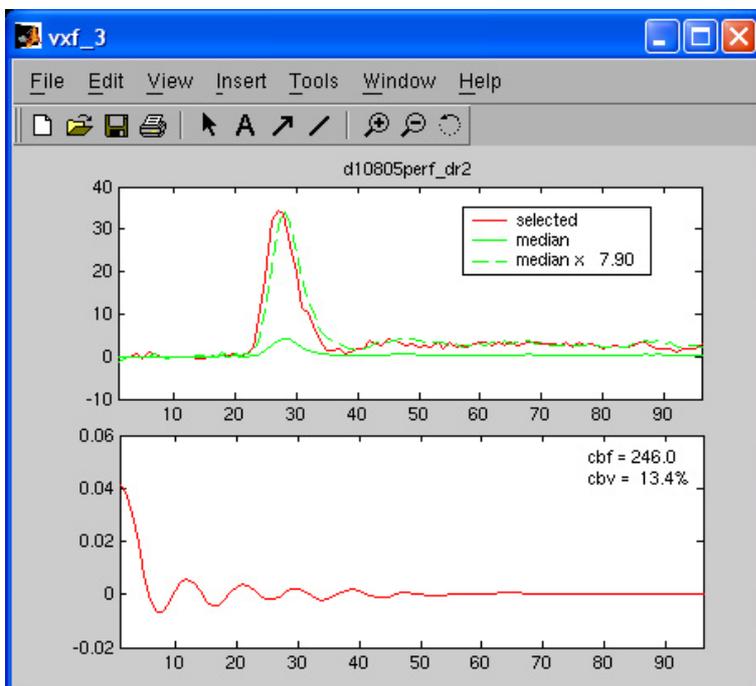- The first window (figure 7) displays the concentration curved in the selected voxels.

Figure 8

- The upper graph in the second window (figure 8) shows the AIF (labelled 'selected'), the median tissue curve (labelled 'median') and median tissue curve scaled to the same amplitude as the AIF (labelled 'median × ...').

- The lower graph shows the deconvolved impulse response function and lists the mean CBF and CBV.
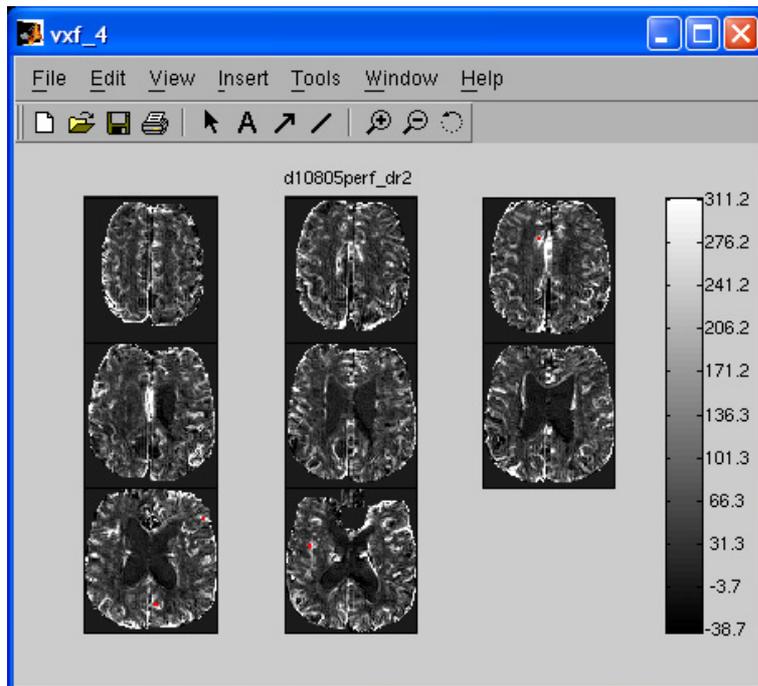

Figure 9

- The last window (figure 9) shows the calculated CBF images.
- Try selecting different voxels (rows) in figure 6 and recalculating CBF and CBV. How does the choice of AIF affect the calculated values? Note that when you select a new voxel, its location is displayed in figure 9 by a small green circle.