THE DCE-MRI PERFUSION MAPPING GUI

SHORT CHECKLIST

PAWEŁ TOKARCZUK

16. I. 2020.

Introduction

This is a short aide-memoire to using the software.

The important action points are highlighted in blue.

A more detailed description is given in the Quick User's Guide, and a fuller technical account will appear in one or more reports, to be produced at the conclusion of this project.

Preparation

If you are intending to use the GUI outside the Steiner Suite, then initialise the paths to the source data and results using the script:

pft_InitialiseFolders

Getting started

Open a ciné-stack using the big green button.

Select a "pickled" MAT file from those on offer.

Use the sliders at the bottom left of the dialog to window the image display and to navigate between Epochs and Slices. You can also change the colormap of the image display using the menus at the upper left, and the resolution using the downsampling options in the lower right corner.

Processing decisions

1. Last Usable Frame.

Begin by navigating to a slice in which some major organs are visible: lungs, liver, spleen and kidneys. Advance the Epoch slider until you see the first unusable frame. Roll back to safety by one epoch.

Set the Last Usable Frame slider appropriately.

2. MPA region of interest.

Navigate to the slice in which the section through the MPA is most nearly circular.

Click the large yellow button to create the ROI.

A circle will appear in the image display. Move and re-size it with the mouse, then double-click to select the visible region.

3. Deconvolution controls.

There are two ways to see the effect of changes in the processing parameters on the deconvolution:

   a. Move the mouse inside the image display axes. You will see a time-course being displayed and updated, and a residue function being calculated in real time, using fixed parameters.

b. Freeze the image display with a click of the left mouse button within the image. If you are unsatisfied with the chosen voxel, unfreeze the display with the ==purple== button and choose another. You can now make changes to the Deconvolution controls in the upper right section of the dialog.

To adjust the deconvolution controls, create a frozen time-course from within the MPA ROI; this is will be very similar to the AIF, so the deconvolved residue function should look a lot like a delta-function at time zero.

Pay attention to the following options:

Deconvolution

Normalisation

Matrix Algebra

SVD

Zero-fill Truncated AIF

You shouldn't need to change any of these, although you're free to experiment.

The really critical controls are:

Retain SV's

Filter (decades)

Note that too little filtering creates a sharp (truncation) step in the data, with evident noise in the residue function. On the other hand, too much filtering results in a loss of information, and constrains the deconvolution excessively: 1.0 decades seems to be a good working value.

The singular values fall into distinct groups (these are plotted at the top of the dialog, with Index running from top to bottom and Value from left to right, in order of decreasing size). Values to the left of the vertical separator are retained (if relevant) and those to the right are discarded. Retaining too many values may create an "over-fitted" noisy residue function, whereas keeping too few yields an oscillatory and clearly wrong result.

Move the separator across the Singular Value plot, pausing at each break between groups to inspect the resulting residue function.

You should find that retaining most – but not necessarily all – the values yields the best result. Note, also, that deconvolution by Left-Division is equivalent to using the Explicit PINV (SVD) with No Action taken in respect of the Singular Values.

Quantitative mapping

Once you have set your deconvolution parameters, press the ==pink== button to create the maps.

It's best to accept any filenames offered by the dialog at this stage; results for a given study are automatically numbered, so that nothing is overwritten.

You will be prompted for a time-course threshold, expressed as a percentage of the maximum in the AIF.

The legal values are in the range 1 – 50 %; the default is 10 %, though even 5 % gives a good result without creating too much background noise.

If you would like to reduce the minimum threshold to zero, please let me know – it's a one-line fix.

The outputs at this stage are:

- An Excel file with a summary of the processing parameters, grouped into several tabs.
- A black-and-white image of the MPA region of interest.
- A MAT-format "pickle" which can be read by other MATLAB applications further downstream.
- A folder of DICOM files, grouped into sub-folders.

The last of these has the following maps:

- Pulmonary blood volume (PBV): both filtered and unfiltered.
- Pulmonary blood flow (PBF): again, filtered and unfiltered.
- Time to peak (TTP).
- Mean transit time (MTT).

Note that the last two "time-like" maps are set on a baseline to distinguish unprocessed voxels from those with physical but low or zero values. Obviously, the TTP map will be "chunked" into just a few bins.

The dialog will keep you informed of progress. A full analysis at the native image resolution may take 5 minutes or so, although every factor of 2 in the downsampling results in a factor of 8 speed-up.

Note that, although there is nothing to prevent you acquiring the AIF at one resolution, and creating the maps at another, you should avoid this, since you won't strictly be comparing like with like in that case.

Documenting your choices

Notice the orange "Capture Display" button; this will save images of all the axes (though it may not catch all the legends).

Obviously, another straightforward route is **Alt-PrtScr, Paint, Ctrl-V and File | Save As.**