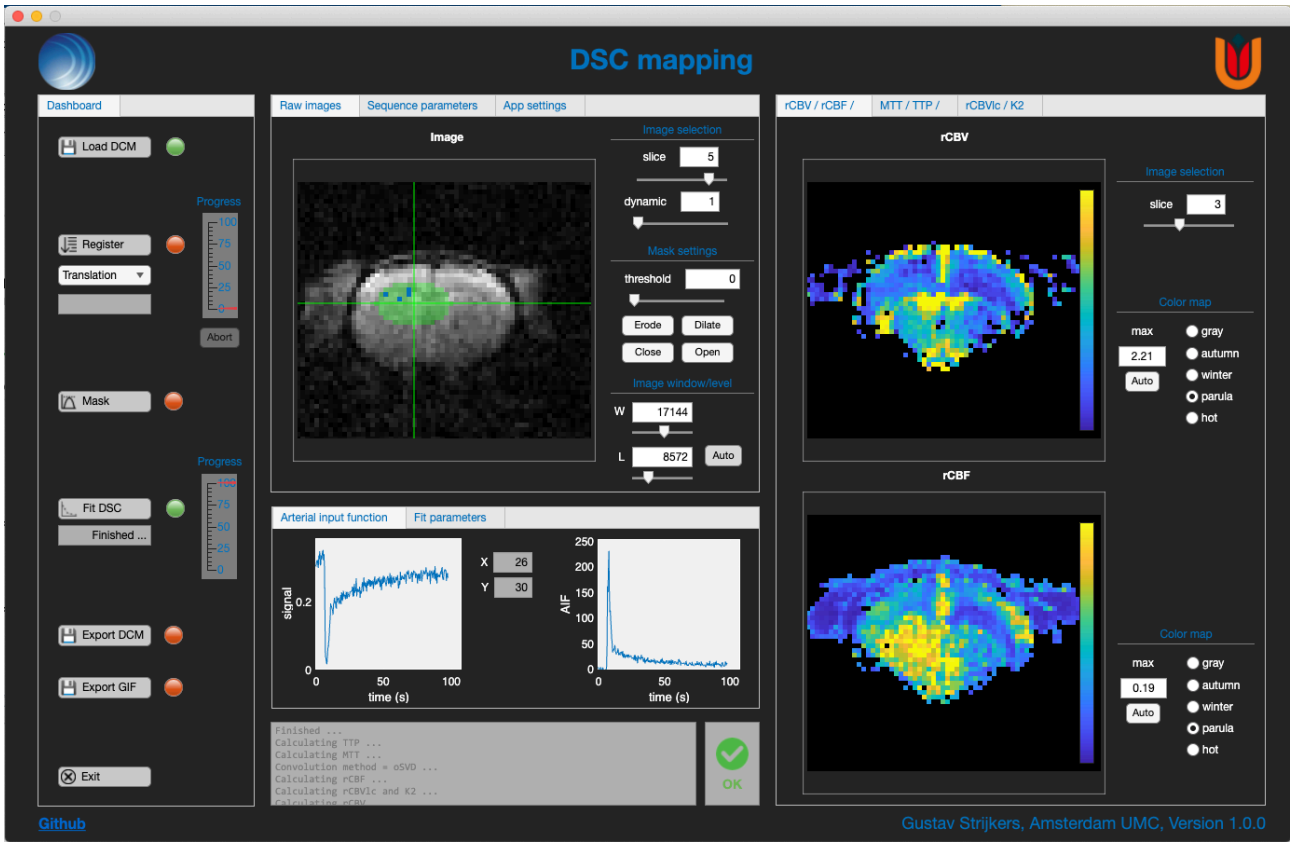


Table of contents

1. Overview

DSCmapp is a software utility and graphical user interface to reconstruct hemodynamic and vascular properties of brain tissue from a Dynamics Susceptibility Contrast (DSC) MRI acquisition an MR Solutions preclinical MRI system.

2. Contact

DSCmapp and this manual are written by:

Gustav Strijkers
Amsterdam UMC
Biomedical Engineering and Physics
Amsterdam, the Netherlands
g.j.strijkers@amsterdamumc.nl

3. Disclaimer

The software has been tested using mouse and rat data acquired with an MR Solutions preclinical 7.0T/24cm system.

However, this does not warrant the functions contained in the program will meet your requirements or that the operation of the program will be uninterrupted or error-free.

In case of questions or issues, please contact Gustav Strijkers.

4. Installation notes

Software download

Matlab source code and a Windows standalone version (using the free Matlab runtime engine) can be downloaded from GitHub:

`https://github.com/Moby1971?tab=repositories`

Installation of the Windows standalone version

`MyAppInstaller_web.exe`

Will install the Matlab runtime engine and the DSCmapp program.

5. Running the software

Running in Matlab 2023a

The DSCmapp software can be started from its root directory from the command line.

```
>> DSCmapp
```

Notes:

Additional licenses may be required.

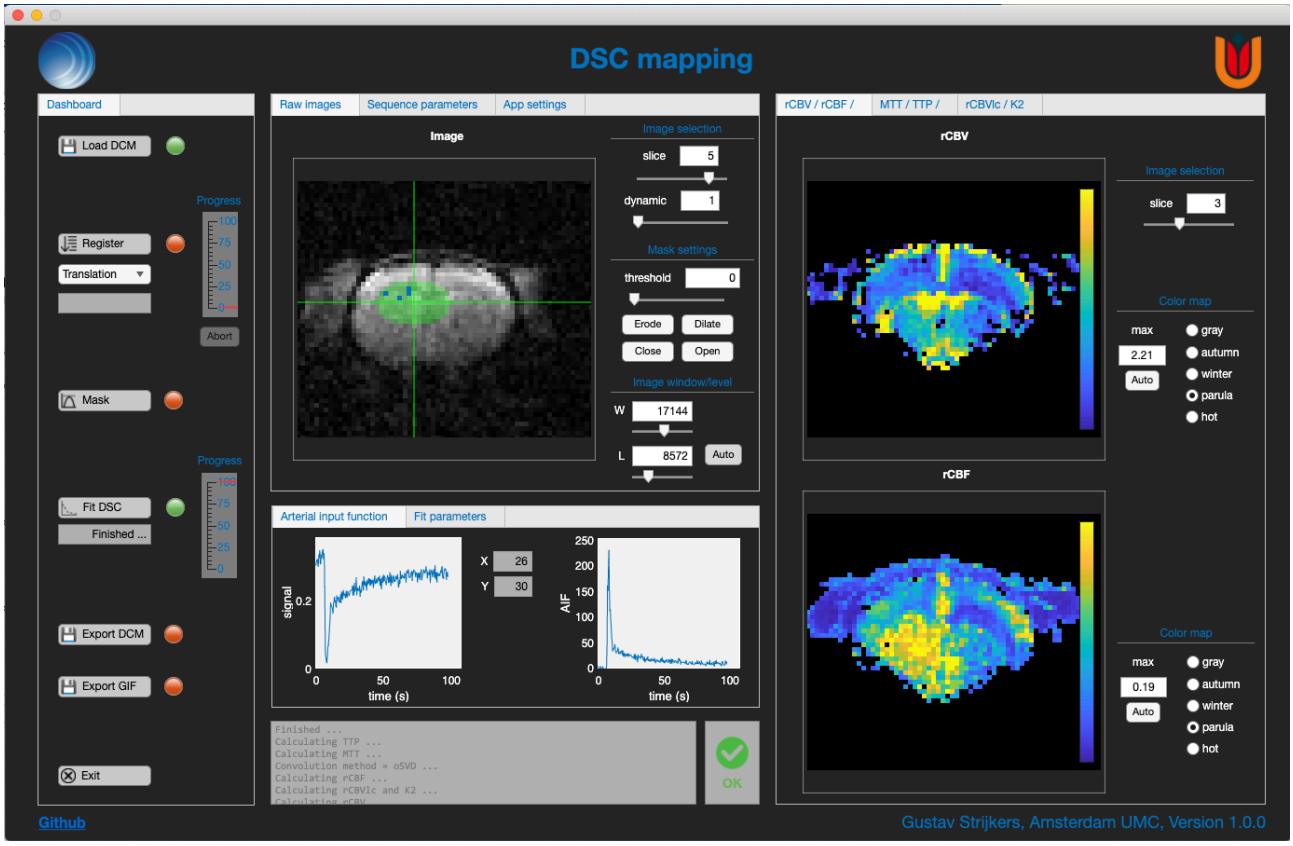
```
>> license('inuse')
curve_fitting_toolbox
image_toolbox
matlab
optimization_toolbox
statistics_toolbox
```

Running the Windows standalone

The Windows standalone version can be run from the start menu or the desktop icon.

6. Basic operation

The DSCmapp program operates from a single window with 5 panels.



Panel 1: Dashboard

This panel contains the task buttons and parameters that control the reconstruction process. A green light next to the task indicates that the task has been completed. Red indicates not completed yet.

Panel 2: Raw images, Sequence parameters, and App settings

This panel has 3 tabs for the raw images, list of sequence parameters, and application settings.

Panel 3: Arterial input function and Fit parameters

This panel displays the arterial input function (AIF) and fit parameter settings.

Panel 4: rCBV/rCBF/MTT/TTP/rCBVlc/K2

Calculated parameter maps.

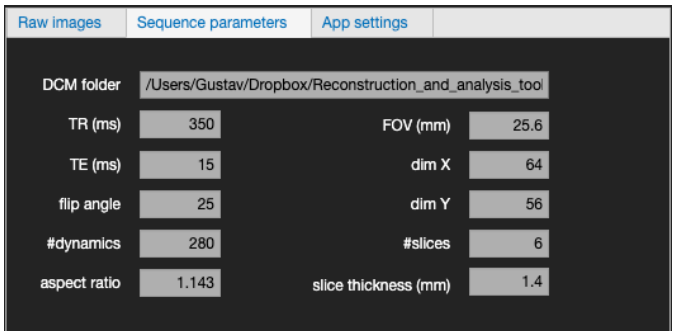
Panel 5: Messages

Displays program status and messages.

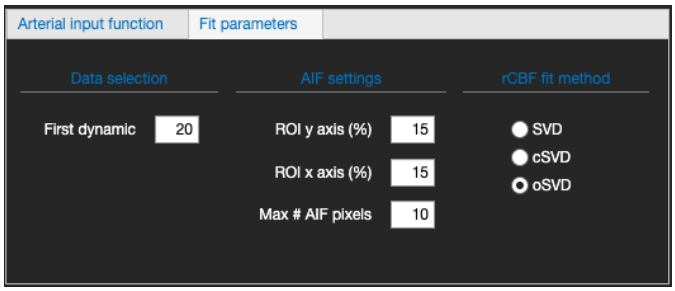
Step 1: Loading data

Press Load DCM to import load the DICOM files.
The app expects a multi- or single-slice brain data with at least 50 dynamics (time-series), acquired during injection of a contrast agent.

Relevant acquisition parameters will be shown in panel 2.

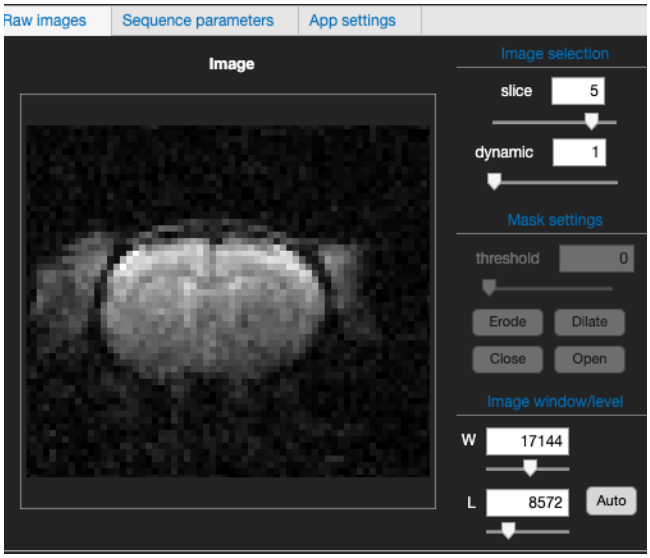


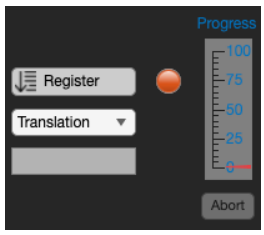
Standard, the first 20 dynamics will be omitted to remove the transient signal during the acquisition of the first dynamics. If needed, this parameter can be adjusted in the Fit parameters panel.

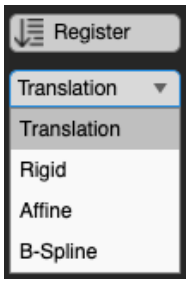


Step 2: Image registration

Use the sliders and/or edit-fields to inspect the slices and dynamics. The image scale can be adjusted with the Window (W) and Level (L) edit fields and sliders.







In case the images not perfectly registered, press 

to perform a registration. Available registration methods are: translation, rigid, affine, and b-spline.

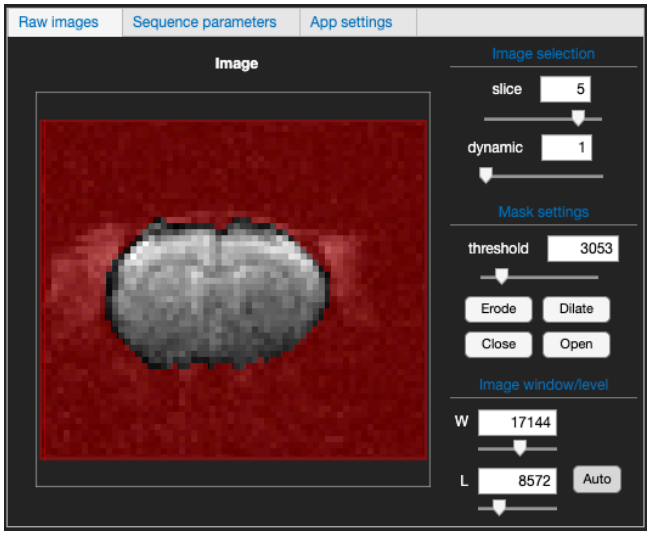
NOTE: this step usually can be omitted and might take very long for large datasets.

Step 3: Segmenting the images

To isolate the brain the images can be segmented. Press 

to perform an automatic thresholding.

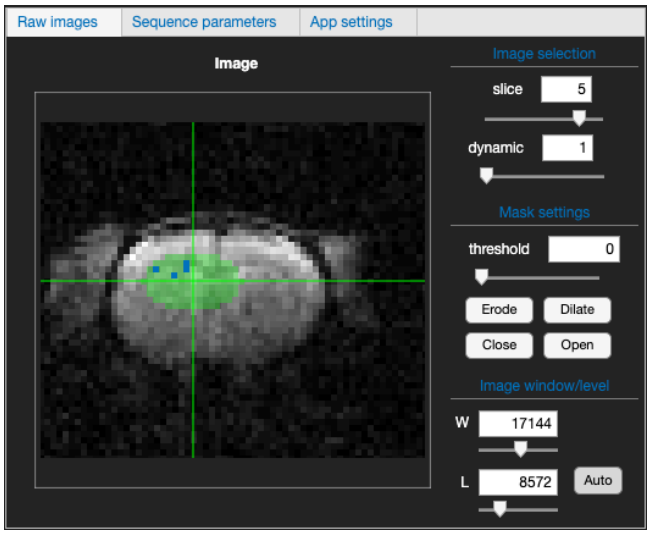
The result will look something like the figure below in which the red pixels indicate the regions that will be set to zero in the DSC parameter maps.



In case automatic thresholding is not optimal, the threshold can be manually adjusted per slice. The segmentation will be applied to all dynamics. The segmentation can be optimized by erode, dilate, close, and open morphological operations.

Step 4: Selecting an arterial input function (AIF)

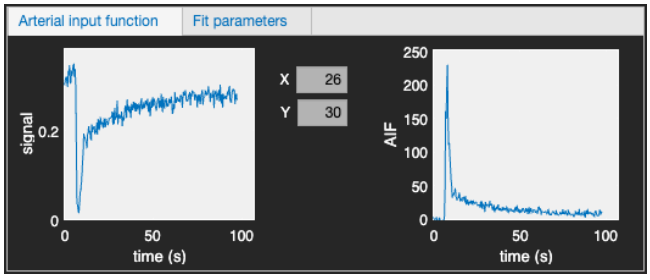
To semi-automatically determine an arterial input function, mouse-click on the brain in the image.



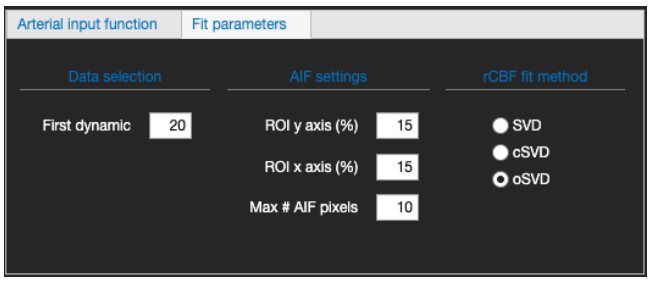
To determine the correct AIF the following approach should be considered. Make a selection for which the signal change is early (first to respond), deep (substantial signal loss), and narrow. Selecting a voxel within an artery might not always be advisable because of signal dephasing by a high contrast agent concentration in the artery. It is acceptable to select voxels adjacent to the artery as long as the local signal drop is early, deep and narrow.

The AIF is automatically selected from the green-shaded area following a set of criteria (based on: Peruzzo et al., Comput Methods Programs Biomed. 2011;104(3):e148–57).

The AIF may look something like this.



The size of the green-shaded AIF search area and the maximum number of selected AIF pixels can be adjusted in the Fit parameters panel.



Step 5: Fitting the hemodynamic parameters

The app estimates the CBF by solving the following convolution equation:

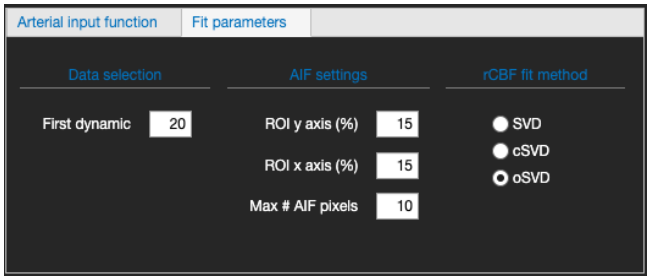
$$c(t) = CBF \cdot AIF(t) \otimes R(t)$$

with:
c(t) = the tissue contrast concentration
AIF(t) = the arterial input function
R(t) = the fraction of contrast agent present in the volume of interest (residue function)

The app uses a model-independent singular value decomposition (SVD) deconvolution approach and makes no assumptions on the CBF and on the residue function shape, thus treating them as complete unknowns to be estimated from the data.

SVD is based on the decomposition of a matrix AIF to compute the inverse AIF^{-1} and then derive the residue function and the CBF.

Three types of SVD can be chosen in the Fit parameters panel: standard SVD, circular Singular Value Decomposition (cSVD), and oscillation index Singular Value Decomposition (oSVD).



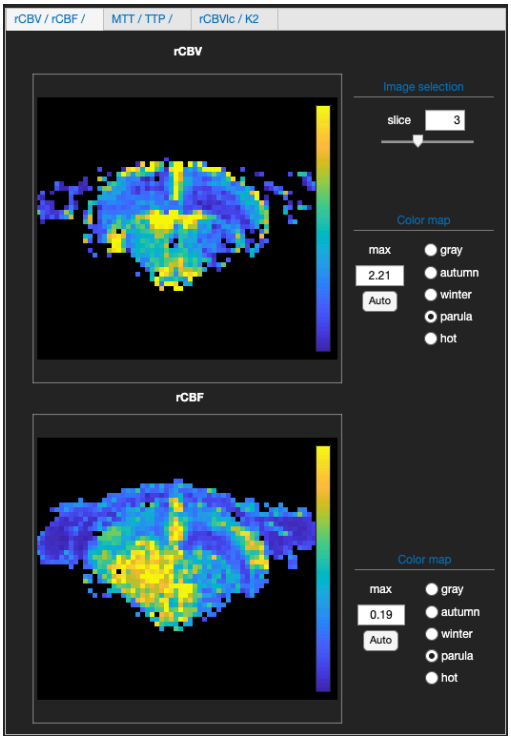
To start the fitting, press  .

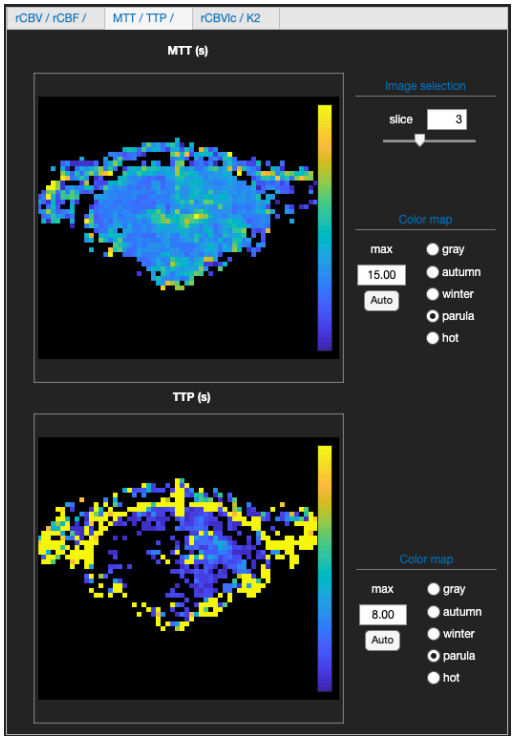
The application will produce the following maps:

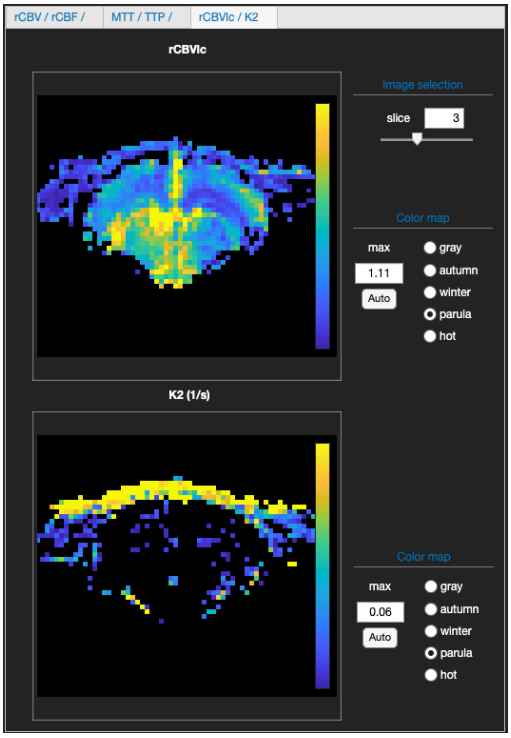
rCBV	=	relative CBV [-]
rCBF	=	relative cerebral blood flow [1/s]
MTT	=	mean transit time (s)
TTP	=	time to peak / delay between AIF and tissue response (s)
rCBVlc	=	relative CBV with leakage correction [-]
K2	=	leakage parameter (1/s)

Step 6: Inspecting the results

The hemodynamic parameter maps will be shown in the panel on the right.







Step 7: Exporting the maps

There are two ways to export maps.

(1) **Export DCM** 

Exports the data in DICOM format for further processing in 3rd party software.

(2) **Export GIF** 

Exports the data in GIF format.

Step 8: Exit

Press 

to exit the program.

Credits

Code

- The app uses code from this DSC MRI toolbox https://github.com/FAIR-Unipd/dsc-mri-toolbox.

AIF selection

- Peruzzo et al. Automatic selection of arterial input function on dynamic contrast-enhanced MR images. Comput Methods Programs Biomed. 2011;104(3):e148–57.
- Calamante et al. Arterial input function in perfusion MRI: A comprehensive review. Prog Nucl Magn Reson Spectrosc. 2013;74:1–32.

Vascular permeability

- Skinner et al. On the Use of DSC-MRI for Measuring Vascular Permeability. Am J Neuroradiol. 2016;37(1):80–7.

CBF calculations

- Peruzzo et al. Stable spline deconvolution for dynamic susceptibility contrast MRI. Magn Reson Med. 2017;78(5):1801–11.
- Zanderigo et al. Nonlinear Stochastic Regularization to Characterize Tissue Residue Function in Bolus-Tracking MRI: Assessment and Comparison With SVD, Block-Circulant SVD, and Tikhonov. IEEE Trans Biomed Eng. 2009;56(5):1287–97.

AIF correction for quadratic R2* dependency on contrast agent concentration

- van Dorth et al. Dependency of R2 and R2* relaxation on Gd-DTPA concentration in arterial blood: Influence of hematocrit and magnetic field strength. NMR Biomed. 35, e4653 (2022).