**DCE and DSC Toolbox**

**DCE Tool**

Designed for the analysis of DCE data, based on Tofts et al. (Tofts and Kermode, 1991).

The software package includes:

* DUSTER: DCE Up-Sampled Temporal Resolution Analysis Method - A proposed method for improving the extraction of AIF and PK parameters and estimates the BAT parameter (BAT ref).
* DCE Perfusion Analysis Method - For perfusion calculation from DCE data, incorporating the delay estimation allows to visualize another important parameter (Guys Ref).

**DSC Tool**

* DSC perfusion tool - for perfusion analysis based on DSC data, incorporating the boxerman weishoff correction for leakage

**Installation**

**Requirements**

Operating system: Was tested on Microsoft Windows 7 and LINUX

System requirements: Matlab 8 + SPM8

**Software Installation**

Download the "Code" and "Tools" folders.

In Matlab, add the SPM8 and the code and the Tools path:

Matlab->File->Set Path...->Add with subdirectories->

**Data Import and Analysis Configuration**

Data Structure

DCE - All image files that form a data set for analysis should be located in a single directory.

The mandatory folders are: the dynamic data must be in a single series, and at least one series with different flip angels from the dynamic data.

DSC - The mandatory folders are: the dynamic data must be in a single series

**Team members:**

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**New DCE GUI Options – V2.6 (Gilad)**

[**\\FMRI-GUY2\SourceForge\Stable\_Versions\code\Version\_2.6**](file:///\\FMRI-GUY2\SourceForge\Stable_Versions\code\Version_2.6)

GUI Activation:

Activate Matlab and type:

cd \\fmri-guy2\Dropbox\University\Msc\Thesis\SourceForge\Stable\_Versions\code\Version\_2.6

DCEInit

setComputerParamM('temppath','D:\Temp\')

dbstop if error

MainGUI

To forget stuff that auto-loads into MainGUI

delete([fileparts(getComputerParams('infosfn')) filesep 'LastMainGUI.mat'])

**DCE Maps**

**>>DCE maps:**

**Ktrans** - map of the transfer coefficient of concentration between the bloood plasma and extravascular extracellular space (EES) given in 1/min.

**Ve** - map of total EES volume. Given in arbitrary units (0-1).

**Vp** - map of otal blood plasma volume. Given in arbitrary units (0-1).

**Kep** - map of the rate of consentaion ("Invers premability" - What returns blood vessels). given in 1/min.

**BAT** - map of bolus arrival time Ve. Given in secounds.

**RMS** - map of root mean squareerror map per voxel relative to the AIF

**rRMS3D and RMStoNoise** - normelized RMS maps

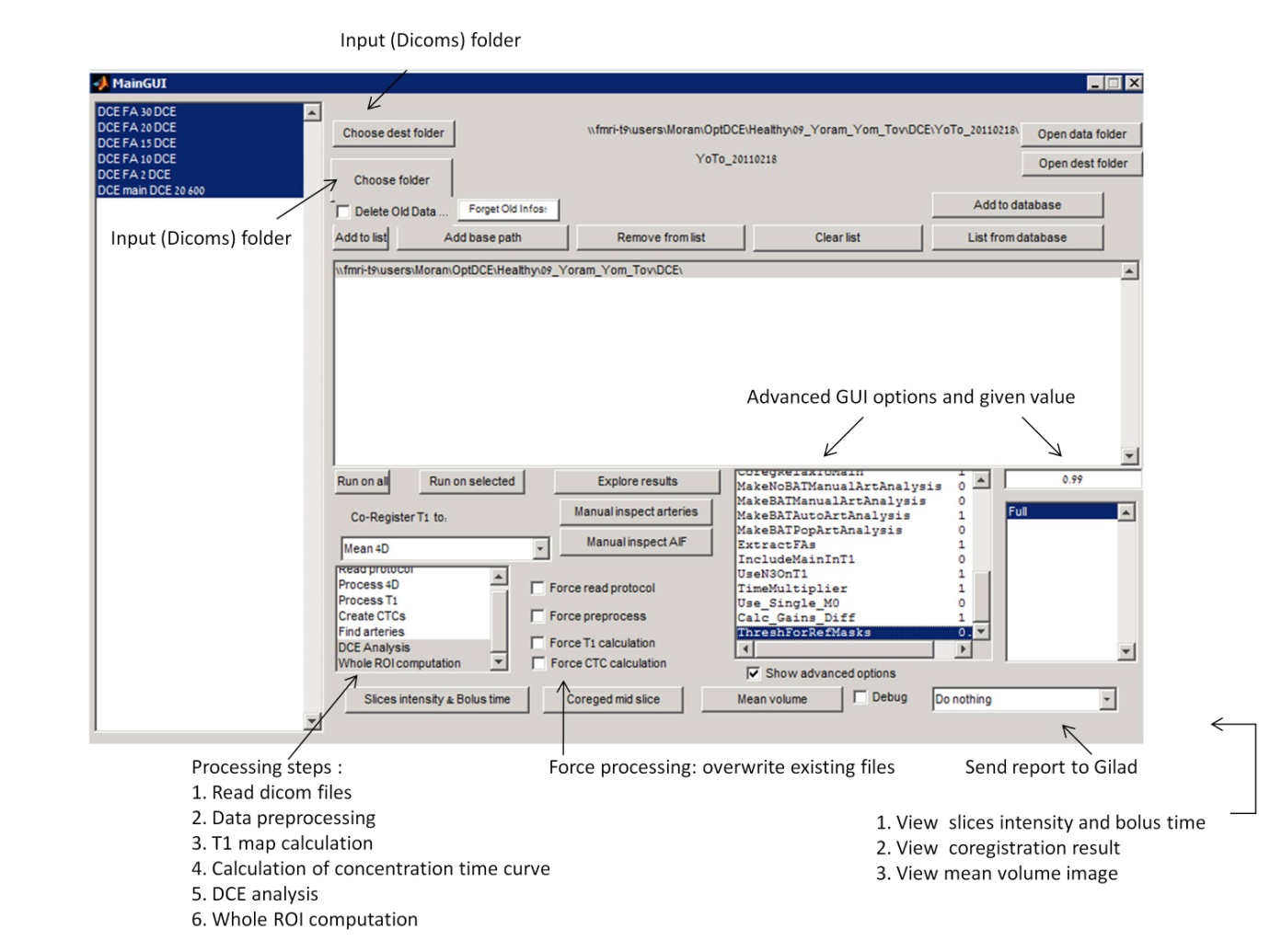
**>>Relaxometry folder:**

**T13DOFA** - T1 map

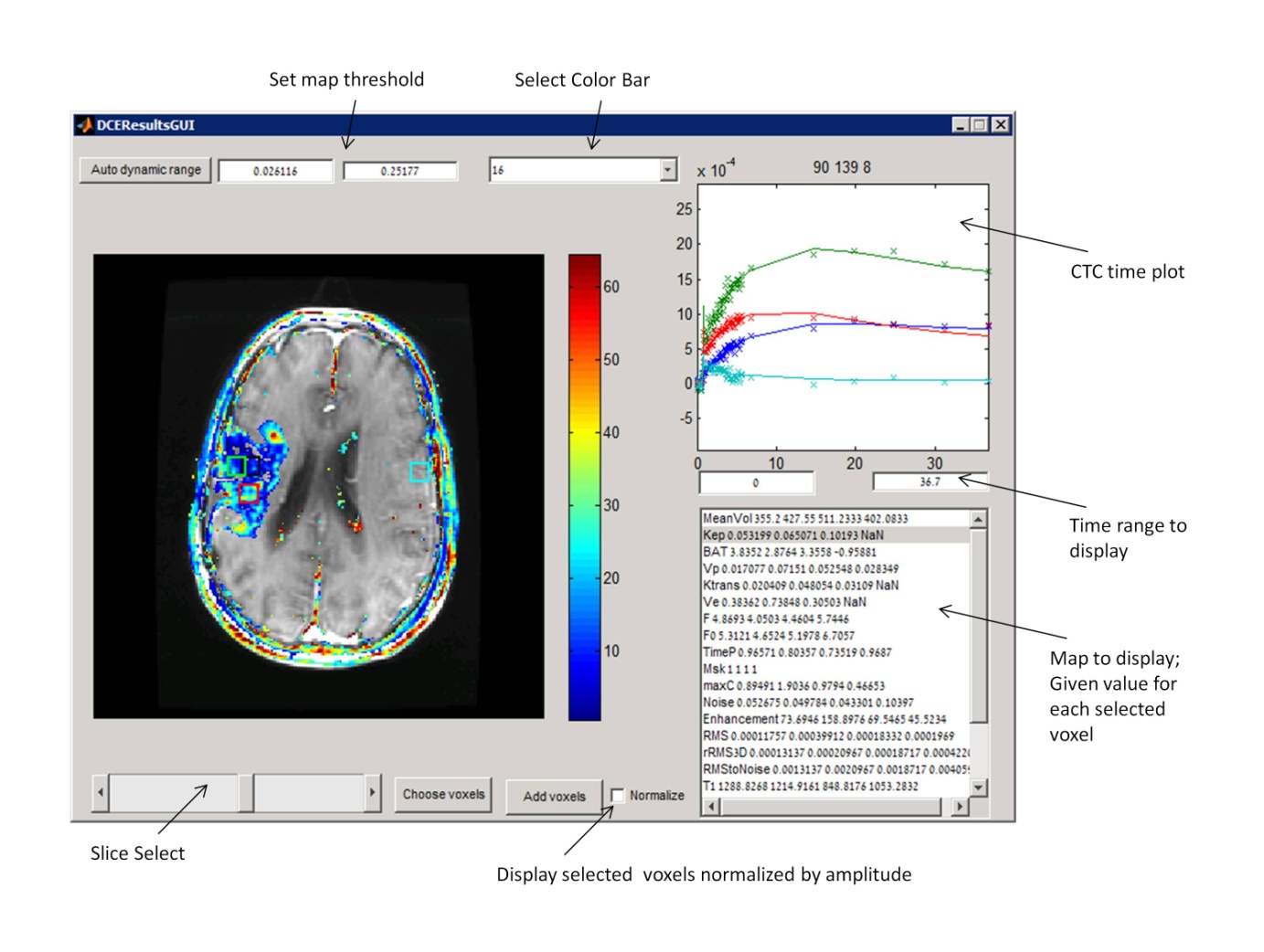
**PD3DOFA** - PD map

**RMS3DOFA** - RMS of relaxometry map

**Main GUI**

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**Main GUI**

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**Advanced DCE GUI options**

1. **SubSampling** – Allowing to sub-sample the original data (use lower temporal resolution)

Default: 1. DO NOT CHANGE (used for high resolution data). 3= for HTR change from 2sec to 6sec

1. **nVolsToRemoveFromEnd** - Cut the last volumes of the test (sometimes the last volumes are distorted). Default: 0
2. **SubSecondResolution** - Number of sub seconds parts for super resolution ("2" means 1/2 of a second). Default: 2
3. **MinFirstBolusStd** - The minimum width of the bolus (standard deviation of the Gaussian that represents the first bolus). Default: 2
4. **FMS\_TolFun** - Function Minimum Search's (Matlab's) parameter. Tolerate Function – minimal improvement for continuing the search. Default:
5. **FMS\_MaxFunEvals** – Number of possibilities for the F Mean Search at each step to change. Can think of it as in the case of 2-D vector f(**X**) ( How many 2-D points to move to from the current one). Default: 10000
6. **FMS\_MaxIter** - Maximal Number of iterations for FMS algorithm. Default: 10000
7. **MaxTDif\_ForAIFSearch** - The possible shift in time for the AIF of the representing voxels (in seconds). Default: 3
8. **MaxTDif\_ForWholeVOI** - Same as MaxTDif\_ForAIFSearch, just when allowing shifting in time for all voxels in VOI (and not just representing voxels). Default: 6
9. **Rep\_MaxAroundBolus** - Number of clusters around the bolus (for finding representing voxels). Default: 10
10. **Rep\_RatioToEnd** - Number of clusters around the end of the test (for finding representing voxels). Default: 10
11. **Rep\_nPerSet** - Number of total clusters will be MaxAroundBolus \*Rep\_RatioToEnd. This option will determine how many representing voxels we will choose from each cluster. Default: 1
12. **Mask\_Thresh** -Set threshold for masking (the general mask of where to work).

For positive values (0-1) uses SPM for masking.

For negative values (0 to -1) uses BET for masking.

The absolute value is passed to the SPM or BET.

Default: 0.5 (i.e., positive, uses SPM and the thresholds with 0.5).

1. **Run\_On\_All** -Default: 0?
2. **TimeDelayToMaskVeins** – Delay from Bolus peak. Default: -0.5
3. **WeightForAIFMeanVesses** –Similarity to the selected AIF Default: 0?
4. **MainCoregistration** - Choose between 1-realignment, 0-no motion correction and >=2 – coregister to that volume. Default: 1
5. **CoregRelaxToMain** - Do coregistration between Relaxometry and main. Default: 1
6. **MakeNoBATManualArtAnalysis** – If "1" and manualArt.nii exists, take the arteries from that file, take their average and make a regular calculation (we have AIF so we simply use Murase to get the PK parameters) without the possibility to shift BAT. Default: 0
7. **MakeBATManualArtAnalysis** - If "1" and manualArt.nii exists, take the arteries from that file, calculate the parameters using F Min Search on the picked arteries (instead of finding representative) and allow the possibility to shift BAT. Default: 0
8. **MakeBATAutoArtAnalysis** – The default mode of choosing the arteries automatically. Default: 1
9. **Extracted FAs** - Correct the flip angles of the scan (we assume there is an error).Default: 1
10. **IncludingMainInT1** - Default: 1. Include the DCE main (FA 20) in T1 calculation. (DO only if the DCE main acquired with the same calibration as the DESPOTs)
11. **UsingN3T1 –** Do inhomogeneity correction. Default: 1
12. **TimeMultiplier –**Default: 1
13. **Use\_Single\_M0 –** Enable calculating T1 using a single angel.Default: 0
14. **Calc\_Gains\_Diff –** Enable/disable gains calculation made by Gilad. Default: 1
15. **ThreshForRefMask.** Default: 0.99 – threshold for the segmented WM mask (used as reference for T1 and Vp cakculation).

**Relaxometry coregistration - Use the list box:**

Can coregister to DCEMean ('Mean 4D'), use no coregistration (' No coreg’) or coregister to the median angle. Anyway will coregister the T1 map o DCE mean.

**To force AIF shape (parameters) calculated before:**

InspectedAIFParams.mat

**To add reference files insert NIFTI files named:**

RefVp\_WM\_830.nii

RefT1\_WM\_830.nii

Manual\_BrainMask.nii

For artery selection, either

InspectedRepVox.nii - Takes exactly what's there, or

ManualArtMask.nii- Looks for arteries only inside that mask.

**Supplementary scripts**

1. **Fast Vp:** Run FastVpMap.m script (after changing into the subject output folder )

Make maximum in the bolus area and extract FastVp.nii map into the subject AutoArtBAT folder

2. **Compare between Ewing and Sourbron's normalization:** Run NormalizeByVeinsN.m script

Takes the Veins AUC and normalize to it

Gives figure with Jims normalization in blue and Sourbron normalization in Red and Magenta.

(The new normalization factor appears in the title)

>> Required input:

* Veins.nii binary mask with selected veins
* DCE output folder

>> Changing into the subject output folder

>> Set the Percent

**DCE – Perfusion [Guy]**

[\\FMRI-GUY2\SourceForge\Stable\_Versions\code\Version\_2.6\Code\DCE\_Perfusion](file:///\\FMRI-GUY2\SourceForge\Stable_Versions\code\Version_2.6\Code\DCE_Perfusion)

* כדי להגדיר path, צריך לשנות את זה ידנית בקובץ ReadRealData.m:

Subject\_name          = 'ReYe';

Subject\_Path          = '\\fmri-t9\users\Moran\DCE\HTR\_STROKE\01\_REMEZ\_YECHEZKEL\Study20140615\_114415';

WM\_mask\_absolute\_path = [Subject\_Path  '\RefAuto1\_WM\_830.nii'];

Art\_Mask              = [Subject\_Path  '\ManualArtMask.nii'];

After\_CTC\_mat         = [Subject\_Path  '\AfterCTC.mat'];

%DCECoregP = [WorkingP 'DCEMainCoreged' filesep];

% \\fmri-t9\users\Moran\DCE\HTR\_STROKE\01\_REMEZ\_YECHEZKEL

DCECoregP = [Subject\_Path filesep 'DCE\_out' filesep 'OrZe\_20130811' filesep];

DCECoregP = '\\fmri-t9\users\Moran\DCE\HTR\_STROKE\01\_REMEZ\_YECHEZKEL\';

* כדי להחליט אם רצים עם תיקון ל - bat או לא, צריך לשנות את השדה הבא ידנית, תחת הקובץ

**Simulation\_Set\_Params.m**

Sim\_Struct.Correct\_estimation\_due\_to\_delay        = true;      % Try to correct for delay

* במידה ויש אפשרות לתקן את הפקטור של ה - AIF מהקוד של גלעד, צריך לשנות את הערך הבא תחת הקובץ **Simulation\_Set\_Params.m**

Sim\_Struct.AIF\_Scaling\_Factor                     = 1;

הפקטור צריך להיות עבור AIF שנבחר כממוצע ה - CTC's של מסכת ה - AIF.

* אופציה לקביעת הטווח של ה- delay ב - dce perfusion בהתאם לתוצאות ה - BAT של גלעד.

(בחולה **סטרוק**, מומלץ לאפשר לטווח ב- dce perfusion להיות עד 20 שניות עם קפיצות יותר גדולות (נניח 0.5 שניות, סה"כ יהיו פי 40 חישובים).

בנוסף יש לו קצת ערכים שליליים (מקדים את ה- AIF), מומלץ לתת אפשרות לדיליי שלילי (נניח שניה אחורה).

גם את זה אפשר לשנות ב **- Simulation\_Sim\_Params.m :**

Sim\_Struct.AIF\_delay\_low                   = 0;   -> -1

Sim\_Struct.AIF\_delay\_max                 = 3;   ->  20

Sim\_Struct.Upsampling\_resolution       = 0.1 / 60;   % Set the upsampling target   -> 0.5/60

**Perfusion\_DCE – output names**

<< to be added >>

**DSC - Perfusion [Chen]**

[\\FMRI-GUY2\SourceForge\Stable\_Versions\code\Version\_2.6\Code\DSC](file:///\\FMRI-GUY2\SourceForge\Stable_Versions\code\Version_2.6\Code\DSC)

GUI Activation:

Activate Matlab and type:

DSCMainGUI

Click on **Init** button on the main Gui