

## Guide for TRUST processing GUI

Note: this code works on a 64-bit Windows computer.

### Step 1: open the GUI

Open Matlab, navigate to the “Pro\_NeoTRUST\_GUI\_Win64\_20190813” folder, and type “trustcode” in the Matlab Command Window. The “trustcode” GUI shows up.

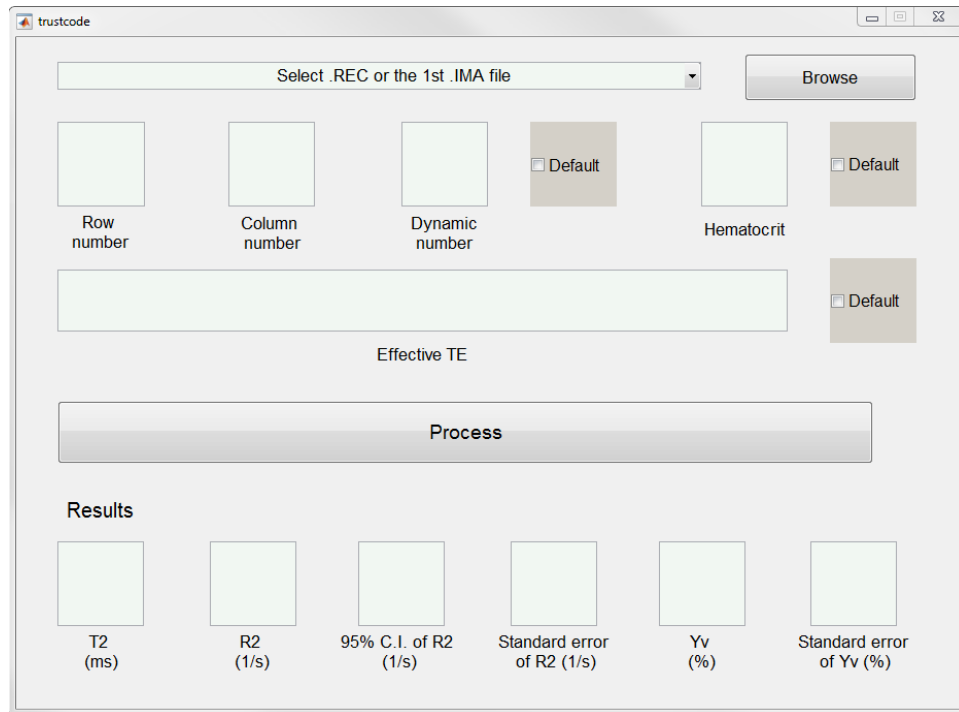


Figure 1: TRUST GUI

### Step 2: select TRUST data

Click on “Browse” button to choose the data to process. This GUI now supports three data formats: *.REC*, *.DCM*, *.IMA*.

For *.REC*, directly choose the *.REC* file to process.

For *.DCM* and *.IMA*, select the first TRUST image of the data to process (Figure 2). Please make sure all the TRUST images to process are stored in the same folder, and no space is allowed in the path, e.g. please name the folder as “TRUST\_sample” instead of “TRUST sample”.

Note: for the Philips Enhanced DICOM format, all TRUST images are stored in a single DICOM file. In this case, just select the DICOM file.

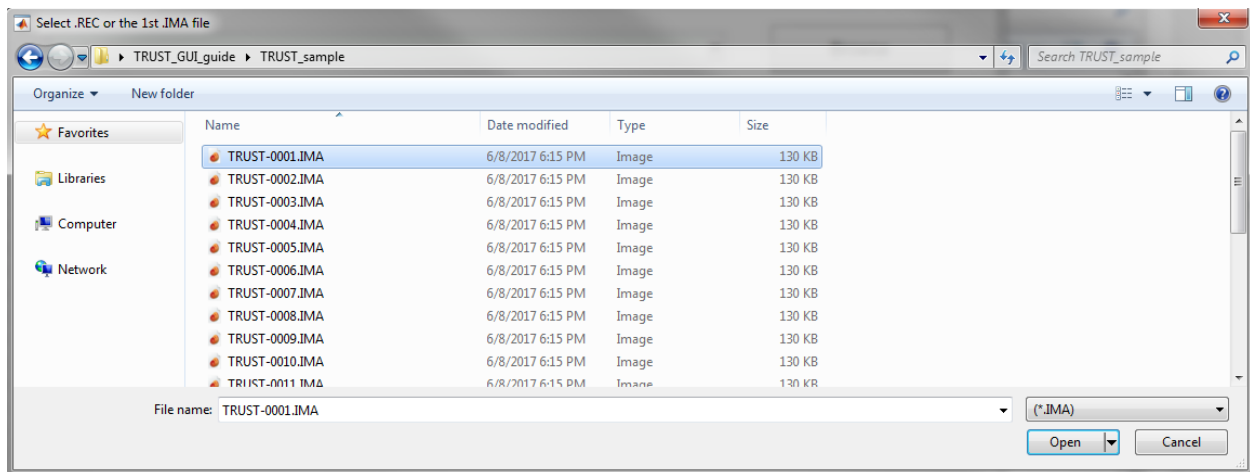


Figure 2: Select TRUST data in .IMA format

### Step 3: set the parameters

Enter the “Row number” (number of rows in the image), “Column number” (number of columns in the image) and “Dynamic number” (number of images), or click on “Default”.

Enter the “Hematocrit” or click on “Default”. If you click on “Default”, it will prompt a dialog window to let the user choose the gender of the subject. The default hematocrit for male, female and unknown are 0.42, 0.40, 0.41, respectively.

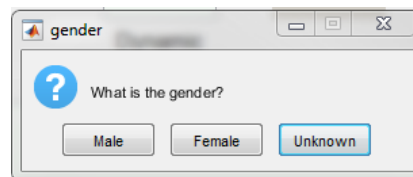


Figure 3: Dialog window for default hematocrit

Enter an array of “Effective TE” (in ms), or click on “Default”. The array of effective TEs must exactly match the actual order of effective TEs of the TRUST images to process. The default array of effective TEs and other default parameters are shown in Figure 4:

The screenshot shows the 'trustcode' software window. At the top, there is a dropdown menu labeled 'Select .REC or the 1st .IMA file' and a 'Browse' button. Below this, there are several input fields and checkboxes for parameters:

- Row number:** 64
- Column number:** 64
- Dynamic number:** 24
- Hematocrit:** 0.41
- Effective TE:** A long text field containing the sequence: 0.44 0.44 40 40 80 80 160 160 0.44 0.44 40 40 80 80 160 160 0.44 0.44 40 40 80 80 160 160

Each of these parameter fields has a corresponding 'Default' checkbox, all of which are checked. Below the parameters is a large 'Process' button. Underneath the 'Process' button is a 'Results' section with six empty boxes for displaying the following metrics:

- T2 (ms)
- R2 (1/s)
- 95% C.I. of R2 (1/s)
- Standard error of R2 (1/s)
- Yv (%)
- Standard error of Yv (%)

Figure 4: Default settings of parameters

#### Step 4: Exclude motion-contaminated images

Click on “Process” button, in a few seconds, the control and difference images of each eTE and each dynamic are shown, as illustrated by Figure 5 and Figure 6.

Type the indices of motion-contaminated images in the Matlab command window and then press enter, as shown in Figure 7.

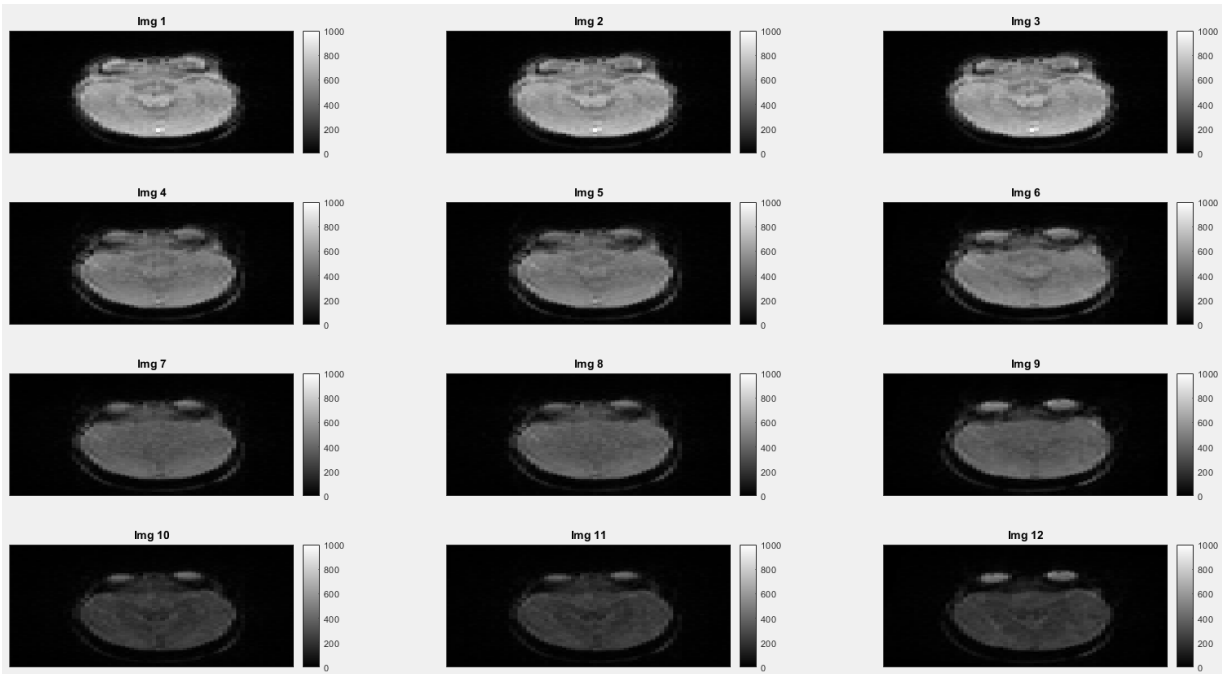


Figure 5: Control images of each eTE and dynamic.

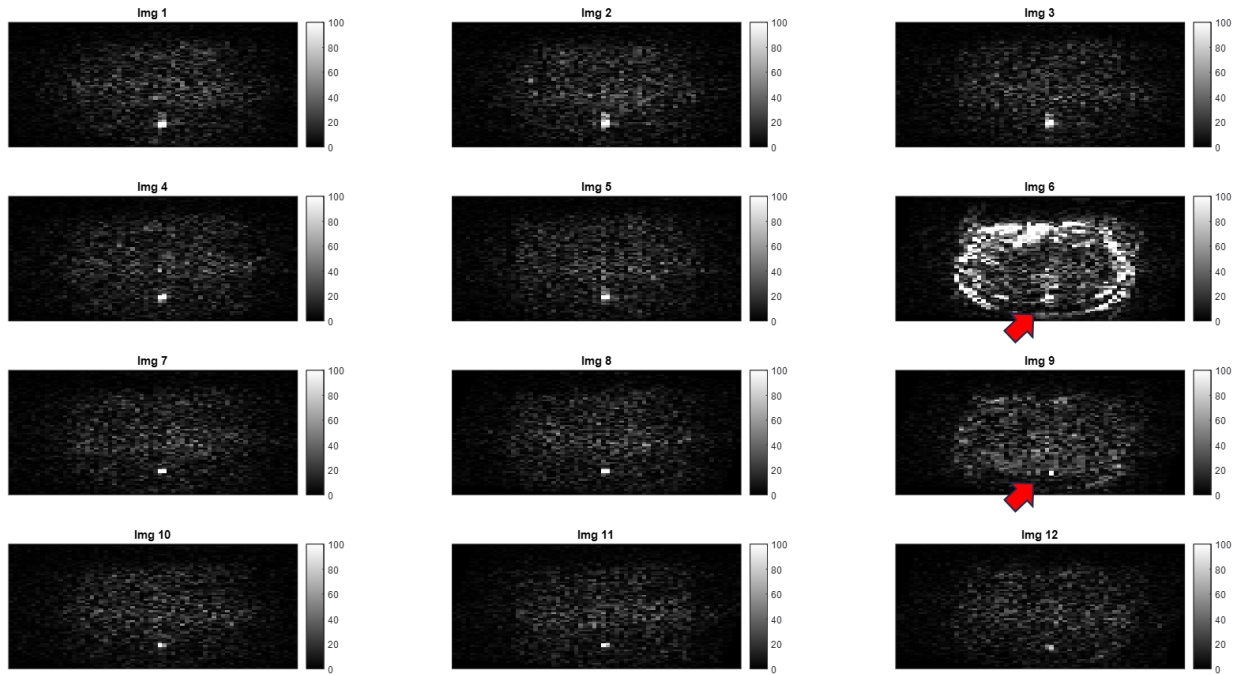


Figure 6: Control-label difference images of each eTE and dynamic. Red arrows point to the difference images with motion contamination.

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fx Manual exclusion: [6, 9]
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Figure 7: Type the indices of images to be excluded in the Matlab command window.

### Step 5: Manually draw preliminary ROI for the superior sagittal sinus

After excluding motion-contaminated images, a figure of the difference image (control – label) will be displayed to let the user draw the ROI for superior sagittal sinus. Please make sure the ROI is large enough to cover the entire sagittal sinus, as shown in Figure 8. After drawing the ROI, double click or right click and then select “Create Mask”.

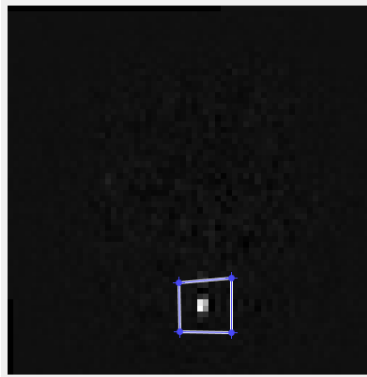


Figure 8: Difference image to draw preliminary ROI for the superior sagittal sinus.

The results will be displayed in the “Results” panel (bottom row in Figure 4). The results will also be saved as a .txt file in the same folder as the REC, .DCM, or .IMA files.