BME33101 Biomedical imaging mid-term project

FID data reconstruction and T_1, T_2, T_2* fitting

Given data information :

- **Matrix size :** 256 x 256, 1 Slice
- **Sample :** Sprague Dawley (SD) Rat brain (age : 6 week, 4 month, 20 month)
- **T_1 sequence :**
  i. Sequence name : RARE-VTR (Rapid Acquisition with Relaxation Enhancement – with Variable repetition time TR)
  ii. Repetition Time (TR) : 50 100 200 300 500 700 1000 2000 3000 5000 [millisecond, ms]. Total number of TR : 10
  iii. Phase encoding array : 0 -1 1 -2 2 -3 3 -4 4 -5 5 -6 6 -7 7 -8 8 -9 9 -10 10 -11 11 -12 12 -13 13 -14 14 -15 15 -16 16 -17 17 -18 18 -19 19 -20 20 -21 21 -22 22 -23 23 -24 24 -25 25 -26 26 -27 27 -28 28 -29 29 -30 30 -31 31 -32 32 -33 33 -34 34 -35 35 -36 36 -37 37 -38 38 -39 39 -40 40 -41 41 -42 42 -43 43 -44 44 -45 45 -46 46 -47 47 -48 48 -49 49 -50 50 -51 51 -52 52 -53 53 -54 54 -55 55 -56 56 -57 57 -58 58 -59 59 -60 60 -61 61 -62 62 -63 63 -64 64 -65 65 -66 66 -67 67 -68 68 -69 69 -70 70 -71 71 -72 72 -73 73 -74 74 -75 75 -76 76 -77 77 -78 78 -79 79 -80 80 -81 81 -82 82 -83 83 -84 84 -85 85 -86 86 -87 87 -88 88 -89 89 -90 90 -91 91 -92 92 -93 93 -94 94 -95 95 -96 96 -97 97 -98 98 -99 99 -100 100 -101 101 -102 102 -103 103 -104 104 -105 105 -106 106 -107 107 -108 108 -109 109 -110 110 -111 111 -112 112 -113 113 -114 114 -115 115 -116 116 -117 117 -118 118 -119 119 -120 120 -121 121 -122 122 -123 123 -124 124 -125 125 -126 126 -127 127 -128
- **T_2 sequence :**
  i. Sequence name : MSME (Multi-Slice Multi-Echo)
  ii. Echo Time (TE) : 8 16 24 32 40 48 56 64 72 80 88 96 104 112 120 128 136 144 152 160 168 176 184 192 200 208 216 224 232 240 248 256 264 272 280 288 296 304 312 320 328 336 344 352 360 368 376 384 [ms]. Total number of TE : 48
  iii. Phase encoding array : -128 -127 -126 -125 -124 -123 -122 -121 -120 -119 -118 -117 -116 -115 -114 -113 -112 -111 -110 -109 -108 -107 -106 -105 -104 -103 -102 -101 -100 -99 -98 -97 -96 -95 -94 -93 -92 -91 -90 -89 -88 -87 -86 -85 -84 -83 -82 -81 -80 -79 -78 -77 -76 -75 -74 -73 -72 -71 -70 -69 -68 -67 -66 -65 -64 -63 -62 -61 -60 -59 -58 -57 -56 -55 -54 -53 -52 -51 -50 -49 -48 -47 -

46 -45 -44 -43 -42 -41 -40 -39 -38 -37 -36 -35 -34 -33 -32 -31 -30 -29 -28 -27 -26 -25 -24 -23 -22 -21 -20 -19 -18 -17 -16 -15 -14 -13 -12 -11 -10 -9 -8 -7 -6 -5 -4 -3 -2 -1 0 1 2 3 4 5 6 7 8 9 10 11 12 13 14 15 16 17 18 19 20 21 22 23 24 25 26 27 28 29 30 31 32 33 34 35 36 37 38 39 40 41 42 43 44 45 46 47 48 49 50 51 52 53 54 55 56 57 58 59 60 61 62 63 64 65 66 67 68 69 70 71 72 73 74 75 76 77 78 79 80 81 82 83 84 85 86 87 88 89 90 91 92 93 94 95 96 97 98 99 100 101 102 103 104 105 106 107 108 109 110 111 112 113 114 115 116 117 118 119 120 121 122 123 124 125 126 127

- **T_2* sequence :**

  i. Sequence name : MGE (Multi-Gradient Echo)

  ii. TE : 2.7 6.1 9.5 12.9 16.3 19.7 23.1 26.5 29.9 33.3 36.7 40.1 43.5 46.9 50.3 [ms]. Total number of TE : 15

  iv. Phase encoding array : -128 -127 -126 -125 -124 -123 -122 -121 -120 -119 -118 -117 -116 -115 -114 -113 -112 -111 -110 -109 -108 -107 -106 -105 -104 -103 -102 -101 -100 -99 -98 -97 -96 -95 -94 -93 -92 -91 -90 -89 -88 -87 -86 -85 -84 -83 -82 -81 -80 -79 -78 -77 -76 -75 -74 -73 -72 -71 -70 -69 -68 -67 -66 -65 -64 -63 -62 -61 -60 -59 -58 -57 -56 -55 -54 -53 -52 -51 -50 -49 -48 -47 -46 -45 -44 -43 -42 -41 -40 -39 -38 -37 -36 -35 -34 -33 -32 -31 -30 -29 -28 -27 -26 -25 -24 -23 -22 -21 -20 -19 -18 -17 -16 -15 -14 -13 -12 -11 -10 -9 -8 -7 -6 -5 -4 -3 -2 -1 0 1 2 3 4 5 6 7 8 9 10 11 12 13 14 15 16 17 18 19 20 21 22 23 24 25 26 27 28 29 30 31 32 33 34 35 36 37 38 39 40 41 42 43 44 45 46 47 48 49 50 51 52 53 54 55 56 57 58 59 60 61 62 63 64 65 66 67 68 69 70 71 72 73 74 75 76 77 78 79 80 81 82 83 84 85 86 87 88 89 90 91 92 93 94 95 96 97 98 99 100 101 102 103 104 105 106 107 108 109 110 111 112 113 114 115 116 117 118 119 120 121 122 123 124 125 126 127

What to do? :

Part 1. FID (Free induction decay) data reconstruction

In this part, you need to reconstruct the MR image by filling the k-space using the given FID data (using only 6 week rat brain data). The number of voxels in each given sequence FID data is :

(x size) x (y size) x (Total number of TR or TE) x 2

The reason for performing "x 2" is that the complex number FID is divided into real number and imaginary number. For example, given RARE-VTR FID data has 1310720 voxel numbers (1310720 x 1), which is the result of calculating 256 (x size) x 256 (y size) x 10 (Total number of TR) x 2 (real & imaginary numbers) as shown in figure 1. If the real number and imaginary number are combined in the form of

a complex number, the number of voxels in result RARE-VTR FID data is 655360 (655360 x 1). Therefore, the first step in FID reconstruction is to combine the given fid data into complex number data type (figure 1).

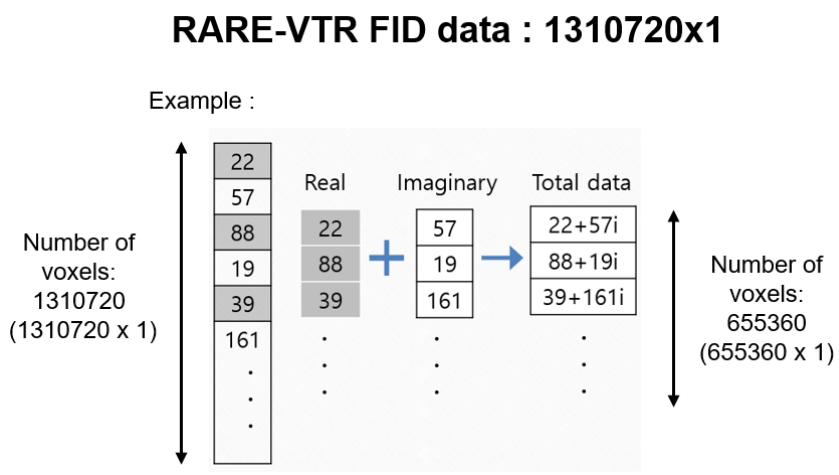

Figure 1. Example of combining RARE-VTR FID data.

The next step is to fill the k-space with FID data according to the given phase encoding array and derive MR images using 2D Inverse Fourier transform. In case of RARE-VTR FID data, the voxels are arranged in order from the smallest TR (= 50 ms) to the largest TR (= 5000 ms). The complete k-spaces (256 x 256 x 10) are obtained by repeating the method of filling all parts of k-space according to the phase encoding array coordinates and moving to the next k-space (figure 2).

For MSME and MGE FID data, the method of filling k space is different from RARE-VTR FID data. In these cases, the complete k-spaces (256 x 256 x 48 or 15) are obtained by repeating the method of filling each part of all k-spaces corresponding to one phase encoding array coordinate and moving to the next phase encoding array coordinate (figure 3).

After filling all the k-spaces, apply 2D Inverse Fourier transform to derive the result MR images (figure 2 and 3). If the MR images are rotated, you can use the imrotate function to reset the images.

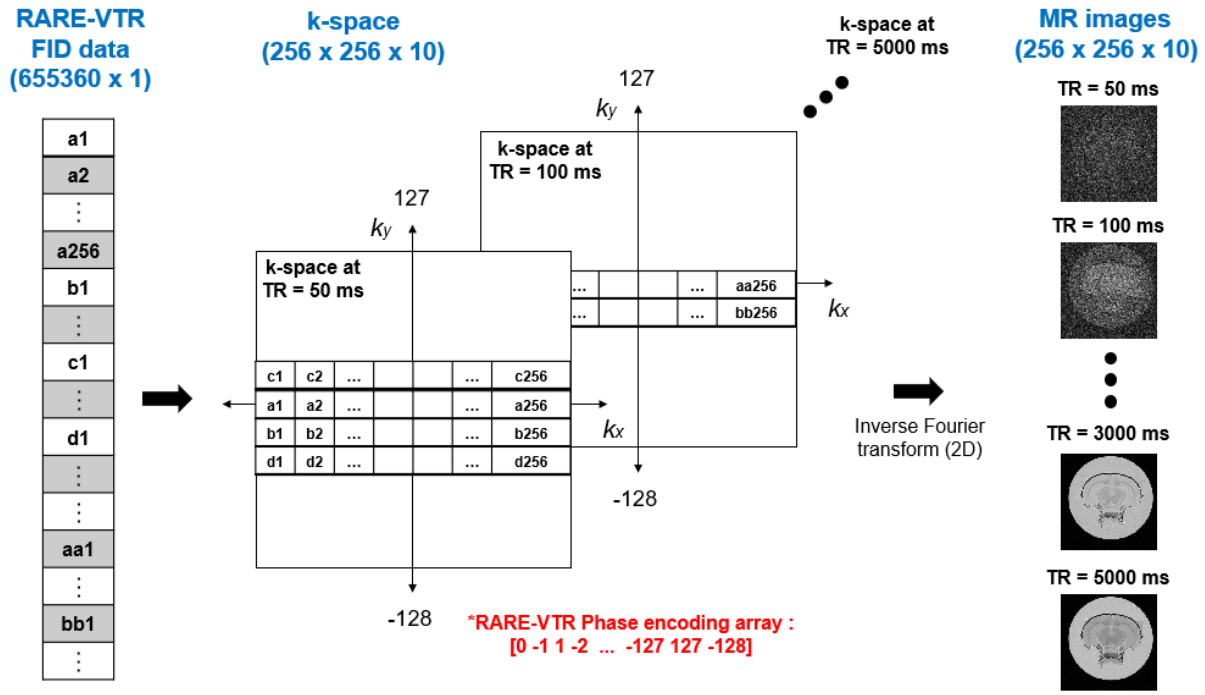

Figure 2. Example of RARE-VTR FID data reconstruction process.

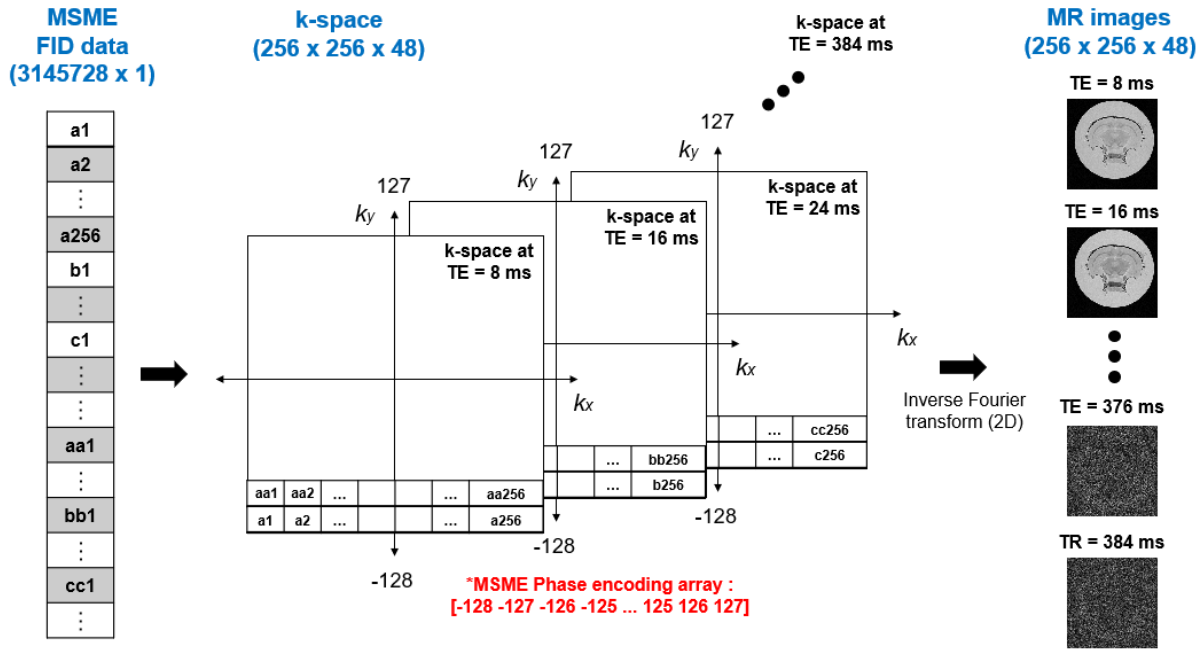

Figure 3. Example of MSME FID data reconstruction process.

Part 2. T_1, T_2, T_2* fitting and fitting quality check

In this part, you need to perform fitting process to obtain T_1, T_2, T_2* values and check the fitting quality. The longitudinal relaxation time T_1 and transverse relaxation time T_2 (acquired by spin echo method) equations are represented in figure 4. T_2* is expressed by "T_2 + local field inhomogeneity" and acquired by gradient echo method.

So, what you need to do in this part is to derive the values of T_1, T2 and T2* through the fitting process from one selected point using the result MRI data obtained in part 1 and equations in figure 4. It is also necessary to evaluate the quality of the fitting through the R-squared value (R^2, the statistical measure of fit). The coordinates used for this part are freely selectable within the brain area. The example of fitting result using RARE-VTR sequence is shown in Figure 5.

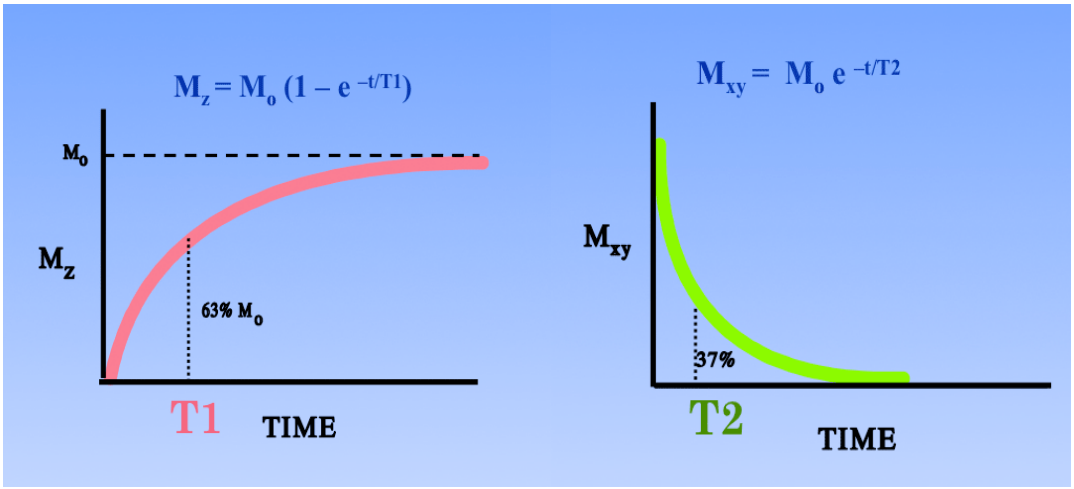

Figure 4. Graphical representations of T_1 and T_2.

(figure reference : http://www.mriquestions.com/bloch-equations.html).

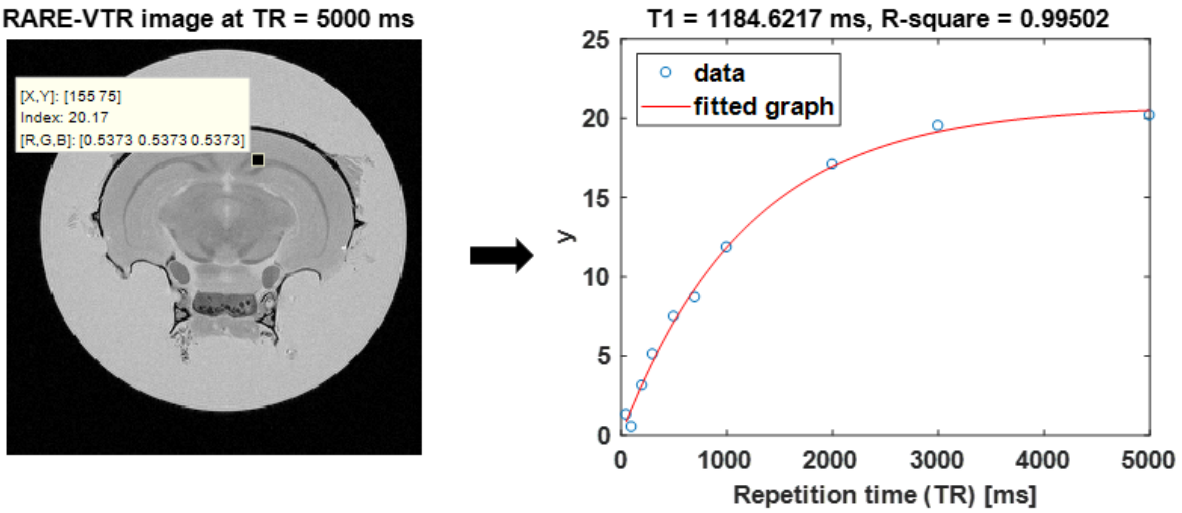

Figure 5. Example of RARE-VTR data fitting process and fitting quality at one specific point.

Part 3. T_1, T_2 and T_2* mapping

In this part, you need to fit all voxels to make T_1, T_2 and T_2* maps of rat brain. Using the fitting algorithm used in Part 2, you can derive the result maps as shown in Figure 6. Depending on your computer's performance, it may take from a few minutes to several hours to draw a map. If you want, you can reduce the time by fitting only the voxels in the brain region through the ROI (region of interest) function.

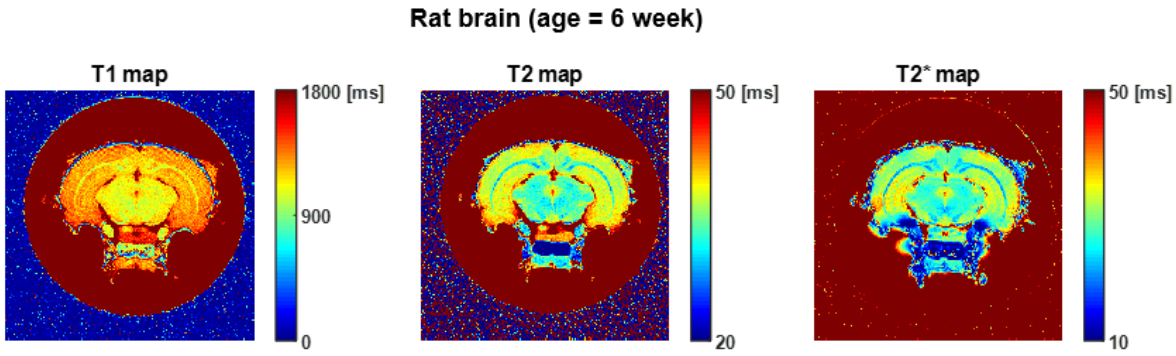

Figure 6. Example of T_1, T_2 and T_2* maps of 6 week rat brain data

★Optional★ Part 4. Analysis of T1, T2 and T2* by age

This part is optional, but if you complete it correctly, you will get extra points. In this part, you need to map additional 4 month and 20 month rat brain data along with the 6 week rat brain maps generated in part 3. Then you need to target specific brain regions to analyze how the values of T1, T2 and T2* of those regions change with age. The region of the rat brain does not matter which region you choose, but it is better to look at the substantia nigra or corpus callosum region as shown in figure 7. Various methods, such as bar graphs, histograms, and box plots, can be used to show and explain changes in brain regions by age.

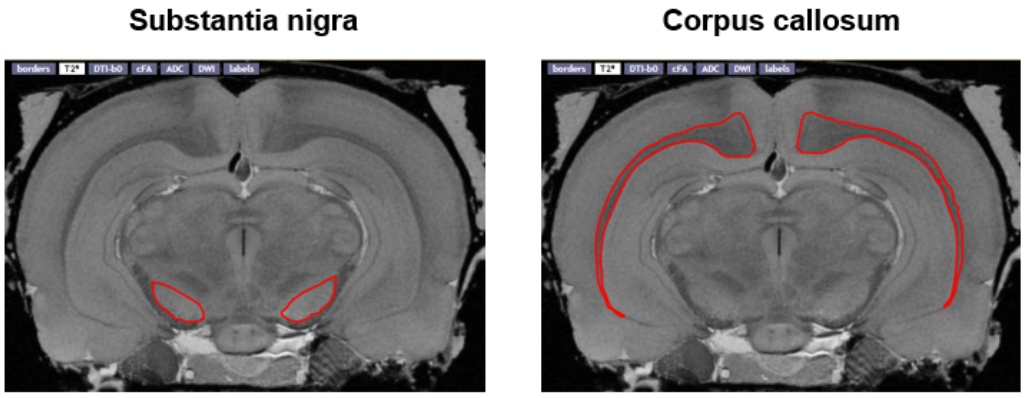

Figure 7. Substantia nigra and corpus callosum regions of rat brain (red line).

(figure reference : https://scalablebrainatlas.incf.org/rat/PLCJB14)

Report form :

Theory

: Explain theory you applied.

Method

: Describe the code structure in detail.

Results

: Show the results of each part

Discussion

: Your opinion of your results.

*Notice: When you submit the report, you should attach the full version of code and result mat files. (I will compare your results with our results.)