PROJECT PAPER

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INTERPOLATION OF T2 RELAXATION TIME UNDER THE EMC* FIT ALGORITHM SIMULATION DATABASE FOR A MULTI-SE* PROTOCOL

Laurène Bouskila

Purpose:

T2 mapping has demonstrated various benefits in applications for non-invasive diagnosis. Moreover, the EMC fit algorithm provide optimal matching T2 values with relatively high accuracy and precision. Unfortunately, simulations are very impractical in terms of time consumption.
In order to reduce this amount of time, we are looking to set a mathematical model of interpolation for the ETL* values and evaluate its performance over the T2 mapping on a brain sample.

Methods:

It is needed to explore the EMC curves in a given simulated dictionary of curves, in order to find an interpolation pattern for the T2 EMC curves, thus saving computational time in simulations. This model will define a new database (containing the interpolated lines) that will be tested to generate the corresponding T2 map of the brain sample. Several parameters can alter the analysis of the error between the original database and the interpolated one: mathematical model of interpolation, order of interpolation, number of interpolated lines … We will try to give a complete analysis and draw conclusions on the effect of the number of interpolated lines on the propagation of the error in the mapping.

Results:

There is a tradeoff between time saving benefits on the number of interpolated lines and the level of propagation error into T2 mapping. Obviously, the speed of interpolation over simulations increases as the amount of lines is significant, but this will cause inaccuracies in the T2-mapping due to the rise of the relative error. As a matter of fact, there is an optimal value if we take into account a certain bound of acceptable error (usually defined by the percentage of error in the measurement devices themselves).

Conclusion:

As a matter of fact, one should conclude about an optimal value regarding the number of interpolated lines by taking into account a certain upward limit of acceptable error (usually defined by the percentage of error in the measurement devices themselves). However, the system will benefit from a consequent decrease in the computational time over simulations.

Context

Nowadays, T2-relax-based contrast is widely used for non-invasive diagnosis. Unfortunately, this only allows visually qualitative mapping. We would rather be interested into getting the actual values of the T2 relaxation times in order to get T2-mapping.

Although quantitative T2-mapping through single-echo SE has demonstrated merit for various applications, it stills remains challenging in the case of the guenine to get T2 relaxation time values.

In the case of a single-echo SE, the signal decays exponentially (so called FID=free induction decay) and so will be used as values of reference for our research.
Despite its benefit of reducing the diffusion effect, Multi-echo SE bring into play side effects/parameters that will distort the decay form of the signal. Among them, the strong signal contamination that splits the signal into three coherence pathways (leading to indirect echoes, and consequently deviation from the correct T2 values).

Therefore, we won't be able to consider the exponential decaying form of the signal and we will have to perform simulations under the EMC fit algorithm to get the corresponding T2 relaxation time values. Note that multi-echo SE consequently elongates the T2 curve (because of the echoes due to refocusing pulses at FA (=flip angles) chosen in a range around an optimal value of 180 degree).

It has been demonstrated that the EMC fit algorithm get optimal matching T2 results (high accuracy and precision) for our purpose (see reference 3).
However, simulations are very impractical in the sense of computational time efficiency.

*
EMC=echo modulation curve *SE=spin echo* *ETL=echo train length*

Methods

We will explore the EMC curves in a given simulated dictionary of curves, in order to find an interpolation pattern for the T2 EMC curves, thus saving computational time in simulations.
We expect a non-linear interpolation (or partially linear) since the decay approaches a similar tendency to an exponential form. This implies that a difference between short relaxation-time values will lead to significant change in the echo amplitude compared to the same difference, examined for long relaxation-times (due to logarithmic scale).
We thus need to investigate for an appropriate and non-uniform interpolation.

When fitting datas for the brain sample DICOM, the following database is fetched to the GUI that produces corresponding T2 maps:
'2014_05_18MID149s_T2_1_300_1000__B1_50_130_400um_L_20mm.mat'.
The matrix under analysis, called echo_train_modulation, contains 5 dimensions [B0,B1+,T1,T2,ETL] and belongs to the dictionary database that resides in the EMC database folder.
For simplicity, we'll restrict this research to a 2D matrix by restraining the three first parameters. That is to say that we assume a total homogeneous magnetic field, and a fixed value for the longitudinal relaxation T1 time as described in the following figure.

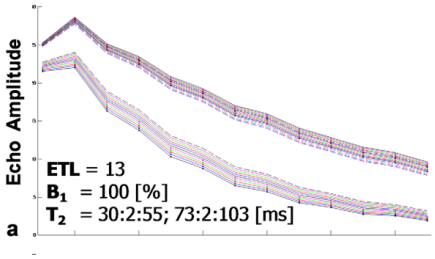


FIG. 1. Examples of a simulated echo-modulation-curve (EMC) database for a multi-SE protocol. a: Simplified database containing two ranges of consecutive T2 values.

This investigation will contain two main steps:
First we will perform interpolation on one over two lines starting from the T2=10ms line.
Next, we'll try to expand this interpolation to 2 lines interpolation for each original line in the dictionary of curves.
For now, we also restrict ourselves to a simple interpolation mathematical model to get the missing curves.
In order to evaluate the efficiency of our model: we'll examine the relative error between the interpolation to the actual simulated datas.
Theoretically, the rejection criteria should be the overcoming of the EMC measurements errors themselves (in %).

Project Conduction

Analysis of the database parameters

The echo_train_modulation[B0,B1+,T1,T2,ETL] matrix contains T2 parameters of size 440 and ETL of size 20.
This implies that for each T2 relaxation time, ie. each EMC line, there will be 20 sampled values that will define the echo amplitude values.
The 440 T2 times array contains two different scales of segmentation:

- From T2=1ms(1st value) to T2=300ms (300th value), the steps are of 1ms
- From T2=305ms(301st value) to T2=1s (440th value) the steps are of 5ms.

The interpolation was performed on the following mathematical models:

$$Vinterpolated(T_2(i)) = Voriginal(T_2(i-1)) + \frac{|Voriginal(T_2(i-1)) - Voriginal(T_2(i+1))|}{2}$$

(a) *48.86%=100*(215/440)= interpolation mathematical model*

$$Vinterpolated(T_2(i)) = Voriginal(T_2(i-1)) + \frac{|Voriginal(T_2(i-1)) - Voriginal(T_2(i+1))|}{3}$$

$$Vinterpolated(T_2(i+1)) = Voriginal(T_2(i-1)) + 2*\frac{|Voriginal(T_2(i-1)) - Voriginal(T_2(i+2))|}{3}$$

(b) *65%=100*(286/440)= interpolation mathematical model*

By comparing the matrices of the original and modified database, the relative error is calculated under the following definition:

$$error_R = 100 * \frac{Voriginal(T_2 = i) - Vinterpolated(T_2 = i)}{Voriginal(T_2 = i)}$$

All the relative errors are stored in a matrix error(1,:,1, :, :).

The brain sample is selected as a DICOM for the two dictionaries of curves (original vs interpolated) and for each one of them, two resulting files are created (under EMC_results folder).
One of them is under the .mat format and contains the relevant values for each pixel.

The relative error of these two files is then computed in order to get some insight on the propagation of the error into the T2 relaxation time mapping.

Results

Expectations

In this research there exist two parameters that can affect the propagation of the error into the T2 maps, and thus decrease their accuracies.
First of all, we do expect that the number of interpolated lines will cause a change in the mapping. This is because, interpolated lines are constructed thanks to values from a mathematical model (simple interpolation).
For example, in step 2, where about 2/3 of the whole database is interpolated, each ETL value is calculated from two lines: one line that resides next to it, and another one situated two sampled values of T2 away from it. This engenders the error to critically increase. Consequently, increasing the number of interpolated lines engenders a rise in the propagation level of the error into the mapping.

Next, as explained in the introduction, the mathematical model set for the interpolation also plays a role in the impact of the T2 map precision. For simplicity we kept the interpolation to a linear form, but if the interpolation factor increases, or even better: if a non-uniform interpolation (interpolation type differs as T2 changes) is applied to the database, the error should be less propagating to the maps.
Because the decay of the EMC curves behaves as a decaying exponential curve and so the error will be more important when dealing with low T2 values.

Observations

(a)

(b)

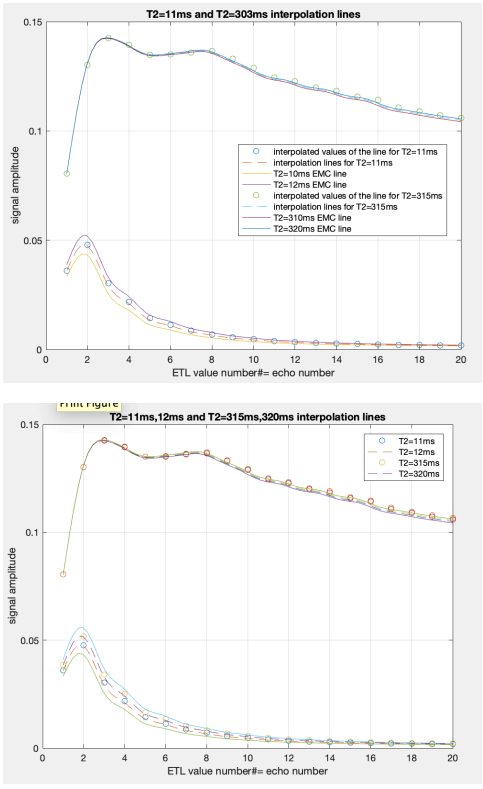


FIG. 2:
(a)Interpolation step 1 (half of the database interpolation starting from T2=10ms) examples for T2=11ms and T2=315ms (b) Interpolation step 2 (2/3 of the database starting from T2=10ms) examples for T2=11;12;315;320ms

(a)

(b)

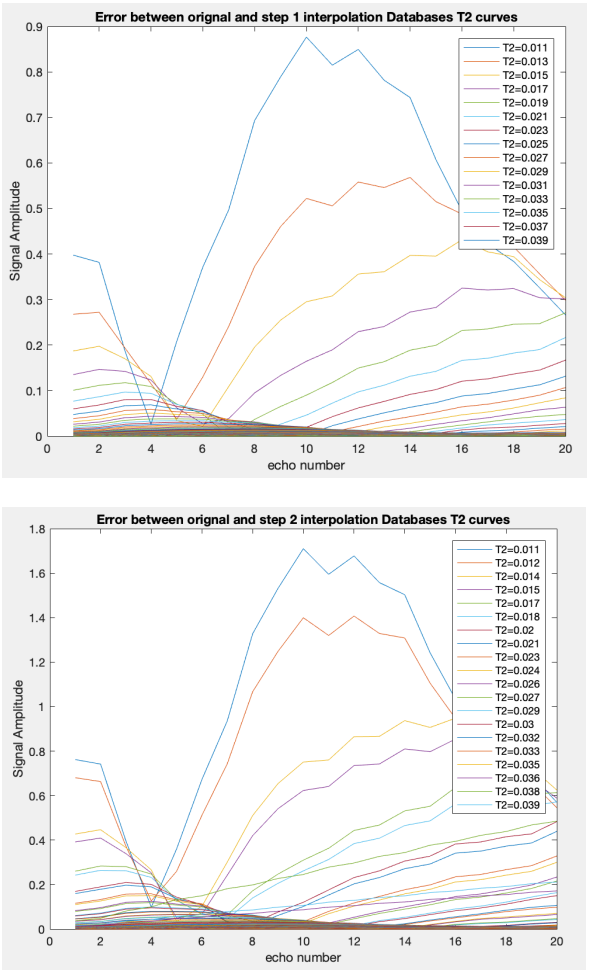


FIG. 3: (a)Relative error in interpolation step 1(b) Relative error in Interpolation step 2

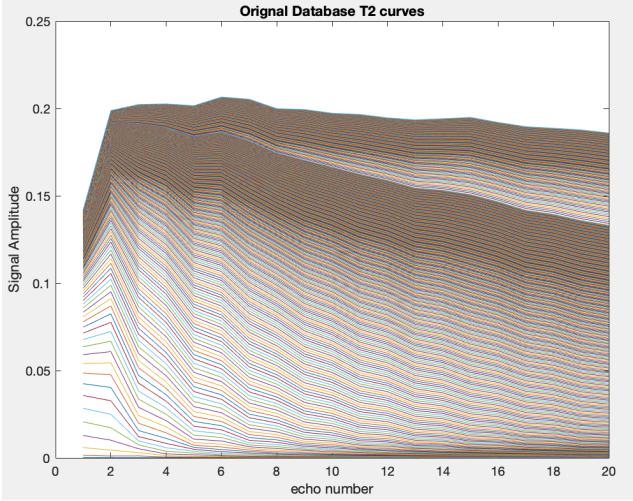
As can be observed from FIG2, the interpolated lines are depicted with dash and circles for the sampled values. In (a) there's one interpolated line between two simulated ones. Whereas in (b) we interpolated two lines between every two simulated lines.
In both cases, the difference is greater when dealing with low T2 values compared to high T2 values lines.

This is the reason why FIG3 depicts a relatively higher error for the line T2=11ms (lower T2 lines) compared to the T2=315ms (higher T2 lines) line which is closed to 0%, and this is valid for both interpolation steps.
Beside that, we also notice that for the same line (T2=11ms for example), the relative error increases (from 0.9% to 1.7%) between step1 to step2 interpolation. This is because, as expected, the number of interpolated lines increased and so the tracking of the values is less accurate.

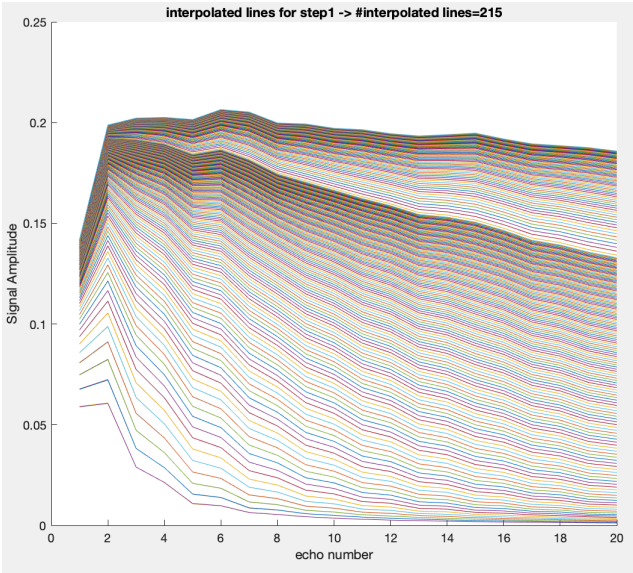
At later stages, this error will determine the level of propagation to the T2 maps. That's we will see next. From there, we can establish an analytical rejection criteria: Is the level of propagation too high? Does it affect considerably the accuracy of the T2 map?

Pay attention that FIG2 was just a 'zoom-in' on some specific curves, the overall database should look like FIG4 for the original database and for the interpolated lines.

(a)



(b)



(c)

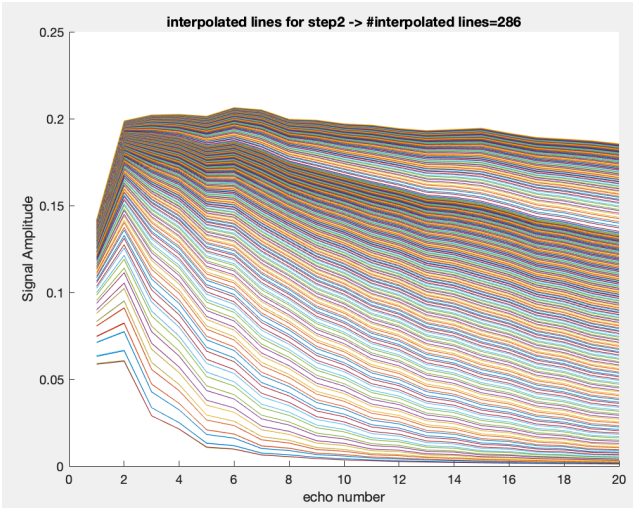


FIG4: (a) Original DB T2 curves (b) interpolated curves for step1 interpolation (c) interpolated curves for step 2 interpolation.

We can see that the graph (c) is more dense than (b). This is because the number of interpolated lines is increased in step2.
Note that whereas graph (a) depicts the 440 T2 lines of the database, graphs (b) and (c) depict only the interpolated lines.

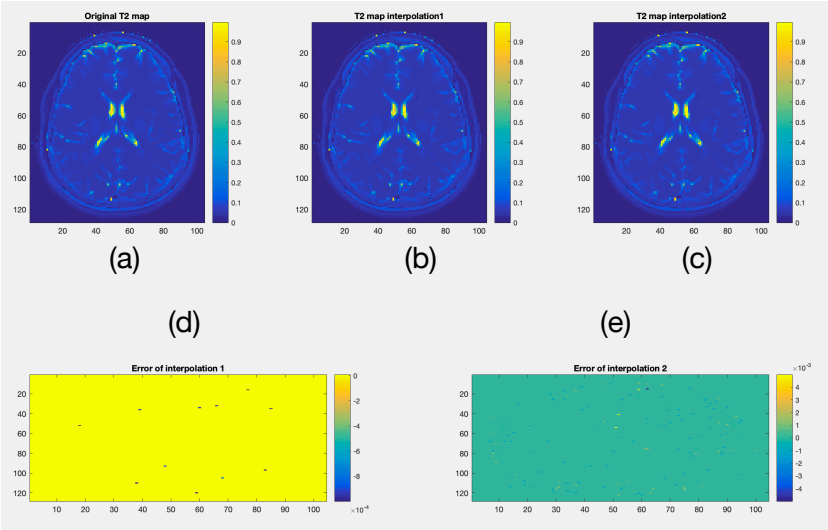


FIG5: (a) Original DB T2 map (b) step 1 interpolation T2 map (c) step 2interpolation T2 map (d) Difference between maps (a) and (b) =Relative error of interpolation 1 (e) Difference between maps (a) and (c) =Relative error of interpolation 2

The above figure confirm our expectations: The three first graphs depict the T2 maps on a brain sample for original, step 1 and step 2 interpolations respectively.
As expected, it can be observed from graphs (d) and (e) that the relative error between the interpolated and original maps increase as the number of lines interpolation is greater.
As a matter of fact, in for step 1 interpolation, only a few errors are distinguishable; whereas in step 2, the errors are more important (pay attention to the order of magnitude of the colour bar), numerically greater than before, and of various magnitude.

Eventually, as the error increase, it can propagate into the T2 map and alter its use and readability.

Proposal for further work

It is interesting to extend this research forward by bringing attention to the interpolation form: One should get smaller error between diluted and original databases by creating a non-uniform interpolation pattern depending on the line under interpolation (low or high T2 value).

A compromise for the tradeoff between speed of interpolation and precision of simulations may be determined by criteria of selection such as measurement error.

Depending on the material used, we can eventually define a rejection criteria. As a matter of fact, the error of the measurement devices can be used as an upward limit for accepting the interpolated datas as accurate enough, and by doing so, prevent from harming the reading of the T2 maps unreasonably.

Obviously, this method extends to various databases on different organs. The brain is used in this research as an example of work.