A Learning method to Estimate Multi-Compartmental T2 Distributions with low Data Requirements

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Synopsis

The estimation of intravoxel distributions of T2 values based on multi-echo MR data is a challenging task. Interestingly, the information above is quite useful for detecting damage in brain tissue, i.e. for estimating myelin-water-fraction changes associated with the demyelination process. Currently available methods typically require a long train of echoes, which are not always feasible to acquire. In this work, we tackle the problem using state-of-the-art neural network architectures based on attention mechanisms such as Recurrent Neural Networks (RNN) with attention and the newly proposed Transformer architecture, widely used in Natural Language Processing Tasks and Computer Vision. We test our model on limited data (5 echoes and 4 TR). The methodology identifies myelin abnormalities in a rodent model of a neurological disorder with demyelination.

Introduction

The estimation of multi-compartmental T2 distributions P(T2) from multi-echo MR data allows the determination of myelin water fraction and therefore the identification of demyelination. The performance of classic inversion approaches has been investigated in recent studies, as well as approaches based on supervised learning techniques. Those techniques require a long train of echoes (e.g 60 measurements are reported in (Yu. Et. Al 2020)). This proposal uses state-of-the-art Artificial Neural Networks (ANN) and T2 decay synthetic signal generators to investigate the feasibility of enabling a low-requirement-clinically-feasible acquisition setting for this problem. We use in-vivo data from rats with a genetically defined neurological disorder called TAIEP characterized by mutant tubulin genes, conditioning de- and hypo-myelination of the CNS, and atrophy of basal ganglia and cerebellum.

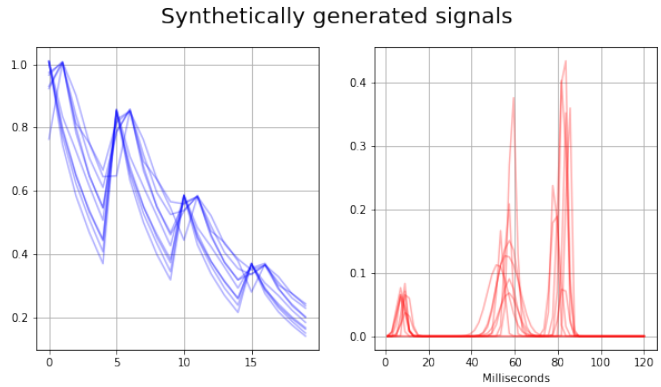
Methods

Rats (3 Control and 3 TAIEP, all 2 months of age) were scanned on a 7T Bruker 70/16 US scanner, selecting a single coronal slice showing the corpus callosum with a plane resolution of 0.13 x 0.14 mm^2 and slice thickness of 1mm. Five echoes were acquired (TE={7,21,35,49,63} ms) for each 4 different repetition times TR={800,1500,3000,5000} ms. The white matter analysis was carried out on the corpus callosum of the rats.

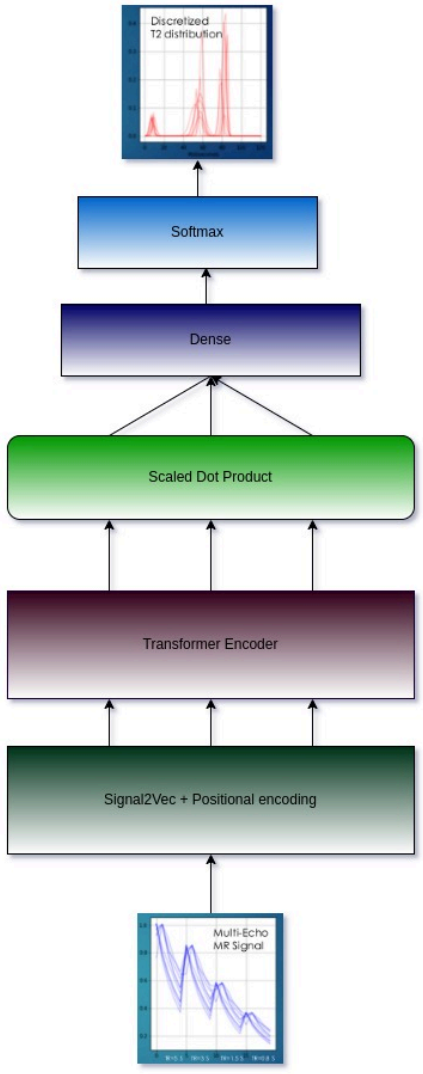
The first step is to create a training database of MR signals from multi-echo T2 based on the acquisition protocol. We use the EPG formalism such that the MR signal is defined as

$$S(TE_i) = M_0 \int EPG(TE_i, T1, T2, \alpha) P(T2) dT2.$$

T1 value was set to 2000 milliseconds (about 2 seconds). The refocusing angles α are generated with a uniform distribution from 90 to 180 degrees. In synthetic signals, we set $M_0 = 1$ and the real signals are normalized to their maximum value to mitigate the scaling effect. ***P(T2)*** is parametrized from 1 to 120 milliseconds to cover for T2 values associated with myelin and intra/extracellular water spaces at 7T. We generate the T2 distributions using 20000 equally spaced points in the interval [1,120] ms. We then down sample the generated signals to a distribution of 60 bins. The down-sampled distribution is used as the target distribution intended to be predicted by the network. We added Rician noise with SNR=40 to all the synthetic signals (the SNR was estimated on homogeneous ROIs in the ex vivo rodent data). We created 10000 synthetic signals to train the learning model by randomly sampling the uniform distributions for the parameters above.



For the inference machine, we propose a novel Deep Learning architecture based on attention mechanisms. The architecture corresponds to a Transformer (Vaswani 2017) based architecture, using an initial layer to convert a signal into vectors and then using the Transformer encoder to capture relevant information among the distinct parts of the signal. The resulting vectors of the encoding are then joined using the scaled dot product (Badhan au), and the resulting vector is then fed into a dense layer with a SoftMax activation function at the end to obtain the desired distribution. The proposed architecture is shown in Figure 1.

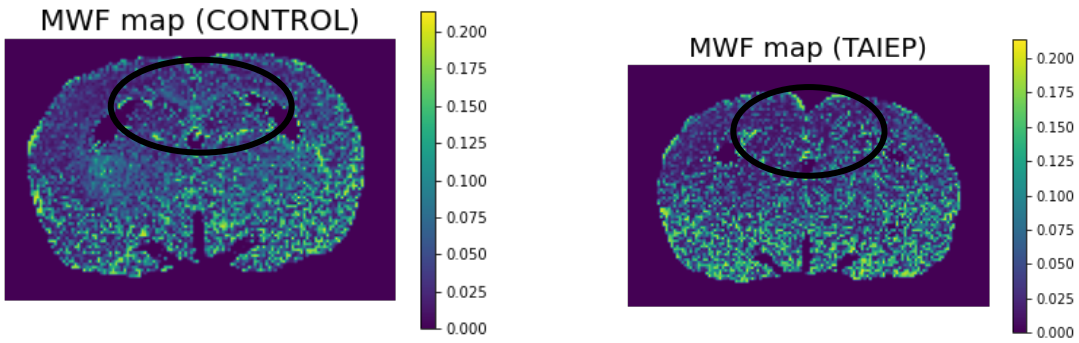


The loss function is the convex combination of the Wasserstein Loss function with the Mean Squared error function (0.55 and 0.45 are the corresponding weights of the function). The model was trained for 200 epochs with a batch size of 200.

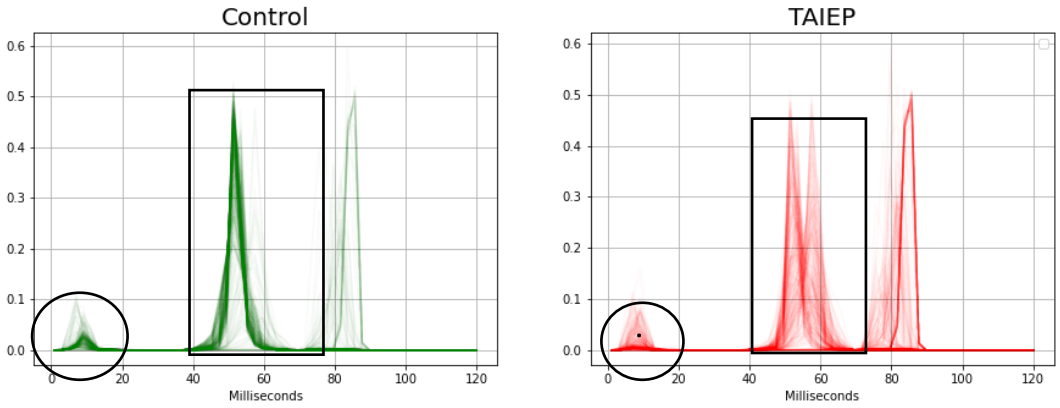
Experiments and results

The proposed model presented high efficiency in the synthetic data presenting a small value of the loss function equal to 6.2. The learning method was also tested with human data just for comparative purposes. Our model outperformed previous supervised learning methods in both human and rat data. We then tested out the model to estimate the Myelin-Water-Fraction (MWF) of each voxel in the rat dataset.

As we see in Figures 3 and 4 the model was able to capture the demyelination process among the corpus callosum



It is worth mentioning that the model was also able to capture the inflammatory process of the TAIEP rats as shown in figure 5.



Conclusions

Our experiments indicate that the use of state-of-the-art supervised learning methods can reduce the number of images required to estimate multi-compartment T2 distributions. The natural extension of this work is to identify the minimum amount of data required to ensure the robustness of the estimation.

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