Magnetic Resonance Spectroscopy (MRS) Reconstruction Using Style Transfer Deep Depth wise Framework

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Abstract

The human brain is a complex and heterogeneous organ composed of distinct compartments such as cerebral cortex, the cerebellum, the brainstem, and the subcortical regions. To analyze the chemical composition of tissues in brain, in vivo magnetic resonance spectroscopy allows non-invasive measurements of neurochemicals in either single voxel or multiple voxels. The reconstruction spectra using 1/3rd of original data than current Edited-MRS scans will not only result in four times faster edited-MRS scans but also extensively reduction in radiations. In this work, we present a deep depth-wise channel attention module (DCAM) based fine-tuned network for magnetic resonance spectroscopy image reconstruction. Besides, we have used channel-wise convolutions and average pooling without dimensionality reduction. We have trained the initial network from scratch on track-1 simulated dataset, however due to the limited dataset, we finetune the network on track-2 and track-3. Experiments are conducted on Edited-MRS-Rec-Challenge dataset1 that showed significantly better performance.

Keywords: Deep Learning, Magnetic Resonance Spectroscopy, Style Transfer, depth-wise channel attention, Reconstruction, Huber loss.

1. Introduction

The brain is a highly complex and heterogeneous organ that consists of many different types of cells, including neurons, glial cells, and endothelial cells. These cells interact with each other in complex ways to perform a wide range of functions, including perception, thought, movement, and emotion. Due to its complexity and heterogeneity, studying the brain is a challenging task that requires a wide range of techniques and approaches. These include anatomical imaging techniques, such as magnetic resonance imaging (MRI), magnetic resonance spectroscopy (MRS) and computed tomography (CT), functional MRI (fMRI) and positron emission tomography (PET). The biochemical processes that occur in the brain are highly complex and dynamic, and involve the activity of numerous neurotransmitters, enzymes, receptors, and other signaling molecules. Magnetic Resonance Spectroscopy (MRS) is a non-invasive imaging technique identical with nuclear magnetic resonance (NMR) spectroscopy. It uses magnetic fields and radio waves to analyze the chemical composition of tissues in the human body such as quantification of Gamma Aminobutyric Acid (GABA), which is overlapped by creatine and glutamate.

MRS provides information about the concentrations of various metabolites within tissues, which can be used to diagnose and monitor diseases. Besides, it can also be used to detect tissue changes in stroke and epilepsy. MRS data is acquired as a series of spectra, each representing the concentration of a different metabolite [2], [3]. The spectra are typically acquired in a 3D volume, with each voxel (3D pixel) in the volume containing a spectrum and can provide estimates of GABA levels in the brain, however, it has limitations and may not always be precise or accurate. Figure 1 shows the different chemical peaks of a suspected brain tumor. Besides, its high-quality data is needed to efficiently estimate GABA which requires long scan times. Hence, Edited-MRS reconstruction challenge is organized to investigate the machine learning models for spectra reconstruct using 1/3rd of data than current Edited-MRS scans, which will not only result in to four times faster edited-MRS scans but also extensively reduction in radiations. In this work, we present a deep depth-wise channel attention module (DCAM) for magnetic resonance spectroscopy image reconstruction. Besides, we have used channel-wise convolutions and average pooling without dimensionality reduction.

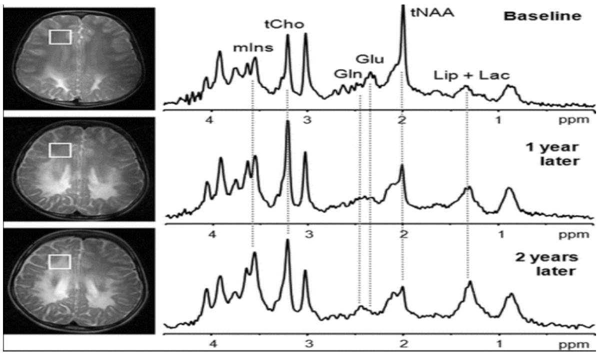

Fig. 1 MRS graph shows the different chemical peaks of a suspected brain tumor [1]

Recently deep learning models have been used in medical image analysis for segmentation, classification, and object recognition [4], [5], [6], [7]. The 2D and 3D segmentation models have been proposed for segmentation of medical imaging [8], [9], [10].

2. Methodology

2.1. Proposed Depth-Wise Edited-Mrs Reconstruction

In this work, we presented UNet based model for MSR reconstruction tasks. Figure 2 and Figure 3 show the proposed reconstruction framework that consists of convolutional blocks, Max-Pooling blocks, Up-Sampling blocks, 1x1 Conv, depth wise channel attention module (DCAM) blocks (see figure 4. The DCAM block is introduced in each encoder block after the convolutional layer block. The convolutional block consists of convolutional layers with Batch-Normalization and ReLU activation function to extract the different feature maps from each block in the encoder side. The 2D max-pooling layer has been used to reduce the input spectral size. The 1x1 convolutional layer with SoftMax function has been used at the end of the proposed model. Spectral input size is reduced with increasing the number of layers in the encoder block and the spectral input size is recovered via a 2D up sampling layer using a bilinear up sampling method in the decoder side. The DCAM block handles the input feature maps extracted from each convolutional block in the encoder side and further passes these feature maps into the decoder block. The output of each encoder block is fed into the proposed DCAM. Later, the outputs of DCAMs are concatenating them with the corresponding decoder blocks. The output of the last encoder block is passed to the DCAM, and the resulting feature maps are directly concatenated with the corresponding decoder block. Each max-pooling layer receives the output from DCAM. In addition to DCAM, we have implemented different other modules such as channel attention module (CAM), spatial attention module (SAM), channel spatial attention Module (CSAM). As we have larger dataset available for task 1, we trained the proposed model from scratch on track 1. However, there are only few samples available for track 2 and track 3, thus we have developed the style-transfer based framework by finetuning the pre-trained model and freezing the parameters of the encoder and decoder layers except the bottom and last two layers where the weights or parameters are finetuned using vivo dataset for track-2 and track-3. Figure 3 shows the block diagram of finetune network for track-2 and track-3.

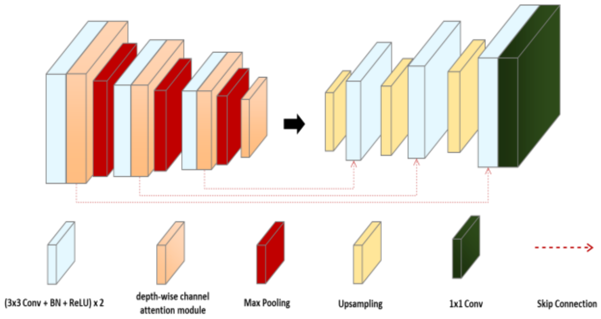

Fig. 2 The proposed model used for track1 simulated dataset

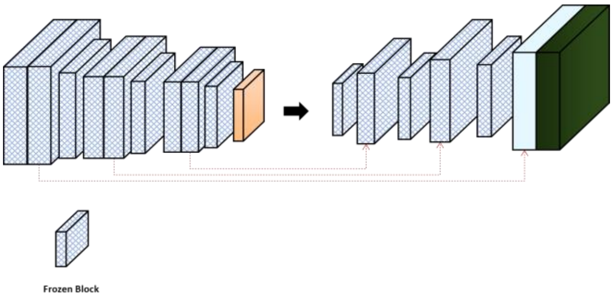

Fig. 3 The proposed model used for track2 and track3 vivo dataset

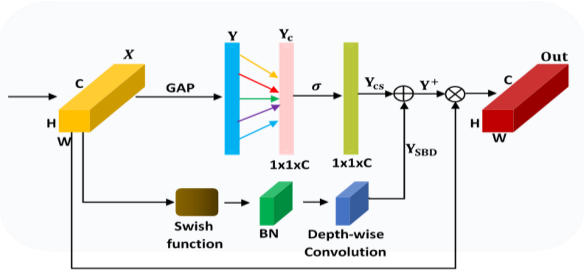

Fig. 4 Diagram of the proposed depth-wise channel attention module (DCAM)

Figure 4 is proposed depth-wise channel attention module (DCAM) used in encoder side of the proposed model. In this experiment, we have used two loss functions: Mean Squared Error (MSE) and Dynamic Huber loss (LHuber). MSE is sensitive towards outliers whereas L Huber is less sensitive to outliers than MSE loss. For N predictions, MSE loss function is defined by;

$$L_{MSE} = \frac{1}{N}\sum_i^N \left(X_i - \breve{X}_i\right)^2 \qquad (1)$$

N and $X = (x_1, x_2, \ldots, x_N)$ are the ground truth MRI spectrum and $\breve{X} = (\breve{x_1}, \breve{x_2}, \ldots, \breve{x_N})$ are their corresponding estimated MRI spectrum. The huber loss function is defined;

$$L_{Huber} = \frac{1}{N}\sum_i^N z_i \qquad (2)$$

Where N is the batch size and z_i is defined by;

$$z_i = \begin{cases} 0.5(x_i - \breve{x}_i)^2, & if\ |x_i - \breve{x}_i| \le \beta \\ \beta|x_i - \breve{x}_i| - 0.5\beta^2 & otherwise \end{cases} \qquad (3)$$

Where β is controlling hyperparameter. In our experiment, β decreases from 15 to 1 during the training for each epoch.

2.2. *Simulation Results*

In this section, we briefly first describe the dataset, followed by evaluation parameters, experimental setting, and evaluation. We have used preprocessing step provided by challenge organizer to convert dataset into Frequency domain spectra and added some noises (random Gaussian amplitude, random Gaussian frequency and random Gaussian phase noise, combined).

2.3 Dataset and Evaluation Matrix

The test set may differ in traditional features, such as by vendor and echo time and it will be lower quality data i.e., lower main SNR or larger frequency and phase shifts. The dataset consists of 5500 spectra (5000 ground-truth spectra and 500 corrupted spectra). The evaluation of the proposed model is performed on an evaluation set which has similar features to that of train set. To evaluate the performance, we have used mean squared error (MSE), signal to noise ratio (SNR), linewidth (FWHM), peak shapes GABA, GLX (PS). Evaluation of model is based on task (simulated, in vivo homogeneous, in vivo heterogeneous) and each metric is ranked individually and well as combined (MSE, SNR, FWHM, PS with ratio of 40%,20%,2 0%, 20%, 20% respectively).

2.4 Parameter Setting

In this work, we β decreases from 15 to 1 during the training for each epoch. We have trained proposed models using Adam optimizer and dynamics Huber loss function using 0.0001 learning rate and 200 epochs. The dataset is normalized using clip [0,1] window. All models use PyTorch and trained on Tesla V100 GPU machine [11], [12]. We have converted all dataset time series into frequency spectrum. The challenge organizers provided simulated and in vivo data training sets representing GABA-edited MEGA-PRESS scans composed of two sub spectra (ON and OFF).

3. Results

We have used scripts provided by organizers to add varying noise, frequency, and phase shifts, that were used for data augmentation purposes. We have developed different variations of proposed framework (depth-wise channel attention module (DCAM), channel attention module (CAM), spatial attention module (SAM), channel spatial attention Module (CSAM)) and compared the performance. The frequency spectrum has been used as input to train our proposed model for task 1, 2 and 3. We have trained proposed model parameters from scratch using 80 percent simulated data in frequency domain and validated using 20 percent of the frequency spectra of simulated dataset. In task two, vivo data (i.e., single-vendor data) in frequency domain has been used to fine-tune the trained model that was trained using simulated dataset. Similarly, for task3, the heterogeneous in vivo data with different frequency spectra has been used to train the proposed model and later fine-tuned the proposed model using different number of epochs. We have used dynamic Huber and Dynamic Tukey loss function for training and optimizing the parameters of our proposed model. The combined loss (Huber and Tukey) loss function provided better performance on validation dataset. Figure 5 shows the comparative analysis. Table 1 describes the evaluation results of proposed edited magnetic resonance spectroscopy reconstruction framework. We can notice that our proposed framework achieved significantly better mean squared error (8.89e-03), signal to noise ratio (4.61e+01), linewidth (9.17e-02) and peak shapes score (9.44e-01) respectively in comparison to baseline method and other methods.

Table 1 Comparative evaluation of proposed framework (depth-wise channel attention module (dcam), channel attention module(cam), spatial attention module(sam), channel spatial attention module (csam)) with baseline results on task 1, task 2 and task 3

	MSE	**SNR**	**Linewidth**	**Shape Score**
Comparative evaluation for track 1				
Baseline	4.37e-02	1.43e+01	2.70e-01	6.89e-01
Proposed DCAM	5.79e-03	3.66e+01	5.50e-02	8.52e-01
Proposed CAM	7.33e-03	4.11e+01	6.44e-02	9.33e-01
Proposed SAM	7.88e-03	5.26e+01	7.37e-02	9.683e-01
Proposed CSAM	6.33e-03	4.01e+01	6.11e-02	8.10e-01
Comparative evaluation for track 2				
Baseline	4.09e-02	1.46e+01	2.56e-01	7.09e-01
Proposed DCAM	5.79e-03	3.66e+01	5.50e-02	8.52e-01
Proposed CAM	7.33e-03	4.11e+01	6.44e-02	9.33e-01
Proposed SAM	7.88e-03	5.26e+01	7.34e-02	9.68e-01
Proposed CSAM	6.33e-03	4.26e+01	6.11e-02	8.12e-01
Comparative evaluation for Track3 with 2048 spectra				
Baseline	9.30e-03	3.77e+05	1.25e-01	9.21e-01
Proposed DCAM	8.26e-04	5.11e+02	8.18e-02	9.92e-01
Proposed CAM	7.12e-04	7.22e+02	5.27e-02	5.12e-01
Proposed SAM	5.32e-04	6.59e+02	4.22e-02	7.12e-01
Proposed CSAM	7.88e-04	6.44e+02	6.22e-02	6.33e-01
Comparative evaluation for Track3 with 4896 spectra				
Proposed DCAM	6.92e-04	5.95e+05	7.68e-02	9.94e-01
Proposed CAM	7.09e-04	2.29e+02	7.63e-02	9.97e-01
Proposed SAM	6.10e-04	3.11e+02	6.41e-02	9.89e-01
Proposed CSAM	6.88e-04	3.89e+02	6.11e-02	8.66e-01
Proposed DCAM	6.33e-04	3.22e+02	6.83e-02	8.98e-01

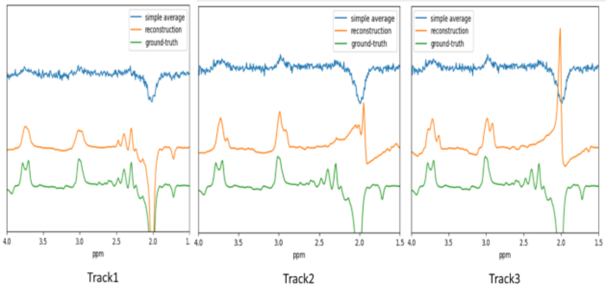

Fig. 5 Comparative analysis: ground truth vs proposes depth-wise channel attention module (DCAM) based reconstruction

4. Conclusion

In this paper, we presented deep depth-wise channel attention module (DCAM) based fine-tuned UNet architecture for magnetic resonance spectroscopy image reconstruction. Due to the availability of large dataset for task 1, we have trained network from scratch on track-1 simulated dataset followed by finetuning the network on track-2 and track-3. Experiments are conducted on Edited-MRS-Rec-Challenge dataset that showed significantly better performance for all parameters i.e. mean squared error (8.89e-03), signal to noise ratio (4.61e+01), linewidth (9.17e-02) and peak shapes score (9.44e-01) respectively in comparison to baseline method and other methods.

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Authors Introduction

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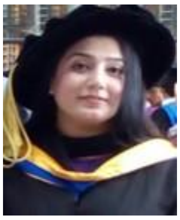

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