Reconstruction of Undersampled Concentric-Ring MRSI k-space data using a Convolutional Graph Neural Network

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Introduction

Magnetic Resonance Spectroscopic Imaging (MRSI) is an emerging medical imaging modality, which is steadily gaining popularity. It allows the acquisition of spectra, which encode the biochemical substances, for each voxel. Compared to other imaging techniques such as Magnetic Resonance Imaging (MRI) its acquisition time is relatively long. This makes its clinical application challenging. The typical approach to decrease the acquisition time is to omit k-space sampling points or trajectories. These are then later computationally reconstructed. In this paper a graph neural network is proposed for the reconstruction of undersampled concentric ring k-space data.

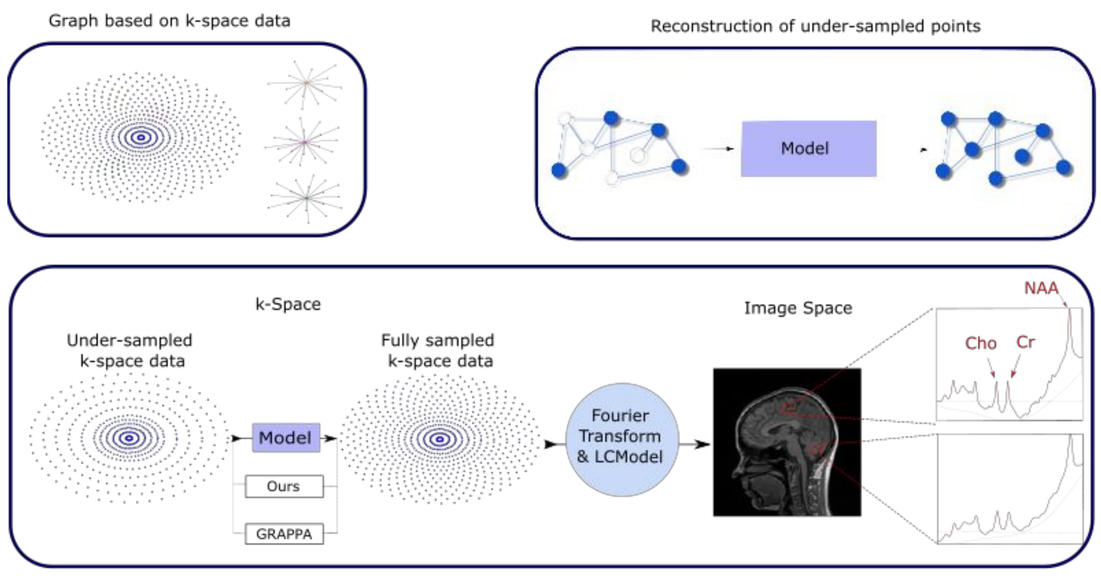

Figure 1: Overview of the method. Data is acquired, undersampled and defined as graph (top left: Neighborhoods of vertices are shown in color). The pre-processed data is reconstructed by ours and GRAPA. Post-processing includes Fourier transformation in all spatial and time dimension and LCModel fitting. The output is a volume of the brain, where each voxel represents a spectrum.

Data and Method

Non-water suppressed whole-brain MRSI data were collected from seven volunteers in ten random head positions. The data of the first six volunteers were used for training and the data of the last volunteer for validation. Water-suppressed, long-TR FID-MRSI data were measured from all volunteers in the tenth position, and was used to evaluate the network. In each scan concentric ring trajectories were used, in total 16 rings with 388 points per ring each are acquired. Graphs are defined by connecting point pairs with a distance less than 1.5 times the Nyqusit criterion. These rings are undersampled, by fully sampling the inner 6 and then skipping every second of the outer rings.
The proposed complex Graph Neural Network (GNN) consists of two graph convolutional layers with a tanh activation function in between. A novel graph convolutional layer is introduced. For this purpose indicator functions are applied

$$\chi_\epsilon(x) = \sigma(n(x-\epsilon))\sigma(n(\epsilon-x))$$

The resulting weighting function is then defined as

$$\omega(p(v,w)) = \chi_\epsilon(p(u,w)-\mu)$$

where μ, ϵ are learnable parameters. Following the framework by Monti et al[3] the patch operator is defined as

$$D_j(v)f = \frac{1}{C_{v,j}} \sum_{w \in N(v)} \omega_j(p(v,w))f(w),\ j = 1,\dots,J$$

where

$$C_{v,j} = \sum_{w \in N(v)} \omega_j(p(v,w))$$

The feature vectors are merged with a complex fully-connected layer. A linear layer with complex weights, following complex addition and multiplication rules.

Comparison of Metrics used for Evaluation						
	SNR	G-Factor	FWHM	tCr CRLB	tCho CRLB	tNAA CRLB
Ours	7.72 (3.95)	1.31 (1.08)	0.091 (0.042)	18.35 (8.22)	19.85 (7.86)	10.94 (7.30)
GRAPPA	8.81 (4.73)	1.29 (1.43)	0.098 (0.042)	18.72 (8.68)	20.22 (8.33)	10.40 (7.19)
GT	11.39 (4.73)		0.077 (0.037)	13.37 (8.76)	13.66 (8.70)	9.30 (7.16)

Table 1: The table shows the evaluation results for our method and GRAPPA comparing them to the Ground Truth (GT) based on fully sampled data. For the assessment several metrics are presented including SNR, FWHM and CRLBs.

Evaluation & Results

The metabolic maps of tCho to tCr and tNAA to tCr, computed by LCModel [2], are shown in figure 2. Here the estimated relative amplitude of each voxel is shown, if its CRLB is lower than 40%. Although the average CRLBs of our method and GRAPPA [1] do not differ dramatically, it can be seen that a our methods leads to a more stable reconstruction of these metabolite maps. The reconstruction of our method still leads to ring-like artifacts in the relative amplitude maps, but compared to GRAPPA, is less noisy. SNR and Full-Width-half-Maxima maps are shown in figure 3. Here our method leads to a slight decrease in SNR, compared to GRAPPA. The average SNR of the volume is 7.72 and 8.81 (Table 1) for our method and GRAPPA. As before, the same ring-like artifact can be observed. The SNR decreases along the edges of the ring.

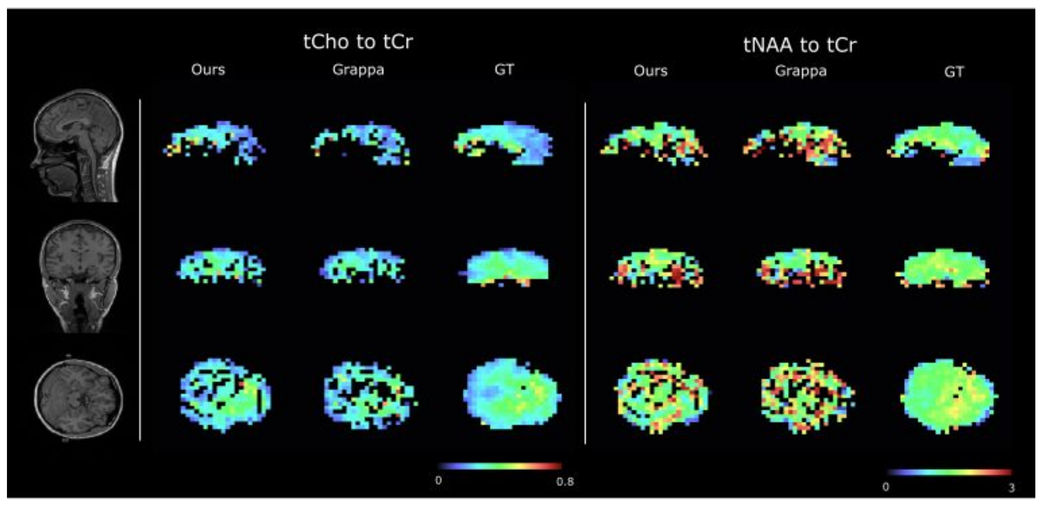

Figure 2: The figure shows the evaluation results for our method and GRAPPA comparing them to the Ground Truth (GT) based on fully sampled data. For the assessment CRLBs of the maps for the metabolite groups tCr, tCho and tNAA.

Discussion

A novel deep learning based method for the reconstruction of undersampled non-Cartesian MRSI data is presented. The introduced model is compared against a state-of-the-art GRAPPA reconstruction algorithm and results in similar reconstructions. Overall, the results suggest that a deep learning based reconstruction is promising, but further research should be done.

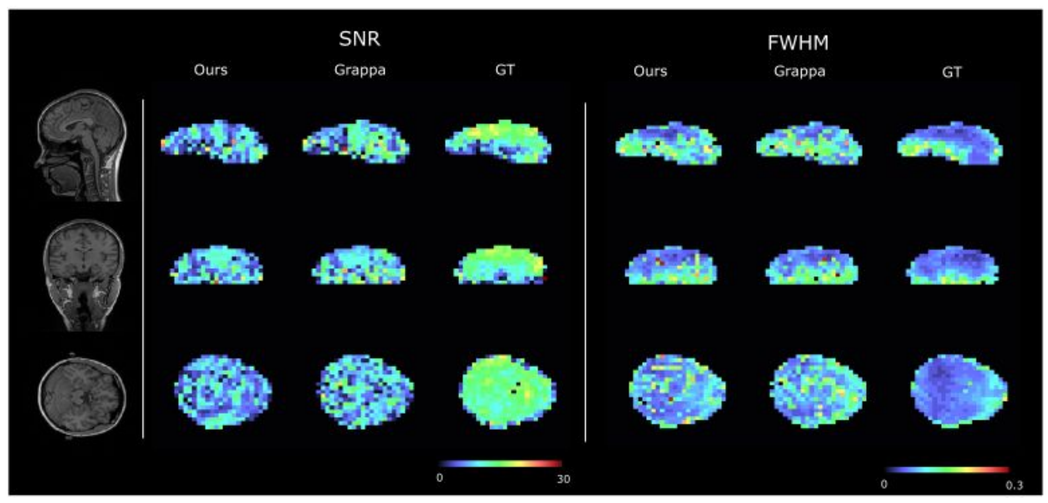

Figure 3: The figure shows the evaluation results for our method and GRAPPA comparing them to the Ground Truth (GT) based on fully sampled data. For the assessment SNR and FWHM maps are presented.

References

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