Direct Estimation of Model Parameters in MR Spectroscopic Imaging using Deep Neural Networks

***Dhritiman Das*[1,2], *Eduardo Coello*[2,3], *Anjany Sekuboyina*[1,4], *Rolf F Schulte*[2], *Bjoern H Menze*[1]**

1. Department of Computer Science, Technical University of Munich, Munich, Germany

2. GE Healthcare, Munich, Germany

3. Department of Physics, Technical University of Munich, Munich, Germany

4. Klinikum Rechts der Isar, Munich, Germany

Introduction

In MRS, accurate quantification of metabolites in the tissue sample is important for diagnosis of in-vivo diseases. For this purpose, non-linear model-fitting tools are widely used amongst which the LCModel[1] is regarded as the gold-standard fitting tool. However, some of its drawbacks include: (1) prior knowledge-tuning and long fitting-times, and (2) high estimation-error for noisy data. Prior work has also focused on using machine-learning for metabolite-quantification[5]. In this study, we present an alternative to the non-linear model fitting using a deep neural-network approach.

Methods

We aim to perform the inverse signal modeling where we have a training dataset $D=(S_i(\omega), Y_i)$, $i \in [1, N]$, where N is the total number of synthetic training spectra. $S_i(\omega)$ represents the synthetic training frequency-domain spectra while Y_i represents the corresponding training labels, $[NAA_i, PCh_i, Glx_i, mI_i]$.

MLP Network A five-layered multi-layered perceptron (MLP)[6] network was constructed to work as a regressor mapping $S_i(\omega)$ to Y_i. Each layer consisted of 300 neurons with rectified linear unit (ReLU) activation. The randomly-initialized network was trained to predict the labels by iteratively minimizing the error using gradient-descent with a learning-rate of 10^{-3}. The predicted concentrations are denoted by $\hat{Y}_j$. The corresponding LCM concentration labels Y_j serve as the ground-truth, $j \in [1,M]$, where M is the total number of test-spectra. For our experiments, given the estimate $\hat{Y}_j$ and the testing label Y_j, the corresponding estimate error can be calculated as, $\hat{E}_j = ||\hat{Y}_j - Y_j||_1 \,./\, ||Y_j||_1$

Data. N = **1-million** spectra were simulated using the data from the ISMRM-Fitting Challenge 2016[8] with variations in concentrations, baseline, lipids, linewidth and SNR. For testing, a standard phase-encoded 2D brain MRSI data of a healthy human volunteer is acquired on a 3T-scanner using a PRESS sequence with voxelsize= 10x10x15mm^3, TE/TR=35/1000ms, spectral width = 2000Hz, 400 points. ppm-cropping and signal-normalization of the training and test spectra is performed as well.

Results

Fig.1 shows the metabolite maps for all the metabolites using both the LCModel and DNN. The mean absolute relative errors for NAA/Cr, PCh/Cr, Glx/Cr and Ins/Cr were **0.19**, **0.16, 0.20, 0.13** while the median absolute relative errors were **0.17, 0.14, 0.18, 0.11** respectively. Training time for the synthetic data is 30 minutes using the MLP. The LCModel takes 10 minutes for the quantification, while our proposed network, after training, takes only 10 seconds leading to a **60x** improvement in speed.

Discussion and Conclusion

A larger training set with more training labels and a stronger network would improve results by providing a robust quantification of real data. Future work would involve using a more diverse network with layer-wise training of spectral features to improve the accuracy of parameter estimation.

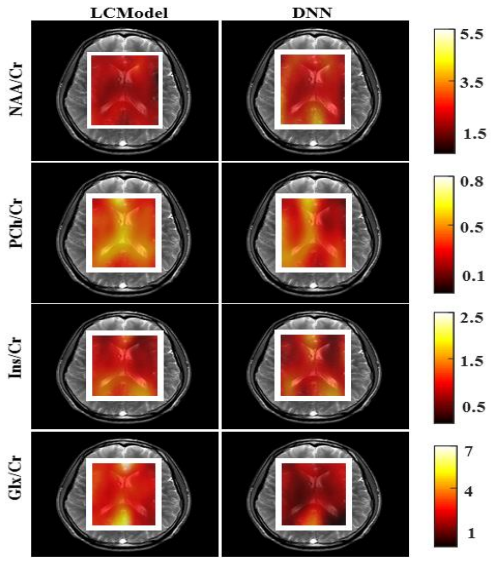

Fig.1: Comparison of the metabolite maps obtained using LCModel (***Left)*** and Deep Neural Network ***(Right)*** for different metabolites (NAA, PCh, Glx, Ins) in a healthy 2D CSI data. Colorbar indicates concentration ratio with respect to creatine for different metabolites.

References

[1] Provencher, S.W.: Estimation of metabolite concentrations from localized in vivoproton NMR spectra. Magnetic Resonance in Medicine (6), 672-679 (1993).

[2] Wilson, M., Reynolds, G., Kauppinen, R.A., Arvanitis, T.N., Peet, A.C.: A constrained least squares approach to the automated quantitation of in vivo 1h magnetic resonance spectroscopy data. Magnetic Resonance in Medicine 65(1), 1-12 (2011).

[3] Vanhamme, L., van den Boogaart, A., Huffel, S.V.: Improved method for accurate and effcient quantification of mrs data with use of prior knowledge. Journal of Mag-netic Resonance 129(1), 35-43 (1997).

[4] Schulte, R.F., Lange, T., Beck, J., Meier, D., Boesiger, P.: Improved two-dimensional J-resolved spectroscopy. NMR in Biomedicine 19(2), 264-270 (2006).

[5] Das, D., Coello, E., Schulte, R.F., Menze, B.H.: Quantification of Metabolites in Magnetic Resonance Spectroscopic Imaging Using Machine Learning, pp. 462-470. Springer International Publishing, Cham (2017).

[6] Widrow, B., Lehr, M.A.: 30 years of adaptive neural networks: perceptron, madaline, and backpropagation. Proceedings of the IEEE 78(9), 1415-1442 (Sep 1990).

[7] Hecht-Nielsen, R.: Theory of the backpropagation neural network. In: International 1989 Joint Conference on Neural Networks. pp. 593-605 vol.1 (1989)

[8] http://www.ismrm.org/workshops/Spectroscopy16/mrs_fitting_challenge

[9] Bland, J.M., Altman, D.: Statistical methods for assessing agreement between two methods of clinical measurement. The Lancet 327(8476), 307-310 (1986).

Acknowledgements

The research leading to these results has received funding from the European Union's H2020 Framework Programme (H2020-MSCA-ITN-2014) under grant agreement n° 642685 MacSeNet.