Towards handling artefacts in Convolutional Neural Networks-based MRS quantification

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Introduction. This work comes within the context of the dazzling development of artificial intelligence and focuses on the design of convolutional neural networks (CNN) deep learning for in vivo MRS data quantification. In previous work [1], we have demonstrated, on a linear combination of metabolites and macromolecular contributions that CNN could correctly learn the metabolite proportion quantification process. In the present work, experiments on simulated data mimicking in vivo conditions, including artefacts/in vivo specificities demonstrate the ability of CNN to handle some artifacts, which usually make difficult the parameter fitting task.

Method. The CNN learns a regression function that, for a given spectroscopic signal returns the relative concentration of the metabolites. The learning is performed on synthetic data which attempts to cover the wide characteristics of real in vivo data. In the present work, our data generation, in addition to usual combination of metabolite, macromolecule (from the ISMRM MRS Fitting Challenge 2016) and noise signals, includes artifacts such as eddy current (EC) effect (time varying phase), frequency shift, first order phase, as well as in vivo specificity such as Voigt lineshapes.
For this study, a 7-layer CNN is implemented in Caffe. The network architecture can be represented as C(64,7)-cr-P(2)-C(64,7)-cr-P(2)-C(64,7)-cr-P(2)-C(64,7)-cr-P(2)-C(64,7)-cr-P(2)-C(64,7)-cr-P(2)-FC(21), where C, P, cr, and FC are convolution (#filters,size), max-pooling, concatenated-relu, and fully-connected layers, respectively. For the network optimization, “Adam” solver used with the learning policy: “multistep", base learning rate: 1e-3, gamma: 0.1, stepvalues: 15k, 30k, 45k, and maximum iterations of 55k. Training, validation and test sets of size 100k, 10k and 10k are generated for this experiment.

Results. The proposed method is evaluated by Relative Absolute Error (RAE=mean absolute difference over mean absolute deviation) and Correlation Coefficient (CC), measured on ground truth (GT) and CNN predicted values of each metabolite. The overall performance of the model is mean(RAE) and mean(CC), averaged over all metabolites. Table 1 gives the best performances corresponding to the main metabolites, for PCr, NAAG, Gln, Pcho and Tau RAE$\in [0.71 - 0.84]$ and CC$\in [0.50 - 0.65]$.

	RAE	CC
Mac	0.176	0.980
NAA	0.197	0.976
Ins	0.287	0.951
Glu	0.351	0.925
Cr	0.522	0.830
GPC	0.588	0.785
GSH	0.669	0.715
mean	0.721	0.571

Table 1: The best performances.

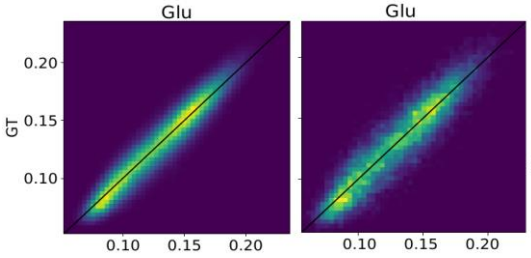

Fig. 1: GT vs. CNN estimation 2D histogram for training (left) and test sets (right).

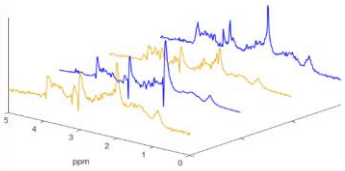

Fig. 2: Illustration of sample spectra with different EC effects.

Conclusion & Discussion. We have presented here our preliminary results on simulated data. Our developments enabled to say, that for our specific implementation data quantification works for the main metabolites even in presence of some important artifacts. Large water residual signal and important lipid signal contamination need still to be added and investigated to fully address in vivo MRSI data quantification.

References. [1] Hatami, N., Sdika, M., Ratiney, H. Magnetic Resonance Spectroscopy Quantification using Deep Learning. *MICCAI 2018*.

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