Application of Wavelets and Machine Learning Based Approaches for Analysis of Magnetic Resonance Spectroscopy Signals

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By

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CHAPTER 6

Conclusions and Future Scope

MRS provides chemical metabolite profile of the organ scanned for diagnosis and serves as a complementary technique to MRI, which gives the anatomical information non-invasively. The presence of different metabolite and macromolecular peaks in MR spectra gives an insight to the changes at tissue level non-invasively, with each peak serves an important biomarker for the diagnosis or pathological progression of a disease. The isolation of MM from the spectra obtained after MRS scan holds many prospects. A single framework for the quantification of individual MMs from isolated spectra along with metabolite components is necessary in a diagnostic setup along with MRI as it has already been reported that with the onset of certain pathological conditions like tumor, multiple sclerosis, and stroke, the variations in metabolite as well as MM components is visible.

The goal of acquiring MR spectra in clinical setting is to obtain quantified concentration values of individual biomarkers for diagnostics and pathological inferences non-invasively. In this thesis, a limited number of *in-vivo* MR spectra and a large set of simulated and augmented spectra, generated using individual basis set matching *in-vivo* acquisition characteristics, has been used for analysis and performance evaluation of methods to tackle issues with MRS quantitation.

In this thesis through a series of studies, we have proposed an efficient approach of peak estimation/concentration computation from post-acquisition MRS spectra by separating the overlapping high molecular-weight MMs from other low molecular-weight metabolite peaks with the idea that the quantified metabolites and MM components can serve in classifying

spectra into normal, benign or malignant based on these quantified metrics accurately, and hence providing better diagnostic inferences non-invasively, as the next step.

A clinical MRS acquisition at moderate static magnetic field is generally low SNR, degraded FID signals with macromolecular components and other baseline components overlapped throughout the metabolite peak range which makes the analysis of such spectra difficult. The goal of post processing an MR spectrum is to retrieve a clean, artifact-free signal to boost the steps of accurate quantification of biochemicals from the spectra, necessary for diagnostic assessment of patients in a clinical set up.

Over the last 2-3 decades, several post-acquisition approaches have been taken to separately address different issues related to MRS to improve the quantitation of biochemicals from the spectra.

Wavelet transform provides multi-scale decomposition of a signal in time-frequency domain which can be used as features for various specific applications. In the present work, for noise-based study and effectiveness of wavelet transform and as feature extractor, a norm-based thresholding approach over sparse wavelet coefficients was used for the noise and artifact removal from the spectra. Norm-based sparsity measures were used to determine the thresholding values with two propositions in mind, specific to MR spectra are: i) noise characteristic of wavelet decomposition coefficients is supposed to have very distinct presentation in multi-scale features making thresholding robust to noise. ii) Norm based parameters are used in machine/deep learning models for regularization during training. Therefore, the denoising of MR spectra based on norm-based method was effective, it was encouraging to make use of these features in further analysis of spectra using ML/DL models.

In the following study, we attempted to address another important aspect of MRS analysis towards accurate quantitation. Isolating macromolecular components from a degraded post-

acquisition MR spectrum is another important but difficult task, mostly addressed by curve-fitting approaches till now. It is an ill-posed inverse problem of estimation where a machine learning model could be used to learn this inverse problem in a regression set up to isolated the fitted macromolecular baseline spectrum. Taking inferences from the previous studies, wavelet features were used for training the XGBoost regression model and L1-L2 norms were used as regularization parameters for efficient isolation of macromolecular baseline. The trained model was highly robust to noisy dataset performing even better than comparable deep learning models.

In the final study, we collected inferences from all the studies we attempted e.g. wavelet multi-resolution features, performances of machine-learning models and a naïve CNN model over these features, and included more effective DL models like UNet, Attention modules, Residual modules, Inception modules for this study to finally build a learning-based model utilizing wavelet transform as a significant feature descriptor and analyse different aspects of MRS signals in a post-acquisition set-up. Addressing the low SNR issues, presence of unwanted artifacts, macromolecular baseline separation from MRS spectra and peak estimation for metabolites as well MM component can be performed with this single framework and can be extended for efficient accurate quantitation and in diagnostics.

As the natural step forward, inclusion of more *in-vivo* spectra to optimize the methods will improve the robustness and generalizability of the learning-based approaches used in this thesis. Based on the encouraging outcomes we have seen for our model, a tumor staging classification model can be designed to provide early diagnostic information in cancer treatment non-invasively. Moving forward, these networks or modified ones can then be applied in specific disease-based research to further solidify the idea that learning-based approaches can have bigger role in clinical MRS based diagnostics and reduce the invasive option of biopsy.