ABSTRACT

MR Spectroscopy (MRS) is a non-invasive, ionizing radiation-free analytical MR technique to obtain information about a range of biochemicals, usually referred to as "metabolites" and “macromolecules” signals, from MR scanner. Proton MRS (^{1}H) is the most common technique used for tissue characterization of an organ in clinical setup complementing with MRI, which provide anatomical information. It presents an effective alternative method to biopsy for diagnosis of the tissues in the region of interest (ROI). The signals obtained are the sum of damped exponentials in time domain, called free induction decay (FID). Each individual exponential is associated with a particular ^{1}H nucleus of resonant frequency, uniquely defined by the local magnetic field depending upon the environment in which the molecule resides. The difference in these resonant frequencies, termed as ‘Chemical Shift’ and is the main basis of differentiation among biochemicals in MRS.

With the advancement in image processing and machine and deep-learning domains, use of image-based methodologies like MRI, CT, USG as non-invasive diagnostic tool in clinical set-up of healthcare has improved drastically. These tools have the shortcoming of generally providing anatomical profile through images. MRS, on the other hand, provides much detailed profile on a bio-chemical level, resembling *in-vivo* conditions non-invasively. This presents a fascinating area to study *in-vivo* condition non-invasively complementing MRI towards highly effective early diagnosis in healthcare. With technological advancements, MRS scan times have reduced exceptionally, increasing its usability and acceptability in the healthcare community. With the availability of more data and developments in the field of signal processing; ML, DL techniques have effectively worked in favour of MRS based research as well as clinical applications post-acquisition.

Biological signals like MRS signals are significant in analysing human physiological conditions. But these signals are susceptible to noise and artifacts and superimposition of a broad

macromolecular baseline with the metabolite components which can cause misinterpretation and subsequent incorrect diagnosis. In this thesis, we have attempted to create a single framework for the non-invasive, post-acquisition quantitation of biochemical components present in the MRS spectra such that it can be used in disease diagnosis. In this thesis, the analysis of degraded MR spectra was performed in three steps: noise and artifact removal, macromolecular spectra isolation from overlapped metabolite spectra, ultimately leading to a quantitation strategy for estimating individual metabolites and macromolecular components.

For different studies in this thesis, a basis-set of 18 individual metabolites [alanine (Ala), aspartate (Asp), creatine (Cr), ɣ-aminobutyric acid (GABA), glucose (Glc), glutamine (Gln), glutamate (Glu), glycerophosporylcholine (GPC), glutathione (GSH), lactate (Lac), myo-inositol (mI), N-acetylaspartate (NAA), N-acetylaspartylglutamate (NAAG), phosphoryl-choline (PCho), phosphorylethanolamine (PE), phosphocreatine (PCr), taurine (Tau)] were identified from literature review. The relative amplitude range for each metabolite was determined from the literature [26, 32-34]. Next, a basis-set for 17 MM components [$M_{0.94}$, $M_{1.22}$, $M_{1.43}$, $M_{1.70}$ (1.63, 1.68, 1.81), $M_{2.05}$ (1.99, 2.04), $M_{2.27}$, $M_{2.54}$, $M_{3.00}$, $M_{3.21}$ (3.11, 3.22, 3.27), $M_{3.71}$+ $M_{3.79}$, $M_{3.97}$] of gaussian lineshape were simulated with amplitude, linewidth and chemical shift parameters obtained from literature. Variation in the relative concentrations of different biochemicals is indicative of a specific medical condition or disease, and act as an important biomarker for detection and diagnosis.

To address the issue of noise and artifacts, a rational-dilation wavelet transform-based signal decomposition and a thresholding criterion designed using L_{pq}-norm-based sparsity measure of the decomposition levels of the signal was implemented and evaluated. Compared to the standard state-of-the-art methods, which are effective in denoising but can cause distortion of the signal at discontinuities, the proposed method can remove artifacts such as spurious echoes present in the MR signals and improve the signal SNR without distorting the signal**.** From this study, we also

took inferences that wavelet based multi-resolution decomposition can be used as an efficient feature descriptor for machine-, deep-learning models.

To address the issue of macromolecular baseline and metabolite spectra isolation from noisy MR spectra, which inherently is an inverse problem (explained in chapter 4), a novel approach of gradient boosted wavelet-feature tree model in a multioutput-regression framework for MRS spectral fitting was adopted, where the inverse problem was learned by training over wavelet coefficients of noisy spectral dataset simulated using basis-set of metabolites and macromolecules. The proposed method performed almost perfectly for the simulated dataset with smaller margins of error, compared to an equivalent CNN model. For the simulated test set, RMSE and SSIM of 0.1623 and 0.9571 respectively were obtained and RMSE of 0.2263 was obtained for *in-vivo* test set. The fitted peak amplitude for individual MM component lies within ±4% of error range over the simulated dataset. From our attempt, we have found that for residual waterpeak height <= 3* Highest peak of training spectra, our model is able to isolate MM spectra with little hyperparameter tuning of our model. The proposed model achieved an RMSE value of 0.2988 and SSIM of 0.8973 when the spectra was contaminated with residual water peak.

From the two previous studies, we understood the effectiveness of combining wavelet features in a learning-based framework for regression tasks. Therefore, for the goal of quantitation of MR spectra in a post-acquisition setup, we introduced more complex but efficient strategies like UNet structure for 1D-signals, residual modules, attention modules, inception module among other for our final study. a novel hybrid deep network of inception module-Unet architecture with residual connection and regression-dense layers has been proposed to isolate and quantify brain metabolites and macromolecules (MM) from a degraded, low SNR with baseline embedded, line-broadened spectra obtained from proton MR spectroscopy (^{1}H-MRS) in a clinical setting. In time domain, peak amplitude of individual biomarkers is directly proportional to their relative concentration. A set of degraded 30000 spectra with equivalent ground truths were simulated mimicking *in-vivo*

characteristics of brain MRS by using basis for individual metabolites and MMs for training and evaluation of the proposed model with train/validate/test set as 70/15/15 % ratio. The model performed accurately in isolating corrected metabolite and MM spectra with an accuracy of 99.19% on a trained model with validation loss of 0.0714 and test-set root mean-squared error (RMSE) of 0.2684. The structural similarity index (SSIM) between ground truth and isolated spectra was calculated with a mean value 0.9427 for metabolites, and 0.9506 for MM spectra. The peak amplitude estimated by regression-dense layer module from isolated spectra gave an RMSE value of 0.1807 for metabolites, and 0.0833 for MMs. For each metabolite/MM relative concentration or peak amplitude estimated, mean absolute percentage error (MAPE) was calculated. For all the 18 metabolites, the overall MAPE calculated was 9.03 %, with Ala, GABA, PCho, and NAAG having highest MAPE at 9.14, 10.44, 11.07, and 9.91 % respectively. For GSH, Gly, and NAA, MAPE were 8.48, 8.60, 7.29 and for rest of the metabolites, MAPE was below 5%. Similarly, for 17 estimated MM peak, the overall MAPE was 4.09% with $M_{1.22}$, $M_{3.27}$, $M_{3.79}$ having values above 5.5%. The rest of the MM peaks ranges between 2.21-3.9% of MAPE. The study results, therefore, support for an end-to-end deep learning model approach in quantitation of clinical degraded MR spectra for diagnostics and pathological studies. Small tests over datasets with water peak removed also gave encouraging results and scope for future developments to further reduce the acquisition times of an MRS scan.

Keywords: MRS, metabolites, signal processing, sparsity, L_{pq}-norm, spurious echo, macromolecules, complex wavelet, gradient boosting, feature extraction, inception model, UNet, attention, residual connection, peak estimation.

Abstract of the Thesis

On Cyclic Codes and Their Generalizations over Some Finite Non-Chain Rings and Construction of Quantum and LCD Codes

The thesis submitted in partial fulfillment

for the Award of Degree

DOCTOR OF PHILOSOPHY

by

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This thesis is devoted to the study of certain algebraic codes like cyclic, constacyclic, skew cyclic, and skew constacyclic codes over some finite non-chain rings. Additionally, it explores their applications in the construction of quantum error-correcting codes, which have become increasingly important in the emerging fields of quantum information and computation. Moreover, it examines another significant class of error-correcting codes called linear complementary dual (LCD) codes over these rings. Consequently, we construct many new codes with either improved parameters codes with good parameters (MDS, AMDS, BKLC) belonging to interesting classes of codes like quasi-cyclic, skew multi-twisted codes etc. Computations are done using SageMath and MAGMA software.

This thesis consists of an **Introduction** and **seven chapters**, including **Preliminaries** as the first chapter and **Conclusion and Future Scope** as the last chapter.

Introduction gives an introductory overview of the contents of the thesis. Includes an extensive literature review on cyclic codes, their generalizations, and their applications in constructing quantum and LCD codes. Additionally, it outlines the motivation and objective of the thesis.

Chapter 1 serves as the foundation of the thesis, introducing essential concepts and definitions from algebra, classical coding theory, and the theory of quantum error correction.

In **Chapter 2**, we study cyclic codes over a non-chain ring $\mathbb{F}_q[u,v,w]/\langle u^3-u, v^2-v, w^2-w, uv, vu, uw, wu, vw-wv\rangle$ denoted as $\mathcal{S}$. We explore several key properties of Gray map on $\mathcal{S}$ and linear codes over $\mathcal{S}$. We find an explicit form for the generator matrix of the Gray image of linear codes over $\mathcal{S}$. Furthermore, we discuss the structural properties of cyclic codes over $\mathcal{S}$ and their duals. Additionally, we present the construction of quantum and LCD codes from cyclic codes over $\mathcal{S}$. Consequently, many new codes with better parameters are obtained.

Chapter 3 investigates skew cyclic codes over a non-chain ring $\mathbb{F}_q[u_1, u_2, \ldots, u_r]/\langle u_i^3 - u_i, u_iu_j - u_ju_i\rangle_{i,j=1}^r$ denoted as $\mathcal{R}$. We explore several key properties of Gray map on $\mathcal{R}$ and linear codes over $\mathcal{R}$. We find an explicit form for the generator matrix of the Gray image of linear codes over $\mathcal{R}$. This chapter examines the structural properties of skew cyclic codes over $\mathcal{R}$ and their duals. Furthermore, it provides methods for constructing quantum and LCD codes from skew cyclic codes over $\mathcal{R}$, leading to the construction of many new codes with improved parameters.

Chapter 4 delves into exploring skew constacyclic codes over a general class of non-chain rings $\mathbb{F}_q[u_1, u_2, \ldots, u_r]/\langle f_i(u_i), u_iu_j - u_ju_i\rangle_{i,j=1}^r$ denoted as $\mathcal{T}$, where $f_i(u_i)$ are monic polynomials which split into distinct linear factors. We establish several key results on the structural properties of skew constacyclic codes over $\mathcal{T}$. We prove that the Gray image of a skew constacyclic code over $\mathcal{T}$ belongs to a class of codes which is a particular case of skew multi-twisted codes and a generalization of quasi-twisted codes.

The findings of Chapter 4 are utilized in **Chapter 5** to construct quantum and LCD codes. This chapter investigates the Euclidean and Hermitian duals of skew constacyclic codes over $\mathcal{T}$. We develop methods for constructing quantum codes from Euclidean and Hermitian dual-containing skew constacyclic codes over $\mathcal{T}$. Moreover, the construction quantum codes over nine different rings (belonging to this class of non-chain rings) is demonstrated. Consequently, many new and improved quantum codes are obtained. Moreover, this chapter studies Euclidean and Hermitian skew constacyclic LCD codes over $\mathcal{T}$, leading to the construction of several MDS, AMDS, and BKLCs as Gray images of these codes.

The construction of quantum codes in Chapters 2, 3, and 5 relies on dual-containing codes. **Chapter 6** deals with the construction of quantum codes based on entanglement that do not require dual-containing codes. In this chapter, we explore the construction of entanglement-assisted quantum error-correcting codes (EAQECCs)

from constacyclic codes over a general class of non-chain rings $\mathcal{T}$. We prove that under a polynomial Gray map, the image of constacyclic codes (for some specific choice of twisting constant) over $\mathcal{T}$ is a cyclic code. Furthermore, we propose a method to construct EAQECCs from these codes. Consequently, we construct many new MDS EAQECCs from the proposed method.

Chapter 7 provides a chapter-wise summary of this thesis. It also outlines the future scope of the research in this direction and proposes several open problems for further investigation.

Keywords: Gray map; Cyclic codes; Constacyclic codes; Skew cyclic codes; Skew constacyclic codes; LCD Codes; Quantum codes; EAQECCs

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