1 CHAPTER

INTRODUCTION

Highlights of the Chapter

- *Identification of the problem*

- *Objectives and contribution of the thesis*

- *Outline the thesis organization*

Identification of disease is an essential prerequisite to secure the best treatment. Modern medical imaging techniques are assisting clinicians, and provide the anatomical and functional information portrayed in the form of images for diagnosis purpose. Radiologists recognize the disease if the spatial location or value of a group of pixels varies outside the normal range. However, the depth interpretation of these images and extracting the vital information of biological tissue requires mathematical analysis, and hence, the field of medical image processing comes into effect. The objectives of medical image processing are ambitious and varying in scopes such as disease diagnosis, the extent of its spread, radiotherapy, and surgery.

Rapid development in the medical imaging techniques helps in the reduction of diagnostic uncertainty. Planner X-ray imaging is the first and one of the most popular modality of medical imaging [1]. The differential attenuation of x-rays in the body generates the contrast

between different tissues. This imaging technique suffers from overlapping soft tissue or complex bone structures and hence often challenging to interpret. X-ray computed tomography (CT) based on the similar concept of differential attenuation and overcame the drawback of planner X-ray imaging [2]. Multi-slice CT enabled with higher technology can acquire the full three-dimensional images in a single patient breath-hold. However, the fact that planner X-ray and CT uses the ionization radiation, which is the most significant disadvantage of these imaging modalities. Ultrasound imaging is a non-radiation and inexpensive diagnostic modality [3]. It produces the image with the help of backscattering of mechanical energy. The biggest disadvantages of this imaging modality are relatively poor tissue contrast. Further, positron emission tomography (PET) and single photon emission tomography (SPECT) are mainly used for the determination of functional information of the organ rather anatomical [4].

The present thesis selected MRI data as an application because of its importance in the diagnosis of different diseases [5-7]. The following are the advantages of MRI modality: (i) It has the ability to provide superior soft tissue contrast, which makes it ideal for the examination of the brain, spine and other soft tissues [8, 9]. (ii) The different pulse sequences are used to characterize the specific pathological conditions and can reveal significant pathological information [10]. (iii) The availability of contrast agents improves the differentiation between the normal and unhealthy tissues [11].

The present study includes the designing of post-processing algorithms for analysis of different sequences of MRI data instead of work on dynamic contrast based study or expensive medical imaging technology for scanner.

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1.1   Challenges in the analysis of MRI data

MRI data suffers from noise, artifacts and low contrast [12]. These degradations are the primary cause that affects the diagnose quality of diseases [13]. MRI data contains noise due to the heating effect in receiving coils. The artifacts in MRI data may be produced by the scanner hardware or by the interaction of the patient's body with the hardware [17]. Artifacts degrade the information of the MRI data and hence the diagnosis. Sometimes artifact could be misinterpreted if clinicians do not become familiar with the medical history of patients and face postoperative/other images. Motion artifact and intensity inhomogeneity artifact are prevalent artifacts as appeared on MRI data. The ability to provide MRI data with least noise, minimum artifacts and high contrast is often constrained by acquisition time and highly-expensive scanner.

Apart from optimal acquisition strategies, the degradation can be encountered with the help of medical post image processing techniques. Further, the primary visual nature of medical images may be limited by inter-observer variation even after analysis by the experts. The computer analysis algorithms such as automatic segmentation designed with the suitable logic can help in this regard to accurately segregate the lesion and its extent.

De-noising is the first and critical preprocessing step used to improve the image quality by reducing the noise component while preserving the image features. Improvement of the signal value in MRI data without sacrificing the contrast and spatial resolution can improve the diagnostic value. Further, the enhancement of tissue contrast makes easy differentiation of soft-tissues. However, the contrast enhancement techniques are highly susceptible to noise and artifacts. Hence, there is a requirement of the highly controlled contrast enhancement algorithm.

The information of cluster location is difficult to decide in prior, as there is absence of ground truth for new MRI data, and the pathology may appear in the form of unknown cluster(s). Hence, it becomes challenging to fulfill the requirement of automatic and accurate image segmentation. In this regard, the unsupervised methods of segmentation play the vital role. However, these methods need the number of clusters as the input, and the task to choose the number of clusters in prior is difficult to decide in most of the practical conditions.

In the view of above discussed challenges, MRI processing algorithms are aimed to target at:

1. Image de-noising with least blurring [14, 15]

2. Contrast enhancement without amplification of noise [16, 17]

3. Artifact corrections without loss of the fine structure details [18, 19]

4. Reliable segmentation of tissue of interest [20, 21]

Further, MRI data has different weighted sequences such as T1, T2, diffusion-weighted and fluid-attenuated inversion recovery (FLAIR). Each of the sequences contains exclusive information about the anatomy of the interest, and the image properties of these sequences are different regarding their computational analysis. Hence, across different weighted MRI sequences, it is difficult for a single conventional algorithm to achieve all the above objectives successfully, hence, possess uncertainty in achieving desired results. In this view, there is a requirement to establish the methodology that can process the input image adaptively.

1.2   Objectives of the Thesis

The ultimate objective of the thesis is design algorithm to improve image quality and segmentation which will help to achieve accurate diagnosis. In this view, the thesis aims to develop algorithms based on evolutionary computation techniques for:

1. Noise estimation followed by de-noising of MRI data

2. Contrast enhancement of MRI data

3.   Intensity inhomogeneity correction of MRI data

4. Automatic segmentation for MRI image data

The development methodology of these algorithms ensures to address the multiple degradations of an image simultaneously.

1.3   Contribution of the Thesis

This thesis contributes to the necessary theory and implementation of new optimization-based analysis of MRI data. The thesis has shown different clinical applications and has developed the following algorithms:

1. Development of adaptive noise estimation approach for de-noising along with feature enhancement of MRI data

2. Implementation of different DSR models for optimum contrast enhancement of MRI data

3. Correction of intensity inhomogeneity artifact in diffusion-weighted MRI data of neonatal/infantile brain

4. Formulation of cluster quality index for unsupervised clustering

5. Development of an improved fuzzy c-means algorithm based on multiple cluster quality indexes

The present work has tested and validated the proposed algorithms on the standard dataset, further, the inclusion of pathological real MRI data in the study has shown the clinical significance of these algorithms.

The advantages of the algorithms based on evolutionary computation techniques are:

(i) The adaptive search of positions in the search space (variables) make algorithms robust to the analysis of different sequences of MRI data

(ii) The change/addition of the objective functions can control the quality of de-noising, contrast enhancement and segmentation of MRI data.

1.4   Organization of the Thesis

The remainder of this thesis describes in more detail what has been anticipated in this introduction. The structure of the thesis is given as follows:

Chapter 2 provides the background and literature review. This chapter discusses the significance of noise estimation in de-noising and application of Dynamic Stochastic Resonance for contrast enhancement. The chapter presents a brief overview of segmentation algorithms and cluster quality measures for automatic segmentation. Further, the importance of evolutionary computation has been discussed.

Chapter 3 presents the multi-objective Particle Swarm Optimization (MOPSO) for the application of noise estimation from the MRI data. Further, this chapter proposes the non-local Kalman filter for de-noising of MRI data. The proposed algorithm has been compared with other popular filters.

Chapter 4 presents the quartic bistable DSR system for the contrast enhancement of diffusion-weighted MRI data. The dynamic parameters of the quartic bistable model have been tuned with the help of MOPSO. Further, this chapter presents the bistable neuron model of the DSR system and modified this model of DSR for the contrast enhancement of T1, T2, FLAIR, and diffusion-weighted MRI data. The dynamic parameter of this neuron model has been tuned with the help of Bat optimization algorithm. After the implementation of optimization on two different DSR models, this chapter also presents the cascading approach of these two different DSR models. The proposed algorithms have been compared with other popular contrast enhancement algorithms.

Chapter 5 presents the multi-stable model of a DSR system for the contrast enhancement of pituitary microadenoma. The dynamic parameter of the tri-stable model has been tuned with the help of Antlion optimization algorithm. The proposed algorithm has been compared with other popular contrast enhancement algorithms. This chapter also compares popular evolutionary computation algorithms.

Chapter 6 presents the algorithm for correction of intensity inhomogeneity/Shading artifact present in MRI data. This chapter deals explicitly with the diffusion-weighted neonatal brain MRI data. The algorithm has been validated on the standard dataset and compared with popular inhomogeneity correction algorithms.

Chapter 7 presents the improved FCM based on multi-objective optimization. Further, this chapter formulates an efficient cluster quality index based on multiple properties of the cluster. This index is very effective and helps FCM in the selection of a number of clusters and make it automatic segmentation algorithm. The results have been compared on a vast standard dataset in the presence of a different level of Rician noise.

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Chapter 8 summarizes the overall contribution and point out the main achievement of the thesis along with its future directions which might be the interest in further research.

2 CHAPTER

THEORETICAL BACKGROUND

Highlights of the Chapter

- *Understanding of noise estimation and de-noising of MRI data*

- *Classical MRI enhancement approaches and importance of Stochastic Resonance based enhancement technique*

- *Outline of segmentation methods and the need of fuzzy c-mean for the segmentation of MRI data*

- *Significance of cluster quality index for unsupervised segmentation of real MRI data*

- *Overview of evolutionary computation based optimization and its requirement in medical image processing*

This chapter covers the background ideas of de-noising, contrast enhancement and automatic segmentation of MRI data. The discussion on noise estimation follows the popular de-noising algorithms, and the contrast enhancement follows the some facts necessity of the DSR. The present chapter discusses fundamentals of evolutionary computation techniques and most importantly the role of optimization techniques in the area of medical image analysis.

The acquired *k-space* data is a Fourier transform data, which is commonly known as raw data. This raw data is complex and known to be corrupted by white Gaussian noise. After the