

Chapter 10

A Modified High Speed Hopfield Neural Model for Perfect Calculation of Magnetic Resonance Spectroscopy

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ABSTRACT

In this chapter, an automatic determination algorithm for nuclear magnetic resonance (NMR) spectra of the metabolites in the living body by magnetic resonance spectroscopy (MRS) without human intervention or complicated calculations is presented. In such method, the problem of NMR spectrum determination is transformed into the determination of the parameters of a mathematical model of the NMR signal. To calculate these parameters efficiently, a new model called modified Hopfield neural network is designed. The main achievement of this chapter over the work in literature (Morita, N. and Konishi, O., 2004) is that the speed of the modified Hopfield neural network is accelerated. This is done by applying cross correlation in the frequency domain between the input values and the input weights. The modified Hopfield neural network can accomplish complex signals perfectly without any additional computation steps. This is a valuable advantage as NMR signals are complex-valued. In addition, a technique called “modified sequential extension of section (MSES)” that takes into account the damping rate of the NMR signal is developed to be faster than that presented in (Morita, N. and Konishi, O., 2004). Simulation results show that the calculation precision of the spectrum improves when MSES is used along with the neural network. Furthermore, MSES is found to reduce the local minimum problem in Hopfield neural networks. Moreover, the performance of the proposed method is evaluated and there is no effect on the performance of calculations when using the modified Hopfield neural networks.

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INTRODUCTION

Applications of magnetic resonance imaging were started in magnetic resonance imaging (MRI) which is a technique imaging the human anatomy, and they include various specialized technique such as diffusion-weighted imaging (DWI), perfusion-weighted imaging (PWI), magnetic resonance angiography (MRA) and magnetic resonance cholangio-pancreatography (MRCP). Functional MRI (fMRI) that is an innovative tool for functional measurement of human brain and that is a technique imaging brain functions, also became practical and has been widely used in recent years. In contrast with MRI and fMRI, magnetic resonance spectroscopy (MRS) is a technique that measures the spectra of the metabolites in a single region, and magnetic resonance spectroscopic imaging (MRSI), which obtains the spectra from many regions by applying imaging techniques to MRS, has also been developed. Although ^{31}P -MRS was widely performed in MRS before, proton MRS is primarily performed recently. ^{13}C -MRS using heteronuclear single-quantum coherence (HSQC) method has also been developed recently. MRS and MRSI, however, have remained underutilized together due to their technical complexities compared with MRI.

At present, MRS is technically evolved and its operation has remarkably improved. The measurement of MRS also has started to be automatically analyzed and indicated, and there are some representative analysis software introduced in the Internet, LCModel: an automatic software packages for in-vivo proton MR spectra including the curve-fitting procedure (Provencher, S.W. 2001), and MRUI: Magnetic Resonance User Interface including the time-domain analysis of in-vivo MR data (Naressi, A., Couturier, C., Castang, I., de Beer, R. and Graveron-Demilly, D., 2001). The technique proposed in this chapter is also used for in the time-domain. It probably a better result of the analysis is obtained by combining the algorithms

of MRUI with our technique, because both of them are performed in the time-domain.

MRSI has the big feature that is not in MRI and fMRI, that is, it can detect internal metabolite non-invasively, track the metabolic process and perform the imaging. Thus the importance of it is huge. Furthermore, MRSI is also expected as an imaging technique realizing the molecular imaging. I believe that MRSI has the value beyond fMRI, because of its potential.

For commonly performing the MRSI, it is an indispensable technique to quantify NMR spectra automatically, and it is also expected to progress the automatic analysis techniques. Therefore, it is necessary to develop a novel method introducing neural network techniques including our proposing method, as well as existing analysis software. Consequently, it is important to proceed with the research of this territory.

MRS is used to determine the quantity of metabolites, such as creatine phosphate (PCr) and adenocine triphosphate (ATP), in the living body by collecting their nuclear magnetic resonance (NMR) spectra. In the field of MRS, the frequency spectrum of metabolites is usually obtained by applying the algorithm of fast Fourier transform (FFT) (Cooley, J.W. and Tukey, J.W., 1965) to the NMR signal obtained from the living body. Then, quantification of the metabolites is carried out by estimating the area under each spectral peak using a curve fitting procedure (Maddams 1980, Sijens et al., 1998, Mierisová et al., 2001). However, this method is not suitable for processing large quantities of data because human intervention is necessary. The purpose of this chapter is to present an efficient automatic spectral determination method to process large quantities of data without human intervention.

This chapter is organized as follows: first conventional determination methods of NMR spectra are described and a brief outlines of the proposed algorithm is given. Second, an over efficient view of NMR signal theory; a mathematical model

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