Application of SVD-Based Metabolite Quantification Methods in Magnetic Resonance Spectroscopic Imaging

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Abstract. MRSI can reflect the abnormal metabolites information of different diseases in clinical diagnosis. We made research on the application of SVD-based metabolite quantification methods in 2D MRSI by comparing two different SVD algorithms. In the quantification process, first, the FID signals are rearranged into a data matrix. Then, we can make full SVD by Golub algorithm or partial SVD by Lanczos algorithm. Last, the parameter estimation on each metabolite can be acquired by the definition of the linear parameter model. The ordinary full SVD must decompose all the singular value, with a big cost of the time. The partial SVD just needs to calculate the less singular by the character of the Hankel matrix to improve the estimation speed. When the SNR of MRS signals is higher than ten, the computation time on partial SVD is decreased by thirteen times of the ordinary method. But the speed of quantification is only half of the ordinary one when the SNR is lower than one. Improvements of speed and accuracy in metabolite quantification are key factors for 2D MRSI to be a clinical tool in the future.

1 Introduction

As an important application and a noninvasive imaging method in NMR, magnetic resonance spectroscopic imaging (MRSI) has been proposed as a method to diagnose and localize the brain tumor [1], temporal lobe epilepsy [2] and many other diseases in the early stage. It can present information in the form of spectrum for each voxel and in the form of metabolite map for each metabolite, the latter represents not only simply anatomy but also local metabolic states or local tissue abnormalities.

In vivo 2D MRSI suffers generally from long imaging time and poor SNR of spectrum. After spatial reconstruction on MRSI raw data, the MRS parameter in each voxel needs to be quantified to observe the difference between the normal and abnormal tissues. Different from the single voxel MRS, except the accuracy, the speed of the quantification process for MRS data in multiple voxels is also an important factor for MRSI to be a clinical tool. The least-square (LS) algorithm is usually used to estimate the nonlinear model parameters in single voxel MRS [3]. But it requires a number of iteration steps, and start values must also be set for the nonlinear parameter, which is very long time consuming and thus prohibitive in clinical application for MRSI. Based on that the MR signal can be fitted with the exponential

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decay model, a linear model avoiding iterative calculation can replace the nonlinear model to improve the speed of quantification. We make research on the application of SVD-based metabolite quantification methods in 2D MRSI by comparing two different SVD algorithms using the linear parameter model.

2 Theory

The sampled raw data signal $M(k_x, k_y, t)$ in *k*-domain for 2D MRSI [4] is given by

$$M(k_x,k_y,t)=\sum_{k=1}^{K}\int_x\int_y m_k(x,y)\exp[i2\pi(k_x x+k_y y)]\exp[(-\lambda_k+i2\pi f_k)t]dxdy \tag{1}$$

where $m_k(x, y)$ is the density in the position and λ_k is the decay constant of the k 'th metabolite, $\lambda_k = 1/T_{2k}$. f_k is the chemical shift frequency.

After the spatial reconstruction on MRSI raw data with a similar algorithm on MRI, we get the spatial-domain signal $m(x, y, t)$ in each voxel position, which is a summation of FID signals of different metabolite.

$$m(x,y,t)=\sum_{k=1}^{K} m_k(x,y)\exp[(-\lambda_k+i2\pi f_k)t \tag{2}$$

And we know, the FID signal with only one kind of metabolite can be expressed by

$$s(t)=a\exp(-\frac{t}{T_2})\exp[i(2\pi ft+\varphi)] \tag{3}$$

Considering the implied phase in a position (x, y), we can express equation (2) by

$$s(t)=\sum_{k=1}^{K} a_k\exp(i\varphi_k)\exp[(-\lambda_k+i2\pi f_k)t] \tag{4}$$

The task of the quantification of metabolites is to estimate four parameters a_k, λ_k, f_k and φ_k for the *k'th* metabolite.

2.1 Linear Model and Parameter Estimation

A linear parameter model [5] avoiding the iterative calculation can replace the nonlinear equation (4) to improve the speed, with the following type

$$s_n=\sum_{k=1}^{K} c_k\zeta_k^{n+\delta}+\varepsilon_n \qquad n=0,1,...,N-1 \tag{5}$$

where $c_k = a_k\exp(i\phi_k)$ denotes the *k'th* complex-valued amplitude, $\zeta_k = \exp[(-\lambda_k + i2\pi f_k)\Delta t]$, δ is the delay time $t_{beg} = \delta\Delta t$, ε_n is the noise.