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Decomposition of Magnetic Resonance Images by Estimating MR Physical Parameters

WANG Wei-dong [1,2], BAO Shanglian [2]

（1.The Center of Biomedical Engineering, Chinese PLA General Hospital, Beijing 100853 ;
2.The Beijing Key Lab of Medical Physics and Engineering, Peking University, Beijing 100871, China)

Abstract - Tissue segmentation of single and multi-spectral magnetic resonance (MR) images has been widely studied for the applications on normal aging brain, as well as on the diagnosis studies of Alzheimer's disease (AD), brain trauma and tumor in the recent years. But, the most of proposed methods in the published papers, the tissue segmentation was considered as problems of statistical decision[1], pattern classification, cluttering[2], image processing and analysis[3]. The parameters used for tissue segmentation in those methods were the gray scalar/vector in single/multi-spectral images, which indirectly reflected the physical characteristics of the tissue. And those methods addressed the problems of tissue segmentation as the partitioning concourse of the components in a pixel in finite sets. So the results of the tissue segmentation obtained by conventional methods were unreasonable in some sense. This paper presents a new method of tissue segmentation based on the principle of spectroscopic decomposition of MR images, which consider the tissue segmentation as the problem of the estimation of MR physical parameters of the issues. This method can be used for suppressing not only fat MR signal in magnetic resonance imaging (MRI) but also water signal in magnetic resonance spectroscopy (MRS). Thus, this method is called the spatial and spectral MR imaging.

Key wors: magnetic resonance imaging (MR)；tissue segmentation; parameter estimation; multi-spectral images

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通过磁共振物理参数估计 实现磁共振图像的分解

王卫东[1,2] ， 包尚联[2]

（1. 解放军总医院生物医学工程研究室 北京100853；
2. 北京大学医学物理和工程北京市重点实验室 北京100871）

摘要：近年来，单谱与多谱磁共振图像的分割方法研究已经取得了很大进展，并应用于正常年龄的脑发育和脑疾病的诊断研究，例如老年痴呆综合征、脑损伤、脑肿瘤等的临床研究等。据此可以通过多谱MR图像获得多种对比度信息，更加准确表达人体组织及其病理情况。现已提出的大多数方法，把组织分割问题考虑成统计决策、模式识别和聚类、图像处理和分析等问题。 在这些方法中用于组织分割的特征主要是单谱/多谱图像的灰度值/矢量，它们不能直接反映组织的物理特征。而且，这些方法将组织分割问题表述成组织磁共振图像中像素不同成分的有限集合。所以，这些组织分割的方法所取得的结果在某种意义上是不够合理的。这篇论文提出了一种基于磁共振图像谱分解的新的组织分割方法，该方法将组织分割问题考虑成组织的磁共振物

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理参数的估计问题。这个方法不仅用于磁共振成像中脂肪信号的抑止，也用于核磁共振谱中的水信号抑止。因此，这个方法可以称为空间和谱MR成像。

关键词：磁共振成像、组织分割、参数估计、多谱图像

1 Introduction

Magnetic resonance imaging (MRI) offers an excellent differentiation among tissues such as the cerebral white and gray matters, as well as the cerebrospinal fluid (CSF) regions in human brain, and the water and fat molecules within other organs. So that it is possible efficiently to segment the tissue into different partials by computers. MR image segmentation methods have been proposed for quantitatively assessing subtle changes in tissue volume or tissue parameter distribution characteristics for the applications, such as normal aging brain, and the diagnosis studies of Alzheimer's disease (AD), brain trauma and tumor et al. The desired attributes of those segmentation methods should produce reliable and reproducible measurement values, which should be stable over time for longitudinal measurements, and be less depend on the observer input.

The MRI segmentation methods published in the literatures were mostly belonged to single and multi-spectral MR image segmentation methods. The quantitative evaluations of the performs for the methods are the measurement accuracy, of the regional areas or volumetric of brain, as well as for the results stability and reproducibility. For the most cases, the segmented results were fluctuated very much. A summary of the performance for these methods was published elsewhere. People think that the multi-spectral segmentation shows that the one of the great advantages of MRI over other radiological imaging modalities is the potential to provide specific chemical information in vivo. However, the conventional segmentation methods for proton MR images integrate, rather than separate the signal from chemical distinct protons within the pixels. As a result, in the segmentation of multi-spectral MR images, the signal intensity recorded for a given image pixel is a weighted average of the bulk relaxation time T1 and T2 and the proton density contribution from several distinct proton species.

Our purpose in writing this paper is to develop the technique for tissue segmentation via the estimation of MR physical and chemical parameters in tissue. This paper presented a new method for automatic tissue segmentation by estimating tissue parameters, which well overcame the shortcomings of the conventional segmentation methods and gave an effective suppression of overlapped tissue signals.

2 Theories and Method

It is well known that the MR signal of the protons in same position of a molecular in tissue is usually an exponentially damped complex sinusoid. No loss of generality, we assume that the transverse relaxation time is constant in the case that main magnetic field is fixed and has very good uniformity. Then the MR signal of multiple kinds of the protons in different positions in a molecular structure or in different molecules (following simplified as “proton specie”) in the tissues can be represented as the sum of multiple exponentially damped complex sinusoids in the form of

$$s(x,y,t)=\sum_{i=1}^{M}A_i(x,y,t)e^{-\frac{t}{T2_i}+j\int_0^t dt\omega_i(x,y,t)}, \tag{1}$$

where M is the number of the proton species in the tissues, and $T2_i$, ω_i and A_i are the transverse relaxation time, the proton's resonance frequency in radian per second and the magnetization of the i-th kind of proton specie respectively. And there exists $\omega_i(x,y,t)=\gamma B(x,y,t)(1+\delta_i)$, where γ is the gyromagnetic ratio of proton, and δ_i is the chemical shift of the i-th kind of proton specie which is determined by the chemical environment of protons in tissues, generally, the chemical shift of water is set up as zero. Usually, A_i is a complex, whose phase is the initial phase of the magnetization.

It is well known that the gray of pixels can be partitioned into the contributions of the different kind of proton species in frequency domain by using the Fourier transform (FT) of MR data. However, actually, a number of the samples were required for estimating different tissue gray weight in a pixel by the FT technique, which makes FT technique flooey. Therefore, we present a new method, which estimats the weight of each proton specie in tissue by least square Prony method. Take an example of spin echo (SE) pulse sequence, the spectroscopic decomposition formula are derived in the below.

Let $B(x,y,t)=B_0+xG_x(t)+yG_y(t)$, where B_0 is the main-field, and G_x and G_y are the gradients, then the MR signal in accordance in the equation (1) was rewritten as

$$s(t)=\sum_{i=1}^{M}\iint dxdyA_i(x,y)e^{-\frac{t}{T2_i}+j\gamma\left(B_0t+\int_0^t dtxG_x(t)+\int_0^t dtyG_y(t)\right)(1+\delta_i)-\gamma B_0t}. \tag{2}$$

Let $k_x=\gamma\int_0^t dtG_x(t)$ and $k_y=\gamma\int_0^t dtG_y(t)$, which are the data element in k-space, then the k-space signal was represented as

$$s(k_x,k_y,t)=\sum_{i=1}^{M}e^{(-1/T2_i+j\gamma\delta_iB_0)t}\iint dxdyA_i(x,y)e^{j(xk_x+yk_y)(1+\delta_i)}. \tag{3}$$

According to the scheme of data acquisition shown in Fig. 1, where exists $k_x=(\gamma G_x^{read}\Delta T_x)n_x$ and $k_y=(\gamma G_y^{step}T_y)n_y$ with $n_x,n_y=\cdots,-1,0,1,\cdots$, where G_x^{read} is the read gradient field, ΔT_x is the interval of MR echo signal acquisition, and G_y^{step} is the step of phase gradient field with the width T_y. Meanwhile, there are also $t=TE+\Delta T_xn_x$, i.e., $t=TE+(\gamma G_x)^{-1}k_x$. Thus, the equation (3) can be represented in the form of

$$s(k_x,k_y,TE)=\sum_{i=1}^{M}e^{(-1/T2_i+j\gamma\delta_iB_0)TE}e^{(-1/T2_i+j\gamma\delta_iB_0)(\gamma G_x^{read})^{-1}k_x}\iint dxdyA_i(x,y)e^{j(xk_x+yk_y)(1+\delta_i)} \tag{4}$$

where TE is the echo time.

Let $x_i=(-1/T2_i+j\gamma\delta_iB_0)(\gamma G_x^{read})^{-1}$, which is called the complex spatial shift, and $p_i=-1/T2_i+j\gamma\delta_iB_0$, which is called the complex chemical shift, then we have

$$s(k_x,k_y,TE)=\sum_{i=1}^{M}e^{p_iTE}\left(e^{jx_ik_x}\iint dxdyA_i(x,y)e^{j(xk_x+yk_y)(1+\delta_i)}\right). \tag{5}$$

Let $TE=TE_0+(\bar{n}^{-1}-1)\Delta T$, then a series of MR images $I(x,y,n)$ for $n=1,2,...,N$

($N > 2M$) may be acquired by shifting the radio frequency (RF) pulse and read gradient field shown in Fig. 1, where ΔT is the interval of MR image acquisition. And this series of MR images, which is obtained using the inverse Fourier transform of equation (5), can be described as

$$I(x,y,n)=\sum_{i=1}^{M} e^{p_i TE_0} e^{p_i (n-1)\Delta T} \iint dk_x dk_y \left[e^{-j(xk_x+yk_y)} \left(e^{jx_i k_x} \iint dxdy A_i(x,y) e^{j(xk_x+yk_y)(1+\delta_i)} \right) \right], \tag{6}$$

Therefore, we obtained

$$I(x,y,n)=\sum_{i=1}^{M} (1+\delta_i)^{-2} e^{p_i TE_0} A_i((x-x_i)/(1+\delta_i), y/(1+\delta_i)) e^{p_i (n-1)\Delta T} . \tag{7}$$

Let $\overline{A_i}(x,y)=(1+\delta_i)^{-2} e^{p_i TE_0} A_i((x-x_i)/(1+\delta_i), y/(1+\delta_i))$, usually, $\delta_i << 1$, then it was approximated $\overline{A_i}(x,y)=e^{p_i TE_0} A_i(x-x_i, y)$. Thus, the equation (7) was rewritten as

$$I(x,y,n)=\sum_{i=1}^{M} \overline{A_i}(x,y) e^{p_i (n-1)\Delta T} . \tag{8}$$

From the above equation (8), we estimated the MR physical parameters of $T2_i$, ω_i and A_i for $i=1,2,...,M$ in different tissue as the feature parameters for segmenting MR images. To estimate these parameters, an intermediate variable $I_s(n)$ was first calculated by $I_s(n)=\iint dxdy I(x,y,n)$. Then one gets

$$I_s(n)=\sum_{i=1}^{M} \tilde{A}_i e^{jp_i (n-1)\Delta T} , \tag{9}$$

where $\tilde{A}_i=\iint dxdy \overline{A_i}(x,y)$. The gradient of slice selection was omitted in the figure.

For estimating the ptissue arameters, the following equations were structured

$$\mathbf{I}_{f0} a = I_{M+1}, \tag{10}$$

where the matrix $\mathbf{I}_{f0}=[I_M I_{M-1} \cdots I_1]$ is called the Toeplitz matrix with $I_n=[I_s(n) I_s(n+1) \cdots I_s(n+N-M-1)]^T$, $n=1,2,...,M$. The coefficient vector a can be obtained by solving the equation (10), which is used for computing the relaxation times and the chemical shifts.

Constructing the polynomial equation in the following

$$z^M + \sum_{i=1}^{M} a_i z^{M-i} = 0, \tag{11}$$

where $a=[a_1 \quad a_2 \quad \cdots \quad a_M]^T$. Let the roots of the polynomial equation (11) be z_i, $i=1,2,...,M$. Usually, the complex chemical shifts z_i, $i=1,2,...,M$ should not be dependent with the spatial coordinates (x,y). Hence, we obtain $T2_i=-\{\text{real}[\ln(z_i)]/\Delta T\}^{-1}$ and $\delta_i=\text{imag}[\ln(z_i)]/(\gamma B_0 \Delta T)$ for $i=1,2,...,M$.

Constructing the matrix equation of the following for the spectroscopy decomposition in MR image space

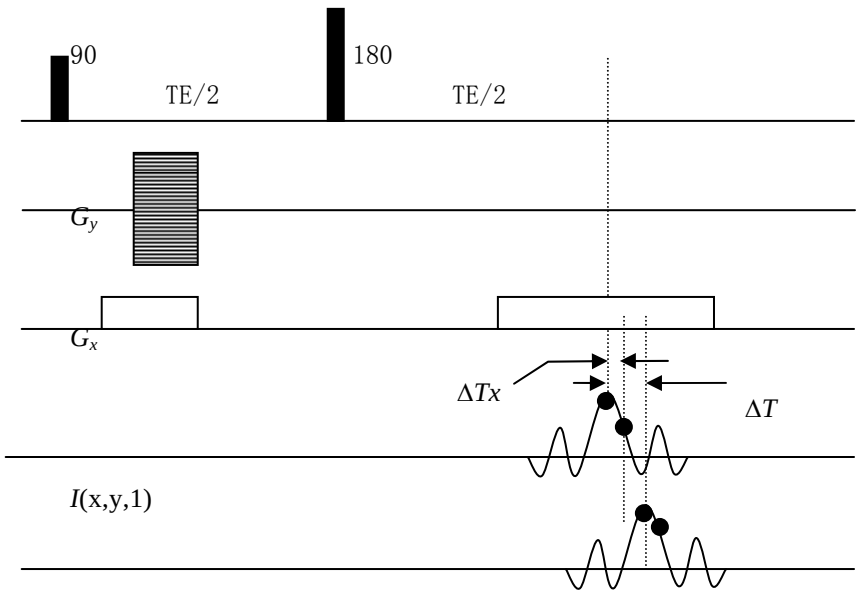

Fig. 1 The scheme of MR image acquisition by using spin echo RF pulse sequence

$$\begin{bmatrix} z_1 & z_2 & \cdots & z_M \\ z_1^2 & z_2^2 & \cdots & z_M^2 \\ \vdots & \vdots & \ddots & \vdots \\ z_1^N & z_2^N & \cdots & z_M^N \end{bmatrix} \begin{bmatrix} \overline{A}_1(x,y) \\ \overline{A}_2(x,y) \\ \vdots \\ \overline{A}_M(x,y) \end{bmatrix} = \begin{bmatrix} I(x,y,1) \\ I(x,y,2) \\ \vdots \\ I(x,y,N) \end{bmatrix}, x,y=1,2,...,K, \tag{12}$$

where K is the size of MR images. Let the solution of the above equation be $\overline{A}_i(x,y)$, $i=1,2,...,M$. These images are expected to obtain the images $A_i(x,y)$, $i=1,2,...,M$ of the different tissues by the transition and scaling the corrections of chemical shifts.

For improving the precision of the estimation of the MR parameters, the number of the acquired images N and the dimension of equation (10) M should be enlarged. Generally, M = [N/2] is recommended. However, the residues of complex chemical resonance frequencies must be removed. And the singularity value decomposition may be used for reducing noise. Some other methods for the estimation of the parameters of exponentially damped complex sinusoids are also used for computing MR physical parameters[4] [5] [6].

The MR image has been partitioned into the MR images of water and fat, and other chemical molecules by the method proposed in the paper. The basic principle of the solution of this problem is

that the distinguishable chemical shifts of fat and water, and other molecules are used for computing t he corresponding their magnetization intensities, and, similarly, the components of cerebral white and gray matters and fluid were decomposited with the distinguishable difference in their relaxation times. In other word, the method can also be applied to the suppress a certain MR signal of the given tissue, such as water and fat.

After estimating the MR physical and chemical parameters in tissues, the given tissue signals from MR image can be derived using the technique of adaptive cancellation. No loss of generality, we assume that the complex chemical shift of the given tissue is p_M. Then a new series of MR images is calculated by the cancellation method in the following

$$\bar{I}(x,y,n+1) = I(x,y,n+1) - e^{jp_M \Delta T} I(x,y,n), \ n = 2,3,\ldots,N, \tag{13}$$

then one gets

$$\bar{I}(x,y,n+1) = (1 - e^{jp_M \Delta T}) \sum_{i=1}^{M-1} \overline{A_i}(x,y) e^{jp_i n \Delta T}, \ n = 2,3,\ldots,N. \tag{14}$$

So continue, we obtained the results on MR images.

3 Results and Discussion

The segmentation of the tissue with different relaxation times is excellent method of their relaxation time measurement. These tissues possess the same chemical shifts. We simulated with the computer simulation software. Usually, it is very difficult to identify the relaxation times of the tissues with the same resonance frequency in the frequency domain by Fourier transform. But it is possible to estimate them by the method proposed in the paper. The segmentation of the tissues for different chemical shifts is identical for chemical shifts. These tissues possess the different resonance frequencies.

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Brief Introducing for Author: WANG Weidong (1964-), male, getting Engineering PhD Doctor degree (1994), Title: Professor, as the director of the Center of Biomedical Engineering and Technical Support, Chinese PLA General Hospital.

作者简介：王卫东(1964-)，男，工学博士(1994)；解放军总医院生物医学工程研究室研究员，医学工程保障中心主任。