Multivariate Image Analysis of Magnetic Resonance Images with the Direct Exponential Curve Resolution Algorithm

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Purpose
The purpose of this study was to develop a postprocessing algorithm capable of calculating the concentration of spins having different decay constants in multiexponential data.

Introduction
Hydrogen NMR spin-lattice and spin-spin relaxation times, \( T_1 \) and \( T_2 \) respectively, have been used to characterize living tissues [1-3]. These biological samples are complex spin systems and several models have been proposed to explain their spin relaxation behavior [2]. Tissues may be composed of different non-exchanging spin types and therefore possess multiexponential (ME) relaxation behavior characteristic of the sum of the individual components. For water alone there have been as many as five different types proposed [3]. At the opposite extreme, different spin types can be coupled by strong exchange, and hence possess one characteristic pair of \( T_1 \) and \( T_2 \) values. In the middle of these two extremes are tissues exhibiting weak exchange and possessing ME relaxation characteristics different from that of the pure spin components. There is no reason to believe that all tissues behave as one of the three possibilities, or that a given tissue will be spatially homogeneous. Clearly more studies are needed to determine an optimum model for each tissue.

This study describes the application of the direct exponential curve resolution algorithm (DECRA), previously used to extract components of NMR spectral and diffusion data [4], to study pure components in magnetic resonance images.

Methods
DECRA was modified to analyze both exponential decay and growth data. The algorithm was applied to magnetic resonance images of a two component wedge phantom and the human brain of a normal age 43 y male. The wedge phantom consisted of opposing wedge shaped compartments filled with different concentrations of aqueous NiCl₂.

MR images were acquired with a 1.5 T whole body imager (Signa, GE Medical Systems) employing a single-slice, single-echo, spin-echo sequence and quadrature birdcage style RF head coil. The image plane passed through the wedge phantom such that the concentration of the two components varied linearly across the image. For the brain images, the axial slice contained six primary tissue types: CSF, gray matter, white matter, meninges, adipose, and muscle.

Two sets of images were acquired for each image plane: a variable TE set used to calculate \( T_2 \), and a variable TR set used to calculate \( T_1 \). The \( T_2 \) image set consisted of 14 images with a fixed TR=1000 ms, and a TE which varied between 15 and 210 ms in 15 ms steps. The \( T_1 \) image set consisted of 15 images with a fixed TE=15 ms, and a TR which varied between 200 and 3000 ms in 200 ms steps. Each 24 cm field of view, 5 mm slice thickness image was acquired with 256 phase encoding steps to form a 256x256 pixel image.

Results
The algorithm correctly found two \( T_1 \) and two \( T_2 \) components in the wedge images (see Table 1). Decra also correctly determined that the concentration of these components varied linearly across the image of the phantom.

<table>
<thead>
<tr>
<th>Component</th>
<th>( T_1 ) (ms)</th>
<th>( T_2 ) (ms)</th>
</tr>
</thead>
<tbody>
<tr>
<td>1</td>
<td>159</td>
<td>30</td>
</tr>
<tr>
<td>2</td>
<td>319</td>
<td>150</td>
</tr>
</tbody>
</table>

The algorithm identified three \( T_2 \) and two \( T_1 \) components in the brain images. Images of the components are presented in Figure 1. The \( T_2 \) and \( T_1 \) values define six unique hydrogen signal bearing environments with densities, \( p_{ij} \), where \( i \) is the \( T_1 \) index and \( j \) the \( T_2 \) index. Owing to the fact that not all of the environments are present in a tissue, it is possible to identify the relative amounts of each environment in a tissue found in the brain images. (See Table 2.)

![Figure 1. Images, from left to right, of the three \( T_2 \) (22, 64, 290 ms) and two \( T_1 \) (0.92, 7.0 s) components found by the DECRA algorithm.](image)

Discussion
We have demonstrated that DECRA accurately determines the \( T_2 \) and \( T_1 \) components and their spin densities in a two component phantom. This algorithm identified three \( T_2 \) and two \( T_1 \) environments in MR images of the brain. Six unique hydrogen signal bearing environments and the relative concentration of each in a tissue were identified from this data. Assuming a relationship between tissue or pathology type and hydrogen environment, these results demonstrate the potential of DECRA to identify tissues and study the changes in tissues affected by disease.

References