A MATHEMATICAL MODEL OF BLOCH NMR FLOW EQUATION FOR FIELD CYCLING TISSUE IMAGING

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INTRODUCTION

Field-cycling magnetic resonance imaging (FC MRI) allows switching of the magnetic field during an imaging scan[1]. FC MRI has been very successful in relaxometry studies and there arises the need to offer more theoretical supports to the rich experimental results available in NMR laboratories. These theories are expected to offer new ways of interpreting the results for new discoveries. In view of this, we have developed a methodology based on the time – independent Bloch NMR flow equations for calculating the transverse magnetization in terms of the applied RF field.

MATHEMATICAL FORMULATION

In this study, we shall consider fluid whose spins are in a motion in which the transverse magnetization does not change appreciably with time of motion[2, 3]. In a rotating frame of reference, we shall assume that under the influence of RF magnetic field as derived in the earlier studies[2], resonance condition exists at Larmor frequency[2, 3]: $f_o = \gamma B - \omega = 0$

From the Bloch equations, the following equation as been derived[2, 3]:

$$v^2 \frac{d^2 M_y}{dx^2} + v\left(\frac{1}{T_1} + \frac{1}{T_2} + \frac{dv}{dx}\right)\frac{dM_y}{dx} + \left(\gamma^2 B_1^2(x) + \frac{1}{T_1 T_2}\right)M_y = \frac{M_o \gamma B_1(x)}{T_1} \quad (1)$$

B_1 is the spatially varying RF magnetic field and v is the spatial fluid flow velocity. We shall assume that the variable velocity is given as follows:

$$v(x) = \frac{x}{\delta} \quad (2)$$

Therefore, if we sample the MRI signal at the point where the transverse magnetization has the largest magnitude ($M_0 \approx 0$), we have:

$$x^2 \frac{d^2 M_y}{dx^2} + x(1 + \delta T_0)\frac{dM_y}{dx} + \left(\gamma^2 B_1^2(x)\delta^2 + \delta^2 T_g\right)M_y = 0 \; ; \; T_0 = \frac{1}{T_1} + \frac{1}{T_2}, \; T_g = \frac{1}{T_1 T_2} \quad (3)$$

In the presence of magnetic field gradient, we shall write the spatially dependent frequency as follows: $\omega(x) = \omega_0 + \omega_1 = \gamma B_0 + \gamma G x$ and $\alpha = \omega - \omega_0$ (4)

Using Eqn (9), we can easily convert spatial information into frequency information such that:

$$\alpha^2 \frac{d^2 M_y}{d\alpha^2} + (1 + \delta T_0)\alpha \frac{dM_y}{d\alpha} + \left(\alpha^2 \delta^2 + \delta^2 T_g\right)M_y = 0 \quad (5)$$

Eqn (16) is an equation transformable to Bessel equation, whose solution is given as:

$$M_y = \alpha^{-\frac{\delta T_0}{2}}\left[C_1 J_n(\delta\alpha) + C_2 Y_n(\delta\alpha)\right] = (\omega_1)^{-\frac{\delta T_0}{2}}\left[C_1 J_n(\delta\omega_1) + C_2 Y_n(\delta\omega_1)\right] \quad (6)$$

where $n = \delta\frac{\sqrt{T_0^2 - 4T_g}}{2}$, J_n and Y_n are Bessel functions of the first and second kind respectively; C_1 and C_2 are constants. However, since the NMR signal must have finite value even when the RF B_1 field is removed, $C_2 = 0$, and then we have:

$$M_y = C_1(\omega_1)^{-\frac{\delta T_0}{2}} J_n(\delta\omega_1) \quad (7)$$

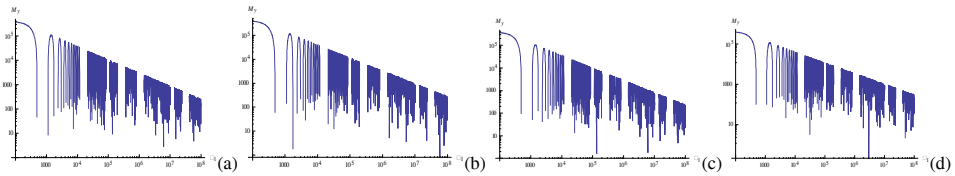

Fig. 1: 2D Plots of the NMR transverse magnetization as function of ω_1 using relaxation parameters (at 1.5T) of [4] (a) Skeletal muscle (b) Heart muscle (c) Liver (d) Kidney. We used δ = 5ms and $C_1 = 5 \times 10^6$.

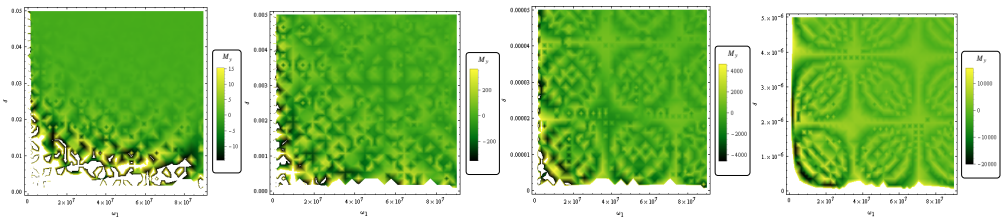

Fig. 2: 3D images of the NMR transverse magnetization as function of ω_1 and the pulse time δ for kidney at 1.5T[4]. We have shown the behaviour of M_y at different ranges of δ and $T_1 = 0.830$s, $T_2 = 0.082$s, $C_1 = 5 \times 10^6$.

DISCUSSIONS AND CONCLUSION

Using Eqn (7) and the relaxation times of selected human tissues, we have shown that it is possible to do computational imaging with relaxometry data. Fig.1 illustrates spectroscopic capabilities of the results we have obtained in this study. The tissues we considered showed unique peaks which correspond to unique values of cycling RF B_1 fields. Fig. 2 shows that the field cycling process can be easily transformed into 3D tissue mapping and it is quite interesting to see that patterns of the signals are very different as the pulse time changes. We also observed that 3D mapping shows very unique signal magnitude and slightly different patterns for different tissues at 1.5T. In conclusion, we see that we can easily use the results in this study to show contrast between various tissues and same tissues with changing T_2 values. We can also use the results to map the changes in tissue molecular dynamics at higher RF field values.

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