Compensating for Metabolite Dynamics in 13C Chemical Shift Separation

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Introduction

Iterative decomposition of water and fat with echo asymmetry and least-squares estimation (IDEAL) method has proven to be fast and efficient for separation of 13C species. However, the underlying least squares chemical shift imaging (LSCSI) technique, which requires multiple acquisitions to resolve metabolites, is not consistent with the fast changing metabolic signal. Total signal contributions from metabolites are assumed to be constant within several acquisitions, which contradicts with the highly dynamic metabolic behaviour. In this work a valid extension to the physical model of signal acquisition in 13C chemical shift imaging (CSI) is proposed. It uses correcting factors obtained by kinetic modelling of metabolic time curves, combines computational simplicity of the direct inversion with higher accuracy of model-based approaches and eliminates the need for additional regularisation.

Theory and Methods

The MRI signal $s_{m,n}$ of an image $x_q(\mathbf{r}_p)$ of a metabolite q with chemical shift frequency Δf_q acquired with a *k*-space trajectory $\mathbf{k}(t_n)$ and echo times $TE_m = m \cdot \Delta TE$ reads $s_{m,n} = \sum_{p,q} e^{i2\pi \mathbf{k}(t_n)\mathbf{r}_p} e^{i2\pi \Delta f_q (t_n + TE_m)} x_q(\mathbf{r}_p)$ (1) where the first and second exponential terms encode the spatial and spectral information, respectively. In the proposed method the spectral encoding matrix was complemented with the time-dependent factors obtained by fitting the two-site exchange model [1] to the measured metabolic time curves. If metabolite distribution in *k*-space is $\hat{x}_q = \sum_p e^{i\mathbf{k}(t_n)\mathbf{r}_p} x_q(\mathbf{r}_p)$ then for M acquisitions the measured signal in a matrix form reads:

$$\mathbf{s} = \begin{bmatrix} K_{11}C_{11} & \cdots & K_{1Q}C_{1Q} \\ \vdots & \ddots & \vdots \\ K_{M1}C_{M1} & \cdots & K_{MQ}C_{MQ} \end{bmatrix} \begin{bmatrix} \hat{x}_1 \\ \vdots \\ \hat{x}_Q \end{bmatrix} = (\mathbf{K} \cdot \mathbf{C})\hat{\mathbf{x}},\ C_{mq} = e^{i2\pi \Delta f_q (t_n + TE_m)},\ K_{mq} = M_z^q(t_{m,n}) \qquad (2)$$

where $\mathbf{C}$ is a matrix of CS encoding and $M_z^q(t_{m,n})$ denotes the sample on the fitted time curve of q^{th} metabolite taken at t_{n+m}, with t_n being time of the first excitation. Without correction this would be a basic formulation of the least squares chemical shift imaging technique (LSCSI) [2], currently being employed for separating contributions of distinct metabolites into the measured signal. Its major limitation is inability to account for the change of longitudinal magnetisation in a course of M excitations. We attempted to compensate this non-valid assumption in our method. The unknown images can then be found by conventional direct inversion of modified CS encoding matrix and the gridding reconstruction.

Animal experiments were conducted on a 3 T GE Signa Excite scanner (GE Healthcare, Milwaukee) with healthy outbred Wistar rats and tumour-bearing female inbred Fischer rats. To resolve up to 5 metabolites IDEAL Spiral CSI pulse sequence [3] consisting of a slice-selective RF pulse followed by an imaging module was repeated 7 times with a relative echo-time shift of 1.12 ms. 13C NMR spectra (Fig.1 (a)), reconstructed from slice-selective FID measurements, preceding each of the imaging modules, were quantified and fitted with piecewise exponential kinetic equations described by Zierhut et al. (Fig. 1 (b)) to obtain components of the correction matrix $\mathbf{K}$ from (2).

Results and Discussion

Effect of model-based correction on outcome of reconstruction was quantified by means of signal-to-noise ratio (SNR) and images were compared with ones obtained with the conventional method (Fig. 2 (a)). Noise reduction was observed in alanine and lactate images (55% and 10% SNR increase) and pyruvate and pyruvate hydrate images show elevated signal in kidney (Fig. 2 (b)). The first-order correction requires very low computational resources and only a single additional step of spectra quantification. The major drawback is the current ability to account only for the average signal evolution from the whole slice, which still results in errors in case of heterogeneous kinetic rates within the slice.

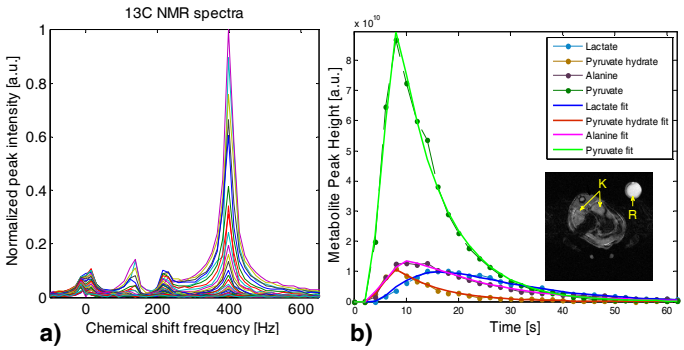

Fig. 1.: **a)** 13C NMR spectra, repetition time = 2 s, number of acquisitions = 32; **b)** Resulting curves of metabolite levels in a slice centered on healthy rat kidney (K) and reference lactate syringe (R). Actual data are represented by filled circles; the estimated fit lines are represented by the solid lines

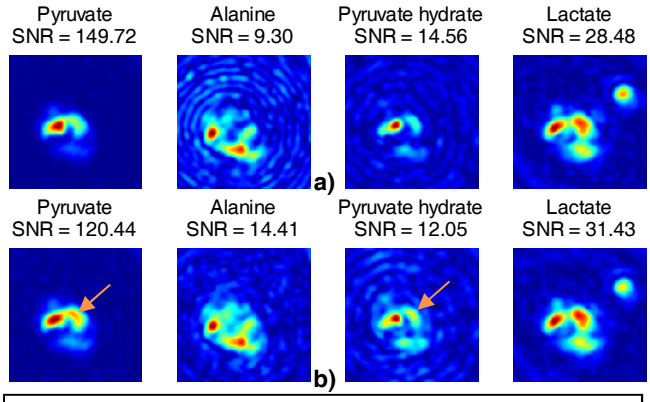

Fig. 2.: **a)** Metabolite images (time-average from 32 frames) reconstructed by direct inversion of the conventional spectral encoding matrix and **b)** the modified one using correcting factors for compensation of metabolite dynamics

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