Combined Reconstruction of Rosette Sampled Data for Hyperpolarised ^{13}C Metabolic Imaging

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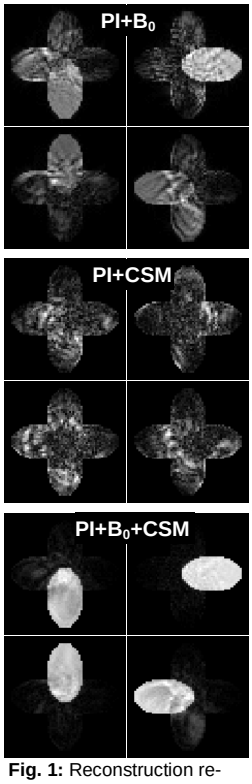

Fig. 1: Reconstruction results for simulated dataset. Parallel imaging (PI) is combined with B_0 correction (top), with CSM (middle) and both (bottom).

Introduction

Imaging of hyperpolarised ^{13}C metabolites requires fast acquisition sequences to encode both the spatial and spectral domain [1]. One of the most efficient single-shot CSI sequences is rosette [2], which samples k-space continuously and traverses the centre of k-space regularly, hence yielding good spectral selectivity. This kind of non-Cartesian sampling requires sophisticated reconstruction techniques, including interpolation onto a Cartesian grid. Coil sensitivities for parallel imaging (PI) can be included by formulating the encoding model in a matrix and inverting this matrix by conjugate-gradient iterative reconstruction [3]. PI was combined with B_0 correction [4], however never with chemical-shift modelling (CSM). The latter denotes the process of including chemical shifts of different chemical species in the reconstruction [5]. However, all published CSM reconstructions require equidistant time-sampling, thus CSM fitting can be solved separately from the actual reconstruction [6]. In this work we propose to include coil sensitivities, B_0 inhomogeneity and chemical shifts in a combined reconstruction, solved iteratively with conjugate gradient optimisation.

Theory and Methods

The MR signal $d_{(\gamma,\kappa)}$ received by coil γ at the κ^{th} sampling point is given by

$$d_{(\gamma,\kappa)} = \sum_{\rho}\sum_{\varphi} \mathrm{E}_{(\gamma,\kappa),(\rho,\varphi)} \nu_{(\rho,\varphi)},$$

where $\nu_{(\rho,\varphi)}$ are the images of the different chemical species φ.
The encoding matrix is given by

$$\mathrm{E}_{(\gamma,\kappa),(\rho,\varphi)} = s_{\gamma}(r_{\rho}) \exp\left(-i\left(k_{\kappa} r_{\rho} + \Delta\omega_{\rho} t_{\kappa} + 2\pi f_{\varphi} t_{\kappa}\right)\right),$$

where s_{γ} denotes the spatial coil sensitivities, $r\rho$ the ρ^{th} pixel position, $k\kappa$ the k-space position, $\Delta\omega_{\rho}$ the frequency offset induced by field inhomogeneities, and f_{φ} the chemical shift frequencies. The images $\nu_{(\rho,\varphi)}$ can be reconstructed by inverting the encoding matrix E, which is usually too large for a direct inversion and thus typically solved by conjugate gradient optimisation [3,7]. The field inhomogeneity $\Delta\omega_{\rho}$ is corrected for by multi-frequency interpolation and its adjoint projector [4,8]. All gridding steps are based on a fast C-implemented gridding routine [9], the rest was implemented in Matlab R2007a.
The reconstruction was evaluated on various datasets sampled along the rosette trajectory, always with n=8192 sampling points, f_1=221 Hz and f_2=71 Hz. A simulated dataset (Fig. 1) includes four resonances at 183.3, 176.6, 161.4, 160.4 ppm, corresponding to $^{13}C_1$-lactate, alanine, pyruvate and bicarbonate at B_0=3T, respectively. The sensitivities of eight coils were simulated with Biot-Savart and added to the dataset together with a 100 Hz Gaussian distributed B_0 off-resonance. The rosette trajectory consists of a single shot with BW=62.5 kHz (t_{acq}=131 ms), and the data was reconstructed to a Cartesian resolution of (64×64).
The ^{1}H *in vivo* rat scan (Fig. 2) was acquired on a 1.5T GE Signa scanner equipped with a dual-tuned transmit-receive rat-sized birdcage resonator [10]. The rosette trajectory consisted of 16 shots with BW=250 kHz (t_{acq}=33 ms), reconstructed to (128×128). B_0 maps were acquired with an SPGR sequence with TE=7 and 9 ms. The ^{13}C phantom scans (Fig. 3) were acquired on a 3T GE Signa scanner equipped with solenoid transmit-receive surface coil. The rosette sequence consisted of 4 shots, 32 averages, BW=125 kHz (t_{acq}=66 ms) and TR=6 s, reconstructed to (120×120).

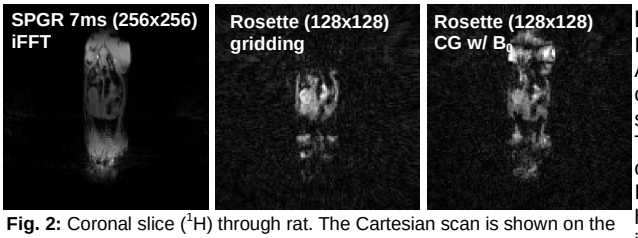

Fig. 2: Coronal slice (^{1}H) through rat. The Cartesian scan is shown on the left for comparison to the rosette scan reconstructed without (middle) and with (right) B_0 inhomogeneity correction.

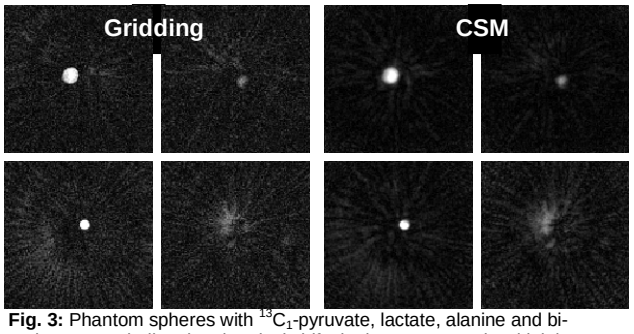

Fig. 3: Phantom spheres with $^{13}C_1$-pyruvate, lactate, alanine and bicarbonate. Including the chemical shifts in the reconstruction (right) reduces spectral-spatial artefacts.

Results and Discussion

Including more physical information in the reconstruction greatly improves image quality. A lot of the signal lost to B_0 inhomogeneities can be recovered (Figs. 1,2). Therefore, we conclude that B_0 correction is a must for robust *in vivo* scans with rosette. Spectral-spatial aliasing artefacts in undersampled rosette data appear as noise in the images. The aliasing is considerably reduced by including the coil sensitivities (Fig. 1) and the chemical shifts (Figs. 1,3) in the reconstruction.
It is possible to include T_2^* in the reconstruction to improve the point spread function, however at the cost of SNR. As ^{13}C metabolic imaging is at the SNR limit, this was not included. Reconstruction times were four minutes (Windows XP laptop with 1.7 GHz Intel Pentium and 1.5 GB of RAM) for the combined reconstruction (Fig. 1; bottom) and less otherwise.

Conclusion

Rosette is one of the most efficient sequences in terms of spectral-spatial encoding. However, rosette is highly sensitive to artefacts such as B_0 inhomogeneity. Extending the encoding matrix to include more physical information (coil sensitivities, B_0, chemical shifts) increases the robustness. Hence, rosette in combination with the proposed reconstruction might become the standard method for metabolic imaging on hyperpolarised ^{13}C.

References

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