Reconstruction of Carbon-13 Metabolic MR Images Using Constrained Optimisation

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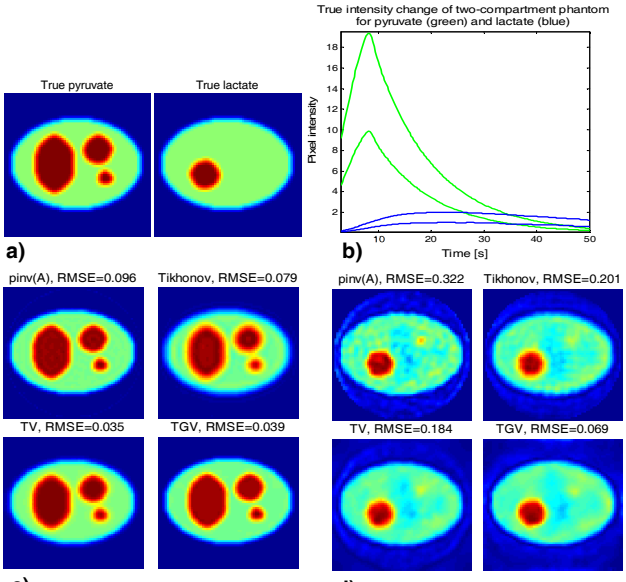
Introduction: Magnetic resonance spectroscopic imaging with hyperpolarised 13C agents is a novel technique that examines the cellular metabolic reactions in a minimally invasive fashion. Being acquired under challenging conditions of rapidly decaying signal and limited injected dose of the hyperpolarised substance, reconstructed images exhibit low signal-to-noise ratio (SNR) and artifacts. The goal of this work is to enhance the quality of the images by means of iterative reconstruction with included regularisation terms.

Theory and methods: The goal is addressed by reformulating the inverse problem as a regularised least-squares, where the solution is chosen to be one that minimises a user-defined objective function consisting of a fidelity term and a regularisation term aiming at penalising noise and non-smooth changes. For the latter, mathematical simulations were performed to investigate the effect of Tikhonov, total variation (TV) and total generalised variation (TGV) penalty [1] terms on the outcome of reconstruction when the ground truth was provided. Root-mean-square error (RMSE) served as image quality assessment metric. In case with experimentally acquired *in vivo* animal data, signal-to-noise ratio (SNR) was used to characterise and compare the reconstruction performance. In simulations, time series of 2D images representing maps of two metabolites whose pixel intensities were changing according to the two-site exchange model [2] served as original data (Fig.1 (a, b)). It has then undergone spectral-spatial encoding [3] and the additive white Gaussian noise with zero mean and standard deviation σ = 5 was applied to get the final "measured" signal. We assumed a FOV of 1.0, a pixel resolution of 32x32 pixels, a relative chemical shift of 400 Hz and Archimedean spiral trajectory of 1000 sampling points. Experimental data were acquired on a 3 T GE Signa Excite scanner (GE Healthcare, Milwaukee, USA) using a dual-tuned rat coil, spiral trajectory (FOV=80 mm, nom. resolution 32x32) and 7 echo times (ΔTE=1.2 ms). In each study 80mM solution of [1-13C] pyruvate was injected out of consideration 2.5 mL per 1 kg of body weight.

$$\mathbf{s} = \mathbf{Ax}$$
$$\hat{\mathbf{x}} = arg\min_{\mathbf{x}} \|\mathbf{A}\,\mathbf{x} - \mathbf{s}\|_2^2 + \alpha\|\mathrm{R}(\mathbf{x})\|_2^2$$

$\mathbf{s}$ – measured MR signal
$\mathbf{A} = \mathbf{CSI} \cdot \mathbf{NUFFT}$ – forward encoding matrix (chemical shift imaging + Fourier encoding)
$\mathbf{x}$ – unknown spin density



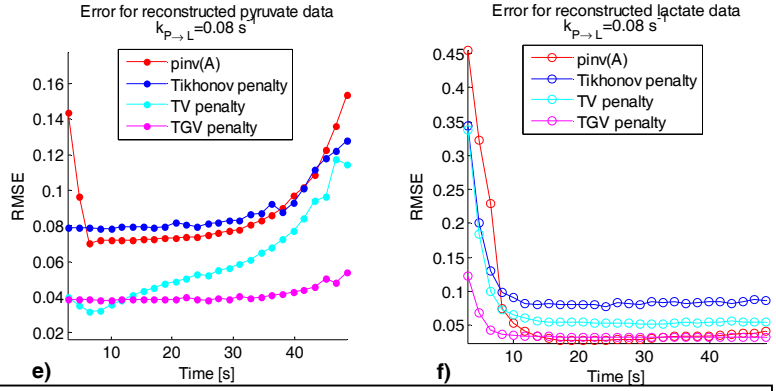


Fig. 1: **a)** True intensity maps; **b)** Signal curves for simulation of time-resolved metabolic images; **c)** Pyruvate and **d)** lactate images (time frame=2) reconstructed with direct method of matrix inverse (pinv(A)) or using iterative reconstruction with Tikhonov, TV and TGV penalty terms; **e)** RMS error versus time for reconstruction of pyruvate and **f)** lactate simulated data using different techniques for the specified conversion rate

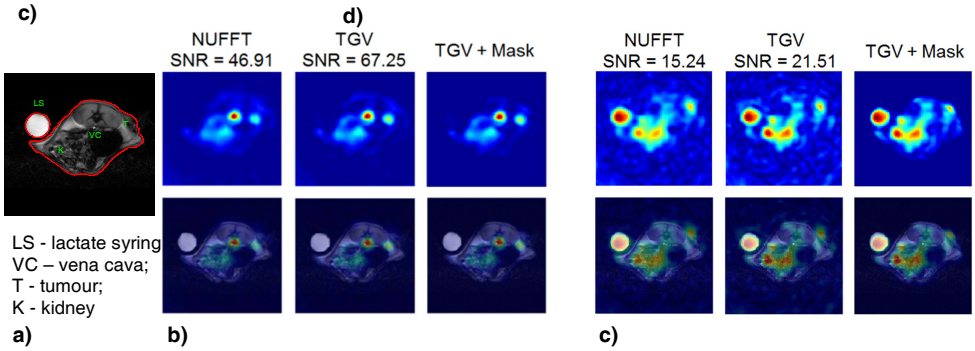


Fig. 2: **a)** Reference anatomical scan; **b)** Pyruvate and **c)** lactate images (sum over 16 time frames) reconstructed with conventional method of non-uniform Fast Fourier transform (NUFFT), iterative reconstruction with TGV constraint and anatomical mask

Results: Simulated data reconstructed by means of conventional pseudoinverse exhibit characteristic "ringing" artifacts and in the lactate data "bleeding" patterns in places of pyruvate distribution (Fig. 1 (c, d)). RMSE plots (Fig. 1(e, f)) show the interval of measurement before the end of injection (tend = 8 s) as the most error-prone. TGV demonstrated clear advantage over both TV and Tikhonov regularisation terms. It has equally good edge-preserving and denoising properties. Longer computational times of TGV reconstruction (270 sec vs. 5 sec for the direct matrix inversion) did not become the obstacle for research purposes, but can be critical for the clinical workflow. TGV constraint was applied to the real *in vivo* data together with the support mask, derived by means of active contour-based segmentation [4], to discard the out-of-object signal (Fig. 2) and improve visualisation of coregistered anatomical and functional images.

Conclusion: This study presents the simulation framework for 13C metabolic imaging with quantitative evaluation of iterative reconstruction performance with several regularisation terms. SNR improvement of up to 40% as well as better delineation of structure borders was achieved with TGV penalty function. Until now it was used in reconstruction of anatomical MR images only and here the applicability of TGV constraint to reconstruction of functional metabolic images and yielded improvement have been shown.

References: [1] Knoll F. et al. Second Order Total Generalized Variation (TGV) for MRI, Magn Reson Med., **65**, 480–491 (2011) [2] Zierhut M. et al. Kinetic modelling of hyperpolarized 13C-pyruvate metabolism in normal rats and TRAMP mice, J Magn Reson, **202**(1), 85-92 (2010) [3] Wiesinger F. et al. IDEAL spiral CSI for dynamic metabolic MR imaging of hyperpolarized [1-13C]pyruvate, Magn Reson Med., **68**(1), 8-16 (2012) [4] Chan T. et al. Active contours without edges for vector-valued images. J Vis Communication, **11**(2):130–141, 2000 (2012)

Acknowledgements: cofunding my BMBF grant #13EZ1114