

Proton-Constrained CMRO₂ Quantification with Direct ¹⁷O-MRI at 3 Tesla

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Introduction

Abnormalities in brain metabolism are found in various diseases: tumors, cerebrovascular diseases and neurodegenerative diseases, such as Parkinson's, Alzheimer's and Huntington's. A useful biomarker of the metabolic brain activity is the cerebral metabolic rate of oxygen consumption (CMRO₂) [1] which can be quantified with ¹⁵O positron emission tomography (PET) [2], and direct or indirect ¹⁷O MRI methods. In direct ¹⁷O MRI the signal change of ¹⁷O nucleus is detected during and after the administration of a ¹⁷O-enriched gas. To overcome the low SNR, ¹⁷O-MRI has so far only been applied at ultra-high fields (B₀ ≥ 7T) [3,4,5]. To make CMRO₂ quantification available at clinical field strengths (B₀ ≤ 3T), where the SNR is smaller [6], prior information from co-registered ¹H MRI can be used in combination with iterative constrained image reconstruction. So far, only the object shape using a binary mask (BM) has been used for constrained reconstruction; however, this mask cannot distinguish different brain tissues. In this work we use an anisotropic non-homogeneous diffusion operator [7] on ¹H MPRAGE data as a constraint to improve the image quality of ¹⁷O images and the localized CMRO₂ quantification in a frontal lobe.

Materials and Methods

For the constrained reconstruction, a dynamic *in vivo* ¹⁷O measurement consisting of 45 3D data sets of the brain was used. The data was acquired with a temporal resolution of 1 min and was obtained in a four phase CMRO₂ inhalation experiment in a healthy volunteer (male, age 49y) at a clinical 3 Tesla MR system (Tim Trio, Siemens). Using a custom-built TxRx ¹⁷O head coil [8], a density-adapted projection sequence (DAPR) [9] and a re-breathing system, the ¹⁷O 3D data sets were acquired during a baseline phase under free breathing (10 min), an ¹⁷O inhalation phase (5 min), a re-breathing phase with a closed breathing circuit (8 min), and a final wash-out phase (22 min), during which the volunteer was breathing room air. In total, 2.5 L of 70% enriched ¹⁷O gas (NUKEM Isotopes) was delivered. The following imaging parameters were used: nominal resolution: (10 mm)³, TE = 0.52 ms, TR = 8 ms, BW = 150 Hz/px, T_{RO} = 6.7 ms, 7500 projections x 128 radial points interpolated to a 128³ matrix.

¹H 3D MPRAGE data (resolution: 0.6x0.6x1 mm³, TI = 1100 ms) were used for co-registration, tissue segmentation, and iterative reconstruction. In addition, after co-registration a numerical ¹⁷O brain phantom was constructed from the segmented WM, GM and CSF compartments of the MPRAGE data with the acquisition parameters of the ¹⁷O-MRI measurement. A T₂-decay (2 ms) and Gaussian noise were applied using a measured SNR of 20. To simulate the dynamic ¹⁷O MRI experiment, the intensities of the WM and GM were modulated with concentration-time curves of a 4-phase kinetic model [4] and literature CMRO₂ values [2].

Both phantom and experimental ¹⁷O images were reconstructed with Kaiser-Bessel (KB) gridding method with and without Hanning filter. Alternatively, an iterative reconstruction was applied by minimizing the objective function

$$J(\rho) = \|A \cdot \rho - y\|^2 - \lambda_D \int \rho \nabla (D \nabla \rho) \quad \text{with} \quad D = \left(1 - \frac{g \cdot g^T}{|g|^2} / \sqrt{1 + \frac{g^2}{a^2}} \right) \quad (1),$$

where **A** denotes the system matrix that maps the image ρ to the corresponding raw data y . In the regularization term the gradient operator g is applied to the ¹H MPRAGE image ($g = \nabla \text{Im}_{1H}$). The factors λ_D and a were chosen providing the best correspondence with PET CMRO₂ values [2] without image distortions: $a = 2 \cdot 10^{-03} \text{Im}_{1H}$, $\lambda_D = 30 / 4000$ for phantom / *in vivo*. CMRO₂ values in the frontal lobe were determined by a fit with the 4-phase kinetic model.

Results and Discussion

Proton-constrained ¹⁷O images show better quality compared to KB regridding (Fig.1-2), since they contain more visible anatomical information (cf. the ventricles). The brain phantom simulations show that decent precision of CMRO₂ values in 1 ml of GM cannot be obtained without filtering. ¹H-constrained reconstruction gives most precise values in phantom simulations and localized *in vivo* CMRO₂ quantification in GM and WM in a frontal lobe (Fig. 4). For GM the value is in a good agreement with literature PET values [2] and has a factor of 1.8-2.8 smaller uncertainty compared to KB gridding. For WM CMRO₂ value is underestimated, since it is affected by partial volume effects (PVE) with other brain tissues. To increase the resolution of the low-SNR ¹⁷O MRI data at 3T, in brain tumor studies ¹H-constrained iterative reconstruction is an interesting alternative to conventional post-processing methods such as filtering, which might also help to overcome limitations due to PVEs.

References

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Financial support from NUKEM Isotopes is gratefully acknowledged.

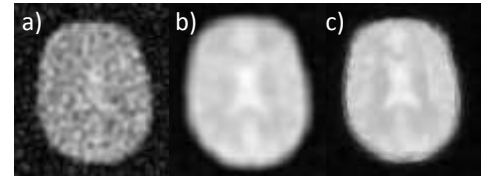


Fig. 1: Transverse slice of the simulated brain phantom reconstructed with Kaiser-Bessel (KB) gridding method without (a) and with Hanning window (b) and with ¹H constraint (c). TA = 10 min.

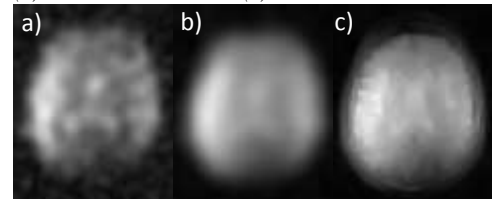


Fig. 2: ¹⁷O MR images reconstructed with KB gridding without (a) and with Hanning window and with proton constraint (c). TA = 10 min

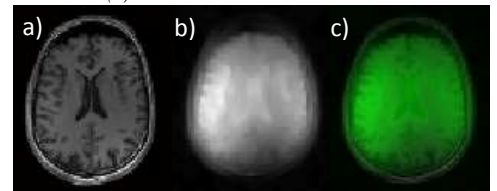


Fig. 3: Comparison of ¹H MPRAGE (a), co-registered ¹⁷O MRI image with proton constrained with TA = 10 min (b and green in c) and fusion of both images (c).

Tissue	CMRO ₂ [μmol/g _{tissue} ·min]						¹⁵ O-PET
	Simulated brain phantom			In vivo ¹⁷ O MRI			
	no Hann	with Hann	¹ H constrained	no Hann	with Hann	¹ H constrained	
GM	1.65±0.63	1,01±0.15	1.12±0.15	1.55±0.34	1.68±0.21	1.56±0.12	1.59±0.23
WM	0.75±0.23	0.80±0.18	0.70±0.14	-*	1.16±0.39	1.12±0.18	0.62±0.10

Fig. 4: CMRO₂ values obtained in the simulated phantom (in 1 ml GM and WM) and with direct ¹⁷O-MRI at 3 Tesla (in 2 ml GM and 4 ml WM) compared with PET literature values from [2]. * was not defined due to low SNR