PET-MRF: One-step 6-minute multi-parametric PET-MR imaging using MR fingerprinting and multi-modality joint image reconstruction

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Target Audience: Researchers and clinicians interested in PET-MR imaging.

Purpose: Despite the extensive opportunities offered by current state-of-the-art PET-MR systems [1], their use is still far from routine clinical practice. While it is feasible to acquire PET data from a single bed position in about 5 minutes, collecting the clinically relevant variety of traditional MR contrasts requires substantially more time. This bottleneck formed by the traditional MR paradigm leads to a relatively inefficient use of the PET component and is particularly prohibitive for multiple-bed-position PET protocols. This work proposes a one-step procedure that merges the MR fingerprinting (MRF) framework [2] with the PET acquisition, and employs a dedicated multi-modality reconstruction exploiting joint information among multiple contrast weightings to enable a 6 minute comprehensive PET-MR exam, which can provide the majority of clinical MR contrasts alongside quantitative parametric maps of the relaxation parameters (T1, T2) together with improved PET images.

Theory & Methods: Although MRF is inherently robust against incoherent undersampling artifacts, there is a limit beyond which the final image quality will suffer. Instead of relaying purely on incoherence between undersampling artifacts and simulated signal evolutions (standard MRF reconstruction), we propose an extension of a recently proposed nonlinear joint multimodality reconstruction [3] to simultaneously reconstruct the series of MRF images and the PET image by enforcing joint sparsity, thereby reducing residual undersampling artifacts in MR while at the same time improving PET reconstruction quality. The joint MRF-PET reconstruction is performed by minimizing the following cost functional:

$$\arg\min_{x_{MR},x_{PET}} \left\{ \left\| E(x_{MR}) - k \right\|_2^2 + \sum_{j=1}^{J} \left((A(x_{PET}))_j - f_j \log(A(x_{PET}))_j \right) + \lambda \left\| \begin{matrix} \Psi(x_{MR}) \\ \Psi(x_{PET}) \end{matrix} \right\|_{2,1} \right\}.$$

In this equation, the first term corresponds to MR data consistency (least-squares), the second term is the PET data consistency (expectation-maximization) and the rightmost term enforces joint sparsity between MRF and PET. Specifically, x_{MR} is the series of 3D MRF image volumes, k is the series of undersampled MR k-space datasets, E maps x_{MR} to k and includes coil sensitivity modulations. A is the PET projection operator [4] mapping the image x_{PET} to the sinogram data f. j are indices of the PET lines of response, and J is the total number of PET lines of response. λ is a regularization parameter and Ψ is the sparsifying transform. The resulting series of MRF images are then matched to the database of signal evolutions to estimate MR parametric maps [2]. Simulated contrast-weightings of interest are then generated from these parametric maps. Experiments were performed on a 3T PET-MR system (Biograph mMR, Siemens, Erlangen, Germany). The study was approved by our institutional review board (IRB), and written informed consent of all patients was obtained prior to examination. 10 mCi 18F-FDG was injected and the exam was started after ~45min of uptake time. A Dixon sequence was run for PET attenuation correction (19s) followed by a 6 min PET list mode scan. During this time window a continuous radial golden angle fingerprinting acquisition was performed [5]. Sequence parameters were as follows: 18 slices with a slice thickness of 5mm, 160×160 matrix covering a FOV of 240×240mm^2, 480 time points each consisting of 5 radial spokes, corresponding to an MR data acquisition time of 3min 10s.

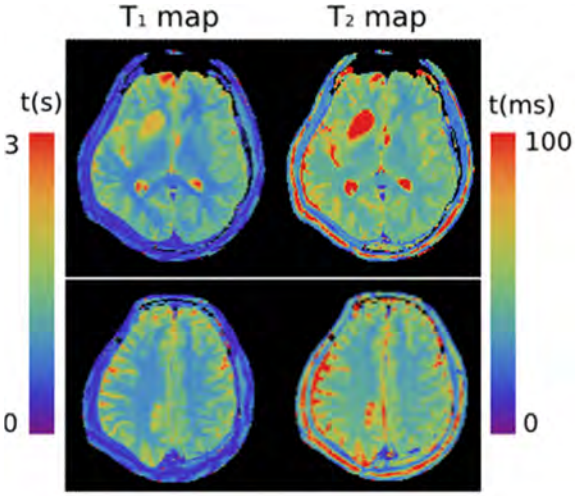

Figure 1: Quantitative parametric maps generated from 5 spokes MR fingerprints reconstructed jointly with the PET data.

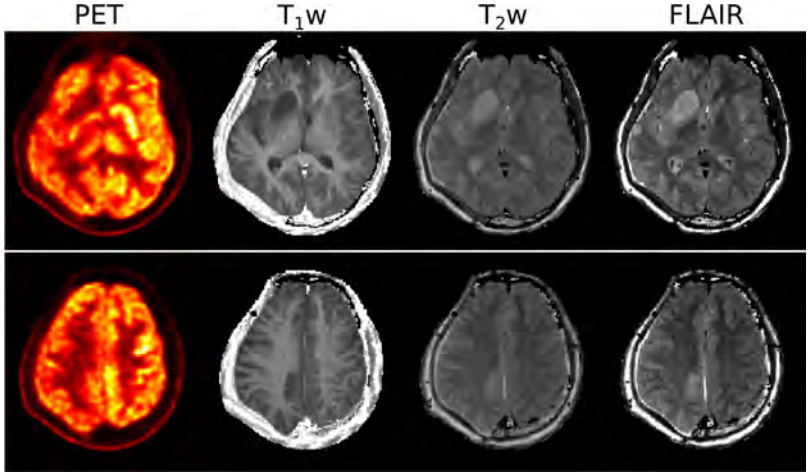

Figure 2: T_1, T_2 and FLAIR contrast, generated from the quantitative parameter maps derived from 5-spoke MRF reconstruction, together with the PET image from joint acquisition and reconstruction.

Results: **Figure 1** shows two slices of quantitative T_1 and T_2 maps of a brain tumor patient generated with the proposed protocol. In addition, our multi-transmit fingerprinting implementation [5] yields spin density and B_1 maps (not shown). From these maps, a multitude of MR contrasts can be generated retrospectively. **Figure 2** shows examples of T_1, T_2 and FLAIR contrast using simulated sequence parameters from the ADNI protocol [6] together with the jointly reconstructed PET data. Joint reconstruction of PET data together with multiparametric MR data is expected to improve PET spatial resolution in areas with significant joint information [3], and indeed quantitative analysis of the jointly reconstructed PET images in comparison to OSEM showed a reduction of 6% PET signal in areas of CSF where no FDG uptake is expected, indicating a reduction of partial volume effect. In gray matter and white matter, the differences were less prominent (GM: 1% signal increase, WM: 1% signal decrease with joint reconstruction).

Discussion & Conclusions: The proposed imaging procedure allows for a "push-button" MR examination comparable to the procedure in PET-CT. The joint reconstruction not only improves the resolution recovery due to point-spread function modeling of the PET images but also assists in the reconstruction of heavily undersampled MR fingerprints, each only containing a minimal number of samples. The joint procedure accelerates and simplifies PET-MR protocol design, and in our experimental protocol continuous MR data acquisition took less time than PET data acquisition. For typical 5-7min PET scans, this additional time can be used to increase the number of MRF slices to provide larger volumetric coverage or increased slice resolution. In addition, the protocol provides quantitative information as well as the possibility to generate numerous different contrasts retrospectively. This allows a post-examination PET-driven virtual MR examination: PET can be used to identify suspicious hotspots and the desired MR-contrast for the target region can then be obtained retrospectively during the process of reading the images. We believe that this has the potential to bring PET-MR one-step closer to daily clinical practice and raises the prospect of routine whole body PET-MR screening on the same time scale as in PET-CT but with a full range of disparate MR contrasts and associated biological information content.

References: [1] Quick HH. JMRI 2014; 39:243–258, [2] Ma et al., Nature 495: 187–192 (2013), [3] Knoll et al., ISMRM 2014 p82, [4] Koesters et al., IEEE NSS/MIC: 4365-4368 (2011), [5] Cloos et al., ISMRM 2014 p542, [6] Mueller et al. Neuroimaging Clinics of North America, 15:869-877 (2005).