In-vivo Tagged-MR based Motion Correction in combined MR-PET

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Combined MR-PET has opened new opportunities to improve PET image quality with MR. With the improvement of spatial resolution in modern PET scanners, patient motion becomes one of the key factors that can deteriorate image quality. Due to the motion-sensitive MR pulse sequences and the natural spatial and temporal alignments between PET and MR, combined MR-PET has a potential to allow accurate PET motion correction without increasing additional radiation dose as compared to PET-CT. Here we report progress in our in-vivo motion correction study, showing results from a free-breathing primate that demonstrates the feasibility of PET motion correction in simultaneous MR-PET.

Methods: An anesthetized monkey was scanned for 32 minutes in an integrated MR-PET scanner at our center (BrainPET prototype PET scanner operating in the bore of a 3T TIM Trio scanner; Siemens, Germany). Air-pressure sensing respiratory bellows was used for gating. We collected tagged MRI and 18FDG PET list-mode data simultaneously. For the MRI acquisition, we used a GRE with TE = 2.41 ms, TR of 164 ms, a flip angle of 25 degree, a FOV of 128x128x128 mm, and a matrix size of 128x64x32 over 3 SPAMM axes (X, Y, Z) [1]. The tagging pattern distance was 8 mm.

Nine phases out of the collected 32 phases in tagged MR study were chosen and motions between adjacent motion phases were estimated by using B-spline nonrigid motion estimation with a motion regularizer that encourages the local invertibility of estimated deformations [2]. We used both the sum of squared difference (SSD) and mutual information (MI) as similarity measures with tagged MR images [3,4]. Tagging patterns can provide additional information for more accurate motion estimation.

We divided the acquired PET data into 8 realizations and used a list-mode Motion-Corrected Ordered Subset Expectation-Maximization (MC-OSEM) PET reconstruction algorithm. Estimated motion was incorporated into the system matrix to reconstruct the list-mode PET data while correcting it for motion [5]. Attenuation correction maps were also deformed by the estimated motion. For simplicity, in this study, attenuation maps were generated by using a simple threshold on images of MR and PET without attenuation correction, followed by a median filtering to fill up hollows of bones. Reconstructed images were smoothed with a Gaussian filter with 1.4 mm FWHM.

Results: With the estimated motion (Figure 1), tagged MR based motion correction with both SSD and MI reduced motion artifacts as compared to uncorrected method and lowered noise as compared to gating method (Figure 2). Our proposed method provides similar image quality to gated PET with 8 times longer scanning time per image (Figure 3 and 4). 18FDG uptake near the white arrows of Gated method was 24% over-estimated compared to the uptake of Gated method with 8 times longer PET acquisition due to high noise and the uptake of Uncorrected method (no motion correction) was 32% under-estimated due to motion artifacts. Our proposed methods achieved 1.2% over-estimated uptake values.

Discussion: Tagged MR based motion correction significantly improved the image quality of the PET data by reducing motion artifacts and lowering noise in our in-vivo free-breathing primate study. With the upcoming whole body MR-PET in early 2011 at our center, in-vivo human study will become possible. For human studies, there are still more challenges.

Indeed, a typical bed position for 18FDG PET acquisition takes about 6 to 7 minutes while our tagged MR acquisition takes, at present, about 24 minutes. One way to improve the acquisition speed will be to use parallel MR acquisition. Another issue is the fading out of tagging patterns. Since human respiratory cycles (~2.5 seconds in our study), it may prove necessary to perform multiple tagging within one respiratory. Tagged MR studies interleaved with navigator can also potentially provide better gating and motion information. Finally accurate attenuation correction with MR for whole body is also challenging and it will require separate MR acquisition [6] or tagging pattern removal strategies [7] / image segmentation for soft tissue, lung, and bones [8].