Simultaneous PET/MR with continuous table motion: The effect of table motion speed on image quality

Harald Braun[1], Susanne Ziegler[1], and Harald H. Quick[1]
[1]*Institute of Medical Physics, University of Erlangen-Nürnberg, Erlangen, Germany*

Target audience: Researchers and physicians working in the new field of PET/MR hybrid imaging.

Introduction: Recently, an innovative acquisition and reconstruction method for simultaneous PET/MR with continuous table motion (CTM) was introduced[1,2]. CTM allows for non-stop PET/MR data acquisition providing seamless field-of-view (FOV) whole-body coverage. In order to develop clinically usable hybrid imaging protocols with CTM, it is necessary to assess how PET and MR image quality change with table motion speed. In this work, MRI protocols that support acquisitions with a moving table and CTM PET data are evaluated with respect to image quality at different table speeds.

Methods: Measurements were performed on a Biograph mMR (Siemens AG, Erlangen, Germany). This hybrid system allows for simultaneous PET and MR data acquisition with a FOV along the z-axis of around 258 mm for PET and 450 mm for MRI.
Two different phantoms were evaluated, one for MR and one for PET imaging: 1. for MR, an “MRI Multi-Purpose Phantom” (Fluke Biomedical, model 76-903) was imaged (Figure 1, top left). This cylindrical fluid filled Plexiglas phantom (diameter: 22.9 cm, length: 11.4 cm) contains different structured inserts that allow evaluation of e.g. SNR, spatial resolution, slice thickness, etc. 2. for PET, a custom-built rectangular fluid filled whole-body phantom (755 x 415 x 180 mm^3) was used[1] (Figure 1, bottom left).
Several MR imaging protocols installed on the scanner support acquisitions with continuous table motion (*syngo* TimCT, Siemens AG): FLASH (2D and 3D), TSE, HASTE and BLADE. The standard clinical protocols as installed on the scanner served as a starting point. Then certain sequence parameters were modified in order to achieve different table motion speeds. In addition to the CTM acquisitions, the sequences were also acquired with the same parameters in multi-station (MS) mode serving as a reference. Table 1 shows the most important sequence parameters for the performed MRI scans. Several image quality measures were evaluated for MRI: SNR, slice thickness, spatial resolution, and artifact behavior.
For PET measurements, the phantom was filled with water and around 400 MBq of the radioisotope ^{18}F. PET data acquisition was then initiated manually via a command line interface to the PET hardware in listmode format allowing using the scanner as in MR-only mode retaining all CTM capabilities. Inherently the scanner does not provide support for CTM acquisitions for PET data. The 2D FLASH sequence was used to control table motion during the PET measurements, as this sequence offers best control of table motion speeds.
The PET data was acquired in MS mode and with CTM using varying table speeds of 0.8, 2.5 and 4.8 mm/s. Rebinning and correction for table motion was performed offline with a custom processing pipeline[2] so that reconstruction could then be performed with the e7-tools (Siemens Molecular Imaging, Knoxville, TN, USA). The e7-tools do not provide inherent support for CTM, so sub-sinograms corresponding to the physical scanner geometry were generated and then reconstructed. For PET scans, SNR, spatial resolution, geometric accuracy, and artifact behavior were evaluated.

Table 1: Measured MR sequences with most important sequence parameters

sequence	orientation	table speed [mm/s]	TE [ms]	TR [ms]	slice thickness [mm]	pixel size [mm^2]
2D FLASH	axial	0.0, 2.0, 4.0, 8.0, 10.7	1.28	150	6.0	1.2 x 1.2
3D FLASH[a]	coronal	0.0, 6.8, 10.2, 13.9	0.98	2.93, 4.00, 6.00	1.2	1.5 x 1.2
HASTE[b]	axial	0.0, 3.6, 7.2, 12.0	80	1000	3.0, 6.0, 10.0	1.3 x 0.9
BLADE[b]	axial	0.0, 1.7, 3.4, 4.8	124	5000	3.5, 7.0, 10.0	1.2 x 1.2

[a] a modification of table speed for 3D FLASH is achieved by varying TR, thus an MS scan for each TR was performed
[b] the table speed for HASTE and BLADE can be modified by changing the slice thickness, thus an MS scan for each slice thickness was performed

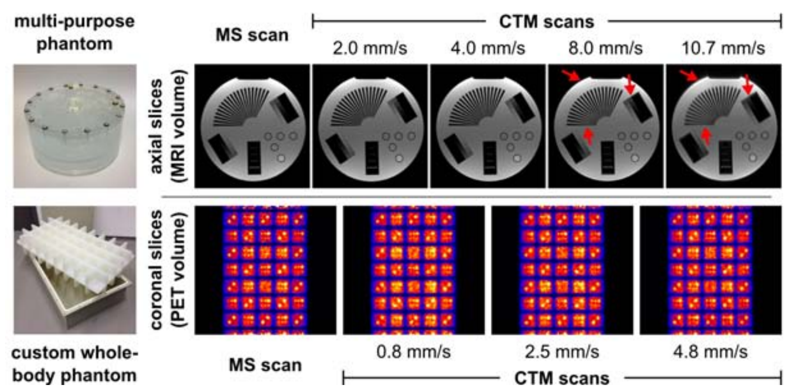

Figure 1: Top: Photography of the Multi-Purpose Phantom and axial slices of the reconstructed MRI volumes acquired with a 2D FLASH sequence at different table speeds showing the insert region. Bottom: Photography of the whole-body phantom and coronal slices of the reconstructed PET volumes at different table speeds showing the resolution insert of the phantom with a voxel size of 4.17 x 4.17 x 2.03 mm^3 (OSEM, 3 iterations, 21 subsets).

Results: MR image quality was found to be mostly superior in MS acquisitions (e.g. SNR was decreased by more than 60% in the 7.2 mm/s CTM HASTE scan). Resolution parameters like spatial resolution and slice thickness were hardly affected by using the CTM approach, however artifacts in phase encoding direction appeared in CTM images that increased with higher table speeds (arrows in Figure 1, top). In contrast, a greater inherent geometric accuracy could be observed in CTM MRI scans as compared to MS MRI scans due to the data acquisition taking place in a more constrained region around the isocenter.
In PET images, spatial resolution was not noticeably affected by table speed (Figure 1, bottom), and resolution drillings down to a diameter of 6 mm could be consistently observed. A slightly crisper delineation of the resolution drillings in the MS scan must be attributed to the greatly reduced randoms fraction due to a later acquisition time. No geometric distortions could be observed in the PET reconstructions.

Conclusion: The CTM approach to simultaneous PET/MR imaging proved to be feasible for various table speeds. While table motion does not seem to have a noticeable impact on PET image quality, the current CTM MR sequences at higher table speeds, however, exhibit a slight decrease in image quality when being directly compared to their MS counterpart. This effect must be balanced to the inherent advantages of CTM data acquisition providing seamless FOV whole-body coverage and simplified workflow when compared to a traditional MS acquisition.
CTM whole-body PET/MR hybrid imaging now has to be evaluated in clinical studies on oncologic patients.

References:
1. Braun H, Ziegler S, Paulus DH, et al. Proc Intl Soc Mag Reson Med. 2012;20:E-Poster #2754.
2. Braun H, Ziegler S, Paulus DH, et al. Med Phys. 2012;39(5):2735-45.