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Fast analytic simulation toolkit for generation of 4D PET-MR data from real dynamic MR acquisitions

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Abstract. This work introduces and evaluates a fast analytic simulation toolkit (FAST) for simulating dynamic PET-MR data from real MR acquisitions. Realistic radiotracer values are assigned to segmented MR images. PET data are generated using analytic forward-projections (including attenuation and Poisson statistics) with the reconstruction software STIR, which is also used to produce the PET images that are spatially and temporally correlated with the real MR images. The simulation is compared with the GATE Monte Carlo package, which has more accurate physical modelling but it is 150 times slower compared to FAST for ten respiratory positions and 7000× slower, when repeating the simulation. The region of interest for mean values and coefficients of variation obtained with FAST and GATE, from 65 million and 104 million coincidences, respectively, were compared. Agreement between the two different simulation methods is good. In particular, the percentage differences of the mean values are: 10% for liver, and 19% for the myocardium and a warm lesion. The utility of FAST is demonstrated with the simulation of multiple volunteers with different breathing patterns. The package will be used for studying the performance of reconstruction, motion correction and attenuation correction algorithms for dynamic simultaneous PET-MR data.

1. Introduction
The improvement of resolution and sensitivity of positron emission tomography (PET) has made apparent the need for motion correction. A critical element for the latter is the accurate representation of real motion vectors. In order to investigate the motion correction with realistic motion vectors, we devise a methodology for generation of simulated PET data with motion estimated from magnetic resonance (MR) images. A Fast Analytic Simulation Toolkit (FAST) has been developed to generate simulated simultaneous PET-MR datasets from acquired MR-derived radioactivity distributions with multiple respiratory positions for multiple breathing patterns and multiple volunteers.

2. Materials and methods
2.1. Simulation toolkit
We use the open-source software package STIR (release 2.1) [1] to generate PET data for the geometry of the Philips Gemini TF PET/CT scanner. The radioactivity (FDG) and attenuation distributions are assigned to segmented images. Multiple gated frames are generated for each
respiratory position. The images are forward projected including attenuation effects to create sinograms.

2.2. Validation of simulation
PET projection data with 65 million and 104 million coincidences, respectively, were generated for one volunteer with FAST and validated against the same number of counts as generated with the Monte Carlo package GATE [2], which has more accurate physical modelling, but it is slower than the analytic method. For both methods, the same reconstruction and correction settings are used: OSEM (10 iterations, 23 subsets) and 3DRP reconstructions including corrections for attenuation and scatter [3] were performed with STIR.

2.3. Demonstration of simulation
A combination of static and dynamic MR acquisitions (35 frames × 0.7 s) is used to segment mainly the lungs from the tissue for multiple frames throughout the respiratory cycle [4]. Lesions of different sizes are inserted manually in one case. The segmented images, incorporated into FAST and PET images, are generated for five volunteers with different respiration pattern (normal and deep breathing).

3. Results
The results were validated against GATE for one respiratory position both visually (figure 1) and quantitatively in terms of regions of interest (ROI) mean values and coefficients of variation (COV) (Figure 2). Visual differences are noticeable in small regions due to the lack of detector modelling in analytic projections by FAST. Examples are demonstrated in figure 3 simulating multiple respiration positions from multiple volunteers with variable anatomy and breathing pattern. PET images correspond to five volunteers illustrated in descending size order from left to right. Two respiration patterns (normal and deep) have been acquired, showing one coronal slice at the end-inspiration and end-expiration for each case. All images relate spatially and temporally to the corresponding MR images demonstrating the fast generation of realistic simultaneous PET-MR dynamic datasets.

![Figure 1](image_url)

**Figure 1.** Analytic versus Monte Carlo simulations for data with two different noise levels (65 million counts and 104 million counts) reconstructed with 3DRP (upper row) and OSEM (lower row).
Figure 2. Upper row: mean ROI values for three regions (warm lesion, myocardium, liver) after reconstruction with OSEM and 3DRP for both GATE and analytic simulations; GATE-OSEM (dark green), Analytic-OSEM (dark blue), GATE-3DRP (light green), Analytic-3DRP (light blue). The error bars show the standard deviation of the mean ROI values. Lower row: COV values after reconstruction with OSEM and 3DRP for GATE and analytic simulations. Simulations are illustrated for two noise levels: 64 million counts (left column) and 104 million counts (right column).

4. Discussion
The analytic simulation method for two different noise levels was compared with GATE simulations at image level showing good agreement in terms of ROI and COV values for OSEM and 3DRP (figure 2). However, in figure 1 some visual difference is observed in small regions such as the three lesions or the myocardium, especially for 3DRP. This is attributed to the mismatch of detector response model in the two packages. The quantitative differences are, in 104 million counts, for OSEM liver 10%, OSEM myocardium and warm lesion (i.e. figure 1 - right side) 19%, while for 3DRP liver are 12%, 3DRP myocardium 17% and 3DRP warm lesion 12%. The COV, which is a measure of noise in the image, is similar for both simulations. In particular, the COV difference between the two methods is for OSEM liver 10%, OSEM myocardium 9%, and OSEM warm lesion 6%, while for 3DRP liver 10%, 3DRP myocardium 15% and 3DRP warm lesion 8%.

Figure 3 illustrates a sample of a PET-MR database of multiple simulated PET studies from real MR acquisitions, with different anatomy, and potentially different physiology. In this figure, two breathing patterns are shown (deep and normal), at two respiration positions for each cycle (end-inspiration, end-expiration). The advantage of using multiple dynamic MR images is that they provide a fast method for creating multiple frames of realistic simultaneous PET-MR data.

5. Conclusions
The importance of the results presented in this investigation is that analytic simulations can replace the time-consuming Monte Carlo simulations for emission tomography. The computational speedup factor is 150× from GATE to FAST and this is a clear advantage of this approach. Moreover, the speedup for repeating multiple realizations is 7000×. This provides the advantage of rapidly producing multiple simulations with different anatomical and physiological circumstances for any kind of clinical PET...
Figure 3. Multiple 3D dynamic PET-MR images with different respiration pattern: normal and deep breathing. In the figures, the two extreme positions of inspiration and expiration are shown. All images are displayed in a fused style with the same colour scale for PET, and grey scale for MR.

scanner. Although there is no claim that FAST can replace the accuracy of GATE or other Monte Carlo packages, it is expected that it will be useful for the evaluation of different reconstruction and correction strategies, especially for simultaneous PET-MR acquisitions.

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References
[1] Thielemans K, Mustafovic S and Tsoumpas C 2006 STIR: Software for Tomographic Image Reconstruction Release 2 IEEE Nucl. Sci. Symp. Conf. Rec. 4 pp 2174-76
[2] Jan S et al 2004 GATE: a simulation toolkit for PET and SPECT Phys. Med. Biol. 49 4543-61
[3] Tsoumpas C, Aguiar P, Nikita K S, Ros D and Thielemans K 2004 Evaluation of the single scatter simulation algorithm implemented in the STIR library IEEE Nucl. Sci. Symp. Conf. Rec. pp 3361-5
[4] Tsoumpas C, Buerger C, King A P, Keereman V, Vandenberghhe S, Schulz V, Schaeffter T and Marsden P K 2009 Simulation of dynamic PET data from real MR acquisitions IEEE Nucl. Sci. Symp. and Med. Imag. Conf. pp 3065-68