Flexible Numerical Simulation Framework for Dynamic PET-MRI

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Synopsis

A numerical simulation framework for dynamic simultaneous PET- MR is presented, which allows for simulated data acquisition of different anatomy with cardiac and respiratory motion and dynamic contrast changes (due to MR contrast agent or PET tracer changes over time). The output of the simulation framework is provided in ISMRMRD and PET interfile raw data format and can be directly used in a range of available reconstruction packages. The reconstructed PET and MR images of the simulated data were compared to an in-vivo patient scan demonstrating that the simulation framework yields realistic data.

Introduction

Realistic numerical simulations of dynamic processes (e.g. respiratory and cardiac motion and dynamic contrast uptake) play an important role in the development of advanced image reconstruction and post-processing methods[1,2,3]. To assess the accuracy of motion estimation and correction techniques, ground truth (GT) motion information is required. For simultaneous PET-MR, MR and PET simulations require hardware-dependent parameters (e.g. MR receiver coil sensitivities or PET detector geometry) to ensure realistic output. Several PET and/or MR simulation frameworks have been proposed, which take physiological motion (e.g. breathing, heartbeat) into account[4,5]. However, they commonly are developed for a very specific task and rely on custom reconstruction software. The input parameters are chosen for a certain application, making them often challenging to adapt for other purposes[4]. In this study, a novel framework to generate simulated dynamic PET-MR rawdata is presented. It provides simultaneous PET and MR rawdata in standardized MR (ISMRMRD) and PET (Interfile) rawdata format[6,7]. Cardiac and respiratory motion and dynamic uptake of contrast agents and PET tracers can be simulated and GT motion information is provided. Chemical shifts between fat and water are also correctly simulated.

Materials and Methods

An overview of the framework design is given in Fig. 1. One input for the simulation is a standardized rawdata file (ISMRMRD format for MRI, Interfile for PET). All hardware-related parameters (TE, TR, flip angle, sequence type, number of receiver coils, k-space trajectory for MR or detector geometry for PET) are taken from the header information and the data part is replaced by the generated simulation data to ensure a valid rawdata file is generated. In this manner, the simulation can emulate the acquisition of already available in-vivo data while simultaneously providing GT information. In addition to the rawdata file a tissue segmentation combined with an XML descriptor detailing the tissue parameters in each voxel of the segmentation (T_1, T_2, spin density, chemical shift for MR, and activity and attenuation values for PET) must be supplied. Based on these parameters combined with those from the input rawdata, the MR simulation generates k-space data using multiple receiver coils, and the PET simulation forward projects the accumulated activity. Motion or contrast changes can be added to the simulation to dynamically modify the segmentation. Each of these contains a model of the dynamic process and its temporal progression which are incorporated into the signal model during the acquisition simulation. An example is given in Fig. 2. These elements are integrated into the open-source software project Synergistic Image Reconstruction Framework[8] (SIRF). It is implemented entirely in C++ employing the functionality of the open-source MR and PET reconstruction engines Gadgetron9 and STIR[10] and provides a Matlab and Python interface for easy usability. Experiments An XCAT-based tissue segmentation and motion model of the thorax and abdomen were used to simulate an FDG-PET-MR exam on a 3T Siemens Biograph mMR. The simulation was performed using rawdata files from a patient data examination with the patient's self-navigator and ECG signal as dynamic signal input[3]. Continuous MR data acquisition during free-breathing was simulated for a triple-echo prototype Dixon-based GRE Golden angle Radial Phase Encoding[11] sequence (T_E=1.2/2.7/4.2ms, FA=10°). The spatial resolution of MR was 1.9x3.2x3.2mm^3 and 2x2.1x2.1mm^3 for PET. Fat-water separation was carried out on the MR data using an iterative chemical-shift approach[12]. The following comparisons were carried out:

- Free-breathing PET and MR acquisition with and without respiratory and cardiac motion correction[3].
- 3D Fat-water imaging for MR-based AC map calculation.
- Evaluation of PET-based motion estimation for different image registration[13].

Results

All simulated images displayed in Fig. 3 to 5 are reconstructions from the rawdata output of the simulation using the same reconstruction software as for the in-vivo data. Fig. 3 demonstrates realistic image quality and motion artefacts. A fat-water separated reconstruction of the simulated MR data, commonly used for attenuation correction estimation in PET, is displayed in Fig. 4. Cardiac motion fields obtained from PET images are compared to GT motion fields in Fig. 5.

Discussion and Conclusion

A framework to simulate realistic PET-MR data with motion and contrast changes was presented. We demonstrated that this framework can be used to evaluate the effect of different types of motion on MR and PET image quality and assess motion-corrected image reconstruction techniques and fat-water imaging methods. Additionally, GT motion information allowed for assessment of motion estimation approaches. This study used the XCAT model but the framework can be used with any available segmentations and motion information. The standardized output enables reconstruction with open-source reconstruction packages, including BART[14], Gadgetron, STIR and other frameworks able to read ISMRMRD or Interfile format.

Acknowledgements

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References

1. Rank, Christopher M., et al. "4D respiratory motion-compensated image reconstruction of free-breathing radial MR data with very high undersampling." Magnetic resonance in medicine 77.3 (2017): 1170-1183.

2. Küstner, Thomas, et al. "MR-based respiratory and cardiac motion correction for PET imaging." Medical image analysis 42 (2017): 129-144.

3. Kolbitsch, C. et al., 2018. Joint PET-MR image registration for cardiac and respiratory motion correction of simultaneous cardiac PET-MR. In Proceedings of Joint Annual Meeting ISMRM-ESMRMB, Paris, France. p. 478.

4. Polycarpou, Irene, Georgios Soultanidis, and Charalampos Tsoumpas. "Synthesis of Realistic Simultaneous Positron Emission Tomography and Magnetic Resonance Imaging Data." IEEE transactions on medical imaging 37.3 (2018): 703-711.

5. Wissmann, Lukas, et al. "MRXCAT: Realistic numerical phantoms for cardiovascular magnetic resonance." Journal of Cardiovascular Magnetic Resonance 16.1 (2014): 63.

6. Inati, Souheil J., et al. "ISMRM Raw data format: a proposed standard for MRI raw datasets." Magnetic resonance in medicine77.1 (2017): 411-421.

7. Todd-Pokropek, A., T. D. Cradduck, and F. Deconinck. "A file format for the exchange of nuclear medicine image data: a specification of Interfile version 3.3." Nuclear medicine communications 13.9 (1992): 673-699.

8. Ovtchinnikov, Evgueni, et al. "SIRF: Synergistic Image Reconstruction Framework."

9. Hansen MS, Sørensen TS. Gadgetron: An Open Source Framework for Medical Image Reconstruction. Magn Reson Med. 2013 Jun;69(6):1768-76.

10. Thielemans, Kris, et al. "STIR: software for tomographic image reconstruction release 2." Physics in Medicine & Biology 57.4 (2012): 867,

11. Prieto, Claudia, et al. "3D undersampled golden angle radial phase encoding for DCE-MRA using inherently regularized iterative SENSE." Magnetic resonance in medicine 64.2 (2010): 514-526.

12. Berglund J, Kullberg J. Three-dimensional water/fat separation and T2* estimation based on whole-image optimization-Application in breathhold liver imaging at 1.5 T. Magn Reson Med. 2012;67:1684-1693.

13. Rueckert, Daniel, et al. "Nonrigid registration using free-form deformations: application to breast MR images." IEEE transactions on medical imaging 18.8 (1999): 712-721.14. Martin Uecker, Frank Ong, Jonathan I Tamir, Dara Bahri, Patrick Virtue, Joseph Y Cheng, Tao Zhang, and Michael Lustig, Berkeley Advanced Reconstruction Toolbox, Annual Meeting ISMRM, Toronto 2015, In Proc. Intl. Soc. Mag. Reson. Med. 23:2486

14. Martin Uecker, Frank Ong, Jonathan I Tamir, Dara Bahri, Patrick Virtue, Joseph Y Cheng, Tao Zhang, and Michael Lustig, Berkeley Advanced Reconstruction Toolbox, Annual Meeting ISMRM, Toronto 2015, In Proc. Intl. Soc. Mag. Reson. Med. 23:2486

Figures

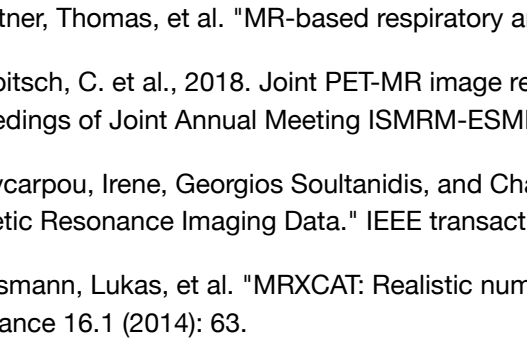

Figure 1. Overview. Standardized rawdata files serve as main input and output. A segmentation together with an XML descriptor defining the MR and PET tissue parameters serves as anatomical input (the XCAT in this case, could be replaced by any segmentation). Based on the simulation parameters and supplied dynamic models the contrast is mapped, motion transformations are applied and data acquisition is simulated. Forward models include coil sensitivities, Fourier transformation and chemical shift for MR and a forward projection including signal attenuation for PET. The parameters and simulated data are stored in the output rawdata file header and data part.

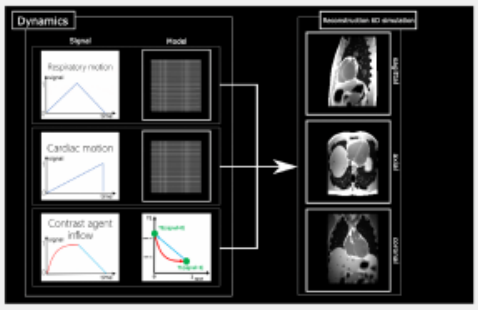

Figure 2. Contrast functionality. Arbitrarily many dynamic processes, either motion or contrast dynamic, can be added to the simulation. The dynamics consist of a signal and a dynamic model. For motion, the models are vector fields, (Dynamics, rows 1 and 2) and for contrast changes, tissue parameter variations (e.g. T1) is mapped over time according to the signal (Dynamics, row 3). The right column shows the reconstruction of the simulation of a cartesian 10-dynamics-acquisition during a synthetic single cardiac and respiratory cycle while contrast agent flows in and out the myocardium. Note the appearance of artifacts due to k-space-data inconsistencies.

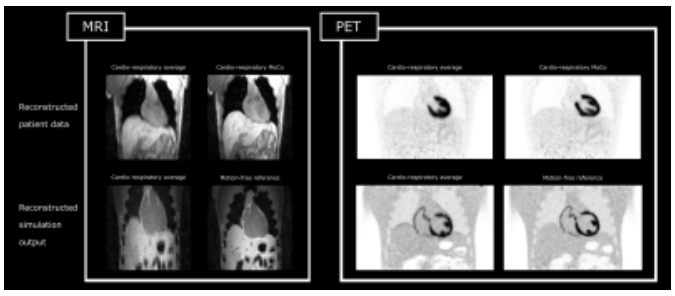

Figure 3. 5D simulation MR and PET. Top row: reconstructioned patient data with motion-averaged, and respiratory and cardiac motion corrected images. Bottom row: reconstructions of rawdata from simulation output in Interfile format with cardio-respiratory motion and without motion. Noise and motion artifacts in the MR and PET reconstructions are comparable to the one in patient data.

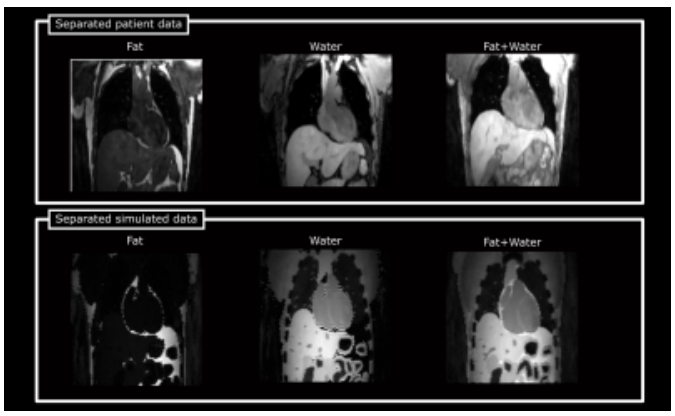

Figure 4. Fat-water separation. The chemical shift simulation allows for a voxel-wise assignment of chemical shift which is incorporated into the signal model. Simulations of multi-echo MR data thus allow for separation into fat and water. Top row: separation of motion corrected patient data. Bottom row: fat-water-separation applied to rawdata from a static simulation. Similar to the patient data, pericardium, abdominal and skin fat separates from the other chemical components of the body.

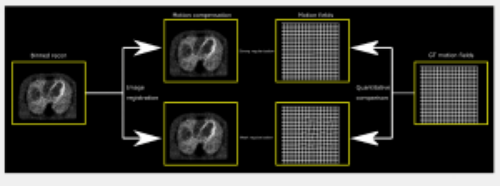

Figure 5. Comparison of motion fields estimated of cardiac motion-resolved PET data (Binned recon) using strong and weak regularization. Both regularization parameters yield comparable motion compensation of the dynamic images. However, comparison with ground truth (GT) motion field show clear benefit (closer to GT) of stronger regularization. GT motion information therefore allows for benchmark testing of image registration and motion compensation algorithms.