CCP PET-MR Exchange Report

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From: Physikalisch-Technische Bundesanstalt (PTB), Berlin

To: University College London (UCL), London (Supervision: Kris Thielemans)

Purpose

The purpose of the exchange was the integration of a numerical simulation framework for dynamic PET-MR data into the Synergistic Image Reconstruction Framework (SIRF).

The exchange was part of a larger effort to implement a simulation framework able to produce MR and PET rawdata in a format which makes simulation results compatible with standard image reconstruction packages such as SIRF. In addition, the simulation framework should also provide ground truth motion information on the displacement of organs due to respiratory and cardiac motion to validate image registration and motion correction methods.

After implementing the MR part of the framework at PTB, Berlin, the simulation was able to simulate the MR acquisition process. The goal of the exchange was to integrate the PET rawdata simulation and to design and implement the software structures to simulate dynamic processes (e.g. respiration, heart beat, contrast uptake) for both modalities.

Activities

General design

In preparation of the exchange, the general design of the framework was developed. A schematic overview is given in Fig. 1.

The design was guided by the principle that simulation results should be easily shareable, i.e. the output of the simulation is provided in a standard raw data format (e.g. ISMRMRD). Hence, the simulation was designed to replace the data part of standardized rawdata formats in PET and MR, while leaving the header information intact. This way, the simulation result can be easily shared and is closer to the real situation of getting rawdata from the scanner and having to process it in a pipeline.

Assignment of tissue parameters (e.g. T1, T2 for MR, or attenuation and activity concentration for PET) to the input tissue segmentation was implemented using an XML file format and corresponding parser.

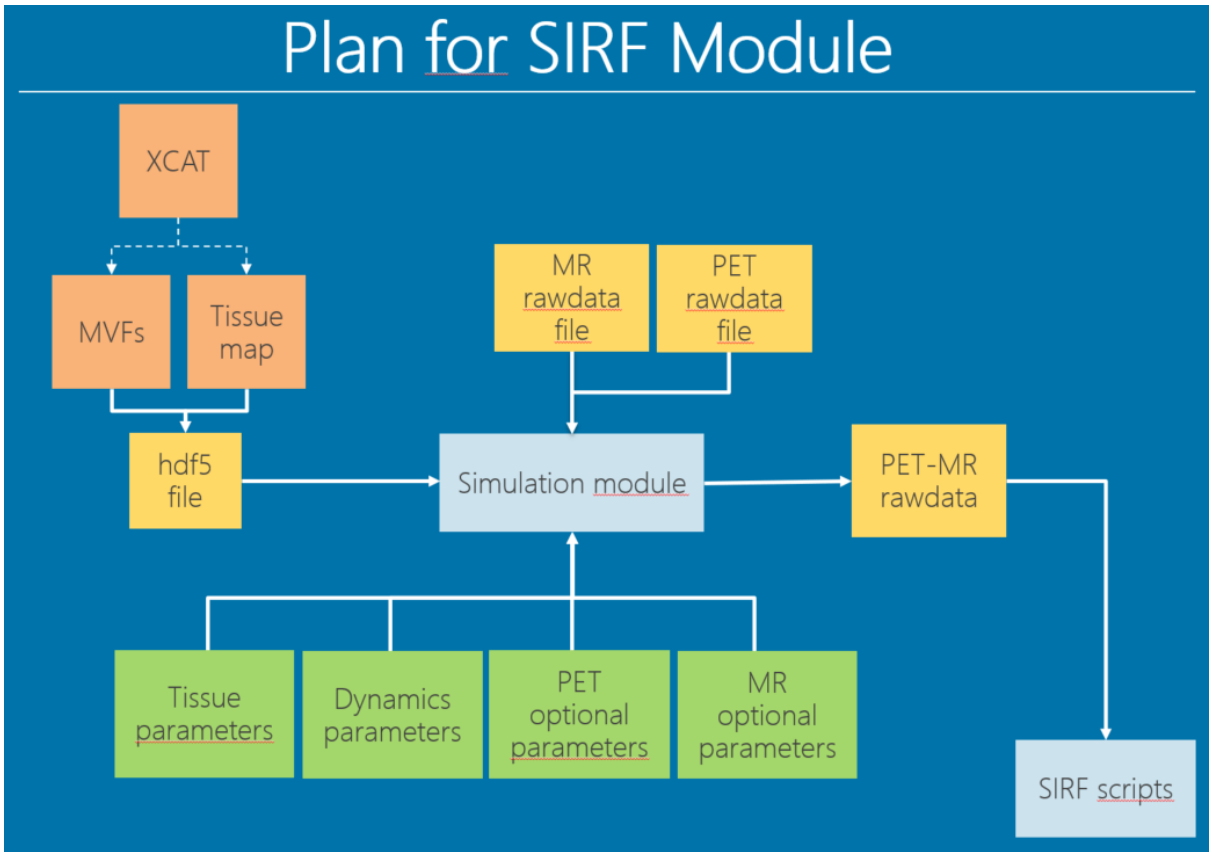

Fig. 1, Simulation framework design. The simulation module takes formatted hdf5 input containing the tissue segmentation and motion vector fields (MVFs). Based on MR and PET rawdata files the acquisition process is simulated. Additional variable parameters enable simulation customization beyond the ones defined in the rawdata files. The output is given in a standardized format and can be reconstructed using SIRF.

Dynamics

Ben Thomas, Richard Brown and Kris Thielemans of UCL helped me design the dynamic end of the framework.

To enable flexible simulation of dynamics a software structure was implemented which contains a signal (i.e. a series of pairs of a time point and associated signal normalized to [0,1]) and rawdata.

A first implementation was done for MR simulations. The dynamic can be manifested as a motion (e.g. cardiac or respiratory motion) or change in tissue parameters, (e.g. T1, T2 values) and hence in image contrast during the acquisition.

This enables the user to add arbitrary dynamics to the simulation, i.e. cardio-respiratory motion with simultaneously changing image contrast can be simulated, effectively enabling an arbitrary number of dynamic processes of type motion- or contrast-variation without structural restrictions.

The UCL group suggested a way to efficiently simulating PET tracer kinetics exploiting the linearity of the acquisition process. That is forward projecting tissue segmentation maps filled with 1 prior to contrast mapping and multiplication by the corresponding contrast after the rawdata generation might save computational effort since the multiplication can be done easily for different respiratory states. In the first step, however, this has not been implemented due to the larger developmental efforts.

PET Simulations

The simulation framework was supplemented with a module simulating static PET data. To this end, the software was implemented assigning PET tissue contrast based on the tissue parameters assigned in the XML file accompanying the segmentation. Also, an attenuation map simulation was implemented. However, the simulation does not contain the simulation of scatter as such a module is not available in SIRF.

Noise

A simple noise generator adding noise to simulated rawdata was implemented. It wrapped STIR functionality to add Poisson noise to PET sinograms, and Gaussian noise to MR rawdata.

Incorporating Simulation into SIRF

A large part of the exchange time was spent on merging the simulation framework with the PET functionality of SIRF (i.e. STIR). Two problems arose, the first being the appearance of linking errors due to circular dependencies in STIR, and the second one due to a namespace confusion resulting in the need to correct large amounts of code for lacking namespace.

A second large effort was undertaken to incorporate SIRFReg, an at the time not yet merged deformation and resampling module in SIRF, to enable motion dynamics.

Results

- Static PET rawdata was successfully simulated by first developing the contrast generating mechanisms for the PET simulation and afterward coupling it to the PET data acquisition model already incorporated in SIRF.
- Noise generation was implemented.
- The dynamic processes software structure was successfully designed and implemented.
- The branch SIRFReg was successfully merged into the simulation which enables simulation of motion during the acquisition.
- In work succeeding the exchange, the dynamics were successfully simulated for MR data.

An application of the dynamic simulation of MRI data can be seen in Fig. 2. The images show *reconstructions* of the simulated rawdata whilst contrast inflows into the vascular system, changing the T1 value of blood, and with a different T1 effect in the left myocardium and atria. The right atrium stays dark, as no contrast inflow was simulated showing how each tissue type can be assigned contrast variations over time during the acquisition independently and how pathologies might be simulated.

Conclusion and Outlook

The exchange program led to a large leap forward in the implementation of the proposed simulation framework. Especially the aid provided by the UCL and SIRF developer group to help correct linking errors and other bugs was of high value and without their insight and help the resolution process would have been prolonged many times over.

Over the course of the exchange, the goals of implementing structures to simulate dynamics, enable motion simulation and the simulation of static PET data were achieved.

However, there are still things missing from the framework which will be subsequently incorporated. These include

- Application of motion and tracer dynamics to PET data.
- Simulation of scatter in PET data. This is dependent on the implementation of a scatter simulation in SIRF itself.
- The implemented code is of modular character and very well tested. However, the use of the array and image data classes in the implementation must be made consistent with the SIRF container classes.
- The speed of the simulation may be improved when simulating many different dynamics.
- After the conclusion of the programming effort in C++, the software needs to be interfaced with Matlab and Python.
- Dynamic simulations will easily enable simulation of attenuation change in lung tissue with respiratory motion.

Acknowledgment

I would like to state that it was very nice to come to London and meet the other people involved with the SIRF project. Everybody was very keen on providing me with help for my tasks and very interested in the project. Especially the technical part of resolving the errors due to linking problems really speed things up and advanced the project very much.

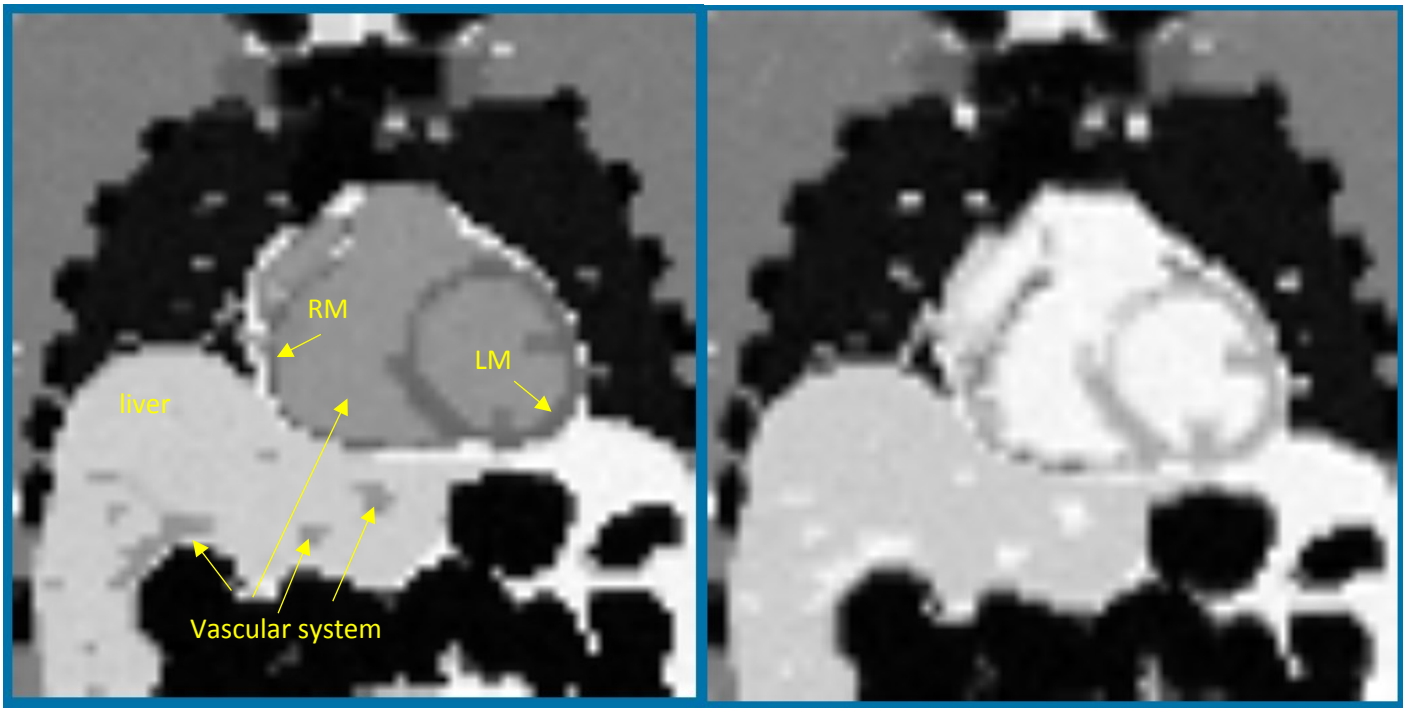

Fig. 2, 7D MRI simulation using the XCAT. Left: reconstruction of simulated rawdata in exhale, with no contrast uptake. Right: reconstruction of simulated rawdata in inhale, with contrast agent uptake in vascular system, and different uptake in the left myocardium (LM) and both atria. No contrast uptake was simulated for right ventricle myocardium (RM) to mimic a pathology. Cardiac motion is also simulated, however both images are in a similar cardiac state and differences are subtle.