CCP SyneRBI Exchange Programme

*Report following exchange with the Institute of Nuclear Medicine,
University College London, London, UK*

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Supervision

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Exchange supervisor: Dr. Kris Thielemans

1 Purpose

Initially written for support of PET and MR data, the Synergistic Image Reconstruction Framework (SIRF) was extended in v3.3.0 to handle SPECT data with parallel-hole collimators using the 'SPECTUB' projector class from the Software for Tomographic Image Reconstruction (STIR). A 3D SPECT system matrix modelling library specific for *pinhole collimators* was recently developed for STIR to enable corrections for the spatially variant collimator-detector response and attenuation by incorporating their effects into the system matrix. The inclusion of the pinhole-SPECT library in SIRF could greatly benefit the research community given the recent advancements in imaging technology, namely in the preclinical setting. This opens up exciting potential for synergistic imaging with pinhole-SPECT systems. Therefore, the objectives of the exchange were as follows:

1. Finalize the integration of the pinhole-SPECT library into STIR,
2. Expand SIRF by adding a new pinhole-SPECT acquisition model, and
3. Investigate the use of SIRF in multi-radionuclide pinhole-SPECT acquisitions.

To elaborate on Objective 3, multi-radionuclide SPECT data reconstructed with conventional energy windows can contain cross-talk which refers to undesired γ-rays detected in an energy window. Cross-talk can be caused by down-scattered photons from higher energies or direct overlap of photopeaks in an energy window. My previous work explored the triple energy window cross-talk correction method to subtract undesired events from the primary window. While the subtraction of presumed cross-talk events improved contrast between simultaneously acquired radionuclides, it also increased noise and reconstruction uncertainty due to compromised count statistics. Thus, a multi-radionuclide reconstruction method was desired to optimize cross-talk correction without compromising count statistics.

2 Summary

A pinhole-SPECT library was successfully integrated and released in STIR v5.1.0 on January 14, 2023, making it the first open-source code available for reconstructing pinhole-SPECT datasets. SIRF was subsequently expanded in v3.4.0 by adding a `PinholeSPECTUBMatrix` acquisition model to allow for the use of SIRF's advanced optimization algorithms when reconstructing pinhole-SPECT data. The extension of SIRF was successfully tested with a proof-of-concept application in multi-radionuclide SPECT using a GATE Monte Carlo model of the Cubresa Spark single-pinhole preclinical SPECT system.

A previously simulated multi-radionuclide acquisition using ^{99m}Tc and ^{123}I in separate capillary tubes was reconstructed in a novel cross-talk correction approach with a simple preconditioned gradient descent algorithm. The objective function to minimize was implemented with the Core Imaging Library (CIL) and constructed with a mixing matrix that defines the relative contribution of counts from a given radionuclide in an energy window. The reconstruction uses the mixing matrix to optimize the distribution of detected γ-rays between the radionuclides. Preliminary results were compared to previously reconstructed images using primary energy window data containing the maximal amount of cross-talk, triple energy window data corrected for cross-talk, and gold standard data free of cross-talk. While the gold standard data yielded a perfect contrast of 1.00 between capillary tubes, the conventional primary energy window contrast was 0.26 $\pm$ 0.15, the triple energy window correction contrast was 0.74 $\pm$ 0.07, and the novel method provided the greatest improvement to cross-talk correction as indicated by a contrast of 0.88 $\pm$ 0.04.

3 Activities

The onsite activities relevant to Objective 1 included:

- General software cleanup followed by commits to STIR including source code, test scripts, LaTeX documentation, and sample files (see UCL/STIR GitHub PR #1100),
- Verification of coordinate systems and general testing with single- and multi-pinhole collimators, and
- Drafting of an article for submission to the Frontiers in Nuclear Medicine journal research topic *Advances in Image Reconstruction for Nuclear Medicine Tomography*.

Objective 2 onsite activities involved:

- Creation of functions to expose STIR's pinhole-SPECT library along with accompanying methods in SIRF (see SyneRBI/SIRF GitHub PR #1154).

While working within the time constraint of the exchange, Objective 3 onsite activities allowed for:

- Understanding Sam Porter's precursor dual-energy SPECT implementation and objective function in SIRF/CIL,
- Building upon the dual-energy SPECT code to enable multi-radionuclide reconstruction using Dr. Thielemans's concept of the mixing matrix, and
- Initial testing of the novel multi-radionuclide reconstruction method using mixing values calculated from the ratio of the total counts in a given energy window to the counts from a given radionuclide in that window using Monte Carlo data.

Aside from the completion of Objectives 1-3, activities made possible by the exchange programme were:

- Presentations on the "Integration of advanced 3D SPECT modelling for pinhole collimators into the open-source STIR framework" at the 2022 IEEE Medical Imaging Conference and STIR User's and Developer's Meeting,
- Participation in various UCL Institute of Nuclear Medicine (INM) physics meetings and social events,
- Regular discussions and meetings with Dr. Thielemans, Dr. Daniel Deidda, and Sam Porter which were crucial for the completion of all objectives, and
- A tour of the National Physical Laboratory (NPL) organized by Dr. Deidda which included a seminar on the "Development of simultaneous multi-probe imaging using a novel SiPM-based preclinical SPECT scanner" to present my overarching thesis work.

4 Results

The main deliverables following the exchange were:

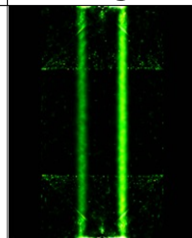
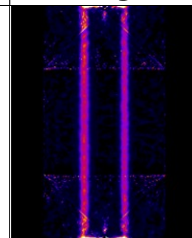
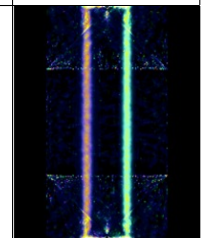
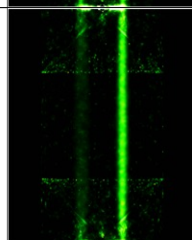
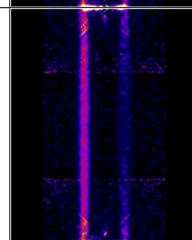
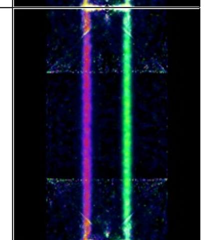
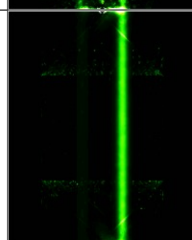
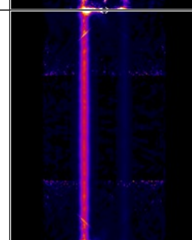
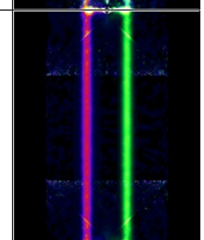
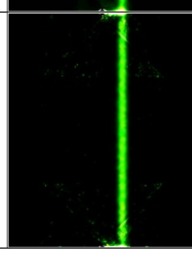
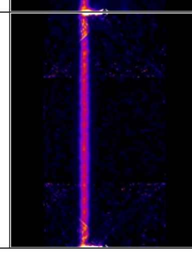
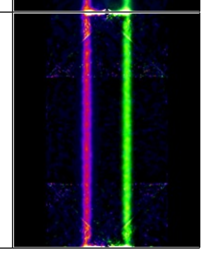
- Integration of the pinhole-SPECT library written by Dr. Carlés Falcón into STIR,
- Expansion of STIR's pinhole-SPECT library to SIRF, and
- Submission of the article "Integration of advanced 3D SPECT modelling for pinhole collimators into the open-source STIR framework" to Frontiers in Nuclear Medicine on December 30, 2022.

Objective 3 showcases the efforts of Objectives 1 and 2 since the simultaneous reconstruction of multi-radionuclide distributions would not be possible here without the successful integration of pinhole-SPECT software into STIR and SIRF. Two capillary tubes containing 5 MBq each of ^{99m}Tc and ^{123}I were simulated in an acquisition with the Spark. These radionuclides present a challenging case with the Spark due to their 19 keV photopeak separation that results in indistinguishable photopeaks. Previous work used STIR to reconstruct radionuclide distributions in a variety of approaches using primary energy window data containing the maximal amount of cross-talk, triple energy window data corrected for cross-talk, and gold standard data free of cross-talk. Radionuclide distributions were reconstructed independently with the OSEM algorithm using 64 projections, four subsets, and 16 subiterations. Previous results were compared to the novel SIRF preliminary results in which the radionuclide distributions were simultaneously reconstructed with a gradient descent algorithm using two energy windows (32 keV wide centered at 135 keV and 167 keV), 64 projections, one subset, and 25 iterations. Table 1 presents the contrast between capillary tubes and maximum intensity projections to illustrate preliminary cross-talk correction results.

5 Discussion and Conclusions

The novel mixing matrix method shows a clear improvement in image quality according to contrast and noise compared to conventional primary energy windows and cross-talk correction with the triple energy window method. This improvement relies on the initial determination of mixing values which can be obtained with Monte Carlo data or carefully measured and independently acquired activity distributions in the fully sampled

Table 1: Contrast and maximum intensity projections from a simultaneous acquisition of ^{99m}Tc/^{123}I in capillary tubes displaced by 10 mm. Images illustrate the improvement in contrast with cross-talk correction.

Reconstruction	**^{99m}Tc**		**^{123}I**		**^{99m}Tc/^{123}I**
	Image	**Contrast**	**Image**	**Contrast**	**Fusion**
Primary energy window		0.40		0.11	
Triple energy window		0.78		0.64	
Mixing matrix		0.91		0.84	
Gold standard		1.00		1.00	

FOV. Although two energy windows were used in this work, multiple energy windows can be used to exploit the spectrum of each radionuclide and utilize counts from multiple photopeaks including those from multi-emission radionuclides such as ^{111}In or ^{177}Lu. However, additional energy windows increase reconstruction time. Given that these results are preliminary and proof-of-concept, there is significant potential to improve the mixing matrix method using other reconstruction algorithms and data subsets, for example. Future work aims to perform a literature review of similar cross-talk correction methods, investigate different priors, improve system matrix energy dependence modelling in STIR, extend the method for quantitative SPECT, and model scatter in the objective function. The current application in preclinical SPECT provides a best-case scenario due to minimal attenuation effects in small-animal imaging.

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