SIRF: Synergistic Image Reconstruction Framewo

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On behalf of CCP PETMR

Abstract- The combination of positron emission tomography (PET) with magnetic resonance (MR) imaging opens the way to more accurate diagnosis and improved patient management. At present, the data acquired by PET and MR scanners are essentially processed separately, and the search for ways to improve accuracy of the tomographic reconstruction via synergy of the two imaging techniques is an active area of research.

The aim of the collaborative computational project on PET and MR (CCP-PETMR), supported by the UK engineering and physical sciences research council (EPSRC), is to accelerate research in synergistic PET-MR image reconstruction by providing an open access software platform for efficient implementation and validation of novel reconstruction algorithms.

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In this paper, we present the first release of the Syn Image Reconstruction Framework (SIRF) software suit CCP-PETMR. SIRF provides user-friendly Pythe MATLAB interfaces to advanced PET and MR reconst packages written in C++ (currently this uses STIR, Softw Tomographic Image Reconstruction, for PET and Gadget MR, but SIRF will be able to link to other reconstruction in the future as appropriate). The software is capa reconstructing images from real scanner data. Both available integrated clinical PET-MR systems (Siemens a are being targeted, and a suitable data format exchange i negotiated with the manufacturers.

Index Terms- Positron Emission Tomography, M Resonance Imaging, Research Software Engineering, So Programming

I. INTRODUCTION

MR images usually provide excellent anatomic de and high soft tissue contrast of the investigated area, b lack sensitivity for imaging probe detection compared images. The latter in turn can clearly show regi abnormality thanks to the distribution of radiotracer whereas normally functioning areas may not be seen Recognition of the complementarity of the two in modalities prompted the development of integrated PET-MR scanners, which as yet has not been paralleled development of an integrated software platform for prodata acquired by such scanners.

CCP-PETMR (https://www.ccppetmr.ac.uk) is a n established in April 2015 with the aim of facilitati investigation of novel synergistic PET-MR reconstruction methods, as investigated by various [1][2], by providing the PET-MR research community software development platform that would be simple to use for research and education purposes and, at th time, powerful enough to be able to handle (in reas time) raw medical data acquired by PET, MR and PI scanners. Both of the available integrated clinical PI systems are being targeted (Siemens and GE) in this so platform, and a suitable data format exchange is negotiated with the manufacturers.

This paper describes the first release of our synd image reconstruction framework (SIRF), an open software platform.

SIRF follows object-oriented principles, which mea most functions callable by a user's code are member fu (or methods) of a platform's objects.

As an example, a Python script using ordered maximum a posteriori one step late (OSMAPOSL) alg for PET reconstruction would involve the following (among others, not shown for brevity):
 # create reconstructor object

- recon = OSMAPOSLReconstruction()
- set reconstructor parameters
- recon.set_num_subsets(num_subsets)
- # prepare reconstructor for use recon.set_up(image)
- # perform reconstruction
- recon.reconstruct(image)

The above exemplifies the simplest level of user's involin PET reconstruction. While it is the most perform efficient way of using the STIR library for reconstr some users may prefer to have more control over compu For example, given an existing iterative algorithm, the wish to run a loop containing the following lines: # perform one iteration recon.update_current_estimate()

- # get current image as Python array img_arr=recon.get_current_estimate().as_array()
- # process image using own processor
- img_arr=my_image_processor(img_arr)

make processed image a new image estimate
recon.set_current_estimate(image.fill(img_arr))

On a still higher level of involvement, the user may a their own or a third-party optimization algorithm

instance, a simple gradient ascent could use a loop: # compute the gradient of objective function

- grad=obj_fun.get_subset_gradient(image,subset)
- # get gradient as Python array
- g=grad.as_array() # get current image as array
- x=image_as_array()
 # define a line search function
 f=lambda t: -obj_fun.get_value(image.fill(x+t*g))
 # maximize f
- t=scipy.optimize.fminbound(f, 0, maxstep)

Similarly, for MR reconstruction, one can use the follow

script that requires no user's input (and no knowledge of reconstruction engine):
 # get access to input data
 input_data=AcquisitionData(input_file)

- # remove oversampling
- processed_data=preprocess_acquisitions(input_data) # create reconstructor
- recon=SimpleReconstruction()
- # reconstruct

image=recon.reconstruct(my_processed_data) A user familiar with Gadgetron's chains is likely to use

efficient, explicit two-gadget chain instead: input_data=AcquisitionData(input_file)

- # create a chain to remove oversampling and reconst recon=Reconstructor(['RemoveROOversamplingGadget', 'SimpleReconGet']) # do all processing
- image=recon.reconstruct(input data)

Again, while this is the most performance-efficient using Gadgetron, some users may prefer to try the acquisition processor in addition to the remov oversampling, in which case the above chain can be sp two, with the user's processing in between: input_data=AcquisitionData(input_file)

PET MR PET MR

. Example reconstruction from simulated PET-MR data (Poisson noise for PET, Gaussian noise for MR, radial sampling with 15 lines). Left ident reconstructions. Right: joint-reconstructions using Quadratic Parallel Level sets prior (after fig 5 in [1]).

II. SOFTWARE DEVELOPMENT STRATEGY

We strive to make our platform useful for as wide a research community as possible. An important choice is the programming language that the users of our platform will need to adopt for their own software development. Two languages and environments that are widely used by researchers with limited software development experience, are MATLAB and Python, basic knowledge of at least one of which we expect our users to have. To handle the conflict between the simplicity of development and the efficiency of the developed software, we use advanced programming languages such as C++ for the actual development and provide simple Python and MATLAB interfaces to building blocks that the users of our platform may use in their own software development. For ease of interfacing into MATLAB, Python and other prospective languages, we wrap C++ code into a C interface.

SIRF is the product of a joint effort of a number of developers from various UK and European Universities. To manage SIRF development efficiently, we use GitHub with its issue tracking, milestones and release management facilities (visit https://github.com/CCPPETMR/SIRF). We also employ the Travis Continuous Integration system: every GitHub commit is compiled and tested automatically, the build/test status is reported in an e-mail and can be checked online at any time.

III. CURRENT SOFTWARE STRUCTURE

SIRF is built upon existing open source software. At present, we employ two well-known libraries: STIR (software for tomographic image reconstruction) [3] for PET and Gadgetron [4] for MR, and we refer to particular reconstruction software packages as 'engines'. Current software structure is reflected by the SIRF file structure, as follows:

RF	:	root
data	:	raw data
examples	:	Matlab and Python demo scripts
src	:	sources
common	:	utilities common to all engines
iUtilities	:	C-interface utilities
xGadgetron	:	Gadgetron extensions
cGadgetron	:	C/C++ interface to Gadgetron
mGadgetron	:	Matlab interface to cGadgetron
pGadgetron	:	Python interface to cGadgetron
XSTIR	:	STIR extensions
CSTIR	:	C/C++ interface to STIR
mSTIR	:	Matlab interface to cSTIR
pSTIR	:	Python interface to cSTIR

create a chain that removes oversampling ap=AcquisitionProcessor(['RemoveROOversamplingGadget'])
remove oversampling

remove oversampling
processed_data = ap.process(input_data)
apply your own data processing
my_processed_data = my_processor(processed_data)
create a reconstruction chain

recon = Reconstructor(['SimpleReconGadgetSet']) reconstruct

image = recon.reconstruct(my_processed_data)

V. INSTALLATION

SIRF is available (under the Apache 2.0 license) at https://github.com/CCPPETMR and the user has the following options for obtaining and installing SIRF (see the SIRF Wiki for detailed instructions):

1. Download a Ubuntu Virtual Machine with all the necessary software (except MATLAB) preinstalled from https://www.ccppetmr.ac.uk/downloads.

2. Linux/MacOS: Download the sources of SIRF, STIR and Gadgetron and build using instructions on the SIRF Wiki.

3. Windows: as above but use Gadgetron installed on VM.

4. Linux/MacOS: Use SIRF-SuperBuild project, based on CMake. The major benefit of this approach is that specific versions of the required dependencies are built (to ensure consistency) without user intervention.

VI. EXAMPLE RESULTS

In this section, we show some preliminary results of reconstructed data of clinical scanners. Support for PET and MR data is mostly complete for the Siemens mMR, while for the GE Signa, only the PET data are handled. PET-TOF support is currently under development [5][6].



Fig 2. Reconstructed images from an anthropomorphic torso phantom experiment for GE SIGNA PET/MR scanner with attenuation (conducted with MR-based Dixon segmentation) and normalisation correction, and without scatter correction using STIR: (top left) OSEM, 28 subsets and 3 iterations (top right) OSMAPOSL with Quadratic Prior, penalty factor 10, (bottom left) OSSPS-PSF, (bottom right) ToF-OSEM acquired from console.

Fig 3. Example images of cardiac patient data acquired on Siemens mMR reconstructed with SIRF. Data from [7].

VII. CONCLUSION AND FUTURE WORK

This software suite will offer a simpler tool for a established researchers to actively and quickly partici the research of PET and MR image reconstruction members of a larger consortium. This should lead to e and robust translation of novel ideas into clinical practic

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