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Motion estimation and correction for simultaneous PET/MR using SIRF

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Abstract

SIRF is a powerful PET/MR image reconstruction research tool for processing data and developing new algorithms. In this research, new developments to SIRF are presented, with focus on motion estimation and correction.

SIRF's recent inclusion of the adjoint of the resampling operator allows gradient propagation through resampling, enabling the MCIR technique. Another enhancement enabled registering and resampling of complex images, suitable for MRI. Further, SIRF's integration with the optimisation library CIL enables the use of novel algorithms. Finally, SPM is now supported, in addition to NiftyReg, for registration.

Results of MR and PET MCIR reconstructions are presented, using FISTA and PDHG, respectively. These demonstrate the advantages of incorporating motion correction and variational and structural priors.

1. Introduction

Multi-modality imaging has enabled a leap forward in medical imaging. The combination of information obtained from two or more physical processes can provide powerful information for diagnosis, disease staging and/or therapy monitoring. One relatively recent example of this is the combination of positron emission tomography (PET) and magnetic resonance (MR) systems into one integrated device. The first modality allows for obtaining quantitative information on function and metabolism *in vivo* by measuring the distribution of molecules ("radiotracers") labelled with positron-emitting radionuclide. The second modality measures magnetic moments of ^{1}H to obtain anatomical and functional information, such as blood perfusion, blood flow velocities or diffusion. The combination of these two modalities has opened a range of new clinical applications and research opportunities, with current emphasis on brain [1–3] and cardiovascular [4] imaging. There is a growing number of these high-end devices (currently eight in the UK).

It is being increasingly recognised and demonstrated that information from complementary modalities, and from multiple time points, can be successfully combined to deliver image quality benefits compared to conventional independent processing. One particular feature of PET/MR is that the acquisitions can be carried out truly simultaneously, giving the opportunity to use information from both modalities to characterise motion, see [5] and [6] for reviews. Many methods exploit the simultaneity of MR and PET acquisitions, and the different properties of the two modalities for mutual benefit. MR generally provides superior structural contrast and better spatial and temporal resolution. Hence, advanced MR sequences combined with iterative reconstruction methods are often used to obtain images for motion estimation via registration. Such techniques allow time-resolved – or more often – gate-resolved (with a "gate" corresponding to a motion state) images to be obtained, with recent advances for joint cardiac and respiratory motion estimation and correction [7,8]. However, the flexibility of MR means that often additional diagnostic acquisitions are required, precluding continuous MR motion acquisition, whereas PET data are available throughout the acquisition. Hence, other methods build motion models parametrised by surrogate signals derived from the PET or interlaced MR navigator data [9]. These models can be estimated on part of the data such that other MR sequences can be used while PET data can still be collected, allowing correction for quasi-periodic motion due to respiration [10] or head movement [11].

From a researcher perspective, implementing these methods or developing new methods is very challenging. Although PET/MR manufacturers provide tools for data manipulation and image reconstruction, these tools may not have all the desired capabilities and are generally not flexible to customisation due to their proprietary nature. There is therefore strong interest in open source software (OSS) that can be used for some or all of the data processing.

Examples of MR or nuclear medicine image reconstruction OSS are given in Table 1.

Software	Modalities reconstructed
Gadgetron [12,13]	MRI
BART [14]	MRI
STIR [15]	PET and SPECT
NiftyPET [16]	PET
RTK [17]	CBCT, CT and in the future SPECT
CASToR [18]	PET, SPECT and some CT support
MIRT [19]	PET, CT, SPECT, MRI (simulated data)

Table 1: Examples of established OSS for biomedical tomographic image reconstruction and the individually supported modalities.

However, none of these packages can reconstruct both PET and MR data, and although it would be possible to use independent reconstruction frameworks, the onus would then be on the user to deal with file types and orientation conventions, as well as potentially registration and resampling. Furthermore, a combined framework also allows for multiple image modalities to be optimised simultaneously for truly synergistic reconstructions, as well as the simultaneous estimation of motion fields.

We are therefore developing an OSS framework called the Synergistic Image Reconstruction Framework (SIRF) [20]. This development is led by the Collaborative Computational Platform on Synergistic Reconstruction for Biomedical Imaging CCP SyneRBI `www.ccpsynerbi.ac.uk`.

SIRF was developed for synergistic PET/MR image reconstruction, aiming to exploit the rich cross-modality information during the reconstruction of both the PET and MR images. SIRF provides researchers with an enabling platform to develop and test novel algorithms on PET/MR patient data, and aims to eliminate the significant technical challenges when interfacing with data from different vendors and proprietary software. SIRF integrates with another OSS called the Core Imaging Library (CIL) [21,22], which provides advanced optimisation and regularisation methods. In addition, SIRF has capabilities for image registration and motion management, as outlined in sec. 2, that are crucial for multi-modality data. Operator Discretisation Library (ODL) [23] is similar in concept to CIL+SIRF, in that it provides a framework for algorithm development relying on other OSS packages for actual computations. However, there is currently no support for complex data (needed for MR), nor registration.

This paper briefly describes additional functionality and the enhanced integration with CIL added to SIRF since the publication of a previous article on the software [20], and describes an application of this work in the context of respiratory motion correction for simultaneously acquired PET/MR. Firstly, the use of a regularised reconstruction of gated MR data is illustrated, allowing derivation of high quality motion fields, which can then be used for a motion-compensated image reconstruction (MCIR) of the MR data with the fast iterative shrinkage-thresholding algorithm (FISTA) to reduce motion artifacts. These motion fields are then used in an MCIR for the PET data together with a convex optimisation algorithm, the primal-dual hybrid gradient (PDHG) algorithm.

2. Motion estimation and correction in SIRF

Many image reconstruction methods can be formulated as an optimisation problem:

$$\hat{x} = \underset{x \in \mathbb{X}}{\arg\min}\, D(Ax, d) + g(x), \tag{2.1}$$

where $x \in \mathbb{X}$ is the discretised image (represented as a vector), $\hat{x}$ is the estimated optimal reconstruction, A is an operator modelling the system (in SIRF, the "`AcquisitionModel`"), d is the measured data (represented as a vector), D is the data fidelity function that measures data goodness-of-fit (often chosen as the negative of the log-likelihood for PET or the L2-norm for MR), and g is a regularisation function imposing desirable properties on the image. In many modalities, the acquisition model is an affine operator:

$$Ax = Kx + b, \tag{2.2}$$

with K the system matrix and b a background term. Details for MR and PET will be given below.

To be able to do motion correction, the data are split into several motion states, usually called "gates", resulting in multiple vectors d_i. There are numerous techniques for performing motion correction. Two of the most common methods are the reconstruct-transform-add (RTA) scheme [24,25], in which correction is performed after reconstruction, and the MCIR scheme [26–31], in which the motion is incorporated into the acquisition model, one for each gate, resulting in the following equation:

$$\hat{x}_{\text{MCIR}} = \arg\min_{x \in \mathbb{X}} \sum_{i=1}^{n} D(A_{\text{MCIR}\ i}\, x, d_i) + g(x), \tag{2.3}$$

with n the number of gates and $A_{\text{MCIR}\ i}$ the acquisition model for the i-th gate (see below) which includes motion information between the gate and a reference position. MCIR therefore finds a single image from all the gates.

Both of the RTA and MCIR schemes assume that the motion is known. One common way to determine the required motion information is to reconstruct motion resolved images (i.e., one for each gate) and then estimate the spatial transformation between the gates using image registration [24,32,33].

As mentioned in Ovtchinnikov et al. [20], registration and resampling in SIRF can be achieved by using the wrapped functionality provided by NiftyReg [34,35], including estimation of rigid, affine and non-rigid deformations (modelled via B-splines). This functionality allows the estimation of motion from reconstructed images of one modality, and then the application of the deformation fields on images from another modality. Since our previous publication, SIRF functionality has progressed further, with specific focus on enabling its use with motion estimation and correction. Some of these enhancements are described below.

A Adjoint resampling

In MCIR, the acquisition model for the motion-corrected image, $A_{\text{MCIR}\ i}$, of a given gate, i, is often computed as a composition of the acquisition model for the image at gate i, $A_{\text{acq}\ i}$, and a warp operator, W_i:

$$A_{\text{MCIR}\ i} = A_{\text{acq}\ i} \circ W_i, \tag{2.4}$$

where $\circ$ is the composition operator (see sec. 2B). Here, W_i is a resampling operator that maps an image at the reference position to the image at gate i. The resampling uses interpolation (such as tri-linear or cubic splines) and is a linear operation in terms of the image values.

Many iterative reconstruction techniques rely on the gradient of the data fitting term in eq. (2.1) with respect to x. Using the chain rule, this can be computed in terms of the gradient of the data fitting term without warping and the gradient of the warping operator. The latter is given by the adjoint operation W_i^*. The reader should note that this operation differs from the inverse, W_i^{-1}, which is used for the inverse transform in RTA and in many other registration applications. In the case of motion warping, the adjoint can be thought of as the switching of the interpolation types (from push to pull or vice versa) when reversing the motion.

The adjoint of the warp operator was implemented in SIRF according to McClelland et al. [36]. The resampling can handle images of different sizes, orientation and voxel size. For a given deformation field, a SIRF resampler object will perform the warp using the "`forward`" method and the adjoint warp using the "`backward`" method (in Python, aliased to "`direct`" and "`adjoint`", respectively, for CIL compatibility):

Adjoint resampling with SIRF

```
import sirf.Reg as reg
resampler = reg.NiftyResample()
resampler.set_reference_image(im_ref)
resampler.set_floating_image(im_flo)
resampler.add_transformation(transformation)
resampler.set_interpolation_type_to_linear()
adjoint_im = resampler.adjoint(im_ref)
```

Tests were implemented in SIRF and CIL to ensure that these operators W_i^* and $A^*_{\text{MCIR}\ i}$ (without background term) were indeed the adjoint of their forward operators. For two linear operators A and A^* to be considered the adjoint of one another, the following equality must hold:

$$\langle Ax, y\rangle = \langle x, A^*y\rangle, \tag{2.5}$$

for all x and y, where $\langle .,.\rangle$ denotes the inner product in the respective space. In the case of motion warping, x and y are both images, but in the case of the acquisition model, x is in the reconstruction space (i.e., an image), and y is in the raw acquisition space (such as a sinogram for PET).

B Enhanced integration with CIL

CIL provides a general optimisation framwework for imaging applications [21,22]. Many of the provided algorithms solve the following problem:

$$\begin{aligned}\hat{x} &= \underset{x\in\mathbb{X}}{\arg\min} f(K(x)) + g(x),\\ &= \underset{x\in\mathbb{X}}{\arg\min} \sum_{i=1}^{n} f_i(K_i(x)) + g(x).\end{aligned} \tag{2.6}$$

The MCIR optimisation problem eq. (2.3) can then be implemented by taking f_i and K_i as the data fidelity and MCIR acquisition model for each gate i, respectively, and g as a regularisation function. As discussed in the previous sec. 2A, for each motion gate of MCIR, one needs to compose the acquisition model with the warp operator. This can be achieved by leveraging the "`CompositionOperator`" from the CIL code base, an example of which is given below. The sum over gates can be written using the block framework scheme implemented in CIL:

MCIR problem

```
from cil.optimisation.operators \
    import CompositionOperator, BlockOperator
Ki_list = []
for i in range(n_gates):
    Ki_list.append(CompositionOperator(acq_models[i], resamplers[i]))

K = BlockOperator(*Ki_list)
```

where "`BlockOperator`" constructs an operator from a list that when applied to an input image, computes the output from each operator in the list and stores the results in a "`BlockDataContainer`". Similar code can be used for the data fidelity term using "`BlockFunction`". The user can then choose the algorithm to solve the optimisation problem by taking into account the "smoothness" characteristics of the objective function. With this consideration, for the MR section of this paper FISTA was used, whilst PDHG was used for the PET component. For a detailed description of the CIL framework, please refer to [21,22].

C Registering and resampling complex images

Since MR images are reconstructed from complex data in the k-space domain, the resultant images are also complex. To be able to perform motion estimation and correction with MR images, it was therefore necessary for SIRF to be able to register and resample complex images. Registering MR images is relatively straightforward – in most cases, the anatomical information is best described by the absolute component of the image, and so SIRF was extended to use the absolute part by default. The ability to resample complex images did not previously exist in NiftyReg, and so this functionality was added to SIRF.

D SPM

Lastly, the rigid registration functionality of the Statistical Parametric Mapping (SPM) [37] is now also available in SIRF. SPM is an OSS that has been designed for the analysis of brain imaging data sequences. Since it was created to process modalities of high temporal resolution, such as fMRI, it is capable of performing rigid registrations over many time points both quickly and to sub-voxel accuracy. Registration with SPM requires Matlab [38], which can be cumbersome if the rest of a workflow has been implemented in another language, such as Python. The wrapping mechanism employed by SIRF (described in greater detail in [20]) is advantageous in this regard; the underlying C++ SIRF code interfaces with the Matlab SPM code. This means that, as per the rest of the SIRF code base, the wrapped SPM functionality can be accessed from Matlab, C++ and Python. Furthermore, by changing just one line of code, the user is able to switch between NiftyReg and SPM registration routines:

Interchangeability of registration packages within SIRF

```python
import sirf.Reg as reg
if use_niftyreg:
    algo = reg.NiftyAladinSym()
else:
    algo = reg.SPMRegistration()
algo.set_reference_image(im_ref)
algo.set_floating_image(im_flo)
algo.process()
TM = algo.get_transformation_matrix_forward()
```

3. Motion correction for cardiac PET/MR

In the following, we present an example of the above-described framework using an *in vivo* cardiac PET/MR scan. A non-Cartesian sampling scheme is presented, which allows for the estimation of respiratory motion. This motion information is then utilised in MCIR to improve simultaneously acquired MR and PET data.

The data used throughout this section consist of a 3:18 min PET/MR scan, which was carried out in a patient 182 min after an injection of 341 MBq of ^{18}F-FDG. The MR acquisition used here was a 3D, three-point Dixon scan (echo times: 1.2, 2.7 and 4.2 ms) with a field-of-view of $400 \times 400 \times 400$ mm^3 and a spatial resolution of 1.9 mm along foot-head and 3.2×3.2 mm^2 in the transversal plane. The readout was oriented along the head-foot direction and the number of acquired readout lines was such that the k-space was oversampled in the phase encoding plane by approximately a factor of 2. In the following, only the first echo was used.

A Respiratory motion estimation and correction for cardiac MR

In this section, a demonstration is given of the estimation of respiratory motion from a 3D non-Cartesian MR scan. The motion information is then used in an MCIR to improve the MR image quality. A new acquisition model was combined with the iterative reconstruction schemes available in CIL to ensure high image quality, even for highly undersampled data. 3D non-rigid motion fields are obtained using spline-based image registration and then applied during image reconstruction to minimise respiratory motion artifacts.

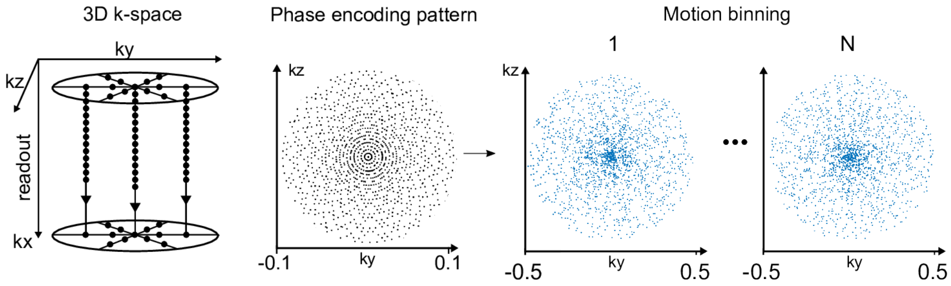

Figure 1: Golden Radial Phase Encoding (GRPE). GRPE combines Cartesian sampling along k_x with radial sampling along k_y and k_z. The Golden radial sampling ensures that the k-space data are well distributed in the $k_y - k_z$ phase encoding space even after splitting the data into N different motion gates (motion binning).

(i) Golden Radial Phase Encoding

Non-Cartesian MR sampling schemes are of great interest for motion-estimation and motion-correction. Even if the data are separated retrospectively into different motion gates (e.g., different phases of the breathing cycle), the k-space data are still well distributed in k-space covering both high and low spatial frequencies. In addition, high image quality can be achieved even from very few acquired k-space points (i.e., high undersampling) utilising iterative image reconstruction schemes. The challenge of non-Cartesian trajectories is that the standard fast Fourier transform (FFT) cannot be applied directly to the data. The non-uniform fast Fourier transform (NUFFT) is required instead, to allow for the transformation of non-Cartesian k-space data to Cartesian image data. Here, as illustrated in fig. 1, a golden radial phase encoding (GRPE) sampling scheme was used [39,40]. This is a 3D acquisition scheme in which frequency encoding (k_x) is carried out along parallel lines. Phase encoding points are obtained along a radial pattern in the 2D phase-encoding plane $k_y - k_z$. All phase encoding points along a radial line are acquired and the angle between two successive GRPE lines is calculated based on the Golden angle of 111.24°. Fig. 1 also shows two examples of the distribution of k-space points after separating it into different motion gates.

The acquisition model A_{GRPE} for this non-Cartesian trajectory implemented in SIRF is, therefore:

$$A_{\text{GRPE i}} = F_i C_c, \tag{3.1}$$

where C is the coil sensitivity map for each coil c and F is the Fourier transform which is used to transform the data of each gate i from image to k-space. For Cartesian sampling schemes, F can be realised by FFT followed by a sampling mask to select the data points for each gate. For the non-Cartesian GRPE, F consists of FFT along the k_x-direction before applying the NUFFT in the

$k_y - k_z$ plane. GRPE allows for the calculation of C from the data itself using the fully sampled k-space centre in the phase encoding plane. The implementations used to realise this acquisition model are wrapped in SIRF from Gadgetron [12,13].

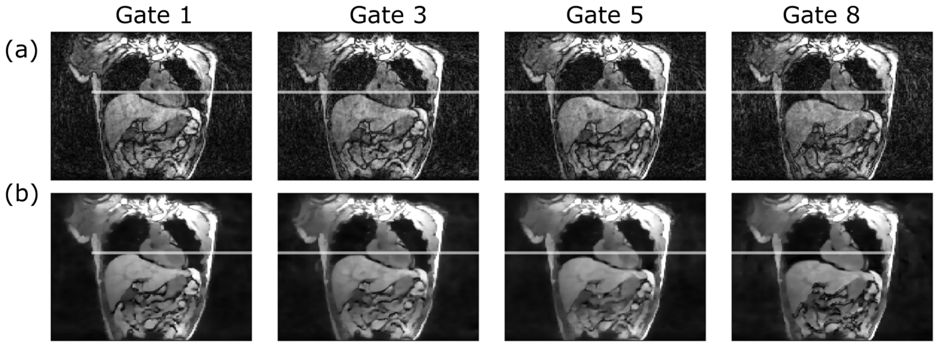

Figure 2: Respiratory-resolved gates reconstructed (row a) without and (row b) with total variation (TV) regularisation. Columns indicate various motion gates. The horizontal line represents the superior-most diaphragm position in the reference gate.

(ii) Reconstruction of respiratory gates

The k-space data were acquired during free-breathing. A self-navigator was extracted from the central k_x-line ($k_y = k_z = 0$). Data were separated into eight different respiratory gates based on the amplitude of the self-navigator [41,42]. A sliding window reconstruction with an overlap of 25% was used, leading to an undersampling factor of approximately three for each gate. Choosing the number of gates is a trade-off between emerging undersampling artefacts and a more accurate motion estimation. Previous studies have shown accurate respiratory motion correction of the liver (where the motion amplitudes exceed those expected in cardiac applications) with as few as five gates [43]. The gates were subsequently reconstructed using the implementation of FISTA [44] in CIL, without and with spatial TV regularisation [45]. We refer to [21] for more information on how to use FISTA via CIL. The MR optimisation problem was mapped to eq. (2.6) using:

- $K_i = A_{\text{GRPE}\ i}$, as described in sec. 3Ai and eq. (2.4);
- the fidelity functions $f_i(x) = ||(K_i(x) - d_i)||^2$ as the least squares function due to the Gaussian noise distribution for MR data, with d_i representing the data for the i-th respiratory gate; and
- g as the TV or total generalised variation (TGV) [46] regularisation function.

Fig. 2 shows four of these eight motion gates comparing both reconstruction algorithms. Changes in the anatomy during the breathing cycle are clearly visible. The TV regularisation leads to suppression of undersampling artifacts and an improved depiction of the anatomy.

(iii) Estimation of respiratory motion fields

The respiratory gates were then used in a non-rigid image registration to estimate the 3D respiratory motion fields, i.e., for each voxel its changes during the respiratory cycle were estimated. This was done via the SIRF wrapper to the NiftyReg spline-based registration algorithm as described in sec. 2.

End-expiration was selected as reference motion gate. Pairwise image registration was carried out to obtain the forward transformation from the reference gate to all other respiratory gates. An example of the estimated motion for a single gate is shown in fig. 3, which is superposed on top of the reconstruction of that gate.

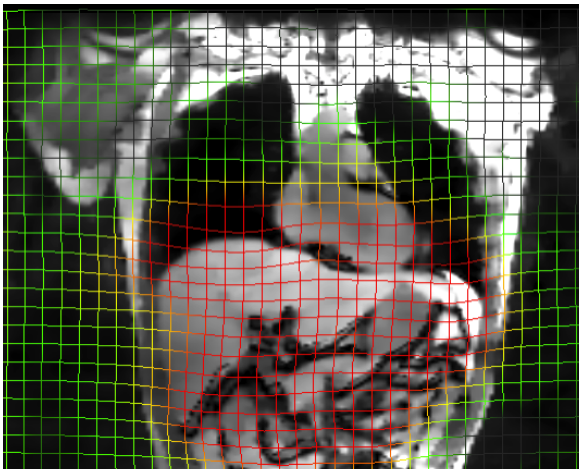

Figure 3: Motion fields estimated for a single gate, represented as a warped Cartesian grid, superposed on top of the corresponding reconstruction of that gate. For emphasis, full inspiration is shown as this has the largest motion compared to the reference state (end-expiration). Here, the colour gradient from green to red describes increasing displacement amplitude.

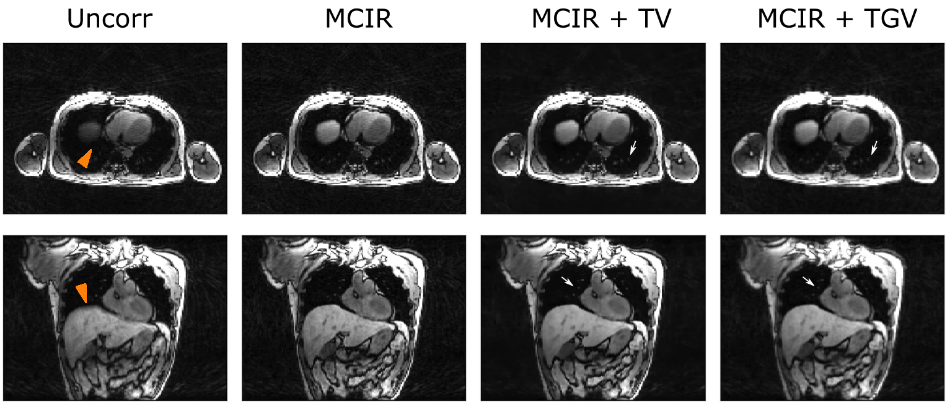

Figure 4: Uncorr: image reconstruction without motion correction with blurring due to respiratory motion clearly visible (orange arrow heads). MCIR: MCIR without regularisation. MCIR+TV: MCIR with TV regularisation. MCIR+TGV: MCIR with TGV regularisation. Regularisation leads to a suppression of undersampling artifacts while preserving even small image features such as lung vessels (white arrows).

(iv) Motion-corrected MR image reconstruction

The MCIR optimisation problem was constructed as in sec. 2B and solved with FISTA. Fig. 4 shows the final MCIR images reconstructed with FISTA without and with additional regularisation. Compared to the uncorrected reconstruction, the minimisation of motion artifacts using MCIR is clearly visible. Further improvement in image quality due to the suppression of residual undersampling artifacts using TV and TGV regularisation can also be seen.

B Incorporating estimated motion into PET reconstruction

As PET/MR acquisitions are simultaneous, the motion fields from the previous section can be used to reconstruct a motion-corrected PET image. In practice, there can be a coordinate transformation between the PET and MR images, for instance due to gantry misalignment. This was estimated by performing a rigid registration between simultaneous MR and PET images, where the PET image was reconstructed without attenuation correction (AC). The MR-derived deformation fields were then transformed into the PET coordinate system.

As mentioned above, the GRPE acquisition was carried out as a three-point Dixon scan. This allowed for the separation of fat and water tissue and the calculation of a segmentation-based AC map [47]. The AC map was obtained from the MCIR MR images to ensure it was also in the reference motion state. The construction of the MR-based AC map was not carried out in SIRF as it required segmentation tools not yet implemented in SIRF.

In PET, A_{acq} is given for gate i as:

$$A_{\mathrm{acq}\,\mathrm{i}} = \beta_i S_i G + b_i, \tag{3.2}$$

where G is the geometric projector (e.g., produced via ray tracing); S_i is the acquisition sensitivity model; b_i is a background term obtained by summing an estimate for the accidental and scattered coincidences; and β_i is the relative time corresponding to gate i, so that $\sum_{\mathrm{i}} \beta_{\mathrm{i}} = 1$. S_i is, in turn, a product of detector and geometric sensitivity and attenuation factors. In the current experiment, the accidental and scatter estimates were computed from the ungated data and $b_i = \beta_i b$. The reader should note this is a simplified assumption that is only approximately valid under small deformations (validated for brain scans in [48]). In other contexts, independent scatter estimates may become necessary. Attenuation factors depend on the motion state. Therefore, for known motion, as is the case with MCIR, attenuation factors are computed by warping the AC maps into the correct position prior to starting the reconstruction, such that S_i is fixed for each gate. The implementations used to realise this acquisition model are wrapped in SIRF from the Software for Tomographic Image Reconstruction (STIR) [15].

The warped forward model $A_{\mathrm{MCIR}\ i}$ is defined in eq. (2.4) and (3.2). We model the data d_i corresponding to gate i as Poisson variables. As the Poisson log-likelihood can be written in terms of the Kullback-Leibler (KL) divergence (up to constant terms), the MCIR problem for PET corresponds to solving eq. (2.3) with D as the KL divergence and $g = \|\nabla \cdot\|_{2,1}$ as the isotropic TV.

In order to reformulate the problem as an instance of the general framework in eq. (2.6), let us define K_i as the linear part of $A_{\mathrm{MCIR}\,\mathrm{i}}$, that is to say $K_i = \beta_i S_i G \circ W_i$, and f_i, g as:

$$\begin{aligned} f_i(y) &= \mathrm{KL}\left(d_i, y + b_i\right), \\ g(x) &= \alpha \|\nabla x\|_{2,1}. \end{aligned}$$

For a convex function f, the convex conjugate function is defined as $f^*(u) = \sup\limits_{x} \langle u, x\rangle - f(x)$. The minimisation problem eq. (2.6) can be solved via the saddle-point problem:

$$\arg\min_{x} \sup_{(y_i)} \sum_{i=1}^{n} \langle K_i x, y_i \rangle - f_i^*(y_i) + g(x), \tag{3.3}$$

which introduces the dual variable $y = (y_1, \ldots y_n)$. In order to solve eq. (3.3), we use the PDHG algorithm [49]. PDHG solves eq. (3.3) by alternatively minimising with respect to the primal variable x and maximising with respect to the dual variable $y = (y_1, \ldots, y_n)$, which it achieves using the proximal operators of g and of f^*. While the proximal operator of the Kullback-Leibler divergence convex conjugate admits an explicit expression, this is not the case for the proximal operator of the TV regulariser, which is approximated with FISTA in inner iterations.

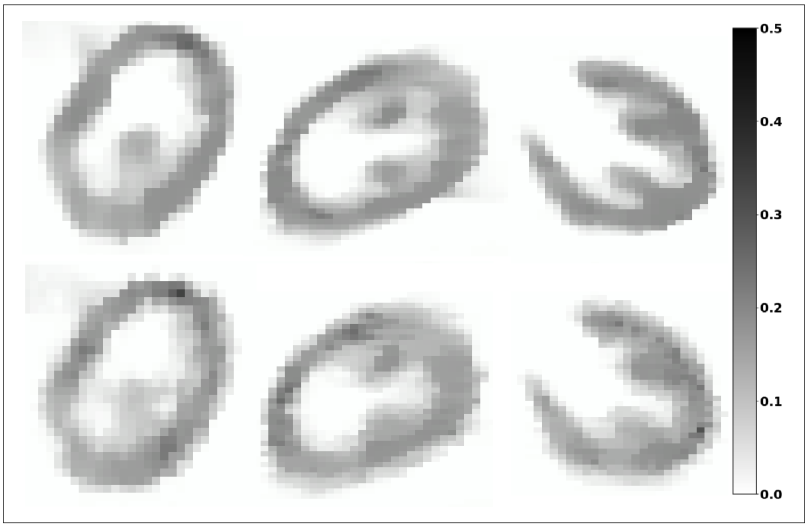

Figure 5: Comparison of TV-regularised PDHG reconstructions with (top) and without (bottom) motion correction for the axial (left), sagittal (centre) and coronal (right) views. Both PET reconstructions were run for 1000 iterations with regularisation strength of $\alpha = 3$. In the motion corrected case, a sharpening of the papillary muscles can be seen.

In order to observe the effect of motion correction, we compare the reconstructions obtained with the forward models $A_{\text{acq}\ i}$ and $A_{\text{MCIR i}} = A_{\text{acq}\ i} \circ W_i$. The reconstructions were performed under identical algorithms schemes (PDHG with the same number of iterations, amount of regularisation and step-size parameters). The results are shown in fig. 5. The effect of respiratory motion correction is that the cardiac structures are sharper, particularly at the level of the papillary muscles. However, these results are preliminary and need further optimisation of regularisation and optimiser settings. For example, we found that the number of iterations required to obtain images of good visual quality was higher in the MCIR context than without gating. This will be studied in future work.

4. Conclusion and Outlook

In this paper we have presented recent improvements of SIRF regarding PET/MR, concentrating on motion correction and in particular MCIR. We have shown how respiratory gates can be reconstructed from a non-Cartesian 3D MR scan and how non-rigid respiratory motion fields can be obtained using the NiftyReg integration in SIRF. These motion fields can then be used for MCIR of both MR and PET. The integration of CIL with SIRF allowed for the use of regularised FISTA and PDHG optimisation schemes.

The modular nature of SIRF and CIL enables rapid prototyping of algorithms. We have demonstrated how MCIR can be implemented in a scheme that is very similar across different imaging modalities. This allows ideas from different communities of imaging and inverse-problem scientists to be conveniently shared. Furthermore, we showed how the consistent interface between SIRF and CIL allows individual components, including regularisers and optimisers, to be interchanged and compared while keeping the remaining components static. This enables researchers to optimise methods for their application.

While we have only utilised spatial regularisation for the reconstruction of the respiratory gates, the application of additional regularisation along the motion dimension should further improve image quality and hence motion accuracy [50,51].

The simultaneous data acquisition and the motion correction using the same motion transformation for PET and MR ensures their optimal spatial alignment. Therefore, the information of one modality could also be applied as guided regularisation for MCIR of the other modality to further improve image quality [52–55], and ultimately joint (or "synergistic") reconstruction [56–59].

In this paper, motion estimation has been carried out as a separate step to MCIR and requires the reconstruction of motion-resolved gates. Although TV regularisation ensured high image quality even for high undersampling factors of the GRPE MR data, this approach still requires that sufficient data are available in each gate to allow an accurate motion estimation. In addition, the information about respiratory motion available from PET was not utilised at all for motion estimation. Registration of multi-modal data has been shown to be beneficial when correcting for both respiratory motion and cardiac contraction [7]. Combining MCIR and motion estimation into a single optimisation would overcome these limitations. By carrying out the reconstruction of a motion-corrected MR and PET image while also optimising the joint motion fields would provide the optimal synergistic use of the simultaneous PET/MR acquisition [26,60–65]. To achieve this, the calculation of gradients with respect to the motion field parameters (e.g., spline weights for the spline-based motion fields used in NiftyReg) is required and will be part of future work on SIRF.

While the use of OSS for prototyping of reconstruction algorithms provides many benefits, there are also limitations to SIRF when compared with vendor's proprietary software. Vendors have often highly optimised their particular algorithms for their system. When using SIRF, the user will need to determine appropriate parameters and hyperparameters, e.g., for regularisation strengths but also for physical properties like system resolution if performing resolution modelling. Similarly, the engines used by SIRF have been optimised for research exploration rather than performance. Hence, computation time when using SIRF is longer than when using vendor software.

There is increasing interest in integrating deep learning (DL) into PET reconstruction [66]. Common DL frameworks include PyTorch [67] and Tensorflow [68] in Python, as well as Matlab's deep learning toolbox [69]. Furthermore, the use DL for image registration is a field that is rapidly expanding [70,71], and which can be leveraged by SIRF. These frameworks can all be used in conjunction with SIRF to implement and explore state-of-the-art methods.

New multi-modality systems are now available or under development, for instance SPECT/MR [72] and (non-simultaneous) SPECT/PET/CT such as the recent Mediso AnyScan clinical system and pre-clinical Bruker Albira Si, enabling opportunities for multi-radiotracer studies. At the same time, top-of-the-range multi-modality systems are expensive and combining single-modality scans from different time-points and systems can provide more cost-effective solutions and faster worldwide adaptation, which again demands the ongoing developments in spatial alignment. While imaging research and software methods are both developing rapidly, the challenging opportunity for cross-modality synergistic methods remains open. We intend to continue to develop SIRF for researchers to be able to exploit synergy in multi-modal, multi-contrast, multi-time point information for a greater range of applications.

Ethics. Patients gave written, informed consent to take part in the study and to undergo a PET/MR scan after the original PET/CT scan without any additional injection of a radionuclide tracer. The study was approved by National Research Ethics Service Committee at King's College London (No. 15/LO/0978).

Data Accessibility. Reconstruction scripts and installation instructions for the specific versions of code used in this research can be found in our contributor's GitHub page. This resource includes information of supported python versions and CI/CD testing.

Authors' Contributions. RB developed PET and registration functionality, co-developed the PET MCIR reconstruction script, ran PET experiments and drafted part of the manuscript. EPas developed the interoperability between SIRF and CIL, co-developed the PET and MR MCIR reconstruction scripts and ran the PET reconstructions on the STFC cluster. EPap co-developed the PET MCIR reconstruction script. CK and JMa developed the GRPE acquisition model, the MR MCIR reconstruction script, carried out the MR reconstruction and drafted this part of the manuscript. RN helped with the development of used MR

sequences with CK. CD co-developed the PET MCIR reconstruction script, carried out PET experiments and drafted this part of the manuscript. JMc and BE implemented adjoint image resampling functionality. EO developed the core of the SIRF code base. CdCL aided with code infrastructure, example scripts, testing and continuous integration. AG developed code for handling patient orientation as well as aiding draft the PET and motion correction sections of the paper. MJE aided with mathematical theory behind PDHG. KT provided general oversight of the project and software and drafted part of the manuscript. All authors read and approved the manuscript.

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