Nuclear Instruments and Methods in Physics Research A 734 (2014) 162–165

Contents lists available at ScienceDirect

Nuclear Instruments and Methods in Physics Research A

journal homepage: www.elsevier.com/locate/nima

Framework for the construction of a Monte Carlo simulated brain PET–MR image database

B.A. Thomas [a,*], K. Erlandsson [a], I. Drobnjak [b], S. Pedemonte [b], K. Vunckx [c], A. Bousse [a], A. Reilhac-Laborde [d], S. Ourselin [b], B.F. Hutton [a,e]

[a] Institute of Nuclear Medicine, UCL, London, UK
[b] Centre for Medical Image Computing, UCL, London, UK
[c] Department of Nuclear Medicine, Katholieke Universiteit Leuven, Leuven, Belgium
[d] Australian Nuclear Science and Technology Organization, Sydney, Australia
[e] Centre for Medical Radiation Physics, University of Wollongong, NSW, Australia

ARTICLE INFO

Available online 14 September 2013

Keywords:
Positron emission tomography
Partial volume correction
Monte Carlo simulation
Brain PET–MR

ABSTRACT

Simultaneous PET–MR acquisition reduces the possibility of registration mismatch between the two modalities. This facilitates the application of techniques, either during reconstruction or post-reconstruction, that aim to improve the PET resolution by utilising structural information provided by MR. However, in order to validate such methods for brain PET–MR studies it is desirable to evaluate the performance using data where the ground truth is known. In this work, we present a framework for the production of datasets where simulations of both the PET and MR, based on real data, are generated such that reconstruction and post-reconstruction approaches can be fairly compared.

1. Introduction

Positron emission tomography (PET) images suffer from a degrading phenomenon known as the partial volume effect (PVE). PVEs are caused by the finite spatial resolution of the scanner and result in a blurring of the observed data. Techniques that correct for PVEs are known as partial volume correction (PVC) methods [1]. Typically these are performed either during reconstruction or as a post-reconstruction process. The term 'resolution recovery' can also be used to refer to PVC, although this is ordinarily in reference to reconstruction-based methods.

Cross-comparisons of PVC approaches tend to evaluate either within-reconstruction or post-reconstruction methods. To compare across these different approaches, and validate the use of the techniques in brain PET, it is important to have ground truth information which does not favour either side. In this paper, we propose a methodology for the creation of Monte Carlo simulated brain PET, where both the PET and required MR data are generated in such a manner that fair cross-comparisons can be undertaken.

2. Materials and methods

2.1. Patient data

In order to simulate brain PET–MR data, a real reconstructed static brain PET image and associated T1-weighted MR image is required. Optionally, if CT data is available for the subject, this can be used to simulated the effects of attenuation, otherwise attenuation coefficients are assigned to tissues based on the segmentation of the T1-weighted MR.

The patient data used in this work consisted of a static 10-min 18F-FDG epilepsy study and T1-weighted MR image that were simultaneously acquired on a Siemens Biograph mMR and a CT that was previously acquired.

2.2. Image pre-processing

The CT data was rigidly registered to the T1-weighted MR using the block matching technique of Ourselin et al. [2]. The reconstructed PET was rigidly registered to the MR using the same registration method. This registration was performed to remove any patient motion due to the duration of the PET acquisition being longer than the MR. A three tissue class segmentation was performed using NiftySeg [3] to generate probabilistic grey matter (GM), white matter (WM) and cerebro-spinal fluid (CSF) masks. The resulting segmentations were then passed as input to the MR simulator POSSUM [4]. Two T1-weighted MR images were

* Corresponding author. Tel.: +44 20 344 70513.
E-mail address: benjamin.thomas2@uclh.nhs.uk (B.A. Thomas).

0168-9002/$ - see front matter © 2013 Elsevier B.V. All rights reserved.
http://dx.doi.org/10.1016/j.nima.2013.08.063

generated with POSSUM, both simulating different acquisition parameters (TE=5 ms, TR=500 ms; TE=14 ms, TR=540 ms) to produce subtly different contrasts between GM and WM in the two images. The former is used during the formation of the *ground truth* (GT), with the latter being utilised for correction purposes. 5% Gaussian noise was added to each of the simulated datasets. The reason for creating two MR images is to ensure that there is an independence between the generation of the GT and the data utilised to apply the correction methods. This independence is enforced through the use of two different segmentation methods (see Section 2.4), one applied to each simulated MR image.

2.3. Ground truth generation

The aim of this work was to simulate realistic PET uptake that does not make assumptions about the distribution. Assigning uniform uptake within anatomical regions unfairly biases results towards PVC techniques that assume regional uniformity. However, to simulate emission data from real patient data, it is necessary to correct for the spatial resolution in the PET data. To achieve this post-reconstruction, anatomy-based PVC technique, the Müller-Gärtner [5], is applied to the reconstructed patient PET data

$$f_G(x) = \frac{f_O(x) - [C_W p_W(x)] \otimes h(x) - [C_C p_C(x)] \otimes h(x)}{p_G(x) \otimes h(x)}, \quad (1)$$

where f_O is the observed image, f_G is uptake in the GM, p_G, p_W and p_C are probabilistic masks (where $p(x) \in [0,1]$) of the GM, WM and CSF space found by segmenting the patient MR image (the first of the POSSUM simulations), C_W is the estimated WM mean value, C_C is the estimated CSF mean value (usually assumed to be zero) and h is the point spread function (PSF) of the scanner. The PVC was applied using a Gaussian PSF of 6 mm full-width at half maximum.

C_W is typically estimated from a WM region thought to be relatively free of PVEs, such as the centrum semiovale. A sphere (1.5 cm diameter) was placed in this region in order to calculate C_W. The MG technique produces a voxel-wise correction in GM voxels only. To create the GT (f_{GT}) for simulation, a WM region was added to the MG-corrected data by multiplying every voxel in the p_W mask by the value obtained for C_W

$$f_{GT}(x) = f_G(x) + [C_W p_W(x)]. \quad (2)$$

2.4. Data simulation

The GT was used as the activity distribution for Monte Carlo simulations using the PET simulator PET SORTEO [6]. Multiple 2D PET acquisitions of a 10-min (40 min post-injection) FDG study for an ECAT Exact HR+ were generated using SORTEO, including the effects of scatter, randoms and attenuation. The resultant sinogram data can then either be reconstructed using techniques such as FBP or OSEM for use with post-reconstruction PVC techniques or used directly by reconstruction-based PVC methods. For post-reconstruction approaches that require segmented MR data, FreeSurfer [7,8] was used to segment and parcellate the second MR image generated by POSSUM. Whereas, reconstruction-based methods can incorporate the second MR image directly into the reconstruction process.

The complete framework is shown in Fig. 1.

3. Results

The images of the segmented patient MR using NiftySeg and the simulated MR images generated by POSSUM can be seen in Fig. 2. The application of the MG correction to the patient PET data is shown in Fig. 3. An example of two PVC approaches (one reconstruction-based and one post-reconstruction) applied to the simulated dataset [9] can be seen in Fig. 4. The reconstruction-based method is the asymmetric Bowsher prior [10] and the post-reconstruction method is iterative Yang [1].

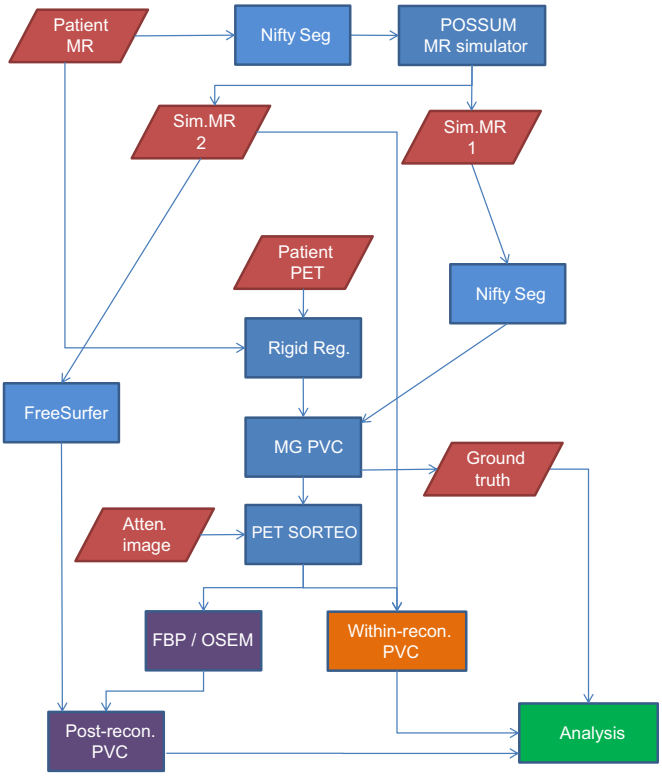

Fig. 1. Flow chart representation of the framework. Red boxes represent images, blue are processes that generate the simulated data, purple are the steps required to apply post-reconstruction PVC and orange represents the reconstruction based techniques. (For interpretation of the references to color in this figure caption, the reader is referred to the web version of this paper.)

4. Discussion

This work reports a methodology for the generation of Monte Carlo brain PET data which facilitates the comparison of PVC techniques. The framework uses real patient data to form GT by applying PV-correction. As demonstrated in Fig. 2, POSSUM can simulate T1-weighted MR images with different acquisition parameters. This is advantageous as it allows multiple segmentations to be generated from the original subject MR image. Independent segmentations are therefore available for the synthesis of the GT and for the application of PVC. This independence removes a potential bias where a perfect segmentation can result in an over-ideal situation for some PVC methods that rely on segmentation. In reality a segmentation will not exactly match the GT and the use of POSSUM in this framework, combined with two different segmentation techniques (NiftySeg and FreeSurfer), aims to recreate this.

The application of the MG PVC technique allows the GT to be derived from real data. The advantage is that no assumption is made about the PET distribution in GM, such as regional uniformity. Were the ground truth to be created with piece-wise constant activity within anatomical regions, PVC techniques that used this assumption would potentially outperform approaches that do not, purely due to the way the GT was created. The MG method will correct one tissue compartment only. In the proposed