Fusing PET and MRI data using super-resolution track-weighted imaging

Fernando Calamante[1,2], Young-Don Son[3], Jacques-Donald Tournier[1,2], Taek-Hyun Ryu[3], Se-Hong Oh[3], Alan Connelly[1,2], and Zang-Hee Cho[3]

[1]Brain Research Institute, Florey Neuroscience Institutes, Heidelberg, Victoria, Australia, [2]Department of Medicine, University of Melbourne, Melbourne, Victoria, Australia, [3]Neuroscience Research Institute, Gachon University of Medicine and Science, Incheon, Korea, Republic of

Introduction: Positron emission tomography (PET) is arguably unique in its ability to provide molecular information about the brain by using a number of specific radioligands. For example, ^{11}C-DASB is a radioligand having a high affinity for serotonin transporters, which regulates sleep and wake, mood, feeding and other essential aspects of normal daily function. However, a major limitation of PET is related to its relatively low spatial resolution. For this reason, PET studies are commonly performed and interpreted in combination with co-registered high-resolution MRI or CT data, and therefore dual PET-CT and PET-MRI systems are becoming increasingly popular. However, in these studies the information is commonly fused by a simple image overlay.

The technique of super-resolution track-weighted imaging (TWI) [1] was recently proposed as a generalized framework to extend the principles of super-resolution track-density imaging (TDI) [2]. In TWI, the information from whole-brain fibre-tracking (the so-called tractogram) is combined with a reference image, to generate a super-resolution track-weighted version of that image. In this study, we apply the TWI formalism to PET data to generate a *super-resolution track-weighted (TW) PET map*. These maps encode the molecular information from PET and display the super-resolution characteristics of the TWI method.

Methods: *Data acquisition:* MRI and PET data were acquired on a healthy volunteer using a 7T Siemens MRI scanner and a high-resolution research tomograph (HRRT) PET system [3]. Diffusion MRI sequence: single-shot DW-EPI (TE/TR=83/6000ms, 1.8mm isotropic resolution, 64 DW-directions, b=2000s/mm^2, 3 repeats); the diffusion data were corrected for geometric distortions using a combined two dimensional PSF mapping method [4]. ^{11}C-DASB data: a bolus injection of 555 MBq of ^{11}C-DASB was administered and data were acquired in a dynamic scan mode for 90min. Note that these MRI and PET data are co-registered because the 2 systems are coupled via a shuttle bed [3].

Fibre-tracking: Whole-brain fiber-tracking was done using a modified version of the MRtrix software (http://www.brain.org.au/), which includes constrained spherical deconvolution to model multiple fiber-orientations [5], and probabilistic streamlines (6 million tracks) using the 2nd order integration over fibre orientation distributions (iFOD2) algorithm [6].

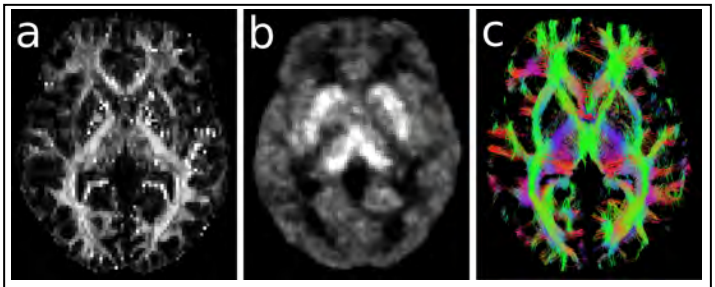

Fig.1: Axial examples of MRI and PET data. (a) The fractional anisotropy (FA) map illustrates the spatial resolution of the acquired diffusion MRI data. (b) ^{11}C-DASB PET image. (c) Example of whole-brain fibre-tracking results, displayed as an axial 1.8mm slab. The colour-coding indicates the local fibre orientation (red: left-right, green: anterior-posterior, blue: inferior-superior). For ease of visualisation, the results from only 100,000 tracks are displayed.

Track-weighted PET: Our particular application of TW-PET involves the following steps: (*i*) the mean PET image intensity along each track j in the tractogram is calculated ($meanPET_j$). (*ii*) For each TWI grid element (note that the grid element can be smaller than the acquired voxel size data [2]), the mean of the $meanPET_j$ values for all the tracks traversing the grid element is computed. (*iii*) This value is assigned as the intensity of the grid element in the TW-PET map. The intensity on the TW-PET map therefore represents the mean PET intensity value for the tracks in the grid element, and therefore 'propagates' the PET information along the corresponding tracks. It will therefore not only visualise the areas with high intensity in the PET image, but also their structural connections. In this study, super-resolution TW-PET maps were generated using a 250µm isotropic grid-size. For anatomical detail, super-resolution TDI maps (250µm resolution) were also calculated from the same whole-brain tractogram [2].

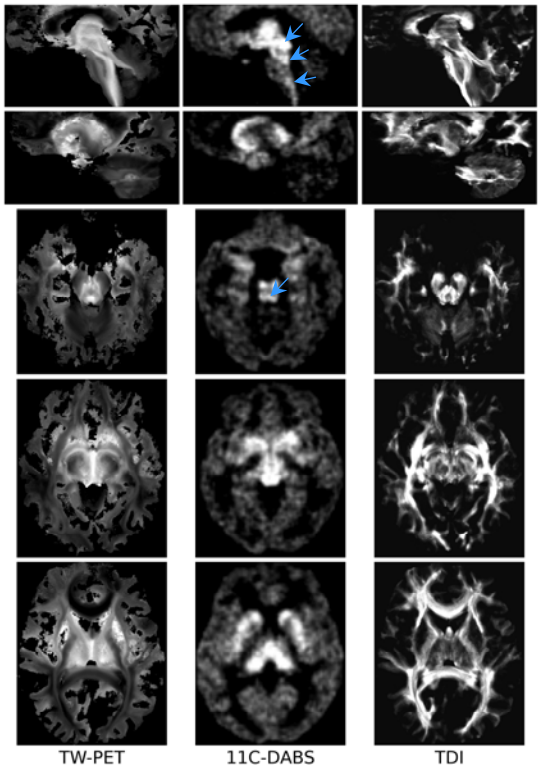

Fig. 2: Examples of super-resolution TW-PET maps (1st column) and corresponding ^{11}C-DASB PET (2nd column). For anatomical reference, the 3rd column shows the corresponding super-resolution TDI maps. The first 2 rows show example sagittal slices; the remaining rows show illustrative axial slices. The arrows indicate the raphe nuclei, where the serotonergic centres are located.

Results: Fig. 1 shows an example of the acquired MRI and PET data, as well as the whole-brain fibre tracking results. Fig. 2 shows illustrative examples of the TW-PET maps (sagittal and axial slices). In particular, the serotonergic pathway can readily be visualised on the sagittal slice through the raphe nuclei (top row).

Discussion: We have presented the first combination of PET and whole-brain diffusion MRI fibre-tracking data, to generate super-resolution TW-PET maps. This approach was shown to produce high-quality maps, with very high resolution, where the intensity represents a track-weighted version of the PET image values (in our particular example, ^{11}C-DASB). This methodology relies on the availability of co-registered diffusion MRI and PET data. Furthermore, the results can be affected by other sources of image mismatch between the two modalities, such as signal drop-out and image distortion in echo-planar imaging. To minimise these effects, we used high-quality distortion-corrected [4] diffusion MRI data at 7T, and a HRRT PET system coupled to the MRI via a shuttle bed with sub-millimetre accuracy [3], leading to improved image quality of the resulting TW-PET maps.

The proposed technique of TW-PET opens up new possibilities in molecular imaging, by combining the high sensitivity to brain biomarkers from PET and the super-resolution capabilities of TWI.

References: [1] Calamante F et al. *NeuroImage*; doi:10.1016/j.neuroimage.2011.08.099. [2] Calamante F et al. *NeuroImage* 2010;53:1233. [3] Cho ZH et al. *Proteomics* 2008;8:1302. [4] Oh S-H et al. *Proc. ISMRM* 2011:2698. [5] Tournier JD et al. *NeuroImage* 2007;35:1459. [6] Tournier JD et al. *Proc. ISMRM*, 2010;18:1670.