Motion-Incorporated Partial Volume Correction: Methodology and Validation

Olivier G. Rousset, Arman Rahmim, and Dean F. Wong

Abstract–**With the advance in PET technology and especially scintillating detectors, spatial resolution in the order of 2 mm FWHM are becoming a reality, allowing a more in-depth exploration of complex organs such as the human brain. Subject movement during imaging has always been a factor contributing to image degradation, but is becoming a major limitation in the achievement of the full spatial resolution potential of modern scanners. We propose to demonstrate that the geometric transfer matrix (GTM) method which is a popular method used for partial volume correction (PVC) can be further extended to head movement correction (HMC) when it is associated with some means of head motion tracking (HMT), and is thereafter referred to as the GTM-HMC method. Computer simulations of arbitrary movements were carried out on in a single magnetic resonance image (MRI) volume that was segmented into various functional regions. Data were analyzed without any correction, after application of the GTM-PVC method alone, and after application of the new GTM-HMC method. Results indicate an excellent recovery capability of the new algorithm in the presence of small movements, with typical root-mean square error of less than 1% over the course of a 90-min study. In the presence of noise, the algorithm did not suffer from increased variance compared to when performing GTM-PVC alone. This method is expected to be of great interest since it can account for all detected movements, does not require the reconstruction of intermediate images with inferior statistics, nor is as computer-intensive as event-driven movement correction methods.**

I. Introduction

With the achievement of PET spatial resolution in the order of 2 mm FWHM, subject movement during dynamic PET imaging is becoming a major limiting factor contributing to image degradation that has an increasingly significant impact on quantitative estimates of regional radiotracer concentration.

Several methods have been proposed to address this important issue of motion correction with various degrees of success and each with their own limitations [1]. We propose here to demonstrate that the geometric transfer matrix (GTM) method [2] used for partial volume correction (PVC) [3], when associated with head motion tracking (HMT), can be further extended as to incorporate *head movement correction* (HMC), and is thereafter referred to as the GTM-HMC method.

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O. G. Rousset*, A. Rahmim and D. F. Wong are with the Russell H. Morgan Department of Radiology and Radiological Sciences, Section for High-Resolution Imaging, Johns Hopkins School of Medicine, Baltimore, MD, USA (*telephone: 410-955-2900, e-mail: olivier@jhu.edu).

II. Materials and Methods

Like GTM-PVC [2], the present GTM-HMC method requires high-resolution structural information such as from magnetic resonance imaging (MRI). In addition, GTM-HMC requires the use of a movement tracking device such as the Polaris motion tracking system (Northern Digital Inc., Waterloo, ON, Canada).

A. Theory

In the case of brain PET presented here, high-resolution MRI are segmented into various functional regions and computer simulations of the PET geometry are carried out to provide PET-like unit-less images of each tissue segment, or regional spread function (RSF) images [2]:

$$RSF_i = \int_{D_i} h(r, r')dr' \quad (1)$$

That is, the convolution integral of the scanner's point-spread function *h(r)* over the spatial distribution of tissue segment D_i [2].

For GTM-HMC, RSF images need to be generated for each recorded head position as derived from the tracking device in terms of rigid body movement parameters such as those given in Table I.

Considering a static image (frame) of duration *t*, let *M* be the number of total detected movements during that frame, each of duration ∂t, then for that frame the resulting RSF is:

$$RSF = \frac{1}{t}\sum_{m=0}^{M} \partial t_m \times RSF_m \quad (2)$$

That is, the sum of RSF images for each head position weighed by their respective duration during that frame. The resulting GTM and corrected estimates are then computed in the traditional fashion as described in [2].

B. Simulation experiment

A typical MRI volume was segmented into 8 functional regions (caudate, putamen, grey, white, braintem, cerebellum, scalp, and other).

Arbitrary movement occurrences were set to have taken place at various point in time during a typical 90 min acquisition during dynamic receptor studies such as with [^{11}C]raclopride which accumulates specifically in the caudate and putamen (striatum). Movements were set to be of either translational in

x, y, and z, or rotational around the same axis. A constant-contrast situation was simulated with a ratio of radioactivity concentrations of 100, 100, 50, 25, 20, 20, 10, 10 nCi.ml^{-1} respectively for the above-mentioned regions (Table I). Analytical simulation of PET tracer uptake in those regions was carried out both in noise-free and noisy conditions (Fig. 1).

TABLE I. TRUE RADIO BIO-DISTRIBUTION

Tissue	Striatum	Grey	White	BrainStem	Cerebel	Other
nCi/ml	10	50	25	20	20	10

Regional time-activity curves as well as the GTMs were extracted using regions-of-interest (ROIs) defined with the 50% RC_{zmin} threshold method [4].

TABLE II. MOVEMENT / TRACKING FILE

M#	time (s)	Tx	Ty	Tz	Rx	Ry	Rz
1	10	0	0	0	0	1	0
2	13	0	0	-1	0	0	0
3	20	0	0	0	2	0	0
4	25	-1	0	0	0	0	0
5	36	0	0	1	0	0	0
6	42	0	1	0	0	0	0
7	207	1	0	0	0	0	0
8	2580	0	1	0	0	0	0
9	2748	0	0	1	0	0	0
10	2772	0	0	0	1	0	0

III. RESULTS

The effect of movement is clearly seen in Fig. 2 where fluctuations in regional radioactivity concentrations reflect the effect of movement alone. Before any correction, bias in regional radioactivity was around 30-35% for all regions (Table III) with variability reflecting the overall effect of the simulated movements over the entire 90-min scan in the constant-contrast situation.

TABLE III. ROOT-MEAN-SQUARE ERROR IN REGIONAL CONCENTRATION

%rms	Observed	GTM-PVC	GTM-HMC[a]	GTM-HMC[b]
Grey	-35.0±0.7	+1.4±0.5	0.9±0.2	+1.3±0.5
Caudate	-36.2±0.5	+5.8±3.4	0.8±0.5	+2.4±2.3
Putamen	-31.6±1.2	+7.6±8.6	0.9±0.4	+2.4±2.7
White	+33.3±0.4	-2.3±0.9	0.2±0.2	-2.7±1.2

[a] noise-free [b] noisy

After GTM-PVC alone, i.e. without taking motion into account, overestimation is observed in the Caudate and Putamen by around 6-8% with an increase in variance due to movement-induced bias present in the GTM (Table III).

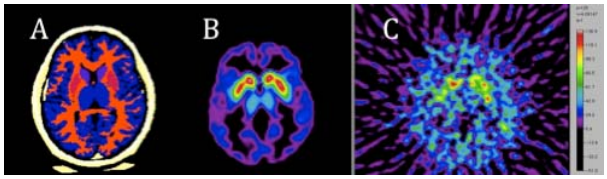

Fig. 1. Segmented MRI (A), after simulation of bio-distribution in Table I, scanner geometry, and movement (B) and in the presence of Poisson noise (C).

When incorporating blurring due to movement in the global GTM, we observed an inaccuracy of less than 1% root-mean-square (Table III).

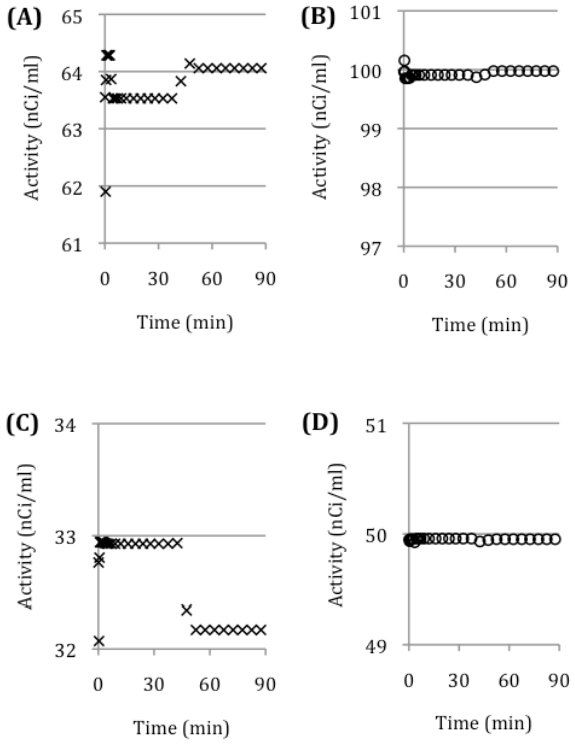

Fig. 2. Actual (obs) and GTM-HMC time-activity curves for the entire 90' in Caudate (A) before and (B) after GTM-HMC, and in whole Grey (C) before and (D) after GTM-HMC. Constant contrast was simulated and in the presence of head movement (Table II.). Scanner's resolution = 6 mm FWHM.

IV. DISCUSSION

A. Accuracy

The relatively small variability of less than 2% observed across all regions reflects the relatively small number (10) and magnitude of movement occurrences simulated (Table II) for a large number of frames (30). However, the *bias* induced by the movement alone can be seen as reaching 5% for smaller regions such as the Caudate (Fig. 2) when e.g., 4 small consecutive movements are simulated (first 30 s of the study,

Table II). Although relatively small, this bias is the result of movement of relatively small magnitude compared to the resolution of the simulated scanner (around 6 mm FWHM). Estimates obtained after GTM-HMC were less than 0.5% off the true values, reaching the limits of interpolation and rounding errors.

B. Precision

In noisy conditions, average bias was preserved, and variance was highly dependent on the number of counts present in each image frame (Fig. 1C).

However, the standard deviation of values corrected with GTM-PVC alone was not increased after incorporation of movement correction, due to being factored in the global GTM.

C. Attenuation

While these data did not account for the effect of difference in attenuation between the emission scan after movement and the mu-map used for attenuation compensation during image reconstruction, this effect can be additionally incorporated within the GTM-HMC matrix for the most rigorous correction.

V. Conclusion

Numerous motion correction methods have been proposed in the literature [1]. In comparison to frame-by-frame movement correction methods [5], the proposed GTM-HMC method has the advantage of accounting for all detected movements, notably intra-frame movements. Unlike the MAF method [6], the present algorithm does not require the reconstruction of intermediate images with inferior statistics. Furthermore, while there exist a range of reconstruction-based motion correction methods; e.g. event-driven methods [7-9] or ones that also modify the system matrix of the reconstruction algorithm [10-15], the proposed technique conveniently operates only on post-reconstruction images and thus does not require access to scanner-specific data-analysis and/or reconstruction tools and is not computationally expensive, while accurately accounting for the effect of motion on the physiological parameters of interest.

While post-reconstruction motion de-blurring at the voxel level is plausible [8], the GTM-HMC formulation results in improved handling of noise amplification. Furthermore, an important consideration with the present method is that we observe a lack of increased variance in the corrected data compared to when correcting for partial volume alone. In noisy conditions, average bias was preserved, and variance was highly dependent on the number of counts present in each image frame (Fig. 1C). At the same time, the standard deviation of values corrected with PVC-alone was not increased after incorporation of movement correction, due to being factored within the global GTM.

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