ELSEVIER

NeuroImage

www.elsevier.com/locate/ynimg
NeuroImage 39 (2008) 1570–1584

# Deconvolution-based partial volume correction in Raclopride-PET and Monte Carlo comparison to MR-based method

Jussi Tohka[a,*] and Anthonin Reilhac[b]

[a]*Institute of Signal Processing, Tampere University of Technology, Tampere, Finland*
[b]*CERMEP, Bron, France*

Received 13 July 2007; revised 10 October 2007; accepted 31 October 2007
Available online 7 November 2007

**In this work, we evaluated three iterative deconvolution algorithms and compared their performance to partial volume (PV) correction based on structural imaging in brain positron emission tomography (PET) using a database of Monte Carlo-simulated images. We limited our interest to quantitative radioligand PET imaging, particularly to $^{11}$C-Raclopride and striatal imaging. The studied deconvolution methods included Richardson–Lucy, reblurred Van Cittert, and reblurred Van Cittert with the total variation regularization. We studied the bias and variance of the regional estimates of binding potential (BP) values and the accuracy of regional TACs as a function of the applied image processing. The resolution/noise tradeoff in parametric BP images was addressed as well. The regional BP values and TACs obtained by deconvolution were almost as accurate than those by structural imaging-based PV correction (GTM method) when the ideal volumes of interests (VOIs) were used to extract TACs from the images. For deconvolution methods, the ideal VOIs were slightly eroded from the exact anatomical VOI to limit the bias due to tissue fraction effect which is not corrected for by deconvolution-based methods. For the GTM method, the ideal VOIs were the exact anatomical VOIs. The BP values and TACs by deconvolution were less affected by segmentation and registration errors than those with the GTM-based PV correction. The BP estimates and TACs with deconvolution-based PV correction were more accurate than BPs and TACs derived without PV correction. The parametric images obtained by the deconvolution-based PV correction showed considerably improved resolution with only slightly increased noise level compared to the case with no PV correction. The reblurred Van Cittert method was the best of the studied deconvolution methods. We conclude that the deconvolution is an interesting alternative to structural imaging-based PV correction as it leads to quantification results of similar accuracy, and it is less prone to registration and segmentation errors than structural imaging-based PV correction. Moreover, PV-corrected parametric images can be readily computed based on deconvolved dynamic images.**


*Keywords:* Partial volume effect; Striatum; Positron emission tomography; Simulation; Richardson–Lucy; Van Cittert; Total variation

## Introduction

The partial volume effect (PVE) is an important degrading factor in quantitative PET brain imaging. The term PVE refers to two factors contributing to blur in images: In the terminology of Aston et al. (2002), the tissue fraction effect is caused by several distinct types of tissue existing in a single voxel. Spill-over (and spill-in) – caused by a non-zero positron range and image reconstruction among other factors – means that the reconstructed image is a convolution of the true image by a point spread function (PSF). The difference between the two sources of PVE for us is that the spill-over and spill-in could be corrected based on the information in the PET image itself and the measured PSF while the correction of the tissue fraction effect requires additional external information. This external information can be in the form of the segmented magnetic resonance (MR) image of the same subject. For the purposes of this paper, there is no need to differentiate between spill-in and spill-over, and therefore the term spill-over is used to mean both spill-over and spill-in.

To date, several methods to correct for PVEs have been proposed. Usually, these methods rely on the availability of a segmented (MR) image of the subject that is co-registered with the PET image. Aston et al. (2002) provided a unifying statistical framework covering many of these methods. The widely applied GTM method (Rousset et al., 1998) utilizes structural information from MRI and assumes regional homogeneity of the radioactivity levels in the PET image. This way a linear system is formed using the structural information and the scanner PSF. The solution to this system then provides the underlying true radioactivity levels based

* Corresponding author.
*E-mail address:* jussi.tohka@tut.fi (J. Tohka).
**Available online on ScienceDirect (www.sciencedirect.com).**

1053-8119/$ - see front matter © 2007 Elsevier Inc. All rights reserved.
doi:10.1016/j.neuroimage.2007.10.038

on the radioactivity levels measured from PVE corrupted data using the structural information. In addition, there exist methods, termed pixel-by-pixel methods, that relax the regional homogeneity assumption for a single (gray matter) structure (Muller-Gartner et al., 1992; Meltzer et al., 1996; Strul and Bendriem, 1999) while assuming that the true radioactivity levels in other brain structures are known. These methods are not routinely applied for Raclopride imaging, and they cannot account for the contamination between two or more different gray matter structures. Therefore, a direct suitability of these pixel-by-pixel methods to striatal imaging with Raclopride can be doubted because there are (at least) two distinct subcortical gray matter structures (caudate and putamen) whose activity level is different from the activity level in cortex.

Because the MR-based PV correction methods rely on the structural information, they are sensitive to the errors in MR-PET registration and volume of interest (VOI) delineation. The effects of mis-registration and mis-segmentation in MR-based PV correction have been previously studied by Baete et al. (2004), Frouin et al. (2002), Meltzer et al. (1999), Quarantelli et al. (2004) and Zaidi et al. (2006). A majority of the above-mentioned works targeted $^{18}$F-FDG-PET imaging of cortical regions. Frouin et al. (2002) and Zaidi et al. (2006) also studied striatal imaging using $^{18}$F-Dopa. Therefore, these studies are of the greatest interest to us. Frouin et al. (2002) studied the effect of the registration and segmentation errors to the GTM-based PV correction with a Monte Carlo-simulated $^{18}$F-Dopa phantom. They simulated various erroneous segmentations and registrations and concluded that both registration and segmentation errors affected the precision of the recovery of the true radioactivity levels. Especially, the variation in the recovered activity levels was found to increase when the extents of the segmentation and registration errors were increased. The segmentation and registration errors were considered separately, and no results about the pooled registration and segmentation errors were provided. Zaidi et al. (2006) studied the effect of several MR tissue classification algorithms to the PV correction with $^{18}$F-Dopa and $^{18}$F-FDG. The delineations of caudate and putamen were performed relying on a segmented brain template, and this template was the same for all tissue classification algorithms considered. Still, it was found that the choice of the tissue classification algorithm could lead up to 10% differences in the activity level of the caudate nuclei in the PVE-corrected PET data. For the putamen, the differences were usually below 1%.

The sensitivity of MR-based PV correction to inevitable segmentation and registration errors leads us to consider purely PET-based PVE correction. As mentioned, the spill-over can be corrected for by utilizing only the PET image itself and the measured PSF. The process is termed deconvolution. For general tutorials about the subject, see Carasso (1999) and Biemond et al. (1990). These methods have not received much attention with brain PET although deconvolution problems share a similarity with the image reconstruction problems (Demoment, 1989). With SPECT (single photon emitting computed tomography), there has been some interest towards deconvolution-based PVE correction (Mignotte et al., 2002; Charalambous et al., 1992). However, the quantification aspects were not considered in the above references. Kao et al. (1997) restored sinograms before the reconstruction. Obviously, spill-over caused by reconstruction cannot be addressed this way. Several sources of the spill-over can be addressed in the iterative maximum likelihood reconstruction algorithms (Leahy and Qi, 2000). Although this would be a favorable avenue to proceed, there are practical difficulties. For example, it is not always possible to choose the reconstruction algorithm or reconstruct the images retrospectively with a better algorithm than the one applied originally. Also, these reconstruction methods call for an advanced modeling of the data acquisition and, in practice, these models are necessarily approximative (see Leahy and Qi, 2000). Still, a recent technique generates the PVE-corrected image based on the multiresolution analysis of the PET and co-registered MRI images of the subject (Boussion et al., 2007). This technique performs the correction using the MRI data but without the need to segment nor to classify the data. Whereas it has successfully been validated for static FDG PET and rCBF SPECT data, this technique still suffers from limitations and is not yet applicable for multi-frame PET data. Moreover, the suitability of this technique for striatal imaging is unknown.

In this study, we evaluate a few well-known deconvolution algorithms and their modifications for their suitability to PV correction in quantitative parametric PET imaging using $^{11}$C-Raclopride. Specific attention is given to the comparison of the deconvolution-based PV correction and MR-based PV correction in presence of segmentation and registration errors. The evaluation is performed by utilizing a publicly available database of Monte Carlo-simulated $^{11}$C-Raclopride images (Reilhac et al., 2005). An important feature of the database is that the normal anatomical variability is modeled in the database. This allows us to draw conclusions about its impact on the variability of regional physiological parameters of interest. The main criteria of the comparison are the bias and variance – with respect to the anatomical variability in the database – in regional binding potential (BP) values. This is an additional novel feature of the present study, since the previous efforts have characterized results mainly with respect to the capability of recovering the true activities rather than the underlying physiological parameters of interest. In addition to regional BP values, we consider the noise level and resolution of the parametric BP images with the deconvolution-based PV corrections as well as the quality of regional time activity curves (TACs).

## Partial volume correction

A beginning note: The BP values in dynamic $^{11}$C-Raclopride are typically computed with the simplified reference region model using cerebellum as the reference region (Lammertsma and Hume, 1996; Gunn et al., 1997). Since the model is nonlinear, the PV correction must be performed separately for each frame of the dynamic image and the PV correction of the parametric image is not reasonable.

### *Deconvolution methods*

#### *Image model*

The task is to restore a 3-D image $t$ which has been deteriorated by a known PSF $h$. We assume that the PSF is symmetric, non-negative, integrates to one, and that $h(0)>0$. A good model for observed image $i$ is $i=\mathcal{N}_2(\mathcal{N}_1(t)*h)$, where $*$ denotes 3-D convolution and $\mathcal{N}_1$, $\mathcal{N}_2$ are noise processes. In practice, we assume a simpler image model

$$i=\mathcal{N}_2(t*h). \tag{1}$$

In other words, we ignore the noise process taking place prior to blurring by the PSF. This is a notable simplification since a part of