

CONDITIONAL PARTIAL VOLUME CORRECTION FOR EMISSION TOMOGRAPHY: A WAVELET-BASED HIDDEN MARKOV MODEL AND MULTI-RESOLUTION APPROACH

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ABSTRACT

The spatial resolution in emission tomography induces partial volume effects, leading to under-estimation of the real uptake and activity spillover. They can be corrected using either region of interest or voxel based approaches. We developed a voxel wise correction, based on the wavelet transform of two co-registered images in order to insert high resolution details of the anatomical image into the functional one. A limitation is the use of a global model which may create artefacts in the corrected image where there is no correlation between the two modalities. The aim of this work was to develop a conditional correction: a comparison between the two modalities using hidden Markov modelling and multi-resolution analysis was developed to allow such a correction. The process was successfully tested on synthetic and clinical images avoiding artefacts.

Index Terms— Wavelet, multi-resolution, partial volume effect, hidden Markov models, PET

1. INTRODUCTION

1.1. Partial volume effects and correction

Partial volume effects (PVE) are consequences of the limited spatial resolution in emission tomography. They lead to a loss of signal in tissues of size similar to the point spread function (PSF) of the imaging device and induce activity spill over between adjacent structures with different amounts of activity.

These effects can be corrected for by using either region of interest (ROI) or voxel based methods. Most of the suggested approaches rely on the knowledge of the point spread function (PSF) of the scanner and *a priori* anatomical information provided by either computed tomography (CT) or magnetic resonance imaging (MRI). Furthermore, they frequently require a segmentation step [1]. Boussion *et al* [2] proposed a new voxel wise based PVE correction methodology based on mutual multi-resolution analysis (MMA) of an emission tomography

image and a corresponding co-registered CT or MRI image. One advantage of this PVE correction approach is that corrected images are generated; not only eliminating the need of a segmentation step but also allowing further image processing and potentially an improvement in the clinical diagnosis.

1.2. The mutual multi-resolution approach

The multi-resolution PVE correction approach consists in extracting some details of a high resolution anatomic image, and adding them through a model in the associated co-registered functional image. Previous work [2] has demonstrated that as long as realignment differences between the two images are within half of the size of the emission system's PSF no significant errors are introduced. The principle of this method is described in detail in [2]. As a first step, discrete wavelet transforms of both the anatomic and the functional images are performed via the "à trous" algorithm, up to the spatial resolution level common to both modalities. As a second step, a linear model is established between the anatomic and functional details at this common spatial resolution level, assuming a correlation between the wavelet coefficients in the two images. In this linear model, a global parameter α is defined as the mean voxel by voxel division of the functional wavelet coefficients by the anatomical ones. As a third step, this model is applied to the high resolution details of the anatomical image in order to obtain the lacking ones in the functional image. Finally, in the last step, these new details are inserted into the initial functional image to obtain the corrected image.

1.3. Limitations and possible improvement

The main drawback of this multi-resolution approach comes from the simple linear model established between the high and low resolution details. As this latter is global, it may introduce artefacts in some cases especially if structures belonging to the anatomical image are not in the functional one. The goal of the present study was to improve this approach in order to avoid such artefacts *via*

a new conditional multi-resolution based correction. Our approach is based on a comparison in the wavelet domain between anatomical and functional decompositions, using statistical hidden Markov models, in order to obtain conditional correction maps (CCM).

These latter represent the main differences between functional and anatomical details, allowing the application of a so-called conditional PVE correction according to the presence or not of similar structures in both anatomical and functional images.

2. MATERIALS AND METHODS

2.1. The Hidden Markov Tree (HMT) model

Since the MMA PVE correction method is based on the use of the wavelet decompositions to obtain the lacking details of the functional image (see left part of fig. 3), the comparison step occurs in the wavelet domain. The technique we chose for the comparison step is based on a special class of nonlinear Markov models. These are defined as discrete Markov random fields (MRF) attached to the nodes of a quad-tree. The main advantage of the quad-tree, whose structure is illustrated in Fig. 1, is its ability to model properties which enable the design of exact non-iterative inference algorithms, like those in the Markov chains. It is consequently possible to link the different scales of a given decomposition using probabilistic and statistical relationships considering a hierarchical structure in which one “father” (level of resolution $j-1$) has 4 “sons” (level of resolution j). In [3], Crouse *et al.* proposed and described such a statistical model in the wavelet-domain, called a Hidden Markov Tree (HMT) model. The HMT model is a tree-structured probabilistic graph that can model the joint statistics of the coefficients of a wavelet transform.

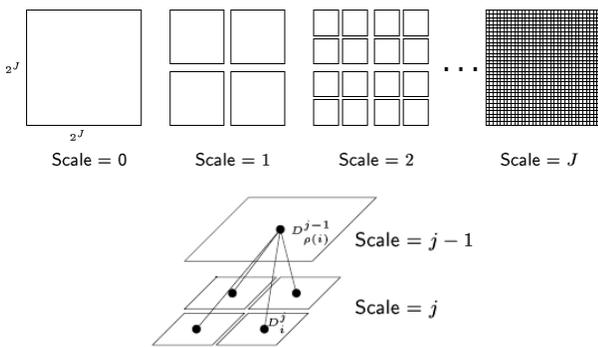


Fig. 1. Quad-tree decomposition of a $2J \times 2J$ image

Due to the compression property of the wavelet transform, we can assume a two-state zero-mean Gaussian mixture model for a random variable W (for each wavelet coefficient). Given a hidden state variable S associated to

the random variable W , and p the probability mass function; $S=1$ leads to a low variance Gaussian probability density function (pdf) and $S=2$ to a high variance Gaussian pdf (fig. 2).

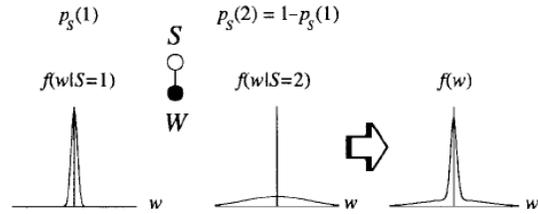


Fig. 2. Two-state mixture model

Considering a wavelet domain quad-tree decomposition of an image and the mixture model previously described, the HMT model can be considered as a multidimensional Gaussian mixture model to which Markovian dependencies between the hidden states along scales are applied. The HMT model is therefore parameterized by:

- (1) $p_{S_j}(m)$: the pmf of the root node S_j
- (2) $\mathcal{E}_{i,p(i)}^{mr} = p_{S_j|S_{p(i)}}[m|S_{p(i)}=r]$, the transition conditional probabilities between scales
- (3) $\mu_{i,m}$ and $\sigma_{i,m}^2$, the Gaussian mixture model parameters

These parameters can be estimated thanks to the iterative Expectation Maximization (EM) algorithm [3, 5]. In order to avoid practical implementation issues regarding the HMT model training for image processing applications [4], we used an initialization scheme from Fan and Xia [6]. This latter is based on a two-step EM algorithm initialization (a within-scale scanning followed by an across-scale counting) improving the main EM step results. Both methods [3] and [6] use HMT models based on the simple Haar wavelet transform and the Mallat’s algorithm [7] due to its natural quad-tree decomposition. However, depending on the application, other wavelet transforms and algorithms can be used. For our new methodology, the “a trous” algorithm with bi-cubic splines interpolation was chosen.

2.2. Wavelet-based segmentation

In order to compare both modalities, our primary objective was to build binary maps (one for each modality) classifying voxels according to the region they are in. Voxels from homogeneous areas were classified as $S=1$ while voxels belonging to boundaries were classified as $S=2$. The first step consists in up-sampling the anatomical image in order to obtain a correlation between the spatial resolution and dimensions of the two initial

images. This is performed using a bi-cubic splines interpolation. The next step consists in applying wavelet decompositions (in the same way used in the multi-resolution approach) and down-sampling in a dyadic way, in order to fill in the entire quad-tree structures. Once the two decompositions obtained, the same levels of resolution are extracted and a HMT model is created on each quad-tree for the segmentation step. Concerning this process, the initial parameters are computed using the two-step algorithm EM initialization [6]. Then, the iterative EM algorithm [3, 5] is applied in order to obtain the parameters optimal values for the HMT model. Finally, the MPM algorithm [3, 5] is used with the previously estimated parameters in order to obtain the segmentation maps (hidden states of each wavelet coefficient) for both wavelet-decomposition images on the quad-tree.

2.3. CCM and conditional PVE correction

In order to perform the comparison between the two segmentation maps (binary images), we use a local dissimilarity comparison method introduced by Baudrier *et al.* [8]. This approach is based on a locally measured and modified Hausdorff distance and allows the main differences between binary dyadic decompositions to be successfully localized and extracted. A CCM is therefore an image in which the grey levels indicate a voxel-by-voxel estimation of the differences between the two binary segmentation maps.

The initial MMA for PVE correction is then modified by (a) computing the linear model parameters using only the wavelet coefficients considered as edge on the two modalities, and (b) discarding the differences defined by the CCM in order to eliminate artefacts. The first step of the method is the same as the previously proposed MMA approach and is based on the wavelet decompositions of both images. Then the HMT model is used in order to compare both decompositions based on the segmentation results, in order to build the CCM maps which define differences between the anatomical and functional images. Finally a conditional correction is performed being applied only where a strong correlation between functional and anatomical information exists. In addition, the parameter α of the global model (see section 1.2) is computed for the rest of the image using only the data for which a correlation has been found, hence avoiding any bias resulting from areas where no correlation exists.

2.4 Evaluation

The whole process and associated results are illustrated in Fig. 3 on a functional/anatomical synthetic dataset. The conditional MMA for PVE correction has also been applied to a clinical MRI/PET dataset as illustrated in Fig.4. It consisted of a FDG brain PET (Philips GEMINI) and corresponding T1-weighted MRI (GE 1.5T, with injection of gadolinium) images acquired on a patient. The images were spatially co-registered by using mutual information maximization and affine transformation. The MRI image shows a hyper intensity signal in the left occipital lobe and the posterior cingulum due to the injection of gadolinium.

3. RESULTS

As illustrated in the figure 3, on the one hand, the classical multi-resolution approach corrects the whole PET image according to a global linear model introducing this way details of the anatomical image that do not correspond to details in the functional image. On the other hand, the conditional approach discards such artefacts by detecting the main differences between images in the wavelet domain.

Similar results are shown in figure 4 for the clinical dataset. Whereas the standard MMA PVE correction introduces artefacts (tumour uptake) in the corrected PET images due to hyper intensity of gadolinium in the occipital lobe (see fig. 4), the conditional approach detects the main differences between images of the two modalities and avoids the insertion of erroneous information in the non-correlated regions (see fig. 4).

4. DISCUSSION AND CONCLUSION

In this paper, we have introduced a new approach to improve a multi-resolution based PVE correction methodology. The wavelet-domain HMT model was used for the segmentation of wavelet transforms of anatomical/functional datasets. Conditional correction maps were then deduced from the obtained binary decompositions. As shown by the preliminary results presented, the new conditional PVE correction algorithm improves the classical multi-resolution approach avoiding over correction and the introduction of artefacts. This is especially interesting in some clinical cases as the one presented in fig. 4. Future work will concentrate on a thorough validation of the approach as well as finer tuning of the HMT model and CCM determination, thanks to larger datasets including simulated and clinical images.

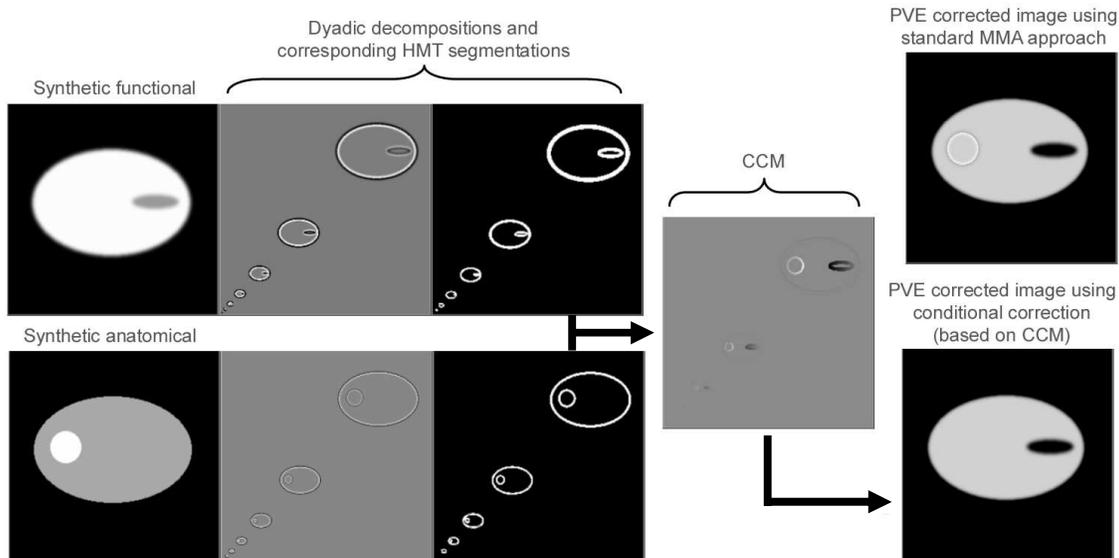


Fig. 3. Conditional and standard PVE correction approaches illustrated on a synthetic dataset

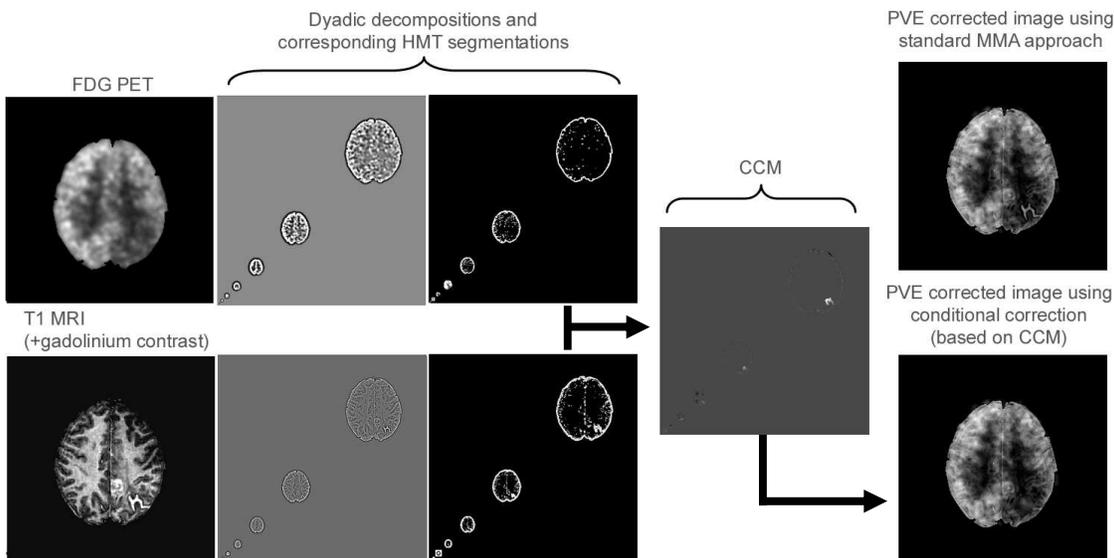


Fig. 4. Conditional and standard PVE correction approaches applied to a clinical dataset

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