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1 A framework based on Hidden Markov Trees for multimodal PET/CT  
2 image co-segmentation

3

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22

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24

25 Abstract

26 Purpose: To investigate the use of a probabilistic quad-tree graph (Hidden Markov Tree, HMT) to provide fast  
27 computation, robustness and an interpretational framework for multimodality image processing and to evaluate this  
28 framework for single gross tumor target (GTV) delineation from both positron emission tomography (PET) and  
29 computed tomography (CT) images.

30 Methods: We exploited joint statistical dependencies between hidden states to handle the data stack using multi-  
31 observation, multi-resolution of HMT and Bayesian inference. This framework was applied to segmentation of lung  
32 tumors in PET/CT datasets taking into consideration simultaneously the CT and the PET image information. PET and  
33 CT images were considered using either the original voxels intensities, or after wavelet/contourlet enhancement. The  
34 Dice similarity coefficient (DSC), sensitivity (SE), positive predictive value (PPV) were used to assess the performance  
35 of the proposed approach on one simulated and 15 clinical PET/CT datasets of non-small cell lung cancer (NSCLC)  
36 cases. The surrogate of truth was a statistical consensus (obtained with the Simultaneous Truth And Performance Level  
37 Estimation algorithm) of three manual delineations performed by experts on fused PET/CT images. The proposed  
38 framework was applied to PET-only, CT-only and PET/CT datasets, and were compared to standard and improved  
39 fuzzy c-means (FCM) multimodal implementations.

40 Results: A high agreement with the consensus of manual delineations was observed when using both PET and CT  
41 images. Contourlet-based HMT led to the best results with a DSC of  $0.92 \pm 0.11$  compared to  $0.89 \pm 0.13$  and  $0.90 \pm 0.12$   
42 for Intensity-based HMT and Wavelet-based HMT respectively. Considering PET or CT only in the HMT led to much  
43 lower accuracy. Standard and improved FCM led to comparatively lower accuracy than HMT, even when considering  
44 multimodal implementations.

45 Conclusions: We evaluated the accuracy of the proposed HMT-based framework for PET/CT image segmentation. The  
46 proposed method reached good accuracy, especially with pre-processing in the contourlet domain.

47

48 Keywords: Positron emission tomography (PET), computed tomography (CT), Bayesian inference, hidden Markov  
49 trees (HMT), wavelet and contourlet analysis, segmentation

50

51

## 52 INTRODUCTION

53

54 The current trend in modern personalized medicine is to acquire and exploit sequential images for a patient during the  
55 course of its treatment (pre-, per-, post-treatment). These images are also more and more frequently coming from  
56 multiple image modalities including Computed Tomography (CT), Magnetic Resonance Imaging (MRI), Positron  
57 Emission Tomography (PET), Single Photon Emission Computed Tomography (SPECT) or UltraSound (US). In  
58 addition, the development of each modality has led to the use of several modes of acquisition, such as various MRI  
59 sequences or the development of several PET and SPECT radiotracers. In clinical oncology and radiotherapy, this has  
60 been especially true, due to the introduction of multimodality imaging integrated devices such as PET/CT and  
61 SPECT/CT, and now the rising development of sequential and simultaneous PET/MRI, which have also led to  
62 significant improvements regarding image fusion and anatomical/physiological data association.

63 On the one hand, multimodality imaging today provides the physicians with an unprecedented potential wealth of  
64 information, both morphological and functional regarding the pathology <sup>1</sup>. On the other hand, the manual and visual  
65 exploitation of the image datasets becomes more and more complex, tedious, subjective and time-consuming owing to  
66 increasing data volumes as well as image characteristics' variability. Automated analysis may thus potentially improve  
67 overall patient management based on the use of multimodality images.

68 From an image and data processing point of view, most recent developments have been focused on a single image  
69 modality, optimizing and adapting algorithms to deal with its specific characteristics. In clinical research, when  
70 multiple images (from one or several modalities) are being considered, they are most often analyzed independently and  
71 the results are then combined *a posteriori*, thereby not exploiting the full potential correlation between multimodal  
72 images. One of the main challenges for semi-automatically handling such multimodal datasets is the large variability  
73 in terms of spatial resolution and definition, noise and texture properties, across as well as within modalities.

74 Several papers have investigated the combination and association of functional and anatomical images for a specific  
75 purpose, such as denoising<sup>2</sup> or reconstruction<sup>3</sup> of PET data using anatomical priors coming from MRI or CT, correction  
76 of partial volume effects in PET or SPECT by exploiting the associated morphological information <sup>4-6</sup>, the use of  
77 associated CT images to spatially register several low-resolution PET images, for instance during treatment <sup>7, 8</sup> or

78 several different radiotracers<sup>9</sup>, or the definition of tumor target volumes in radiotherapy by considering both PET and  
79 CT images features<sup>10,11</sup>.

80 This last application in particular has led recently to the development of several (semi)automated methodologies aiming  
81 at determining a single gross tumor volume (GTV) from fused PET/CT datasets, assuming both modalities provide  
82 complementary information regarding a single contour of the tumor volume<sup>10-16</sup>. Although an alternative approach  
83 could consist in segmenting each image independently and then combine the obtained volumes *a posteriori* using some  
84 kind of consensus, these approaches have mostly considered the first approach and used a variety of tools including  
85 supervised learning using textural features of PET/CT images<sup>10,14</sup>, Markov random field<sup>13</sup>, random walk segmentation  
86<sup>12</sup>, active contours<sup>11,16</sup> and topology integrated within graph-models<sup>15</sup>. The idea underlying all these studies is that the  
87 delineation should benefit from the co-registered modalities' information in order to produce a single, more robust and  
88 accurate GTV. Most of these previous works have indeed highlighted the potential value in considering both modalities  
89 simultaneously in a common mathematical and algorithmic framework. The objective of most of these studies is to  
90 objectively automate the manual and subjective task of GTV delineation by a radiation oncologist visualizing the fused  
91 PET/CT images. We place our present work in the same context.

92 Hidden Markov fields (HMF) are well suited to image processing and have been exploited in a variety of applications,  
93 including medical imaging<sup>17</sup>. They have been used in PET segmentation<sup>18</sup> and two recent studies investigated the use  
94 of HMF to associate PET and CT datasets with the goal of co-segmentation<sup>13,19</sup>. Markov random fields however  
95 require computationally expensive iterative methods for estimating parameters<sup>17</sup>, contrary to hidden Markov chains  
96 (HMC) that have also been explored for PET segmentation<sup>20</sup>. Finally, hidden Markov trees (HMT) share similar  
97 favorable computational properties with chains, while being quite as robust as fields and providing a useful structure  
98 for the association of multiscale and multimodal images<sup>17,21</sup>. HMT proved their efficiency in several fields. For  
99 example, phylogenetic models in biology are diagrams showing the evolutionary relationships between species<sup>22</sup>.  
100 Hierarchical models are also used for aerial image parsing<sup>23</sup>. HMT have found numerous applications in imaging,  
101 including astronomical<sup>24</sup>, remote sensing<sup>25,26</sup> and medical imaging for instance in MRI<sup>27</sup>. However, medical image  
102 segmentation using HMT is quite rare<sup>28</sup> contrary to Markov fields<sup>29</sup>, and to the best of our knowledge, our work is the  
103 first to investigate their use for multimodal PET/CT image segmentation. The present paper is an extension of the first  
104 developments initially presented in a conference proceeding<sup>30</sup>.

105

106 The scope of this work is thus to evaluate the value of a unified framework based on HMT for PET/CT segmentation  
107 with the objective of GTV delineation in radiotherapy planning. Results are provided on 1 simulated case and on 15  
108 clinical datasets with comparison to a statistical consensus of three different manual delineations. Finally, we elaborate  
109 at several potential improvements regarding the framework itself, as well as other applications that may benefit from  
110 its use, and that will be investigated in future studies.

## 111 **MATERIALS AND METHODS**

### 112 **1. Hidden Markov Tree framework**

113 In this section, we present the mathematical methodology used to handle, associate and process multimodal medical  
114 images using different resolutions and modalities within a unified framework based on a HMT.

115 The multiresolution nature of the data can be managed by using the successive scales of the HMT in order to handle  
116 data represented at different resolutions. Another modeling approach consists in using the different levels in the HMT  
117 not to represent data of different resolutions, but rather as an algorithmic solution to model dependencies between  
118 neighboring observations at successive scales, while the data is associated only with the last scale of the HMT. In that  
119 case, different modalities are handled by considering observed data in a given voxel as a vector containing several  
120 values, each vector component representing a modality's observation. This setting was chosen for the present work: in  
121 radiotherapy planning clinical practice, the PET image is up-sampled to exactly the same dimension as the CT, so that  
122 the images can be overlaid for visualization and manual delineation. We used cubic B-spline interpolation to up-sample  
123 the PET image so that a PET voxel exactly corresponds to a CT voxel. Therefore both PET and CT voxels intensities  
124 are associated as a 2-value vector with the leaves of the tree (the level/scale at the bottom of the tree), as illustrated in  
125 figure 1. Note that all the scales/levels above in the tree are only used as calculus and parameters estimation tools and  
126 none of their nodes are associated with PET/CT voxels values.

127 The HMT will exploit conjointly within the same algorithmic framework each couple of voxels' intensities (one PET,  
128 one CT) to take a segmentation decision based on the probability of this couple to belong to a class (tumor) or another  
129 (background). This probability is calculated by combining two different probabilities: the first corresponds to the prior

130 probability of each node of the tree to belong to a given class, which will be based on the fathers-children statistical  
131 transitions in the tree structure (section 1.1). Regarding the segmentation task, the most important probability will be  
132 the one associated with each leaf. Indeed, the probabilities estimated in the above scales are only calculus and  
133 estimation tools to incorporate spatial neighborhood and multiscale information. The second corresponds to the  
134 observation probability calculated based on the voxel couple of values (PET and CT) with respect to the respective  
135 joint generalized normal distribution estimated for the entire PET/CT region of interest containing the tumor and  
136 background (section 1.2). Each case requires automatic estimation of all parameters defining the HMT model and these  
137 estimated parameters are then used to perform the actual segmentation (section 1.3).

### 138 1.1 Hidden Markov Tree model

139 Contrary to HMC, a HMT is a hierarchical hidden Markov model, which is able to take into account the probabilistic  
140 dependencies between scales directly. At a given scale, the probabilistic spatial dependencies among voxels are then  
141 taken into account via dependency on a common ancestor (Figure 1). Similarly to HMCs, HMTs allow fast data  
142 processing owing to their computational efficiency. Despite their simplicity, they are able to produce results with  
143 similar performance as hidden Markov fields <sup>17</sup>.

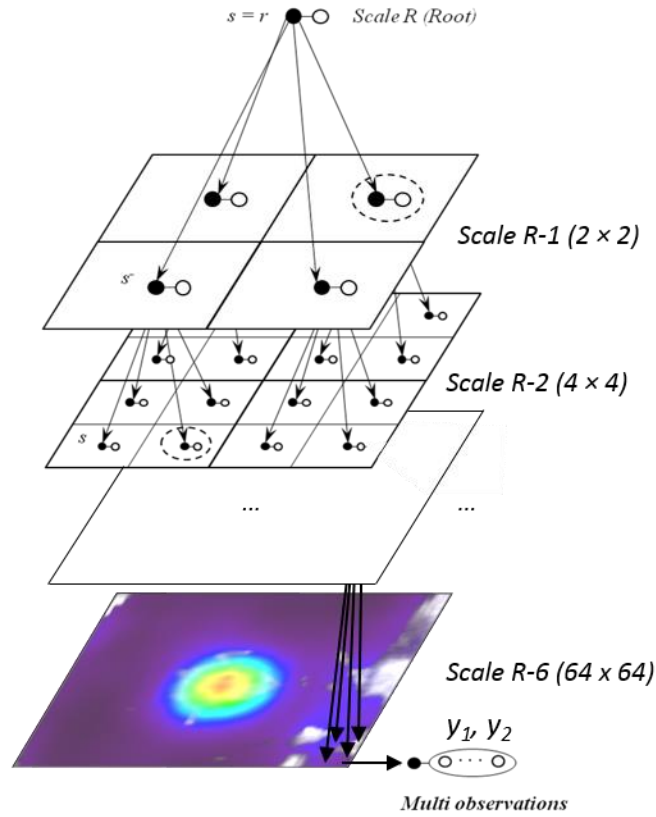
144 The HMT model is defined as follows: let  $S$  be a finite set of points and  $X = (X_s)_{s \in S}$ ,  $Y = (Y_s)_{s \in S_0}$  two random vectors  
145 indexed respectively on  $S$  and  $S_0 \subset S$  subset of observed voxels. Each  $X_s$  takes its values in the finite set of classes  
146  $\Omega = \{\omega_1, \dots, \omega_k\}$  (in this work tumor and background) and  $Y_s$  takes its values in the set of observations (real values  
147 corresponding to voxels' intensities). Let  $S^1, \dots, S^R$  be a partition of  $S$  representing different "generations". Each  $s \in S^i$   
148 admits  $s^+ \subset S^{i+1}$  (called his "children") in such a way that every element of  $t \in S^{i+1}$  has a unique "father"  $t^- \in S^i$  such  
149 that  $(s^+)^- = s$ . We assume that  $S^1$  is a singleton so as its element  $r$  is called "root". Setting  $p(x, y)$  density of the  
150 distribution of  $(X, Y)$ , the random vector  $(X, Y)$  is a HMT if:

$$151 \quad p(x, y) = p(x_r) p(y_r | x_r) \prod_{j=2}^R \prod_{s \in S^j} p(x_s | x_{s^-}) p(y_s | x_s), \quad (1)$$

152 where  $p(y_s | x_s) = 1$  if  $s \notin S_0$

153

154



155

156 Figure 1: Hidden Markov Tree (HMT) Model with the associated PET/CT image (selection centered on the tumor):  
 157 the root, scale R-1 with 4 children, scale 2 with 16, down to scale R-6 with 4096 “leaves” (64×64), each one being  
 158 associated with a vector of 2 values ( $y_1$  and  $y_2$ ) corresponding to the PET and CT intensities. The classification as  
 159 “tumor” or “background” is  $x = (x_s)_{s \in S_0}$ .

160

### 161 1.2 Observation modeling

162 With respect to image segmentation in a statistical setting, a Gaussian distribution is sufficient to model PET voxels’  
 163 intensities and more complex distributions through the use of the Pearson’s system (containing 7 different  
 164 distributions)<sup>31</sup> does not improve accuracy<sup>32</sup>. However, in the present case the framework has to conjointly model PET  
 165 and CT distributions that could be very different, hence calling for a more flexible statistical model. Therefore the  
 166 observation's noise densities  $p(y_s | x_s)$  (for  $s \in S_0$ ) considered are of the generalized normal distribution form<sup>33</sup>.

### 167 1.3 HMT parameters estimation

168 The parameters of the HMT that need to be estimated are listed in table 1. The table also lists how their values are  
 169 initialized, as well as the aspects of these parameters that are not estimated but rather set *a priori*.



HMT parameter category	Parameter	Initialization	Parameter aspects that are not estimated but set <i>a priori</i>
Prior model	Root prior distribution	Equal probability for each class	Each node has 4 children. The number of scales and nodes/leaves are set depending on the size of the input image (e.g. 6 scales for a 64×64 image).
	Parent-child transition probabilities	Calculated using a first rough segmentation through a Fuzzy C-means algorithm	
Observation model (data likelihood)	Mean of distribution for each class		
	Standard deviation of distribution for each class		
	Shape parameter (generalized normal distribution) for each class	The distribution of each class is a generalized normal distribution.	

Table 1: parameters of the HMT

We emphasize that parameters of the HMT are not set or chosen arbitrarily or empirically but all of them are automatically estimated from the observed PET, or CT, or the PET/CT intensities. To estimate the parameters we chose the iterative Stochastic Expectation Maximization (SEM) algorithm<sup>34</sup> which is a stochastic version of the EM algorithm<sup>34</sup>. The EM algorithm has been adapted to HMT<sup>25</sup>, and in the present work we used a SEM version adapted to the HMT model. The parameters are first initialized using a simple fuzzy c-means. The loglikelihood and conditional probabilities involved in the (S)EM rely on the use of backward and forward probabilities, in a similar manner as in HMC. Segmentation (assigning a class to the hidden states based on the tree structure probabilities and the observed data) is then obtained using the estimated parameters with the Modes of Posterior Marginal (MPM)<sup>35</sup> inference, a Bayesian estimator which associates to each site the most probable class given all the data. This estimator requires the computation of the posterior marginals. These are computed through the Baum-Welsh algorithm<sup>36</sup> by propagating information first from the “leaves” to the “root”, and then in the inverse direction, from the “root” to the “leaves”. In this work we used the conditional version of Baum-Welsh algorithm<sup>37</sup> to avoid underflow issues. More details can be found in<sup>25</sup>.

## 2. Pre-processing

The HMT model was applied to three different data representations. Observations in each node were defined as the intensity in each image voxel (as illustrated in figure 1) or its corresponding element in image obtained after pre-processing in the wavelet or contourlet domains.

The spatio-frequential (wavelet or contourlet) transforms provide the ability to exploit image information at different resolutions and directions, in order to better quantitatively describe the information provided by the observed data. The

192 use of images rebuilt after pre-processing in the spatio-frequency domain has been suggested recently for PET image  
 193 segmentation<sup>38</sup>. We thus decided to investigate the potential benefit of such an approach within our context of PET/CT  
 194 segmentation, considering the contourlets in addition to the wavelets.

## 195 2.1 Wavelets pre-processing

196 The wavelet transform (WT) is established as a powerful tool for statistical signal and image processing. In this work,  
 197 we used the isotropic undecimated wavelet transform (IUWT) based on the ‘à trous’ algorithm<sup>39</sup>. The non decimation  
 198 avoids the pseudo Gibbs phenomenon. The “à trous” algorithm decomposes an image  $I_0(x,y,z)$  into a list of wavelet  
 199 planes  $\{w_j(x,y,z)\}$  with intermediate smoothed planes  $\{F_j(x,y,z)\}$ . This approximation sequence  $\{F_j(x,y,z)\}$  is obtained  
 200 through  $N$  successive filtering with a 3D low-pass filter  $h^5$  related to a scaling function  $\phi_{3D}$  which must satisfy a number  
 201 of properties (compactly supported, regularity, symmetry, convergence in the Fourier space and derivability). B-spline  
 202 interpolations were chosen in this work. At each iteration  $j$ , the approximation image  $I_{j+1}$  is given according to equation  
 203 (2).

$$204 \quad I_{j+1}(x, y, z) = \sum_{m,n,o \in [-2;2]} h(m, n, o) I_j(x + m2^j, y + n2^j, z + o2^j) \quad (2)$$

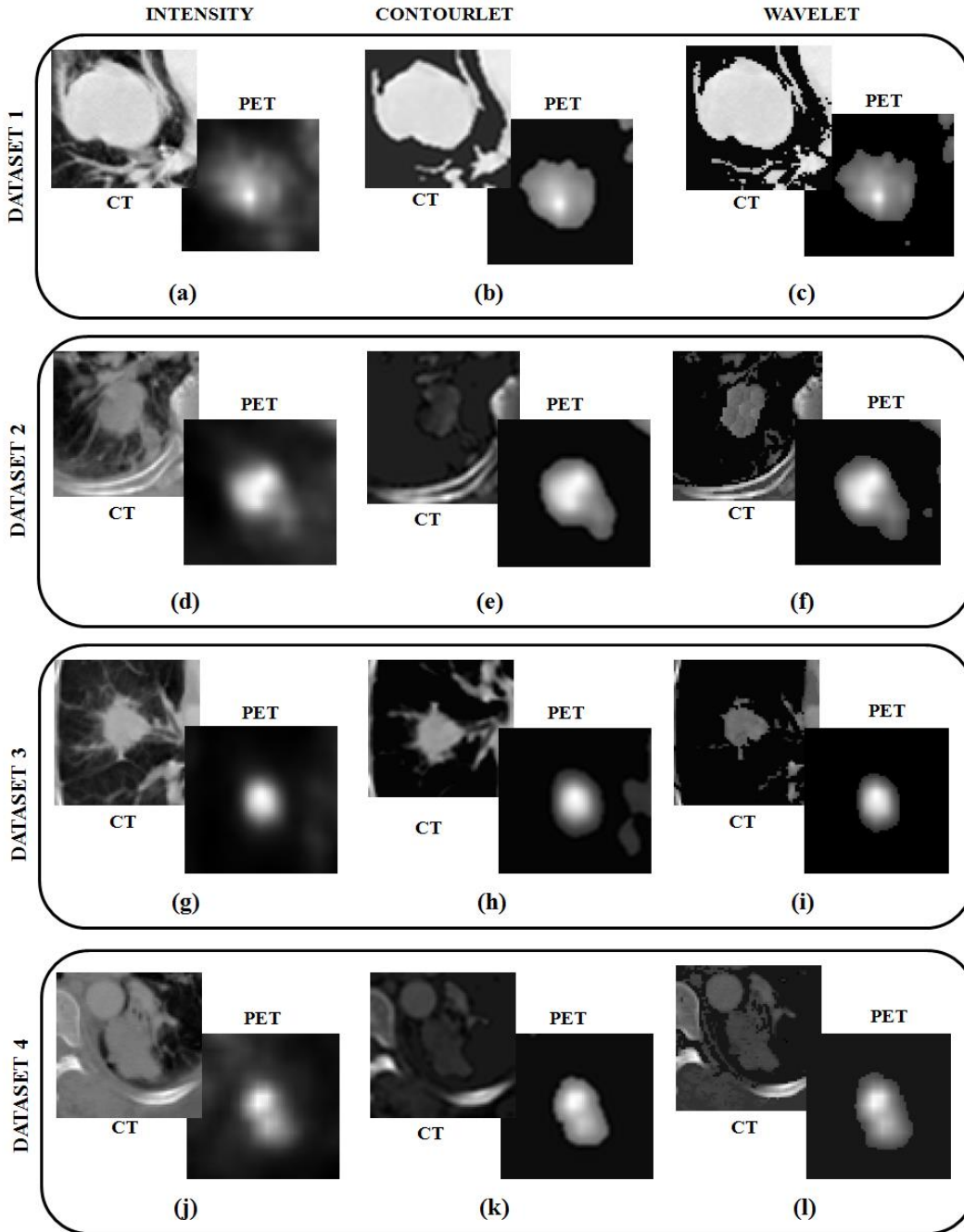
205 The wavelet planes  $w_{j+1}$  are defined as the differences between two consecutive approximations  $I_j$  and  $I_{j+1}$  containing  
 206 the details at a resolution level between  $I_j$  and  $I_{j+1}$  in such a way that the initial image  $I_0(x,y)$  can be rebuilt from its  
 207 details layers as in equation (3).

$$208 \quad I_0(x, y, z) = I_N(x, y, z) + \sum_{j=1}^{j=N} w_j(x, y, z) \quad (3)$$

## 209 2.2 Contourlets pre-processing

210 The Contourlet transform (CoT, to avoid confusion with CT, computed tomography)<sup>40</sup> is an extension of the WT using  
 211 non-separable and directional filter banks. Thanks to its remarkable properties (multiresolution, localization,  
 212 directionality and anisotropy), CoT is a more efficient tool than WT for capturing intrinsic geometrical structures of  
 213 images. CoT is implemented by the pyramidal directional filter bank (PDFB). In a first step, a Laplacian pyramidal  
 214 (LP) decomposition is applied to the image so as to obtain a number of radial subbands. In the second step, each LP  
 215 subband is decomposed into a power of two's number of directional subbands through a filter banks. In this work, we  
 216 used the non-subsampled contourlet transform (NSCT)<sup>41</sup>. First, the M-most significant coefficients from all subbands

217 are retained whereas the rest are set to 0. Second, the image is rebuilt using the selected coefficients. PET and CT  
 218 images and their wavelet or contourlet-based pre-processing results are illustrated in figure 2. In a previous work<sup>38</sup>, the  
 219 value M was arbitrarily set at 200 for PET. In our case we determined these values empirically by exploring values  
 220 between 100 and 3000. The best performance was reached for M=800 for PET images and M=2000 for CT images.



221

Figure 2: Four examples of PET/CT clinical datasets (a, d, g, j) preprocessed in the contourlets (b, e, h, k) or wavelets (c, f, i, l) domains. Note the increased contrast and loss of background details.

222

### 223 3. Evaluation study

#### 3.1 Simulated dataset

224 We have been advocating for a long time the use of realistic simulated datasets with voxel-based ground-truth as part of a rigorous  
225 validation framework for PET segmentation<sup>42, 43</sup> and have contributed in making such datasets available to the community<sup>44, 45</sup>.  
226 However these past efforts were focused on the PET component and did not include CT simulated images. For the present work  
227 in order to investigate the complementary value of PET/CT vs. CT-only or PET-only HMT segmentation, a digital phantom of a  
228 lung tumor located close to the mediastinum and the chest wall was designed and both a PET image and CT image were simulated.  
229 No breathing was simulated. The simulated PET was generated with GATE (Geant4 Application for Tomography Emission) and  
230 reconstructed following the same process as described previously<sup>44, 45</sup>. PET spatial resolution was ~4mm and voxel size of the  
231 reconstructed PET image was  $4 \times 4 \times 4$  mm<sup>3</sup>. The CT simulated image was generated using the same digital phantom used for the  
232 PET simulation. The CT simulation is based on a Monte-Carlo simulation where X-rays are created and tracked individually  
233 through the voxelized phantom using the Siddon projector<sup>46</sup> and attenuated following the Beer-Lambert Law. Compton and  
234 Rayleigh scattering were not computed. The simulation was performed using 360 projections around the phantom (1 projection  
235 per degree), and  $5 \times 10^9$  particles were created to achieve ~10000 counts/voxel in the histogram. The source aperture was 20 degrees,  
236 a focal spot size of 0 mm was simulated, and a mono-energetic at 60 keV was simulated to avoid beam-hardening artifacts in the  
237 final reconstructed image. A line detector composed of 750 pixel elements and 1 mm pixel size, was placed behind the phantom.  
238 The phantom was centered in the image space, the position of the X-ray source was (-700, 0, 0) mm and the position of the  
239 simulated detector was (350, 0, 0) mm. Finally, the simulated histogram was reconstructed using a maximum likelihood for  
240 transmission tomography (MLTR) algorithm based on a gradient-ascent method<sup>47</sup>. For this study, the CT data was reconstructed  
241 using 5 iterations and 72 subsets, 1 mm voxel size, and the final image was blurred with 1 mm Gaussian filter. As explained in  
242 section 1, the reconstructed PET image was up-sampled to be of same size as the CT dataset to be associated within the HMT  
243 framework. Figure 3 shows the digital phantom and the associated simulated PET and CT images.

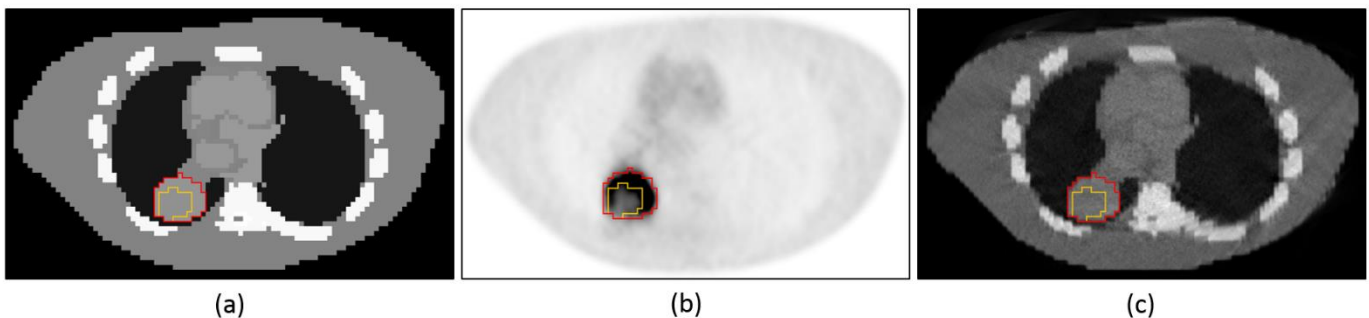


Figure 3. (a) Digital phantom with complete tumor ground-truth contour in red and sub-volume in orange, with a mean value of -5HU and 3 SUV. The rest of the tumor has a mean value of 20 HU and 12 SUV. Background uptake in the lung was set at 0.8 SUV whereas HU were set at -850. Bones were set at 700 HU. The uptake in the surrounding soft tissues (mediastinum) was set at 1.6 SUV and the HU at 40 and -80 (light and dark grey voxels respectively); (b-c) corresponding reconstructed and upsampled PET (b) and CT (c) images.

### 3.2 Clinical Datasets

244 The proposed methodology was evaluated on PET/CT clinical images. Fifteen patients with confirmed non-small cell  
245 lung cancer (NSCLC), stage Ib–IIIb, for which no obvious spatial mismatch between the CT and the PET images (due  
246 to respiratory motion and/or positioning differences between the two acquisitions) was observed, were analyzed. All  
247 patients underwent an  $^{18}\text{F}$ -FDG PET/CT examination for staging purposes before treatment. Patients were instructed  
248 to fast for a minimum of 6 h before examination. Free-breathing PET and CT images were acquired 45–60 min after  
249  $^{18}\text{F}$ -FDG injection. A total of seven 5-min bed positions with overlap were used for whole-body PET (Biograph  
250 PET/CT; Siemens) acquisitions, which were corrected for attenuation using the CT data and iteratively reconstructed  
251 using the ordered-subsets expectation maximization algorithm (4 iterations, 8 subsets). The noise levels in PET and  
252 CT correspond to standard PET/CT clinical acquisitions. Voxel sizes of PET and CT datasets were  $5.31 \times 5.31 \times 5 \text{ mm}^3$   
253 and  $0.98 \times 0.98 \times 5 \text{ mm}^3$  respectively. Spatial resolution of the PET scanner is estimated at 4.5 mm full-width at half-  
254 maximum (FWHM) in the center of the field of view, whereas spatial resolution of the CT scanner is estimated below  
255 1 mm FWHM. The PET and CT images were assumed to be co-registered at reconstruction. The PET images were up-  
256 sampled using a cubic B-spline interpolation scheme<sup>48</sup> so that it corresponds to the dimension of the CT image.

### 3.3 Surrogate of truth

257 In the simulated case, the ground-truth of the phantom was used. In the clinical dataset, all patients underwent surgery  
258 and the maximum diameter was measured on the surgical specimen, as previously described<sup>49</sup>. In the absence of other  
259 surrogate of truth such as histopathological volumes, the validation of the approach consisted in comparing automatic  
260 segmentation of the tumor with a statistical consensus of manual delineations performed by three different experts on  
261 each slice of the fused PET/CT images. The experts were asked to draw contours with the goal of defining a GTV for  
262 radiotherapy planning. The consensus was obtained using the simultaneous truth and performance level estimation  
263 (STAPLE) algorithm<sup>50</sup>, an expectation-maximization algorithm that computes a probabilistic estimate of the true

264 segmentation from a collection of segmentations. In order to strengthen the reliability of this consensus, the maximum  
265 diameter measured in histopathology was compared with the one measured on the STAPLE consensus. The maximum  
266 diameter was not further used for the validation of the proposed algorithm since we are interested here in spatial  
267 PET/CT overlap, which cannot be rigorously evaluated with the maximum diameter only.

### 3.4 PET, CT and PET/CT comparison

268 The proposed framework was first evaluated on the simulated PET/CT dataset, and then on the 15 clinical cases, by  
269 considering either the PET or the CT image only, then using both PET and CT images. Parameters of the HMT model  
270 as described in table 1 were in each case automatically estimated from the input images. They are therefore not set with  
271 the same values for each configuration (PET, CT and PET/CT) but iteratively estimated for each image and each  
272 configuration. Note however that the structure of the tree (1 father, 4 sons for instance) and type of statistical  
273 distributions (set as generalized normal distributions) are the same in all configurations since they are not estimated.

274 Note also that the segmentation algorithms are not applied to the entire whole-body datasets, but rather on a selected  
275 cropped volume around the tumor (as illustrated in figures 2 and 5 for instance).

### 3.5 Other methods for comparison

276 Segmentation results were also generated using the standard fuzzy c-means (FCM) algorithm and the fuzzy local  
277 information c-means (FLICM)<sup>51</sup> for comparison purposes. FLICM is an FCM implementation adding a weighted norm  
278 to account for outliers due to the noise and uses two parameters: a regularization parameter and the size of the  
279 surrounding kernel. We used the recommended parameters values (regularization equal to 1 and kernel radius equal to  
280 3 voxels)<sup>51</sup>. Alternative values for these two parameters were explored without obtaining improved performances.  
281 Both methods were implemented as multimodal, *i.e.* using as input vectors containing the intensities of both up-  
282 sampled PET and CT images. The input regions (cropped from the entire image) were the same for all methods under  
283 comparison.

### 3.6 Evaluation metrics and figures of merit

284 The performance of segmentation was assessed using Dice similarity coefficient (DSC), sensitivity (SE) and positive  
285 predictive value (PPV). Let us denote by  $V_T$  the true lesion volume,  $V_S$  the segmented volume,  $V_T \cap V_S$  the intersection  
286 between volumes  $V_T$  and  $V_S$  and size ( $V$ ) the size of volume  $V$ .

287 The sensitivity (SE) is defined as the ratio between the size of the segmented volume intersecting the true volume, and  
288 the true volume:

$$289 \quad SE = \frac{\text{size}(V_T \cap V_S)}{\text{size}(V_T)} \quad (4)$$

290 The positive predictive value (PPV) is defined as the ratio between the size of the segmented volume intersecting the  
291 true volume and the measured size of the segmented volume:

$$292 \quad PPV = \frac{\text{size}(V_T \cap V_S)}{\text{size}(V_S)} \quad (5)$$

293  
294 The combination of a high PPV and a low SE indicates an under-evaluation of the true volume, whereas the inverse  
295 indicates an over-evaluation of the true volume.

296 The Dice similarity coefficient (DSC) is a statistical measure of accuracy in image segmentation. This metric assesses  
297 the spatial overlap between the segmented volume ( $V_S$ ) and the true one ( $V_T$ ) and is defined as the ratio between twice  
298 the size of the segmented volume intersecting the true volume and the size of the sum of  $V_S$  and  $V_T$ .

$$299 \quad DSC = \frac{2 \times \text{size}(V_T \cap V_S)}{\text{size}(V_T + V_S)} \quad (6)$$

300

301 The Kruskal–Wallis rank test was used (Medcalc<sup>TM</sup>, Medcalc software, Belgium) to statistically compare the  
302 performance of each methods.

303

## 304 **RESULTS**

### 305 ***Validity of the manual consensus***

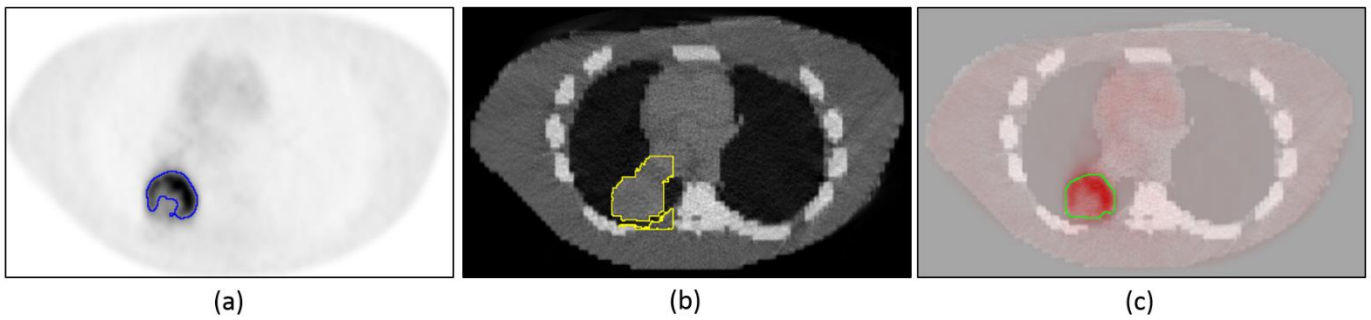
306 The consensus of three manual delineations led to volumes with a maximum diameter very close to the histopathology  
307 measurement, with a correlation of 0.91, and differences of  $9 \pm 7\%$ , which is in line with previous observations on the

308 same datasets by the original authors <sup>49</sup> and other studies <sup>55</sup>. This consensus of manual delineations can therefore be  
309 considered a reliable surrogate of truth for evaluating the proposed methodology.

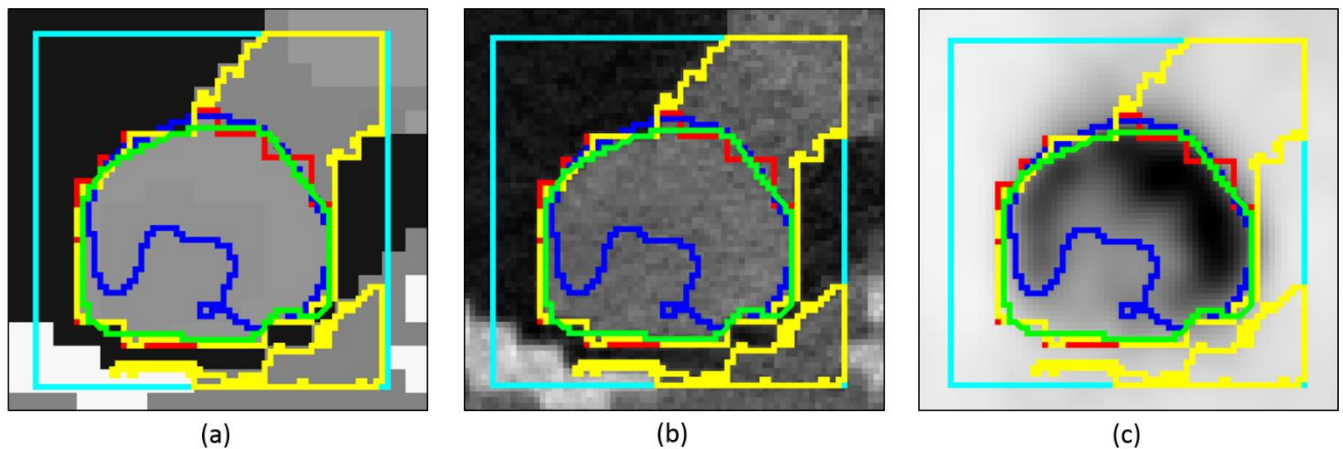
### 310 *HMT segmentation results*

#### 311 *Simulated dataset*

312 Figures 4 and 5 show the IHMT segmentation results considering only the PET, only the CT, or the joint PET/CT. The  
313 PET-only segmentation led to very high PPV (0.96) but low SE (0.65) (DSC of 0.77), due to the heterogeneous uptake  
314 of the tumor, although with no issue differentiating the rest of the tumor uptake from the surrounding normal tissues  
315 uptake. On the contrary the CT-only segmentation led to very high SE (0.98) but low PPV (0.64) (DSC of 0.77) due to  
316 the lack of contrast between tumor and surrounding normal soft tissues. The PET/CT combination led to a better  
317 coverage of the tumor with high SE (0.90) and PPV (0.97) (DSC of 0.93).



319 Figure 4. Simulated (a) PET, (b) CT and (c) overlaid PET/CT images with HMT segmentation on (a) PET only in blue, (b) CT  
320 only in yellow and PET/CT in green.





322 Figure 5. All contours reported to the digital phantom (a), the simulated CT (b) and the simulated PET (c). Cyan box corresponds  
 323 to the initial selection used as input. Red is the ground-truth, blue is PET-only segmentation, yellow is CT-only segmentation and  
 324 green is PET/CT segmentation.

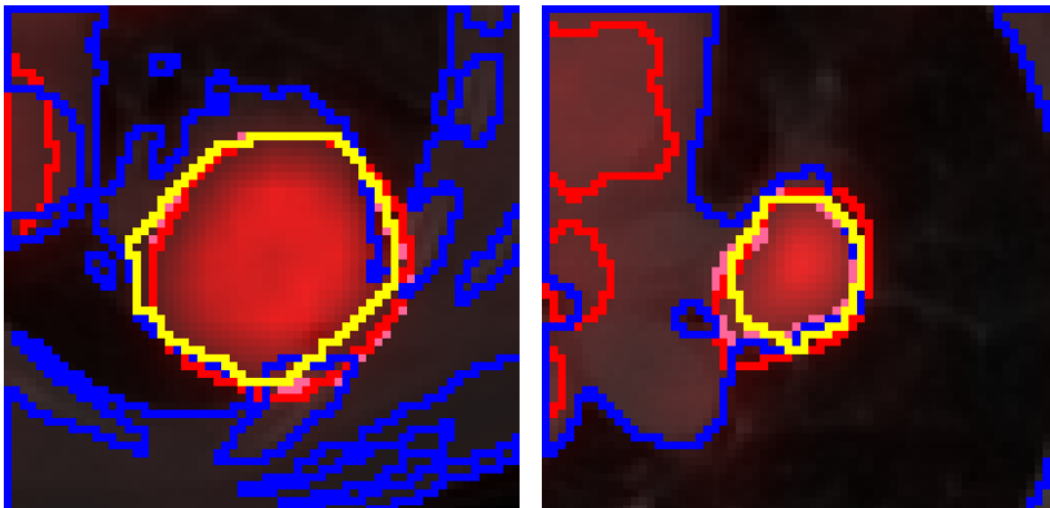
325 ***Clinical datasets***

326 Table 2 summarizes the DSC calculated respectively across the 15 cases, comparing IHMT applied to either PET or  
 327 CT only, or on PET/CT. The HMT on PET/CT obtained the best accuracy with DSC of  $0.89\pm 0.13$  compared to  
 328  $0.50\pm 0.28$  on PET only and  $0.48\pm 0.35$  on CT only. Using WHMT and CHMT the conclusions were similar with the  
 329 same hierarchy, with slightly better DSC, and a small advantage for CHMT over WHMT. The differences between  
 330 IMHT, WHMT and CHMT were not significant ( $p>0.1$ ).

	PET-only	CT-only	PET/CT
IHMT	$0.50\pm 0.28$	$0.48\pm 0.35$	$0.89\pm 0.13$
WHMT	$0.61\pm 0.29$	$0.56\pm 0.31$	$0.90\pm 0.12$
CHMT	$0.64\pm 0.23$	$0.59\pm 0.29$	$0.92\pm 0.11$

331 *Table 2: Performance of IHMT, WHMT and CHMT according to DSC for the 15 cases exploiting either PET or CT*  
 332 *only, or PET/CT.*

333 Figure 6 illustrates two examples of IHMT segmentation on PET only, CT only and PET/CT, showing a similar  
 334 behavior on a clinical case as it was shown on the simulated case.

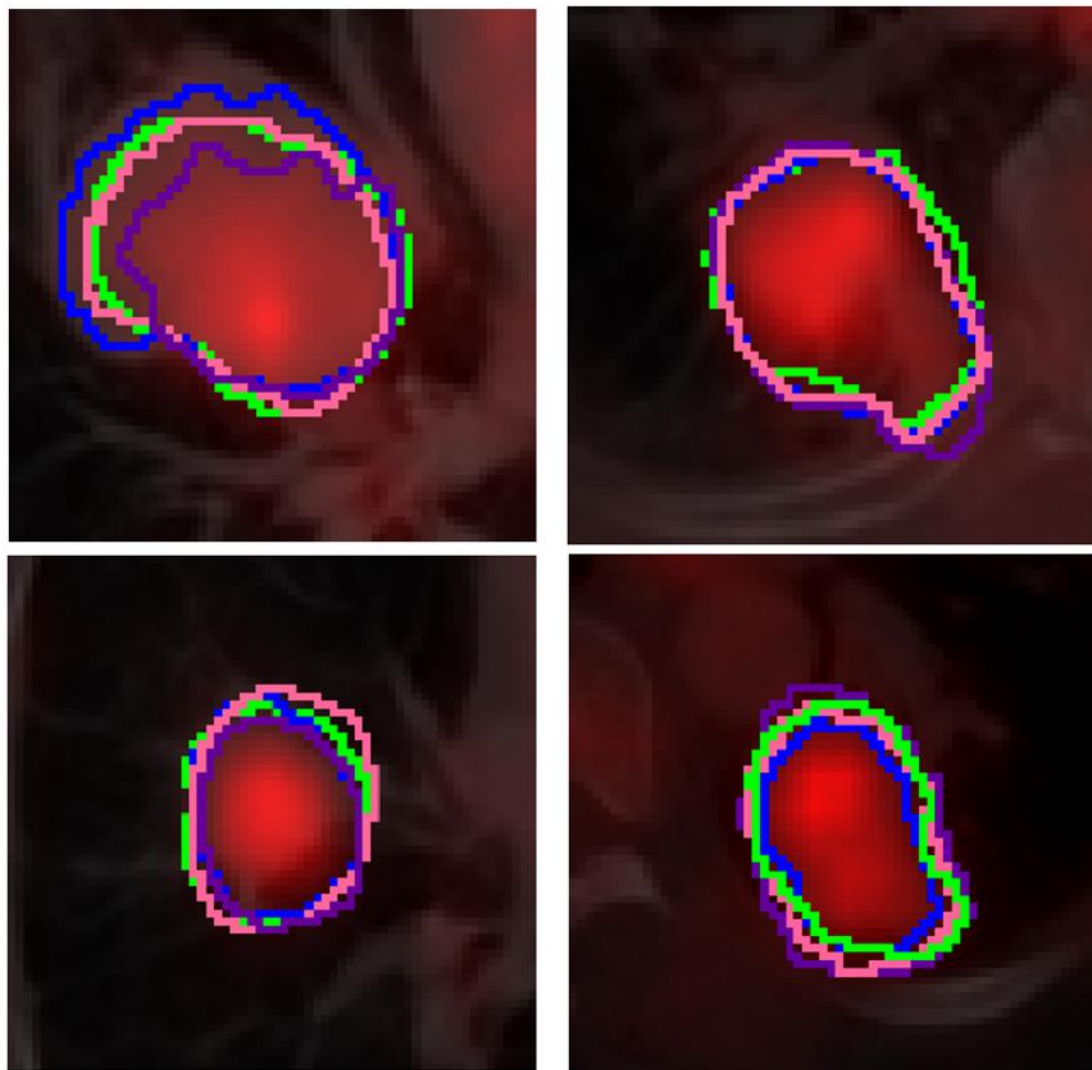


335

336 Figure 6: Comparison of monomodal (PET or CT) segmentation with multimodal PET/CT segmentation using IHMT  
337 on two cases. Yellow contour is the STAPLE consensus, whereas red, blue and pink contours are IHMT segmentations  
338 using PET only, CT only and PET/CT respectively.

339 Figure 7 shows 4 examples of HMT segmentations compared to the consensus of manual delineations for the PET/CT  
340 cases illustrated in figure 2.

341



342

343 Figure 7: Comparison of IHMT (blue), WHMT (purple) and CHMT (pink) PET/CT segmentations obtained on the 4  
344 cases from figure 2. Green contours are the STAPLE consensus.

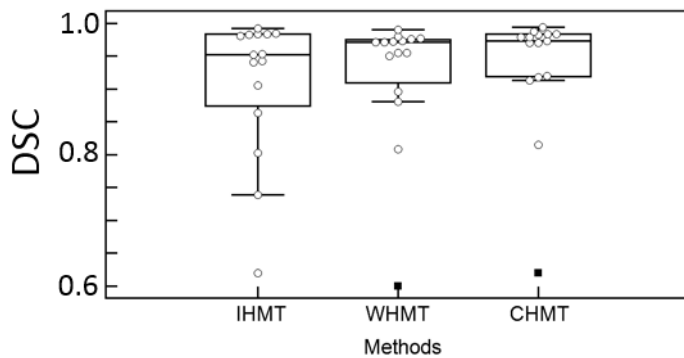
345 Quantitative results of all figures of merit calculated across the 15 cases are summarized in table 3, for IHMT, WHMT  
346 CHMT, FCM and FLICM. The three HMT methods led to an accurate tumor segmentation, characterized by high PPV,

347 SE and DSC values. CHMT slightly outperformed the two other methods with higher mean PPV, SE and DSC values  
 348 along with smaller standard deviations, thanks mostly to an improvement in sensitivity. There was however no  
 349 statistically significant differences between the three approaches. On the contrary, FCM and FLIMC led to significantly  
 350 lower accuracy ( $p < 0.01$ ), with slightly higher PPV but at the cost of a much lower SE ( $< 70\%$ ) resulting in mean DSC  
 351 below 0.8. The difference between FCM and FLICM was on the other hand not significant ( $p = 0.2$ ).

352

	FCM	FLICM	IHMT	WHMT	CHMT
SE (%)	$68.3 \pm 15.1$	$65.1 \pm 14.0$	$85.7 \pm 12.0$	$86.9 \pm 13.1$	$92.7 \pm 5.2$
PPV (%)	$89.9 \pm 7.7$	$92.6 \pm 8.0$	$85.2 \pm 9.3$	$86.3 \pm 16.4$	$86.1 \pm 7.4$
DSC	$0.73 \pm 0.19$	$0.75 \pm 0.16$	$0.89 \pm 0.13$	$0.90 \pm 0.12$	$0.92 \pm 0.11$

353 Table 3: Performance of FCM, FLICM, IHMT, WHMT and CHMT according to SE, PPV and DSC for the 15 patients  
 354 cases.



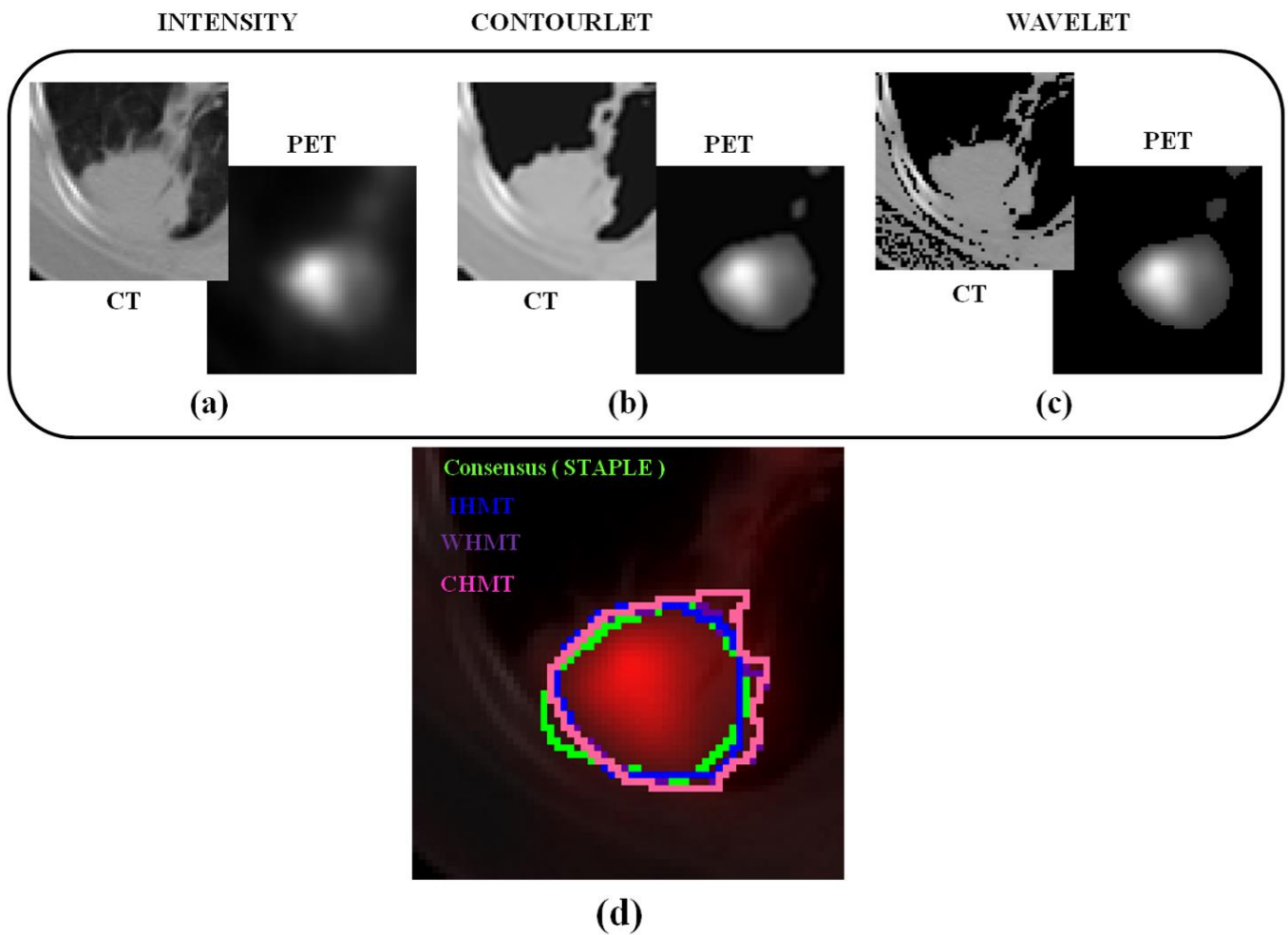
355

356 Figure 8 shows the distribution of the DSC across the entire patient datasets for the three HMT methods. Although the  
 357 differences between the three methods were not significant, smaller spread and higher values were obtained with  
 358 WHMT and CHMT compared to IHMT.

359

360 Figure 8: Distributions of the DSC values obtained by IHMT, WHMT and CHMT on the 15 cases.

361 In figure 9, we show an outlier case for which the DSC is 0.62, 0.60 and 0.62 for IHMT, WHMT and CHMT  
362 respectively. These results may be influenced by the tumor's neighborhood to the ribs and soft tissues in the lung.



363

Figure 9: Illustration of the outlier case: (a) PET/CT clinical dataset image preprocessed in the (b) contourlet or (c) wavelet domain and (d) comparison of IHMT, WHMT and CHMT contours.

364

## 365 DISCUSSION

366 The accuracy of GTV definition becomes crucial in order to exploit fully image-guided, intensity-modulated, motion-  
367 compensated radiotherapy treatment, for which margins that are added to the GTV to derive the clinical (CTV) and

368 planning target volume (PTV) are continuously reduced with each technical improvement. The manual definition of  
369 the GTV by radiation oncologists, which is time-consuming and prone to very high inter- and intra- observer variability  
370 therefore appears to be a major limiting factor amongst the automation efforts occurring in all other steps of  
371 radiotherapy treatment planning and delivery. It has been standard practice for decades to perform manual delineation  
372 of GTV on CT scans. However, over the last few years there has been a growing exploitation of  $^{18}\text{F}$ -FDG PET  
373 functional imaging in the radiotherapy practice. The addition of FDG PET as a complementary information within the  
374 treatment planning step by fusion of CT and PET datasets has been performed in order to improve tumor visualization  
375 and delineation by radiation oncologists. This has led to important changes in practice and guidelines for treatment  
376 planning in several cancer models including lung cancer <sup>56, 57</sup>, including smaller or larger irradiation volumes, higher  
377 inter- and intra- observer reproducibility, and faster delineation <sup>49</sup>.

378 Today radiation oncologists are therefore required to take into consideration complementary visual information using  
379 multimodality imaging when defining GTV. In addition to being used for dose calculation due to the correlation  
380 between Hounsfield units and electron density, CT has always been a modality of choice for manual delineation due  
381 to a high spatial resolution and rather homogeneous tissue densities. PET is intrinsically less well suited to the task as  
382 it suffers from limited spatial resolution, small reconstruction grids (and thus large voxels and limited spatial sampling),  
383 low signal-to-noise ratio and complex uptake distributions shapes and heterogeneities. PET however provides an often  
384 higher contrast between the tumor and healthy background, especially in challenging cases where the anatomical tumor  
385 volume is attached to the chest wall or mediastinum, or in cases of atelectasis. Manual delineation of PET/CT datasets  
386 remains a complex, tedious, time-consuming and less than ideally reproducible task <sup>58</sup>. Efforts to provide automated  
387 PET/CT tumor segmentations are therefore still necessary. This is going to become even more crucial as additional  
388 hybrid imaging is increasingly introduced in clinical therapy with the development of PET/MRI scanners. Despite  
389 these recent developments, the majority of commercially available automated and semi-automated segmentation  
390 algorithms do not usually consider more than one modality at a time.

391 Several works have recently addressed the PET/CT multimodal segmentation <sup>12-14, 19</sup>. A method based on a decision  
392 tree with K-Nearest Neighbors classifiers relying on textural features from both PET and CT images and originally  
393 developed for head and neck <sup>10</sup> was retrained for NSCLC <sup>14</sup>. This approach requires a training dataset to build the  
394 decision tree and is clearly dependent on it as it requires different training for each localization. Compared to a

395 consensus of 3 manual contours generated by STAPLE (similarly as in our study), it demonstrated very high specificity  
396 of almost 1, at the cost of low specificity ( $<0.7$ ) for a mean DSC of 0.61 only.

397 Another framework for the segmentation of multimodal PET/CT/MRI images models functional and anatomical data  
398 in a product lattice and applies simultaneous delineations of tumor regions based on a random walk algorithm<sup>12</sup>. Results  
399 in term of DSC were compared for PET-only, CT-only, MRI-only, PET-CT, PET-MRI and PET-CT-MRI  
400 segmentations, with mean values of 0.832, 0.878, 0.882, 0.914, 0.931 and 0.934 respectively, demonstrating increasing  
401 accuracy with each additional image modality being exploited by the algorithm. Our results comparing segmentations  
402 using either PET or CT only, or PET/CT, are in line with these observations, higher accuracy being obtained when  
403 exploiting both modalities.

404 Another approach used a HMF based segmentation of PET and CT image separately with a regularized term penalizing  
405 the segmentation difference between the two modalities<sup>19</sup>. PET/CT segmentation led to an accuracy of  $0.86\pm 0.05$  in  
406 terms of DSC which is comparable to our results, with however likely lower computational efficiency: HMT ensures  
407 better computational properties and faster estimation of parameters than HMF<sup>17</sup>. A similar approach was evaluated by  
408 comparing PET-only, CT-only and the association of PET and CT images through optimization of a HMF based  
409 segmentation with the graph cut algorithm, where each node is associated with a pair of corresponding voxels in PET  
410 and CT images<sup>13</sup>. More importantly, the method allows obtaining different segmentations on the PET and the CT  
411 through this co-segmentation framework. This original approach was compared with a standard fused PET/CT  
412 segmentation, the surrogate of truth being a manual delineation by a radiation oncologist on CT images with the  
413 guidance of PET images. The proposed method combining PET and CT led to a much higher accuracy than PET-only  
414 and CT-only in a set of 23 lung tumors (DSC of  $0.81\pm 0.08$  compared to  $0.66\pm 0.13$  and  $0.48\pm 0.27$  with PET-only and  
415 CT-only). However, the improvement of the proposed approach compared to a segmentation on fused PET/CT,  
416 comparable to our approach, (DSC of  $0.79\pm 0.08$ ) was not significant.

417 Note that the comparison with our results is challenging since these methods were evaluated on different datasets.  
418 However, we can also observe that the range of overlap values we obtained in the present work compared with manual  
419 delineation, is competitive or even better than those previously reported in similar evaluation settings.

420 In the present work, we developed a HMT based framework allowing the exploitation of several image modalities of  
421 the same object of interest (here, tumors). This framework was implemented under the assumption that the

422 segmentation would benefit from combining both modalities. We aimed at automating the manual task of the radiation  
423 oncologist in defining a single GTV from PET/CT images, contrary to a CT segmentation guided by PET (or the  
424 opposite). The proposed framework was evaluated NSCLC cases previously considered as a reference comparison set  
425 by several other studies<sup>16, 43, 59</sup>. Given our goal (a single GTV derived from both PET and CT images, as is performed  
426 by radiation oncologists), the validation protocol consisted in comparing automatic results with the surrogate of truth  
427 defined by a statistical consensus of three manual delineations, in order to address inter-observer variability. The  
428 accuracy was assessed using 3 complementary metrics in order to provide a full picture of the performance. In addition,  
429 we investigated the potential benefit of a pre-processing filtering step of the PET/CT images using either the contourlet  
430 (CHMT) or wavelet (WHMT) transforms.

431 Our proposed multimodal HMT framework achieved high overlap with the surrogate of truth HMT, providing balanced  
432 segmentation with high PPV and high SE (both >0.80). Overall, the results were slightly improved when applying the  
433 HMT framework on images filtered in the contourlet domain, although the difference was not significant. All HMT  
434 methods significantly outperformed ( $p < 0.01$ ) multimodal FCM and FLICM, which tended to under-estimate volumes  
435 (high PPV, low SE).

436 In this work, we proposed a joint-segmentation framework for anatomical and functional images that has the potential  
437 to combine more than two images (in the present study PET and CT), since extra modalities can be handled and  
438 analyzed simultaneously. As an extension of this work, we thus aim to test the proposed framework on PET/CT rectal  
439 cancer datasets<sup>60, 61</sup>, as well as MRI-PET and MRI-CT-PET datasets.

440 Our work has several limitations. The proposed framework assumes an appropriate co-registration of the considered  
441 images, with an accurate correspondence between PET and CT images. Data were acquired in free-breathing  
442 acquisitions and no correction for respiratory motion was applied. Datasets with obvious mismatches between PET and  
443 CT data were excluded prior to the present evaluation, as they would lead to strong bias in both manual and automatic  
444 segmentations. The inclusion of datasets strongly affected by respiratory motion would require pre-processing  
445 corrections outside the scope of the present study<sup>62, 63</sup>. In our NSCLC cases, bias due to breathing motion cannot be  
446 excluded, even after exclusion of the obvious cases. Other tumor locations with less/no motion could be considered  
447 such as head and neck or brain tumors, however we do not possess PET/CT images for such tumors for which  
448 histopathology measurements are available, the only dataset available to us consisting of head and neck PET images

449 only <sup>64</sup>. We did not use the maximum diameter measurement as an evaluation metric, because it would not allow  
450 differentiating spatial overlap differences between methods. It was however used to check the reliability of the manual  
451 consensus. Another limitation concerns the wavelet and contourlet pre-processing steps: we empirically set the  
452 threshold under which significant wavelets and contourlets coefficients were excluded. In the previous work that  
453 proposed the approach, the value was set arbitrarily at 200 without justification <sup>38</sup>. We found this parameter is quite  
454 robust, as choosing different values only lowered the accuracy of WHMT and CHMT to the level of IHMT. We plan  
455 to further improve the robustness of this step by implementing a case-by-case automated adaptive selection of the most  
456 significant coefficients. Our HMT-based approach could not be directly compared to other previously published  
457 advanced multimodal segmentation methods. These are indeed not freely available and are complex to implement,  
458 which was beyond the scope of the present work. The current efforts of the AAPM Task Group 211 for PET image  
459 segmentation benchmarking <sup>42</sup> are going to be expanded to address PET/CT segmentation. When ready, such a  
460 benchmark will allow a more comprehensive and direct comparison of various multimodal algorithms. We did not  
461 investigate our approach within the context of dose painting or dose redistribution/boosting, as our goal was to automate  
462 the definition of the GTV. Such a GTV could however constitute a starting point for a dose  
463 painting/boosting/redistribution strategy analysis within this GTV.

464 Although the HMT used to build the proposed framework showed interesting properties in terms of overall  
465 performance, robustness and stability, we will further investigate the use of more sophisticated HMT models, among  
466 which we can cite pairwise Markov trees (PMTs) that extend the classic HMT <sup>65</sup>. Another rich recent family of models  
467 are the triplet Markov trees (TMTs) <sup>66</sup>, which extend PMTs and combined with the theory of evidence (Dempster-  
468 Shafer), can be useful when dealing with non-stationary data <sup>67</sup>. These future developments could be exploited to deal  
469 with other applications of the framework such as partial volume effects correction, therapy follow-up using sequential  
470 PET/CT datasets, and fusion of multi tracer PET/CT datasets, or even motion characterization and correction.

471

## 472 **CONCLUSIONS**

473 In this work, we developed a framework based on HMT for multimodal image processing and analysis and investigated  
474 its relevance for multimodal PET/CT segmentation. Tumor delineation was performed by exploiting the hierarchical  
475 and multi-observation properties of a HMT to exploit the CT and the PET image simultaneously. The impact of pre-



476 processing in the wavelet and contourlet domains on the segmentation accuracy was also investigated. The proposed  
477 method led to high accuracy, the best results being obtained after filtering in the contourlet domain, with higher DSC  
478 and the best trade-off between sensitivity and positive predictive value. HMT models could be further applied to  
479 PET/MR and PET multitracer data. Validation of the PET/CT segmentation on datasets with full volume  
480 histopathological reference will also be investigated.

481

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486

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640

641

642 Appendix

643

644 Annex

645

646 Let  $S_0, S_1, \dots, S_N$  be successive scales, with  $S_0 = \{r\}$  containing just the root,  $S_1$  containing four children of  
 647  $r$ , and so on, as showed in Figure 1. Let  $S = S_0 \cup S_1 \cup \dots \cup S_N$  be the set of all nodes. For  $s \in S_n$ , with  $0 \leq n < N$ ,  
 648 we will denote with  $s^+$  the four children of  $s$  (which are in  $S_{n+1}$ ), and for  $s \in S_n$ , with  $0 < n \leq N$  we will denote  
 649 with  $s^-$  the unique parent of  $s$  (which is in  $S_{n-1}$ ). The distribution of the classic HMT  $(X, Y) = (X_s, Y_s)_{s \in S}$  used in  
 650 the paper is defined by  
 651

$$652 \quad p(x, y) = [p(x_r) \prod_{n=0}^{N-1} \prod_{s_n \in S_n} \prod_{s_{n+1} \in s_n^+} p(x_{s_{n+1}} | x_{s_n})] \prod_{s_N \in S_N} p(y_{s_N} | x_{s_N}), \quad (1)$$

653

654  $p(y_{s_N} | x_{s_N})$  are generalized Gaussian distributions modeling PET/CT images  $y_{s_N} = (y_{s_N}^{PET}, y_{s_N}^{CT})$ . Then the problem is  
 655 to compute  $p(x_s | y_{s_N})$  for each  $s \in S_N$ , which is the probability to have  $x_s = tumor$ ,  $x_s = notumor$ . Then co-  
 656 segmenting images  $y = y_{s_N} = (y_{s_N}^{PET}, y_{s_N}^{CT})$  consists of setting at each node  $s \in S_N$  “tumor” if  
 657  $p(x_s = tumor | y) > p(x_s = notumor | y)$ , and “no tumor” if not. Setting  $\omega_1$  as “tumor” and  $\omega_2$  as “no tumor” the co-  
 658 segmentation  $y = y_{s_N} = (y_{s_N}^{PET}, y_{s_N}^{CT}) \rightarrow \hat{x}_{s_N}$  is thus given with  
 659

$$660 \quad \text{For each node } s \in S_N : \hat{x}_s = \begin{cases} \omega_1 & \text{if } p(x_s = \omega_1 | y) > p(x_s = \omega_2 | y) \\ \omega_2 & \text{if } p(x_s = \omega_1 | y) < p(x_s = \omega_2 | y) \end{cases} \quad (2)$$

661

662 The computation of  $p(x_s | y)$  for each  $s \in S_N$  is made on two steps: Backward - Up step, and Forward - Down step.  
 663 For each  $S_n$  and  $s \in S_n$  let  $s^{++}$  be the set of all the descendent of  $s$  (which is the set of leaves of the sub-tree  
 664 having  $s$  for root), and let  $\beta^n(x_s) = p(y_{s^{++}} | x_s)$  for  $s \in S - S_N$ , and  $\beta^N(x_s) = 1$ . Then one shows:  
 665

$$666 \quad \beta^n(x_s) = \prod_{u \in s^+} [\sum_{x_u \in \Omega} \beta^{n+1}(x_u) p(x_u | x_s)], \quad (3)$$

667

668 which makes  $\beta^n(x_s)$  computable for each  $1 \leq n \leq N$ ,  $x_s \in S_n$ .

669 The core point is that the distribution of the whole tree  $X_S$  conditional on both observed images

670  $Y_{S_N} = y = (y_{s_N}^{PET}, y_{s_N}^{CT})$ , denoted as  $p^y$ , also is a Markov tree distribution, with  $p^y(x_r)$  and transitions  $p^y(x_s | x_{s^-})$   
 671 given by  
 672

$$673 \quad p^y(x_r) = \frac{p(x_r) \beta^1(x_s)}{\sum_{x_r \in \Omega} p(x_r) \beta^1(x_s)}, \quad p^y(x_s | x_{s^-}) = \frac{\beta^{n+1}(x_s) p(x_s | x_{s^-})}{\sum_{x_s \in \Omega} \beta^{n+1}(x_s) p(x_s | x_{s^-})} \quad (4)$$

674 Having calculated  $p^y(x_r)$  and  $p^y(x_s | x_{s^-})$  with (3), (4), probabilities  $p(x_s | y)$  for each  $s \in S_N$  are computed by the  
 675 following Forward – Down procedure.

676 Let  $s \in S_N$ . There exists an unique path  $s_1, s_2, \dots, s_N$  such that  $s_N = s$ ,  $s_{N-1} = s^-$ ,  $\dots$ ,  $s_1 = s_r = s_2^-$ . The  
677 distribution of  $X_{s_1}, X_{s_2}, \dots, X_{s_N}$  conditional on  $Y = y$  is then a Markov chain distribution, and  $p^y(x_s)$  is  
678 classically computable by:

679  
680 
$$p^y(x_{s_1}) = p^y(x_r)$$
 given with (4); for  $n = 1, \dots, N - 1$ : 
$$p^y(x_{s_{n+1}}) = \sum_{x_{s_n} \in \Omega} p^y(x_{s_n}) p^y(x_{s_{n+1}} | x_{s_n})$$
 (5)

681  
682 Finally the co-segmentation algorithm runs as follows:  
683

- 684 (1) For each for  $s \in S$  and for  $x_s \in \Omega$  compute  $\beta^n(x_s) = p(y_{s^{++}} | x_s)$  par Backward – Up procedure (3);  
685 (2) For each  $s \in S$  and  $x_s \in \Omega$  compute  $p^y(x_r)$ ,  $p^y(x_s | x_{s^-})$  with (4);  
686 (3) For each  $s \in S_N$  compute  $p(x_s | y_{s_N})$  with the Forward – Down procedure (5);  
687 (4) Perform co-segmentation using (2).