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Segmentation of lymphoma tumor in PET images using cellular automata: A preliminary study

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Abstract

Positron Emission Tomography imaging (PET) has today become a valuable tool in oncology. The accurate definition of the tumor volume on PET images is a critical step. State-of-the-art methods are based on adaptative thresholding and usually require user interaction. Their performances are hampered by the low contrast, low spatial resolution, and low signal to noise ratios of PET images. In this paper, we investigate an automated segmentation approach based on a cellular automata algorithm (CA). The method's results are evaluated against manual delineation on PET images obtained from 14 patients examinations obtained in clinical routine. Its performance is also compared to standard interactive PET segmentation algorithms (fixed or adaptive thresholding). Our method obtains an encouraging average Dice metric of 80.0%, a result comparable to the top methods. In case of small tumors, which are particularly difficult to segment, the method performs best among all of the state-of-the-art methods, both in terms of mean relative error volume (20.4%) and mean Dice metric (79.2%).

Keywords: Image segmentation; Lymphoma; PET images; Tumor segmentation

1. Introduction

Cancer will soon become the most common cause of death worldwide. In particular, the lymphoma, a blood cancer which affects the lymphocytes, is one of the most frequent cancers. Typically, lymphoma cells form tumors in the lymphatic system organs: lymph nodes, spleen and bone marrow. However, as lymphocytes can move to many parts of the body, the cancer can also affect other organs [1]. One of the most important imaging tools for cancer diagnosis and follow-up is Positron Emission Tomography (PET) [2–4]. In this context, the measurement of tumor volume on PET images is a critical step. Despite the poor resolution and low signal-to-noise ratio of PET images [5], many segmentation methods have been proposed for tumor segmentation, in order to automatize this task which can be time-consuming and prone to inter-expert variability when performed manually [6]. The first type of approaches are fixed-value thresholding, with a threshold usually defined in terms of standardized uptake value (SUV). A value of 40% of the maximum SUV (SUV_{max}) is typically used for lung cancer, cervical cancer and head and neck cancer, for instance [7–9]. The second type of approaches gathers adaptive threshold methods, which are among today's state-of-the-art approaches. The principle of these methods is to fit a model of threshold according to a few image parameters. Examples of such methods are Black, Nestle, Vauclin and Fitting, just to name a few [10]. The Black method [11] is based on a linear model. The mean SUV value inside the tumor is computed and iteratively updated thanks to the model. Nestle's method [8,12] proposes to define the threshold according to the mean SUV values of the tumor and the background. Contrary to Black's, this method is not iterative. The method of

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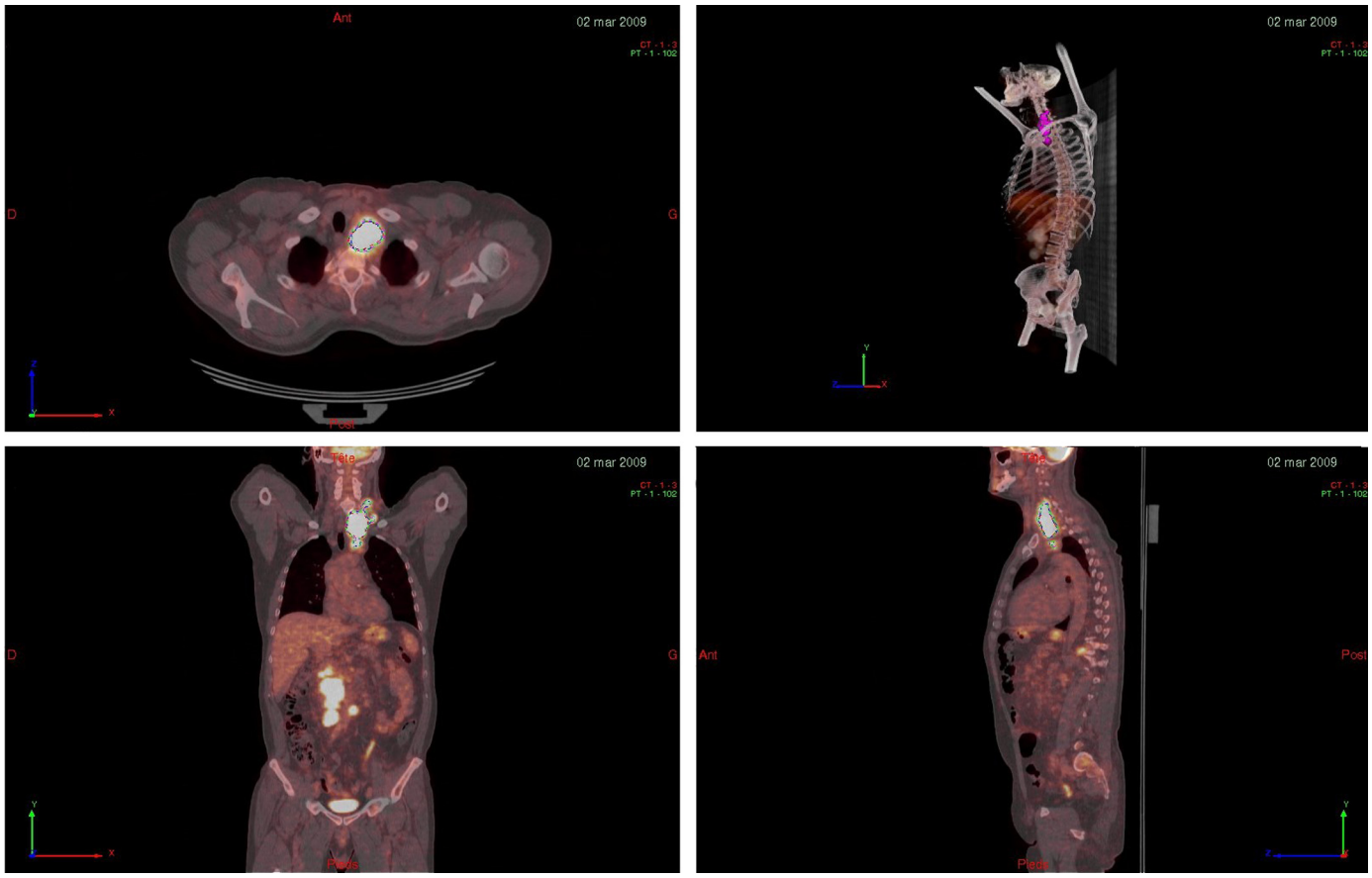

Fig. 1. Segmentation of a lymphoma tumor overlaid on full PET images. From left to right, top to bottom: axial view, MIP (maximum intensity projections) reconstruction, coronal view, sagittal view.

Vauclin et al. [13] uses a nonlinear model to estimate a contrast parameter in an iterative way similar to Black. The contrast parameter is defined as the ratio between the mean background SUV value and the mean tumor SUV value. The Fitting method [14] is based on an iterative algorithm that simultaneously estimates the mean intensities of the lesion and of its local background and also takes into account the spatial resolution of the camera. At last, other methods have been proposed, based on statistics [15], region growing [16], random walker [17,18]. Performances can vary among these methods, depending on the heterogeneous nature of the tumor and its size: in particular, small tumor are known to be challenging to segment [8].

Note that most of these methods have been mainly tested on lung or oesophegal cancer. Only a few methodologies have been proposed for lymphoma image segmentation, as it is particularly challenging: it can be located in various areas of the body, and the SUV decreases quickly after the beginning of the treatment [19]. Thus current works make use of different image modalities, such as CT [20,21], PET/CT [22] or PET only [23]. Typical segmentation for a lymphoma tumor overlaid on PET images is shown in Fig. 1. Inspired by the good properties of the cellular automata (CA) for segmentation of PET images without learning as shown by Kim et al. in a recent publication [23], we investigate the use of this algorithm for the segmentation of lymphoma tumor, and evaluate its performance against state-of-the-art adaptive thresholding algorithms. By using the CA algorithm, we hope that limitations of current state-of-the-art techniques will be overcome: local image properties and spatial neighborhood can be taken into account, contrary to thresholding techniques. The concept of cellular automata, introduced by Von Neumann in the 60s [24], is biologically motivated, based on bacteria growth and competition modeling. It has been used in a wide variety of dynamical models, in various application domains, and in particular in image processing for denoising and edge detection [25,26]. The first use for image segmentation is proposed in [27] for RGB images and the connection of the CA-based segmentation to the graph-theoretic methods has been established in [28]. In medical imaging, CA-based segmentation has been investigated and gave rise to new developments in [28,29] for brain tumor segmentation in MRI, in [30] for breast ultrasound images and in [31] for mammograms, among others. The original proposition of CA is an interactive algorithm [27]. We propose an automated initialization of the CA algorithm, in order to replace the usual user-defined seeds. Note that a preliminary version of this work has appeared in [32].

The remainder of the paper is as follows: in Section 2, we present the CA algorithm and the automated initialization. Sec-