

AUTOMATED REGIONS OF INTEREST (ROIS) TRACKING FOR PET-CT IMAGE SERIES USING CELLULAR AUTOMATA SEGMENTATION

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1. PURPOSE

Multi-modal PET-CT (positron emission tomography – computed tomography) is the preferred imaging technique for determining the extent (staging) of many common cancers, and is increasingly being used to assess treatment response because it can provide functional (PET) and anatomical (CT) information. To assess the response to treatment, scans are acquired at various times during treatment. The conventional imaging approach to evaluate response is to identify regions of interest (ROIs) in particular tumor sites and then manually track changes in size and tracer uptake across the multiple scans over time. The image volume, however, is large and the response to treatment at individual tumor sites is not uniform; hence the assimilation and interpretation of these parameters is not trivial. Other approaches include manually identifying the ROIs and then calculating the overlap among the segmentation of the ROIs from registered image series but such approaches do not take into account the changes in tumors that may occur due to movement, changes in body mass and marked changes in the size of the individual tumors.

In this study, we propose a new automated method to track changes across ROIs from series of PET-CT scans. We introduce the PET response criteria in solid tumours (PERCIST) [1] thresholding approach to automatically detect ROIs in the initial image scan and then use it to track all corresponding ROIs based on Cellular Automata (CA) segmentation [2,3] from the registered image series and exemplify our method to track 30 ROIs across multiple PET-CT scans.

2. METHODS

For each series of d PET-CT scans I^1, \dots, I^d ($I^n \in \mathbb{R}^3$; $I^n = \{I^n(\text{PET}), I^n(\text{CT})\}$) the $I^n(\text{CT})$ for $n=2, \dots, d$, images were registered to $I^1(\text{CT})$, and the resulting parameters were then used in the construction of the transformation indexes $T^1 \leftarrow T^n$. Affine followed by non-rigid B-spline registration algorithms were used to automatically transform the CT pairs. The indices $T^1 \leftarrow T^n$ were then used to transform the co-aligned PET to the CT space. The CT was used in the registration due to its better anatomical definition and higher resolution compared to the PET counterpart.

The registered PET images were then used to detect the ROIs using an automated PERCIST thresholding method [4]. PERCIST is a robust SUV thresholding method that calculates the SUV by combining normalised lean body mass (SUV_{LBM}) with a volume of interest (VOI) reference for the liver or thoracic aorta [1,5]. From the thresholded results, ROIs were derived as the group of voxels that had abnormal tracer uptake.

These ROIs were then mapped to images series T^0 to T^1 denoted as ROI i . For each ROI i , a bounding cube c was constructed and enlarged by 10% (denoted as $c+$) to account for changes in the ROI over the series. Within $c+$, CA segmentation model was applied to detect and segment all the uptake regions. A CA model can be defined as a triplet $A=(S, m, \delta)$ where S is a non-empty state set, m is the neighborhood system (26-voxels), and $\delta:S^m \rightarrow S$ is the transition function. The function defines the rule of calculating the voxels' state at $t + 1$ time step based on the state of its neighborhood at the previous time step t . The segmented ROIs were considered to be the same ROIs from a previous image series, and this process was repeated for all image scans in the series. If the foreground seeds and the backgrounds seeds had a similar average (empirically set to <20% difference), we considered the ROIs to be absent in the following scan in the next series.

3. RESULTS

The test data consisted of 24 whole-body PET-CT scans from 9 lymphoma patients (3 patients with 4 scan series and 6 patients with 2 scan series). The scans were carried out on a Siemens Biograph TruePoint scanner with PET and CT images aligned (hardware co-registration). From these scans, 30 ROIs were identified (including tumours and abnormal lymph nodes) as the ground truth; 3 instances where corresponding ROIs appeared among 4 scans and other 27 instances were an ROI appeared on the first scan but were not present on the following scans. An expert clinician's diagnostic report was used as the ground truth. Our method tracked all 30 ROIs across all the scans compared to the ground truth. An example is depicted in Figure 1 where an ROI was tracked among four image scan series (light blue) and another ROI (dark blue) appearing on the first but not on the second scan. As a by-product of full automation, ROIs belonging to normally occurring high FDG uptake regions, such as the brain, liver, kidney and the bladder were also detected and subsequently tracked; however these ROIs did not interfere with abnormal ROIs.

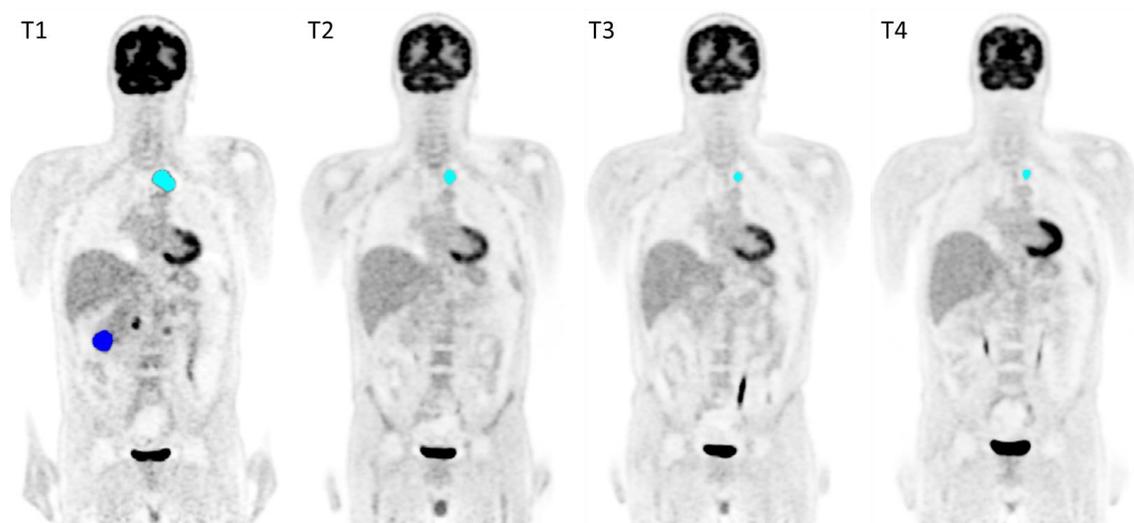


Figure 1. An example of two ROIs (light and dark shade of blue) being tracked among four scan series' T refers to timepoint.

4. CONCLUSIONS

We used an automated method to track ROIs across sequential PET-CT scans in patients with lymphoma who underwent treatment. Our preliminary results identified that our method was robust and in future work we will test our approach on a larger number of studies from different disease types.

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