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Automatic liver detection and standardised uptake value evaluation in whole-body Positron Emission Tomography/Computed Tomography scans

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ABSTRACT

Background and objective: Standardised Uptake Value (SUV), in clinical research and practice, is a marker of tumour avidity in Positron Emission Tomography/Computed Tomography (PET/CT). Since many technical, physical and physiological factors affect the SUV absolute measurement, the liver uptake is often used as reference value both in quantitative and semi-quantitative evaluation. The purpose of this investigation was to automatically detect the liver position in whole-body PET/CT scans and extract its average SUV value.

Methods: We developed an algorithm, called LIver DEtection Algorithm (LIDEA), that analyses PET/CT scans, and under the assumption that the liver is a large homogeneous volume near the centre of mass of the patient, finds its position and automatically places a region of interest (ROI) in the liver, which is used to calculate the average SUV. The algorithm was validated on a population of 630 PET/CT scans coming from more than 60 different scanners. The SUV was also calculated by manually placing a large ROI in the liver.

Results: LIDEA identified the liver with a 97.3% sensitivity with PET/CT images only and reached a 98.9% correct detection rate when using the co-registered CT scan to avoid liver misidentification in the right lung.

The average liver SUV obtained with LIDEA was successfully validated against its manual assessment, with no systematic difference (0.11 ± 0.36 SUV units) and a $R^2 = 0.89$ correlation coefficient.

Conclusions: LIDEA proved to be a reliable tool to automatically identify and extract the average SUV of the liver in oncological whole-body PET/CT scans.

1. Introduction

Positron Emission Tomography/Computed Tomography (PET/CT) is a fundamental tool in oncology, widely used in the staging, restaging and follow-up of different malignant pathologies [1,2].

Several studies [3] prospect the evaluation of PET/CT scans beside the conventional visual assessment, by means of quantitative and semi-quantitative tools. A standard visual assessment is based on the analysis of volumes of tracer hyper-concentration with respect to the surrounding background of healthy tissue. Its principle limitation is the requirement that the background to which the tracer uptake is compared be constant and independent of the patient physiological state [4]. This often is not the case, because either the patient lacks physiological condition or protocol-related factors affect the tracer uptake. The ^{18}F-Fluorodeoxyglucose (^{18}F-FDG) measured uptake, for example, depends on a variety of factors related to the scanning procedure and the actual scanner used for image acquisition [5].

The liver uptake in Standardised Uptake Value (SUV) units has therefore been proposed as a reference for PET/CT scan evaluation in different clinical settings [6], both in a qualitative (e.g., uptake of the lesion higher than that of the liver) and in a semi-quantitative way (e.g. lesion uptake higher than twice the liver uptake) [3].

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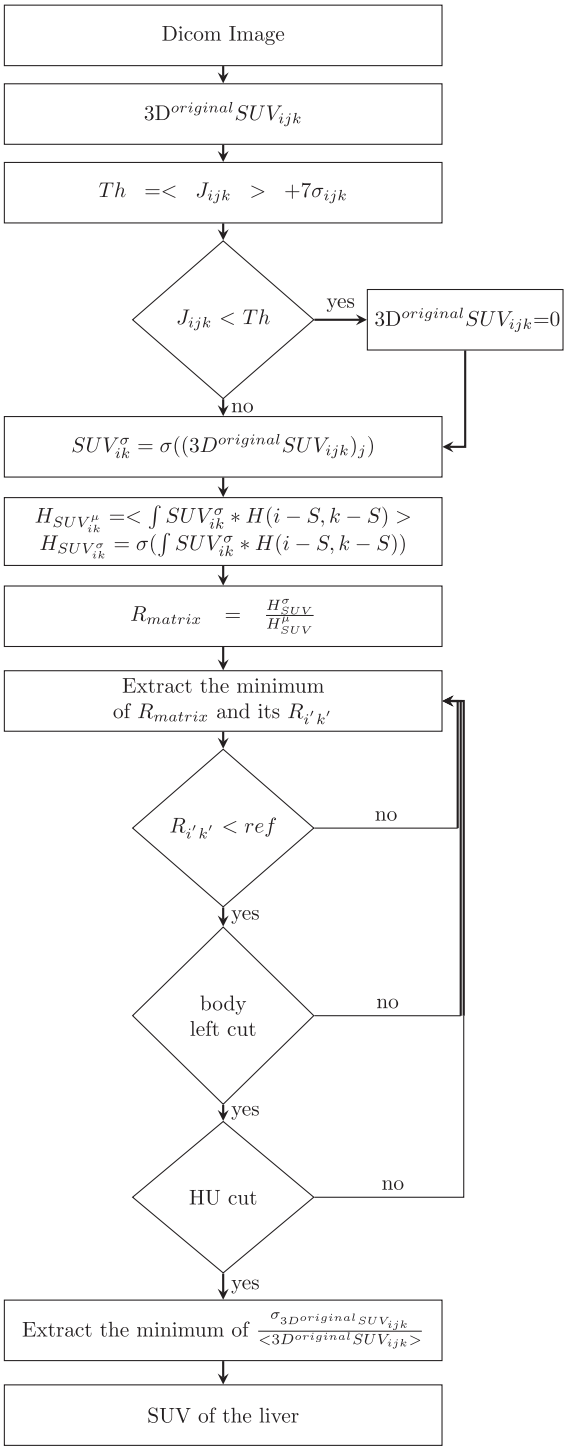

Fig. 1. Flow diagram of the algorithm.

Even though different independent factors such as body mass index (BMI) and blood glucose level (BGL) [7] influence the liver ^{18}F-FDG uptake, the average liver SUV remains nearly constant (within 5% of the maximum value) if the time delay between the tracer injection and the PET/CT acquisition is in the 50–110 min range, with a peak at about 75–80 min [8].

In this work we describe and validate a fully automated approach for the liver uptake measurement in whole-body FDG PET/CT scans, which enables the reproducible calculation of the liver tracer uptake and could become a powerful tool for the tumour-to-reference tissue ratio measurement in multi-centre clinical trials and be adopted for intra- and inter-patient comparison in clinical applications.

The method would be particularly useful in clinical research applications where the physiological variability associated with direct SUV measurements is unacceptably high and a reference value is necessary.

2. Materials and methods

2.1. Algorithm description

The LIver DEtection Algorithm (LIDEA), described in detail in the following, was conceived and structured with the goal of identifying the liver position and evaluating the average liver SUV in a whole-body PET/CT scan.

In order to find a large and homogeneous volume inside the 3D scan of the patient, that is a liver candidate, the following steps are taken:

1. Masking the voxels outside the patient body;
2. Projecting the 3D image on a single 2D coronal image, plane (*x*, *z*), of the patient;
3. Downscaling the 2D coronal image to obtain average and standard deviation values in volumes larger than the single voxel;
4. Finding the *x*, *y*, *z* position of the minimum of the ratio of the standard deviation to average SUV, so as to select a homogeneous volume with relatively high uptake (i.e., a liver candidate).

Initially, the 3D$^{original}SUV_{ijk}$ matrix containing the voxel data from the PET/CT slices is extracted from DICOM images. The SUV in a voxel is defined as:

$$SUV = \frac{[A_{tissue}]w_b}{A_{PET}}$$

where $[A_{tissue}]$ is the tracer activity concentration in the voxel, w_b is the patient body weight and A_{PET} is the total activity injected into the patient evaluated at the acquisition time. All the 3D$^{original}SUV_{ijk}$ matrix are rotated and translated so that the patient in the Head First Supine position. The first step of the algorithm is the removal of voxels outside the patient body from the $3D^{original}SUV_{ijk}$ matrix, that are identified as the exterior to the high gradient region between the patient and the surrounding air. The $3D^{original}SUV_{ijk}$ Jacobian matrix (J_{ijk}) is then computed and voxels with values below a threshold (Th) are masked.

The threshold is defined as the average Jacobian plus 7 times its standard deviation ($Th =< J_{ijk} > +7\sigma_{ijk}$) over two cubic volumes of 5 *cm* side in two different positions (anterior and posterior to the patient head). Starting from the most superior axial plane and moving in the cranial-caudal direction, all the J_{ijk} voxels that fail to meet the $J_{ijk} < Th$ condition are set to 0 in the $3D^{original}SUV_{ijk}$ matrix.

The second step is the $3D^{original}SUV_{ijk}$ projection on the coronal plane in 2D matrix, calculated as the standard deviation $SUV^{\sigma}_{ik} = \sigma((3D^{original}SUV_{ijk})_j)$ of the voxels along the projection direction (*y*-axis).

The obtained 2D matrix is then resampled with a pitch (S) so as to obtain the 2D matrices in (x, z) plane of the average (H^{μ}_{SUV}) and standard deviation (H^{σ}_{SUV}). The new matrices are composed of squared pixels of size S. From the $R_{matrix} = H^{\sigma}_{SUV}/H^{\mu}_{SUV}$ ratio, the $i'k'$ minimum position and its $R_{i'k'}$ distance from the centre of Mass (CoM) are determined.

If the $R_{i'k'}$ distance is higher than a reference value or if the $i'k'$ minimum position is located on the right of the CoM (body left), the $i'k'$ point is rejected. The algorithm iterates the search for the minimum until the conditions are satisfied. This step rejects points