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Automatic recognition of anatomical regions in three-dimensional medical images

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ABSTRACT

This paper presents a method that detects anatomy regions in three-dimensional medical images. The method labels each axial slice of the image according to the anatomy region it belongs to. The detected regions are the head (and neck), the chest, the abdomen, the pelvis, and the legs. The proposed method consists of two main parts. The core of the algorithm is based on a two-dimensional feature extraction that is followed by a random forest classification. This recognition process achieves an overall accuracy of 91.5% in slice classification, but it cannot always provide fully consistent labeling. The subsequent post-processing step incorporates the expected sequence and size of the human anatomy regions in order to improve the accuracy of the labeling. In this part of the algorithm the detected anatomy regions (represented by Gaussian distributions) are fitted to the region probabilities provided by the random forest classifier. The proposed method was evaluated on a set of whole-body MR images. The results demonstrate that the accuracy of the labeling can be increased to 94.1% using the presented post-processing. In order to demonstrate the robustness of the proposed method it was applied to partial MRI scans of different sizes (cut from the whole-body examinations). According to the results the proposed method works reliably (91.3%) for partial body scans (having as little length as 35 cm) as well.

1. Introduction

The application of three-dimensional (3D) medical imaging techniques is widespread in the clinical practice. Computed Tomography (CT) as well as Magnetic Resonance Imaging (MRI) is routinely applied in diagnosis, therapy planning, and monitoring. The number of cases to be processed is continuously increasing [1], so the computer assisted processing of medical images plays a critical role in healthcare. In order to facilitate various clinical workflows several algorithms have been developed for segmentation, registration, or visualization of medical images. These medical image processing methods are usually specialized to anatomy regions or organs. There are clinical applications for lung nodule detection, virtual colonoscopy, cardiac or cerebral vessel analysis, tumor follow-up, etc. Furthermore, many clinical workflows are specialized to a region of interest (ROI). For example, in radiation therapy planning the definition of the organs at risk varies among anatomy regions. Even basic functionalities such as visualization can be specialized to the organ of interest (e.g. lung CT exam is read using different window/level setting in comparison with abdominal or brain cases).

Automated pre-processing functions (e.g. atlas-based organ segmentation) are part of most medical image processing systems. Having no information about the anatomy regions included in the imaging examinations, these functions are usually triggered by pre-defined keywords inserted in the description of the image series. Since the description is filled in by a human operator, simple typos can result in incomplete processing of cases, the correction of which takes expensive time from the physician. The DICOM standard involves tags to specify the anatomy location for each slice of an image series, but it has undefined value in most of the cases [2], so an automated function cannot rely on that.

From the above-mentioned examples one can see that the automated detection of anatomy regions in 3D medical images would have great impact to content-based medical image processing. It would create many opportunities to automate or optimize various types of algorithms (i.e. initialization of segmentation or registration methods), which would save significant amount of time and workload for the clinicians. Therefore, the need for automated detection of anatomy regions does not directly come from the user, but its benefits would be definitely welcomed in medical image processing.

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2. Related work

As early as 1998 the necessity of a well-defined anatomical knowledge representation has been recognized [3]. This idea has revealed that an anatomical ontology could serve well in an automatic medical image processing workflow as a primary source of anatomical information.

The usage of medical Picture Archiving and Communications Systems (PACS) is now part of the daily clinical routines. Florea et al. [4] have compared the automatic image categorization capabilities of different PACSs and have found that these systems are capable to recognize the main anatomical structures even in complex environment. However, the reliability of the recognition has been highly various among the different body regions.

Other research groups have mainly focused on organ or anatomical landmark point detection [5–7]. They have used probabilistic algorithms to automatically define salient landmark points that can be used to navigate through the body scans. Their methods have focused on CT scans only, mainly using full body scans.

Other techniques have been developed to estimate the location of the axial slices in the human body scans [8–10]. They have used various methods and their accuracies varied between 16.6 mm and 28.3 mm, but they have considered CT modality only.

Atlas based registration methods are also available for anatomy detection. The most related approach [11] performs a non-rigid registration to align a statistical model to a full-body MRI scan, but its usability is limited to full-body MRI scans.

The recent VISCERAL challenge [1] has also showed that the automatic anatomy detection is still a very active filed of medical image processing research and could be well utilized in the clinical practice. In [12] He et al. have used a region of interest (ROI) detection for their multi-organ segmentation framework which is a similar task to the anatomy detection. Their work has considered CT modality.

Other works have considered the MRI modality as well. In [13] the authors have used their manifold learning method to classify the axial slices of a low-resolution preliminary scan to estimate the patients position. They have achieved a classification result above 90%. A similar approach have been used in [14] for slice classification and a 94% overall correct classification rate has been reported.

Similar to [5], Criminisi et al. have extended their method to analyze MRI images as well in [15] and [16]. They have achieved high precision in landmark detection in MRI exams.

In summary, the existing methods consider CT and MRI images and focus on landmark point or organ detection. A smaller part of the works has focused on the direct classification of the axial slices of a 3D image. It has not received much attention yet and none of the previous algorithms did consider working with partial body images, where the spatially coherent labeling of the axial slices is even more challenging.

The goal of the presented work was to develop a fully automated method that can label each slice of a 3D image series according to its anatomical location. The method shall recognize the main anatomy regions, shall handle whole as well as partial body series (to cover all clinical scenarios), shall be robust to patient variations (sex, age) and abnormalities (obesity, pathology), shall not have extreme computation demand, and shall be easy to adapt to any common 3D medical image type, so that it can be used in wide range of clinical applications.

3. The data set

The set of 49 full body MRI cases referred in this paper was acquired for research purposes in the University Hospital Zurich. The acquisitions were performed with a Discovery MR750w MRI scanner using the same protocol (LAVA-Flex sequence, T1 weighted, FA/TR$=5°/3.7$ ms, acquisition matrix$=256 \times 128$, 75% phase FOV, scan time 17 s, TE1/TE2$=1.15$ ms/23 ms). The images included all major anatomical regions, the head and neck, the chest, the abdomen, the pelvis, and some part of the legs as well. The test images involved male and female patients of different age (adults only) and level of obesity. The axial resolution of each image was 512×512 pixels. The number of slices varied between 260 and 864 slices (average 447). The pixel size was between 0.39 mm and 1.37 mm (average 0.91 mm), the slice thickness was between 0.47 mm and 8.8 mm (average 5.79 mm). The applied T1 protocol introduces some modality specific image property, but it does not reduce the usability of the method as T1 or some similar protocol is available for all MRI devices and its acquisition is part of the regular MRI examination process.

The image data set was manually labeled. The axial slices were annotated as LEG, PELVIS, ABDOMEN, CHEST or HEAD&NECK. The definition of these classes was based on the basic structure of the human body. The LEG begins at the bottom of the MRI scan and ends where the two legs join, which is the beginning of the PELVIS. The ABDOMEN begins at the top of the pelvic bone and ends at the top of the liver that is the beginning of the CHEST. The HEAD begins at the top of the shoulders and ends at the top of the head. The test dataset involved 21401 manually labeled axial slices. Based on the manual labeling the average size and the variance were calculated for each region, which is presented in Table 1.

Table 2 presents statistics about age, height, and weight of the scanned patients. The data set contained 20 female and 29 male patients.

4. The method

The proposed method consists of three main steps. In the first step the axial slices of the image are separately pre-processed. This is required to eliminate several disturbing image artifacts and to reduce image complexity. In this step the axial images are normalized, so that they can be used in a uniform way in the further processing steps. This is followed by a classical image recognition step that uses 2-dimensional feature extraction and a machine learning approach to classify the individual axial slices of the image by assigning the probability of each label to each slice. To calculate the feature vectors a global shape feature extraction algorithm is applied called the Zernike transform. It is followed by a feature vector size reduction method using Principal Component Analysis (PCA). This way a compact representation is generated for each slice. The feature vectors are further processed by a Random Forest classifier. This machine learning approach assigns a probability for each label to an input slice. The parameters of the PCA transform and the classifier are estimated during the training process. In the final step a post-processing method is applied, a three dimensional coherence inspection method, which takes the valid sequence and the mean size of the anatomy regions into consideration to eliminate the false slice classifications and guarantees the correct order of labels and the correct size of the

Table 1
Size of the anatomical regions.

Region	Average Size (mm)	Variance
LEG	179.56	85.31
PELVIS	206.73	27.19
ABDOMEN	207.83	38.47
CHEST	188.39	33.82
HEAD&NECK	234.08	16.78