3-D TUMOR DETECTION FROM KIDNEYS USING ULTRASOUND IMAGES

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Abstract—*In this review article we describe how 3D ultrasound imaging overcomes these limitations. Specifically, we describe the developments of a number of 3D ultrasound imaging systems using mechanical, free-hand and 2D array scanning techniques. The research presents a work of fiction multifunctional platform focusing on the clinical diagnosis of kidneys and their pathology (tumors, stones and cysts), using a "templates"-based technique. As a first step, specialist clinicians train the system by accurately annotating the kidneys and "3-D golden standard models" is used to compare the results.*

Keywords : *Abnormalities detection, automatic annotation, kidney,kidney pathology.*

I. INTRODUCTION

One of the major goals of computerized medical imaging analysis is to automatically detect, identify and delineate anatomical and pathological structures in 3D medical images. 3D modeling of these structures then allows for easier and more extensive visualization and exploitation of images. In hepatic surgery, medical imaging is used to detect and localize hepatic lesions and their relationship to vascular structures, especially the portal vein that defines the hepatic functional anatomy consisting of several anatomical segments1,2. There are several different definitions for dividing the liver into functionally meaningful parts that represent the resection unit. Different authors have proposed the division of the liver into two *hemilivers*, or into four segments based on the Goldsmith and Woodburne definition3 or into eight subsegments based on the Couinaud definition4 which is today considered the international standard. In order to detect lesions and to localize vascular networks defining the anatomical segments, radiologists currently use helical Computed Tomography scan images with intravenous contrast infusion

(helical CTI). In these images, tumors appear as dark nodules within bright hepatic tissues whereas vessel trees appear as a network brighter than the liver parenchyma. However, detection of the lesion or localization of the vessels is often difficult to process due to a variable image contrast between liver parenchyma and vessels, and also due to an important image anisotropy, the slice thickness being three times

larger than the pixel width.Initially, a clinician invokes a fast version of the region growing segmentation algorithm and a set of advanced correction tools to semi automatically detect and annotate the regions of interest (ROI), and to annotate the organs and their potential abnormalities (tumors, stones and cysts) in a specific MRI dataset. Next, a medical technician defines the rules and parameters for the automatic recognition framework and thus generates 3-D models of the organs and their potential pathology similar to the ones defined by the clinicians. This produces a "template" that includes all the "sensitivity" parameters that govern the dataset that come from a specifically calibrated MRI. The final step is for any user to apply this template's Clinician's [or Golden Standard (GS)] Volume Model versus the Medical Technician's (MT) Volume Model. settings to all other datasets of the same type and automatically identify the organs and their dysfunctions.

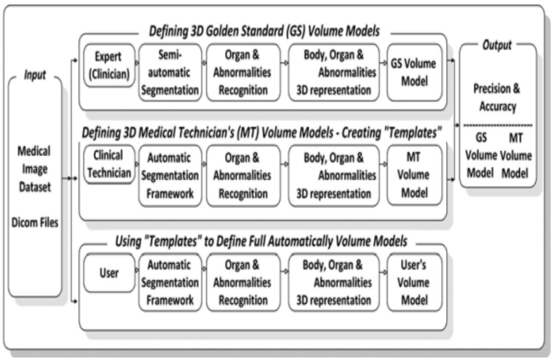

Fig. 1. Methodology used for the evaluation of the automatic segmentation framework

This semiautomatic tumor detection system has a number of advantages over the existing systems given as follows:

1) ATD is not only a method, but a multifunctional platform supporting real-time processing;

2) it simultaneously detects organs as well as their pathology (tumors, stones and cysts) with increased accuracy;

3) Processing time is faster than the existing methods, as the main algorithms and additional controls run “on the fly.” The processing time for a 24 slices MRI dataset is about 1 min;

4) a novel mechanism for the seed pixel method avoids selection of irrelevant isolated pixels (implementing a top-down connectivity analysis between slices);

5) the system achieves more accurate results for the recognition of kidneys compared with the existing methods by implementing additional controls.

Fig 2: 2D ultrasound suggestive of multiple calculi

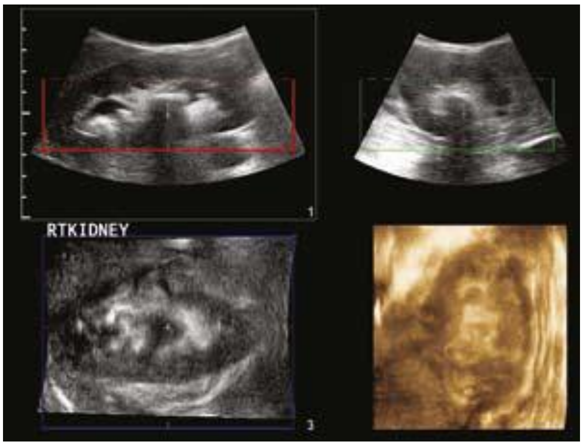

Fig 3: Volume ultrasound

II. FIRST STAGE: KIDNEYS DELINEATION AND IMAGE IMPROVEMENT

Kidney and spleen delineation is more difficult due to their intensity variation. The solution is based on the gray-level histogram analysis of the image limited to regions including the spleen and kidneys. Indeed, the right inferior quarter of the image contains essentially a part of the liver and the right kidney, whereas the left inferior quarter of the image contains only the right kidneys and the spleen. Thus, a comparative analysis of the gray-level histograms allows us to find the intensity range of kidneys, spleen and liver parenchyma, identically localized on both histograms. After delineate the kidneys and the spleen by performing a thresholding followed by morphological operators. After all of these anatomical structures are removed from the original image, then finally extract Kidney . From several existing methods, we chose to use the Montagnat and Delingette method5 who proposed an hybrid deformation framework that consider the global transformations computed in the registration framework as a deformation field similar to the local deformation field of the deformable models scheme. This method applies thus to each *S(i)* vertex of the model with a locality parameter *l*, a combined force *f(i)*:

$$f(i) = (1-l) * GlobalForce(i) + l * LocalForce(i)$$

It is possible to apply to the model in this single framework completely local ($l=1$), completely global ($l=0$) as well as any intermediate ($0<l<1$) force between those two ends. This framework introduces a global constraint in the deformation process that may be scale through the *l* parameter. It makes models more reliable: they are less noise and outliers sensitive. Moreover, the geometric quality of meshes produced by the deformation scheme is better. Application of this method to liver delineation first requires the initialization of a 3D reference model in the image. In order to obtain a liver contour by deformation, it is easier and more reliable to use an initial model with a similar shape. This model is a liver template computed onto visible human data of the *National Library of Medicine*. Delineation is then composed of several stages. Fig. 1 and 2 respectively represent the liver template being bent along each stage and its cut superimposition onto on of the CT scan slides.

III. PROBLEM DEFINITION

In this topic I have studied different problems in multiple forms for semiautomatic 3-d detection of kidney and their pathology in real time. The different types of problems are studied below:

- In medical image analysis, the main problem is that the outcome must be compared with a baseline (Golden Standard model) in order to validate the performance of the image processing algorithms applied to the dataset.
- A problem currently under consideration is the size of the files used to store the different labels and segmented regions.
- The problem with the fuzzy transition zones at the boundaries of the designated areas of interest (e.g., kidney), advanced versions of the pencil and eraser correction tools are integrated in the platform (working with areas and not with pixels), to automatically keep the similar neighboring points connected, providing clinicians with the option to swiftly refine their delineations.
- A problem of detecting the ROI 3-d detection of kidney and their pathology.

IV. OBJECTIVE

To improve the planning of hepatic surgery, we have developed a fully automatic anatomical, pathological and functional segmentation of the liver derived from a spiral CT scan. The following are the objective of project work:

- The main objective is to implement 3-d detection of kidney and their pathology in real time.
- To facilitate the management of the increasing number of medical images using user-friendly tools to ensure accurate and timely diagnosis in the clinical environment.
- The size of the files used to store the different labels and segmented regions.
- Support medical data exchange (telemedicine).
- Assist in the training of clinicians to recognise and treat pathologies.

V. METHODOLOGY

The project is to implement 3-d detection of kidney and their pathology in real time. It is based upon GUI (graphical user interface) in MATLAB. It is an effort to further grasp the fundamentals of MATLAB and validate it as a powerful application tool. There are basically different files. Each of them consists of m-file and figure file. These are the programmable files containing the information about the DICOM and different algorithms to detect the kidney and their pathology in real time.These aims were achieved by carrying out the steps below:

1. The Region of Interest is defined.
2. The parameters used to accurately find the organ and its boundaries are defined: Width (for smoothing the histogram and get the correct boundaries of the organ), ascending and descending (for identifying local minimums), threshold (for removing the noise from the use of erosion—dilation morphological filters) and area (for initial identification of the organ ignoring tiny areas).
3. The parameters to find the correct seeds for the pathology detection to feed to the region growing algorithm are also defined: Grayscale and a tolerance value for the range of values to represent a dysfunction, as well as a threshold value for the erosion filter used to change the sensitivity governing the discard of seeds that are not strong enough.

Parameter to be calculated:

- Accuracy, the proportion of true results (“True Positives” and “True Negatives”) in the total population of the results.
- Precision, the proportion of “True Positives” against all the positive results (“True Positives” and “False Positives”).
- Sensitivity, the ability of the system to identify positive results. It measures the proportion of positives which are correctly identified as such.
- Specificity, the ability of the system to identify negative results, meaning that it measures the proportion of negatives correctly identified as such.

VI. RESULTS

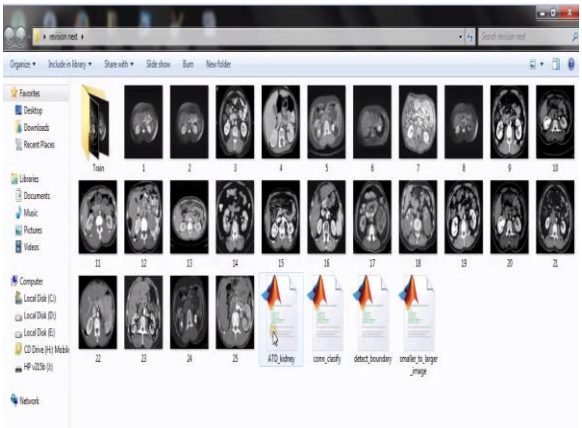

Figure 4: Data set of images

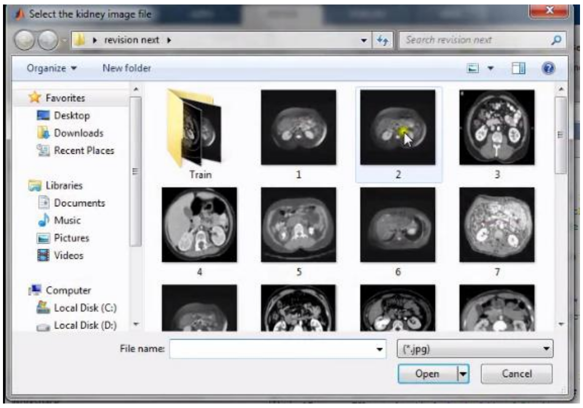

Figure 5 Browse the image from Data set of images

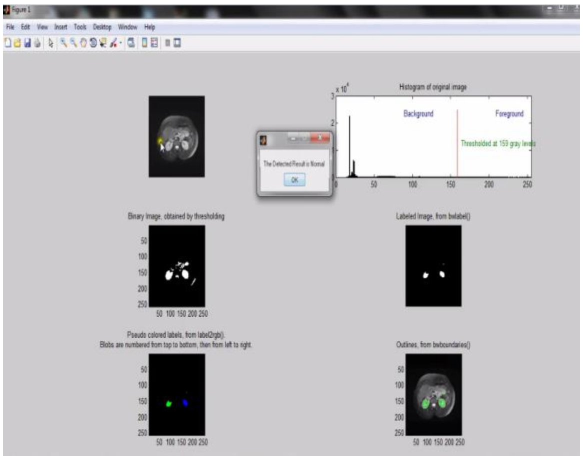

Figure 6:Result without abnormalities

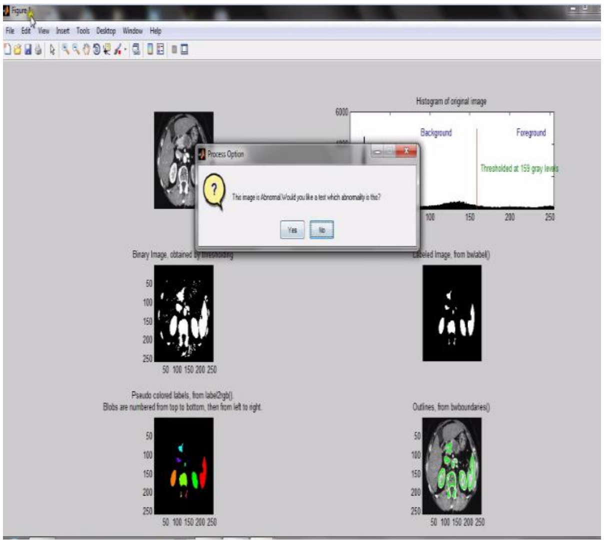

Figure 7: Result with abnormalities

VII. CONCLUSION

The study describes the methodology used to create the automatic segmentation of the kidney with delineation of important anatomical, pathological and functional structures from a routine CT scan. Using the methods proposed in this study, the semiautomatic detection of kidney is performed with the help of ROI algorithm .This work, may allow an improvement in preoperative planning of hepatic surgery by more precisely delineating liver pathology and its relation to normal hepatic structures. In the future this data may be integrated with computer-assisted surgery and thus represents a first step towards the development of an augmented reality surgical system.

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