An Effective Semi Automatic 3D-Detection of Tumors in Kidney's Images

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Abstract

This research presents a novel 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 their abnormalities creating "3-D golden standard models." Then, medical technicians experimentally adjust rules and parameters (stored as "tem-plates") for the integrated "automatic recognition framework" to achieve results which are closest to those of the clinicians. These parameters can later be used by no experts to achieve increased automation in the identification process. The system's functionality was tested on 20 MRI datasets (552 images), while the "automatic 3-D models" created were validated against the "3-D golden standard models." Results are promising as they yield an average accuracy of 97.2% in successfully identifying kidneys and 96.1% of their abnormalities thus outperforming existing methods both in accuracy and in processing time needed.

Index Terms: Abnormalities detection, automatic annotation, kidney, kidney pathology, kidney segmentation, region of interest (ROI), kidney stone and tumor.

INTRODUCTION

The rapid evolution of advanced medical image modalities such as the modern MRI scanners and the large amount of data provided have brought about the need for more automatic processes in computer-aided diagnosis. Clinicians need to examine large numbers of complex medical images to detect abnormalities; a difficult and time consuming task. Hence, there is a need for systems that will automatically detect organs and their possible abnormalities and provide useful metrics.

Several algorithms detect kidney abnormalities, addressing the challenge of increased difficulty in their delineation due to their intensity variation. Prevost et al. [1] had automatically localized the kidney with a novel ellipsoid detector, and then applied deformation of this ellipsoid with a model-based approach in the segmentation process. Using the Dice Similarity Coefficient (DSC) as a metric [2], this system achieved a DSC of 87.5%. Similar to this platform, they calculated the accuracy of automatic segmentation outcome by comparing it with the result of the semiautomatic segmentation method coming from the radiologist's work (golden standard). Lin et al.'s [3] model-based approach for kidney segmentation achieved an average correlation coefficient of 88%, while [4] used Bayesian concepts for a probability map generation to achieve an automatic kidney Parenchyma

volumetry with a DSC of 90.3%. [5] used an automated graph-cuts segmentation technique for dynamic contrast-enhanced 3-D MR renography achieving a DSC of 96% for the kidney and 90% for the cortex and the medulla. Their method was very fast (approximately 20 min) compared with the time needed for a manual segmentation of about 2.5 h, In [6], the authors presented a combination of texture features and a statistical matching of geometrical shapes of kidneys for an automatic segmentation in 3-D MRI images with a mean DSC of 90.6%.

EXISTING SYSTEM:

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

- ATD is not only a method, but a multifunctional platform sup-porting real-time processing;

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

- 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;

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

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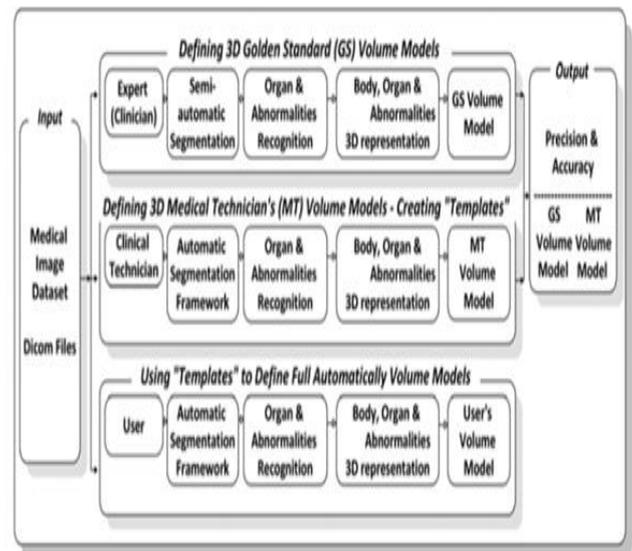

Fig. 1. Methodology used for the evaluation of the automatic segmentation framework Clinician's [or Golden Standard (GS)] Volume Model versus the Medical Technician's (MT) Volume Model.

The platform also supports storage of information in small anonymous xml-structured files (with a 500-kbytes typical file size for a complete dataset) to ensure fast transmission via networks to other clinicians. A typical size of a "template" file is about 2 Kbytes.

PROPOSED SYSTEM:
METHODOLOGY

The method for creating and validating outputs of the ATD platform consists of three steps.

A. Defining "Three- Dimensional Golden Standard Models":

The process calls for clinicians to annotate organs and pathologies in an abdominal MRI dataset in order to define a "golden standard model" for the evaluation. For this process the "manual segmentation panel" integrates an advanced implementation of the "region-growing" semiautomatic segmentation algorithm. Boundary refinement can be achieved by using a custom version of the "pencil" and "eraser" tools

(keeping their neighboring points connected) allowing for the expansion or shrinkage of the selected areas so as to add or remove any mistakenly selected or ignored areas.

The integrated multilevel multifunctional annotation system facilitates the delineation of areas of interest in the selected image. Once the delineation process has been completed, the "3-D volume rendering" option creates and enables the manipulation of the resulting realistic 3-D model of the organ structure and its potential abnormalities.

The implementation uses "visualization toolkit" (VTK) [16], with visualization algorithms in a 3-D interactive process (Fig. 2). Seven dif-ferent views of the 3-D model are available along with corresponding metrics (see Fig. 2 left side). They include MIP. (pH-sensitive Molecu-larly Imprinted Polymer), composite ramp, composite shade ramp, skin, bone, muscle and RGB composite. Newer volume rendering methods are in development [17], [18].

B. Creating Templates With Rules and Parameters to Identify Specific Areas of Interest

By experimenting with the parameters of the "automatic region-oriented segmentation framework," a medical technician attempts to achieve a segmentation result closest to that of the clinician's using a region-oriented segmentation method [15]. A panel enables the inter-active adjustment of the parameters of the framework in a single slide and the checking of the corresponding result in real time.

Once the result is acceptable, the parameters and rules can be saved in a "template" with a name that corresponds to the area identified (e.g., right kidney) and can then be applied automatically to the entire image dataset. For highly complex images, the clinician has the option to define a "working area" where the Framework will be applied (see Fig. 3).

The "validation" panel allows an evaluation by comparing the results for the two models for every

slide. This panel shows the "true positives" pixels which are the common pixels in the two methods (orange), the "false negatives" pixels which are presented only in the clinician's work (blue) and the "false positives" pixels which are presented only in the second image produced by the automatic method (green).

C. Using Existing Templates for Fully Automatic Identification of Specific Areas of Interest

An end user can employ the existing "templates" to find a specific organ (e.g., left Kidney) and its potential abnormalities. The location of the organs can vary from one dataset to another; to identify the initial position of the organ, the engineer loads the "template" in any of the images including that organ and then clicks to verify the already selected organ from a list of objects.

The system's functionality was tested on a dataset of 20 MRIs (522 images) acquired at a local regional hospital and with the following parameters: the MRI machine was a GE Medical Systems, running a scanning sequence of SE and a variant of SK. The slice thickness was 8 mm with a repetition time of 2000 ms. Image frequency was 63.830539 MHz, magnetic field strength was 1.5 T, and spacing be-tween slices was 10 mm.
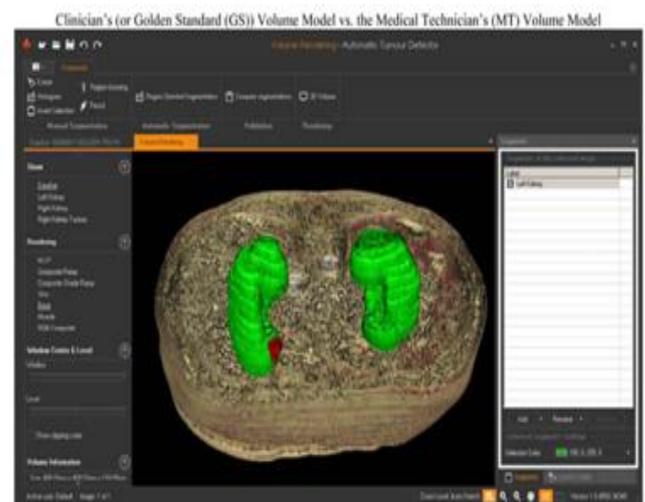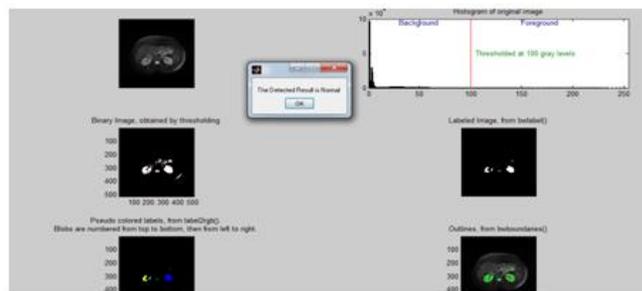

Fig. 2. 3-D model of the body integrating the previously delineated areas. Green represents the kidneys, while red identifies the tumor.
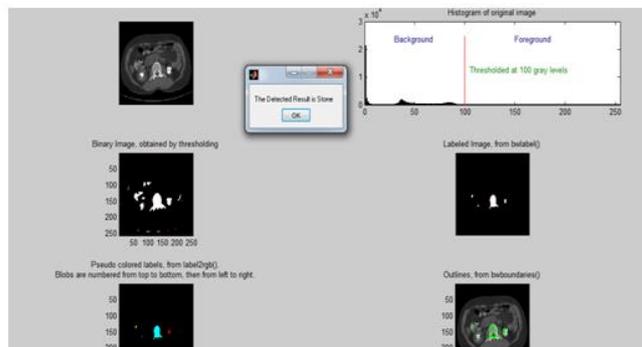
Fig. 3. Defining parameters and rules ("Templates") for the automatic segmentation process.

IV. SIMULATION RESULTS
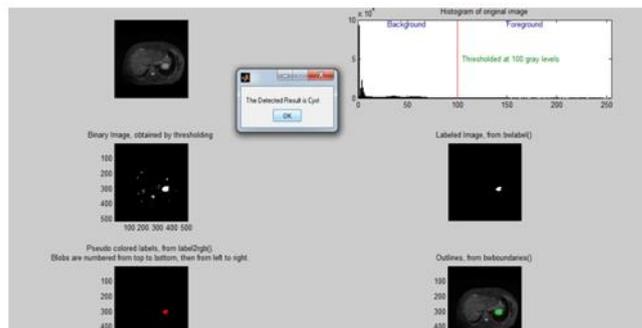
Abnormality detection:

Abnormality detection

Tumor detection:

Tumor detection

Normal kidney:

Normal kidney

Stone detection:

Stone detection
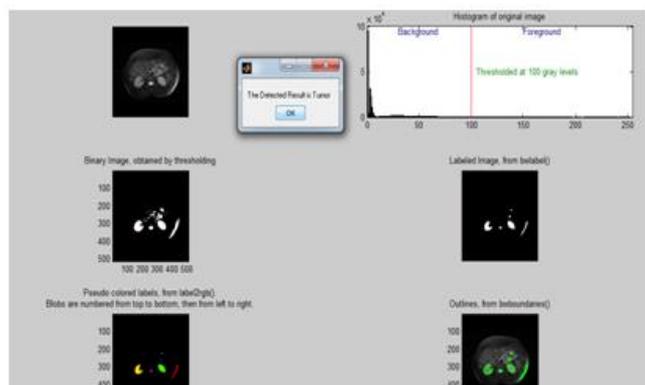
Cyst detection:

Cyst detection

V. CONCLUSION

This research presents a new MRI diagnosis-assistive platform that, after initial creation of a "template," is capable of providing a more automatic 3-D identification of kidneys and their abnormalities (tumors, stones, and cysts). Two methods have been integrated to create "3-D volume models": The first provides clinicians with support (through a user

interface) in order to rapidly identify and delineate areas of interest, with a 3-D view and have real metrics at hand specifying actual physical sizes of organ structures and any abnormal tissue regions. The second invokes a method of increased automation, to identify important areas based on "templates" that are initially created by a medical technician and later on used by a user with no particular prior knowledge of medical image segmentation. These "templates" allow the system to identify organ structures based on their features and look for any abnormalities.

Clinicians who participated in the trials expressed satisfaction with the use of the platform in that it offered better visualization of regions of interest, as it simplified and sped up the image annotation process even in very complex medical image datasets, enabling higher accuracy in organ and abnormality identification.

As using the system requires no previous knowledge of auto labeling, it is easy to support the clinical diagnosis process throughout; from the input stage of the MRI image datasets, to the generation of 3-D models. The fully automated part of the framework (after the creation of "templates") has been tested on 20 MRI datasets corresponding to an equal number of patients (552 Images).

Benchmarking tests of the system have shown promising results. For the recognition of kidneys and their abnormalities, the system outperformed previously reported results with a mean DSC of 97.2% and 96.1%, respectively, compared with other systems with a mean DSC 95% and 91%.

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