Comparison of Lung Nodule Segmentation Technique of Lung Adenocarcinoma Case using MATLAB

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Abstract: Lung cancer has become one of the most significant diseases in human history. By 2030, the worldwide death toll from lung cancer will be 10,000,000 estimated by the World health organization. The 5-year survival rate for advanced Non-Small Cell Lung Cancer (NSCLC) remains disappointingly low. In the current study, computed tomography (CT) scans were used for image feature extraction. The segmentation algorithm in this system played a very important role. A single click ensemble segmentation (SCES) approach is an extension for existing ''Click & Grow'' algorithm. The SCES approach, one seed point will be selected manually as compared with multiple operator inputs, which are typically needed. This results in processing large numbers of cases. By comparing the SCES algorithm with the two readers, the level set algorithm and the skeleton graph cut algorithm, we obtain an average SI of 78.29%, 77.72%, 63.77% and 63.76%, respectively. The proposed automatic lung lesion segmentation algorithm is stable, accurate and automated. So, we concluded by proposing a stable, accurate and automatic single click ensemble segmentation algorithm. The ''Click & Grow'' algorithms were applied multiple times resulting in increase of computational time for each case. Still we saved a lot of manpower.

KEYWORDS: Delineation, Lung tumor, Lesion, CT, Region growing, Ensemble segmentation.

INTRODUCTION

Medical imaging is the technique and process of imaging the interior of a body for clinical analysis and medical intervention, as well as visual representation of the function of some organs or tissues. Medical image processing is a field of science that is gaining wide acceptance in the healthcare industry due to its technological advances and software breakthroughs. It plays an important role in disease diagnosis and in improved patient care. It also helps in decision making by medical practitioners with regard to the type of treatment. Several state-of-the-art equipment produce human organs in digital form which includes X-ray-based devices, Computed Tomography (CT), Ultrasound (US), Magnetic Resonance Imaging (MRI), Positron Emission Tomography (PET) and Single Photon Emission Computed Tomography (SPECT). Irrespective of the equipment used, the raw images produced by such devices have to be processed so that the visual appearance of the image has to be converted to a form which is better suited for image analysis and understanding. The techniques and methods used for this purpose are often termed as 'Image Enhancement Techniques' and are widely used in the research field. These techniques aid in the improvement of an image appearance by enhancing image features or by decreasing ambiguity between different regions of the image.

Lung cancer has become one of the most significant diseases in human history. The World Health Organization estimates the worldwide death toll from lung cancer will be 10,000,000 by 2030. There is a 5 year low survival rate for advanced Non-Small Cell Lung Cancer (NSCLC) [1] . It has been hypothesized that quantitative image feature analysis can improve diagnostic/prognostic or predictive accuracy, and there-fore will have an impact on a significant number of patients [2]. In the current study, standard-of-care clinical computed tomography (CT) scans were used for image feature extraction.

Delineating the lung tumor is the essential step to reduce the variability for future extraction.optimal radiation oncology also deals with Accurate delineation of lung tumors. A common approach to delineate tumors from CT scans involves radiologists or radiation oncologists manually drawing the boundary of the tumor. In the majority of cases, manual segmentation overestimates the lesion volume to ensure the entire lesion is identified [3] and the process is highly variable [4, 5]. A stable and an accurate segmentation of image is critical, as image features (such as texture and shape related features) are sensitive to small tumor boundary changes. Therefore, the developed highly automatic, accurate and reproducible lung tumor delineation algorithm would represent a significant advance. Accurate extraction of soft tissue lesions from a given modality such as CT, PET or MRI is a topic of great interest for computer- aided diagnosis (CAD), computer-aided surgery, and radiation treatment planning and medical research.

The paper structure as follows in section 2 mention the literature survey of Lung Cancer identified with CT scans, and sections 3 and 4 give the proposed methodology, and give an explanation about results. Finally, conclude this paper in section 5.

LITERATURE SURVEY

Lung cancer has become one of the most significant diseases in human history. The World Health Organization estimates the worldwide death toll from lung cancer will be 10,000,000 by 2030. The 5-year survival rate for advanced Non-Small Cell Lung Cancer (NSCLC) [1] remains disappointingly low. It has been hypothesized that quantitative image feature analysis can improve diagnostic/prognostic or predictive accuracy, and there- fore will have an impact on a significant number of patients [2]. In the current study, standard-of-care clinical computed tomography (CT) scans were used for image feature extraction. In order to reduce variability for feature extraction, the first and essential step is to accurately delineate the lung tumors. Accurate delineation of lung tumors is also crucial for optimal radiation oncology. A common approach to delineate tumor from CT scans involves radiologists or radiation oncologists manually drawing the boundary of the tumor. In the majority of cases, manual segmentation overestimates the lesion volume to ensure the entire lesion is identified [3] and the process is highly variable [4,5]. A stable accurate segmentation is critical, as image features (such as texture and shape related features) are sensitive to small tumor boundary changes. Therefore, a highly automatic, accurate and reproducible lung tumor delineation algorithm would represent a significant advance.

Accurate extraction of soft tissue lesions from a given modality such as CT, PET or MRI is a topic of great interest for computer- aided diagnosis (CAD), computer-aided surgery, radiation treatment planning and medical research. However, segmentation of a lesion is typically a difficult task due to the large heterogeneity of cancer lesions (compared to normal tissues), The noise that results from the image acquisition process and the characteristics of lesions often being very similar to those of the surrounding normal tissues. Traditional medical image segmentation techniques include intensity-based or morphological methods [6–9], yet these methods sometimes fail to provide accurate tumor segmentation. A lung tumor analysis (LuTA) tool [10] within the Definiens Cognition Network Technology [11] was developed by Definiens AG [12] and Merck & Co., Inc. It is a prototype application that demonstrates the ability to automatically and semi-automatically identify and recognize organs and tumors in CT images. Its efficacy in automatic lung segmentation is described in [10] and we were able to obtain accurate lung segmentations from LuTA for all cases discussed here.

LuTA is designed to enable fast and easy annotation of lung tumors or other user- defined regions of interest. The user has Flexible controls to choose the annotation of structures. Once a user has clicked on a region of interest, in a single two- dimensional (2D) slice, the application builds out the object three-dimensionally. The results [10] of the first prototype application built using the Definiens Cognition Network Technology provided a proof of concept enabling semi- automatic volumetric analysis of tumors by using CT based scans. However, there are still some drawbacks in the current generation of the LuTA tool . First, although processing time is reduced compared to manual delineation, it still requires substantial operator input. For example, more number of seed points are selected manually for tumor segmentation. Some tumor segmentations will require more than one step, thus additional operations are required (e.g., the radiologist must scroll over the CT slices and find out what part of the segmentation is missing). Additionally, lung tumor boundaries are often found to be incorrect during manual inspection, and thus require manual editing that takes additional time and creates additional sources of error. Finally,

although segmentations can be performed in batch mode, which is appropriate for large studies, it is impractical if manual editing is required.

With the motivation of overcoming the above drawbacks of the ''Click & Grow'' algorithm, we propose a new delineation algorithm based on using multiple seed points with region growing [13]. The new algorithm makes use of the original algorithm by using an original seed point to define an area, within which multiple seed points are automatically generated. An ensemble segmentation can be obtained from the multiple regions that were grown. Ensemble segmentation has played an important role in many medical image applications recently [14–15] and refers to a set of different input segmentations (multiple runs using the same segmentation technique with different initializations) that are combined in order to generate a consensus segmentation. In this paper, we demonstrate that such an approach reduces inter observer variability with significantly fewer operator interactions when compared to the original algorithm.

PROPOSED METHODOLOGY

The overall goal for the LuTA implementation was to accurately, precisely and efficiently enable the analysis of lesions in the lung under the guidance of an operator. A standard analysis workflow was described in detail elsewhere [10]. The workflow is briefly described in the following:

1. A preprocessing step: This was designed to perform a segmentation of the lung as well as other off-line tasks, such as filtering, to improve the interactive performance of the analysis.

2. An optional step with semi-automated correction of the segmented lung. Since lesions are commonly found to be attached to the pleural surface, it was critical to enable efficient correction of the lung boundary in cases where the boundary between juxta pleural target lesions and the pleura had not been correctly determined during the automated preprocessing step.

3. A ''Click & Grow'' step with a user selected seed based segmentation of the lesions.

4. An optional manual refinement step of the semi-automated lesion segmentation to ensure medical expert agreement with any results that could influence patient management.

5. A reporting step generating volumes and statistics about other features, such as average density.

In this project, we focused on how to accurately segment the lung lesion with minimum human interaction; the new algorithm is basically a substitution of steps 3 and 4 above and only requires one manual seed to be entered. The preprocessing and ''Click & Grow'' steps within the LuTA workflow are used by our new algorithm, as described below.

A. Pre-Processing

The preprocessing step performs automated organ segmentation with the main goal of segmenting the aerated lung with correct identification of the pleural wall in order to facilitate the semi-automated segmentation of juxta pleural lesions. In Fig. 1, a CT image of a representative patient is shown segmented after the preprocessing step. The tumor is located in the right lung field.
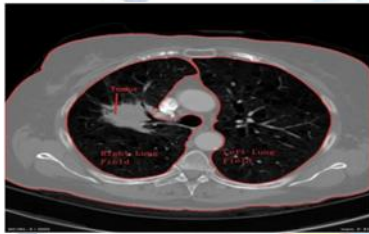

Fig. 1 Lung fields (left and right) were segmented after preprocessing.

B. Click & Grow

After the preprocessing step, the lung lesions must be located in one of the lung fields. In order to segment a target lesion the image analysts identified the lesion within the segmented lung and placed a seed point in its interior—typically at the perceived center of the lesion. Starting from the seed point, an initial seed object was automatically segmented using LUTA's region growing based on similar intensities and proximity to areas with low intensity (''air''). This Definiens proprietary region growing process approximates the object's surface tension Tusingan N3 voxels sized kernel locally by calculating the ratio of the object volume inside a kernel (V_i) to the total kernel volume (V_k), $T \frac{1}{4} V_i = V_k$. With this approach a high relative kernel volume of the objects surface voxels corresponds to a high surface tension. The strength of the surface tension is mainly controlled by the volume of the grown object in order to impose a smoother surface for larger objects. From the grown region, which consists of voxels with similar

density, the intensity weighted center of gravity (IWCOG) was calculated. To decrease inter and intra-reader variability, the seed point was shifted closer to the IWCOG. Additionally, an approximation of the lesion radius and volume, as well as histogram based lower and upper bounds for the intensity were extracted. These parameters were used to define an octahedron- shaped candidate region within the lung. The new seed object was then grown into the candidate region with adaptive surface tension and intensity constraints. The intensity constraints restrict the growth into candidate regions defined by: (1) a pre-computed intensity range of the Gaussian smoothed CT image, where the intensity range was estimated from the intensity statistics of the seed region and (2) a bound on the distance to the seed region which was calculated using a distance map. The distance map was calculated solely for the candidate region within the CNL local processing framework, and provides the minimal distance for each voxel to the seed region as an intensity value. Using the distance map ensures an approximate convexity of the seed object when growing into regions with similar intensities.

C. Single Click ensemble segmentation

The original ''Click & Grow'' algorithm is very useful for delineating the tumor from the lung field in the LuTA application. If the growing process does not sufficiently capture the target lesion, the operator can place additional seed points within the lesion and repeat the growing process outlined above. Upon completion of the segmentation, the individual image objects are merged to form a single image object representing the segmented target lesion. The algorithm also provides the cap- ability for a user to manually edit the segmentation. However, it still has the following drawbacks:

1. The segmentation is not consistent, different readers may generate different tumor regions.

2. It can require many human interactions (multiple clicks) to delineate the tumor in the case where the growing process did not sufficiently capture the target lesion.

3. The tumor boundary is often not satisfactory upon visual examination; sometimes it obviously includes many areas that do not belong to the target tumor.

To overcome the drawbacks of the original method, we propose a new algorithm: the single click ensemble segmentation (SCES) algorithm, which is an advanced version of the previous algorithm. The SCES makes use of the original algorithm by choosing different seed points automatically within a specified area of the lesion and performing region growing with each generated seed point. Thus, an ensemble segmentation is obtained from the multiple regions that were grown, and the final segmentation is based on a voting strategy. In order to better describe the algorithm, we provide first several definitions:

1. Tumor core: the area most likely belonging to the tumor.
2. Manual seed input: the first seed point provided by the user.
3. Start seed point: the seed point randomly selected from the initial tumor region after shrinking.
4. Parent seed point: algorithm selected seed point from a specific location of the tumor core.
5. Child seed point: algorithm selected seed point from the outside of the existing tumor.

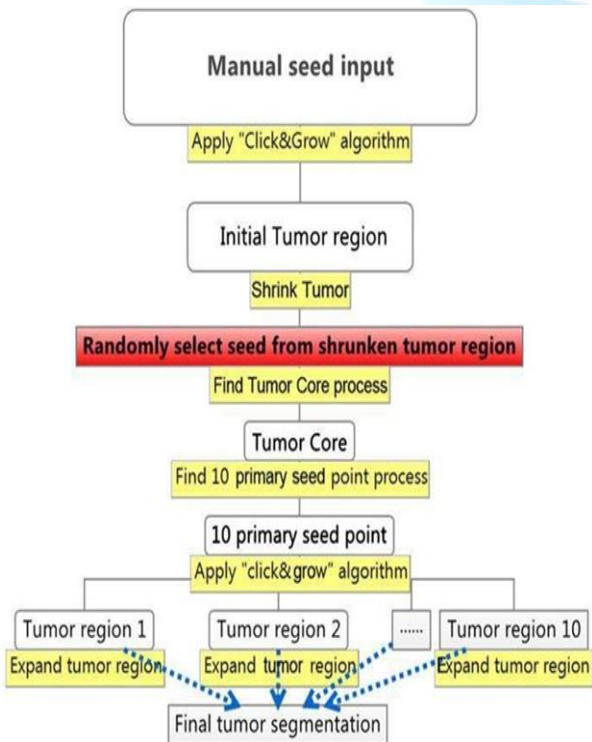The detailed algorithm is described below and the detailed algorithm workflow is shown in Fig. 2:

Fig. 2 Schematic illustration of the flow of the single click ensemble segmentation method.

a. The user provides the manual seed point and calls the ''Click & Grow'' algorithm to create the tumor region.

b. The initial tumor region created was shrunk in the x, y and z direction. (This process is to ensure step c selects a good start seed point).

c. Find start seed point: randomly select seed from shrunken tumor region obtained from step b.

d. Find the tumor core process (Fig. 3): take the center of the tumor region obtained and use it as a new seed point. Perform region growing using the new seed point, and then from the new tumor region, record the pixels which are assigned to the tumor class. Repeat the above step 10 times; we will have10 tumor regions corresponding to 10 different seed points (tumor center).The intersection of the 10 tumor regions is defined as the tumor core. The center of the tumor object is defined as the following: the image object can be treated as the voxel co-ordinates (x, y, and z).
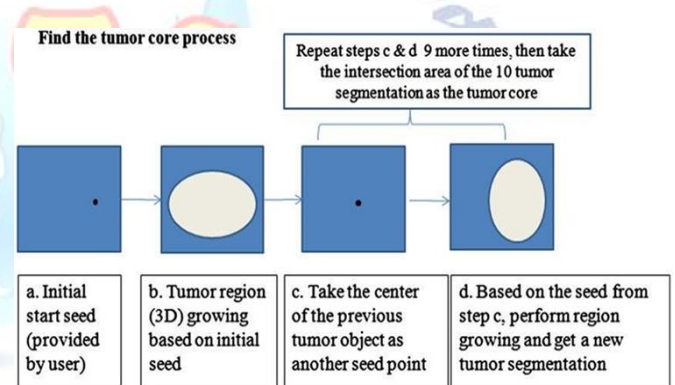

Fig. 3 Illustration of the workflow to find the tumor core process.

e. Locate 10 Parent seedpointsfromthetumorcorein3D: use 3 planes: xy, yz and xz that pass through the center of the tumor core to divide the tumor core into 8 regions, the center of the tumor core in each region is taken as a parent seed point. The 9th parent seed point is the center of the whole tumor core, and the10thoneisrandomlyselected from the tumor core region.

f. For each parent seed point.

(1) Apply the ''Click & Grow'' algorithm and obtain the corresponding tumor region. (2) Based on the tumor region obtained from the parent seed point, the next step involves additional tumor growing as follows:

select 3 slices from the existing tumor region: center slice, center_1 andcenterþ1 slice (Fig. 4.4). The child seed point (24 in total, 8 child seed points for each slice) is 3 pixels away from the existing tumor boundary. For the center slice, the child seed point is placed at a distance of 451 successively, starting from 01 to the x-axis. Similarly, the child seed points of center _1 and centerþ1 slices were placed in a similar fashion. Their starting point is at 151 and 301, respectively. Independently apply the ''Click & Grow'' algorithm to each child point. The ''Click & Grow'' algorithm might not always return a tumor region or in the case of invalid seed points the ''Click &Grow'' algorithm does not return a tumor volume. Even if grown successfully, the region is kept only after several conditions are satisfied. The conditions we added for the rule-set are based on the intensity mean, standard deviation, shape and connection status with the main tumor region produced by the parent seed point.

(3) Merge tumor regions: simply assigns the tumor regions created from 1 parent seed point and 24 child seed points to the same class. We now have a complete tumor segmentation.

g. Finally, we get an ensemble segmentation consisting of 10 (since we have 10 parent seed points that came from the tumor core) different/similar tumor segmentations. We use a voting strategy to determine the final tumor region. A voxel is assigned to the tumor class if in its 3_3_3 neighborhood window half or more of the voxels were labeled tumor voxels in at least half of the segmentations and corresponding flow is shown in Fig. 4.
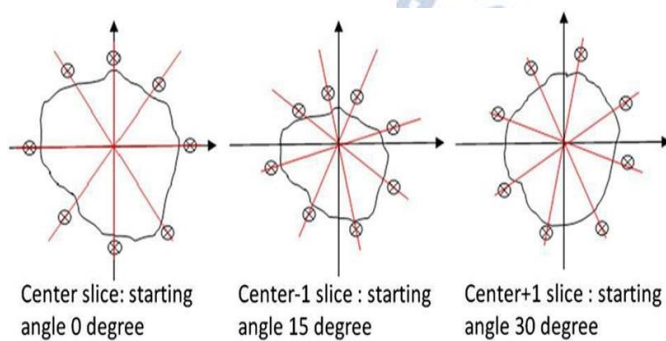

Fig. 4 Expand tumor region: locate 24 secondary seed points: child seed point selection from the existing tumor region.

RESULTS AND DISCUSSION

The proposed algorithm is implemented and tested on some of the CT scan images of lungs using MATLAB software. Fig. 5 illustrate the example figure of CT scan of lungs.
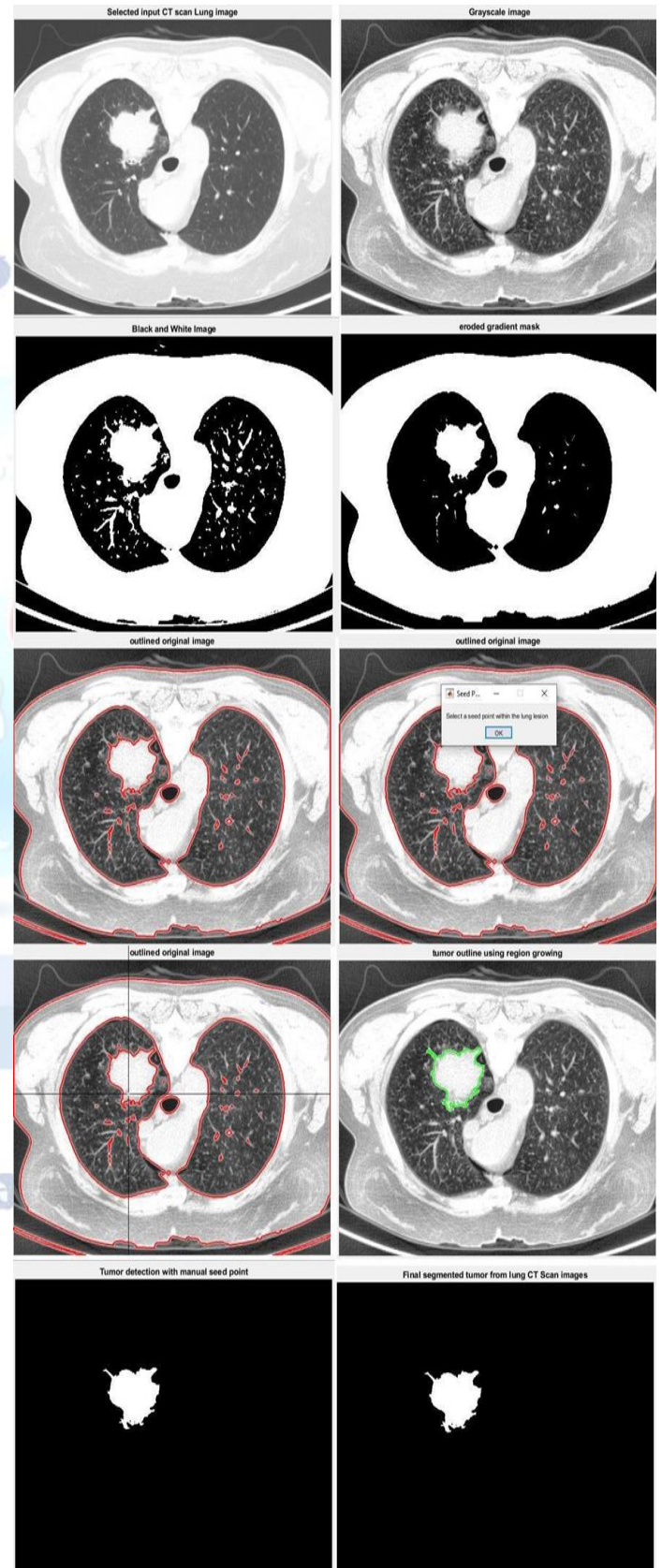

Fig. 5 Example of CT scan lung images

CONCLUSION AND FUTURE SCOPE

We proposed a stable, accurate and automatic single click ensemble segmentation algorithm in this project. The important component of this work is to reduce the human interactions while lesion delineation remains accurate and consistent as a result of ensemble segmentation. Though the computation time was increased for each case since multiple ''Click & Grow'' algorithms were applied, we saved a lot of man power. With the automated batch mode method built in to the Definiens' software platform, the lung lesion segmentation work load has been tremendously reduced (in other words, we can save a significant amount of valuable time for readers/oncologist/radiologists in the segmentation of lung tumors), the only thing requiring human interaction is the choice of the manual seed input. The aim of the algorithm is to provide a delineation tool that can be used by many readers to obtain the same segmentation results. The tumor segmentation should not differ much with different manual seeds provided by different readers. The single click ensemble segmentation algorithm we proposed here is a nice upgrade. As the new algorithm evolves to better address some issues we discussed above, it will become an even more powerful tool that can be further tested in clinical environment and it will be also very useful in future multi-center clinical trials.

Future enhancements will focus on part-solid tumor types, which result in unstable tumor boundaries when given different start seed points. The problem of incomplete tumor segmentation with big tumors is also a remaining challenge.

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