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Multidimensional Interactive Radiology Report and Analysis: Standardization of workflow and reporting for renal mass tracking and quantification

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Abstract

A conventional radiology report primarily consists of a large amount of unstructured text, and lacks clear, concise, consistent and content-rich information. Hence, an area of unmet clinical need consists of developing better ways to communicate radiology findings and information specific to each patient. Here, we design a new workflow and reporting system that combines and integrates advances in engineering technology with those from the medical sciences, the Multidimensional Interactive Radiology Report and Analysis (MIRRA). Until recently, clinical standards have primarily relied on 2D images for the purpose of measurement, but with the advent of 3D processing, many of the manually measured metrics can be automated, leading to better reproducibility and less subjective measurement placement. Hence, we make use this newly available 3D processing in our workflow. Our pipeline is used here to standardize the labeling, tracking, and quantifying of metrics for renal masses.

Keywords

DICOM; renal masses; tumor; image processing; reporting

1. INTRODUCTION

During the last two decades, much effort has been expended to convert all medical imaging files to digital format, and to ensure that these images are available anytime, and anywhere. Yet, a conventional radiology report still primarily consists of a large amount of unstructured text, and lacks clear, concise, consistent, and content-rich information. Many screening, diagnostic, and therapeutic decisions are based on imaging data. Hence, an important unmet clinical need involves better communication of radiology findings and of information that is specific to each patient. For instance, a pool of hospital clinicians revealed a preference for more detailed and index/tabular report [1,2].

Although structured reporting systems have been recognized as desirable for many years, a universal system has yet to be adopted. This is mainly due to the fact that current radiological practice relies on subjective measurements, as well as to a lack of standardized quantitative measures. The Multidimensional Interactive Radiology Report and Analysis (MIRRA) system being proposed combines and integrates advance image processing with medical radiology to help codify renal mass reporting.

2. METHODS

3D Segmentation

Our workflow starts from the reception of images for the CT scanner and consists of a combination of image image-processing steps and quantitative analyses. As such, it relies on adequate image resolution and clarity at acquisition. Although generalizable to any modality, here as a proof of concept we will apply it to renal masses, for which clinical imaging typically consists of contrast enhanced computer tomography (CECT). In particular, standard-of-care at our center involves the acquisition of multiphasic data, including pre-contrast, corticomedullary, nephrographic, and excretory phases. In general, the phase that allows for the easiest delineation between renal mass and normal tissue is the nephrographic one.

In the first step of our pipeline, Synapse 3D (Fujifilm, Stamford, CT) is used to create masks of each individual renal mass, and to segment the residual kidney. Three-dimensional segmentations of renal masses allow for a more standardized set of physical measurements than the 2D analysis that is now used in most clinics. In the current radiological workflow, masses are evaluated by first choosing the largest cross-section on the trans-axial plane and hand drawing a line across the longest linear distance between two borders of the mass. A second measurement perpendicular to the maximum may also be performed. These measurements are used to assess mass size and changes in size. The subjectivity of this method leads to widely varying results which dependent on the skill of the reader. In addition, important 3D information is lost in the process. By demarcating the mass in 3D, measurements such as volume, largest cross sectional measurement, and smallest bounding box can be mathematically generated, thereby improving the consistency of measurements.

Next, segmented renal mass volumes are tessellated into three-dimensional shells. These 3D models will be used for display as well as calculations of new metrics.

The normal kidney tissue can also be segmented in 3D. This volume is used for contact surface area calculations, and is also used as the source image for our atlas standardization process, as explained below.

Automated Quantification

After the extraction and tessellation of both lesion(s) and remaining kidney, a series of automatically derived quantitative metrics can be extracted. The simplest calculated parameter is tumor volume. The current clinical workflow does not include a calculation of total volume, an important marker of tumor evolution. Here volume is extracted simply by

multiplying the size of an individual voxel by the number of voxels isolated through segmentation.

The rest of the auto-generated metrics are based on the tessellated volumes. The next parameters we compute are automated versions of the Tumor Node Metastasis (TNM) staging and the Response Evaluation Criteria in Solid Tumors (RECIST) linear measurements. Standard clinical practice consists of visually locating the largest axial cross-section of a tumor and measuring across the largest width of the cross-section in one of the three standard orthonormal planes. TNM staging looks for the largest cross-section in all three orthonormal planes, whereas RECIST generally stays with the axial plane. These linear measurements are used as clinical measures of mass size. In our workflow, to automate the process, the tessellated object is segmented by slice, and the largest cross section is calculated. Each vertex from the tessellated mass is compressed by slice, leaving only the two-dimensional coordinates of the vertices. The maximum distance between two vertices for all slices is kept as the single dimensional measurement for each orthonormal plane. Although in practice the TNM and RECIST criteria are not applied to all renal masses clinically, our automated process allows for these metric to be calculated with no additional user interaction.

TNM and RECIST criteria have the major limitation of being constrained to only the three planes of imaging, hence results are very dependent on the 3D orientation of the tumor. In our workflow, in addition to the two former measures, the overall linear size of the mass is calculated by finding the minimum bounding box for the tessellated mass. The minimum bounding box for a mass is defined as the smallest rectangular prism which surrounds it. This metric gives a linear size similar to the TNM and RECIST, with the additional advantage of being orientation independent.

Currently, there is no agreed upon metric to describe the degree of to which a mass is exophytic or endophytic. We propose the use of the ratio of contact surface area (CSA) to total surface area of the mass as a quantitative measure to characterize endophytic lesions. The exophytic metric is one minus the endophytic measure. CSA is defined as the area of the mass which physically touches normal kidney tissue. To calculate the CSA, the tessellated surface of the mass is subtracted from that of the kidney. The faces of the mass grid which overlap the area enclosed by the kidney are retained. The CSA is the summation of the surface areas of the faces.

Atlas Standardization

In current radiology reports, masses are identified textually using general language descriptions of position relative to the kidney, with the possible addition of a screen capture of a marking on a multi-planar reformatted (MPR) image. Because of the qualitative and non-standardized nature of masses location reporting, extra care must be exercised by clinicians when reading radiologists reports. In addition, there may be multiple masses in the kidney, which may lead to confounding terminology.

To standardize the reporting of masses, an atlas-based technique is employed to automate mass designation. A voxel based template and a corresponding tessellated 3D surface object

are created for both the right and the left kidneys. We chose to employ the 12 segments Kidney Segmentation System [3]. Using a 12-parameter affine transformation, each kidney is co-registered to the voxel-based template. The centroid of each mass is calculated and warped into template space using the calculated transform. With this method, endophytic centroids lie within one of the segments of the kidney. To find the projection of a mass with an exophytic centroid on the surface of the template kidney, the atlas vertex is chosen to be the one with the minimal distance to the centroid of the mass. Masses can then automatically be labelled by their standardized positions on the atlas. This yields uniformity in tracking and mass labeling.

Reporting

The final MIRRA product is printer/reader friendly PDF document encapsulated in a DICOM format is provided for quick viewing. The PDF document format allows the inclusion of static images as well as interactive 3D models, which adds an important visualization aid for referring physicians. The file format allows the incorporation of 3D scenes within the document itself. The 3D scene can be constructed using stand tessellation language (STL) formatted 3D model files, which is a standard file format used by many 3D processing software programs, including Synapse 3D. 3D PDFs, when opened in a viewer like Adobe Acrobat Reader, allow the user to manipulate the 3D scene with options such as rotating the scene, hiding objects, changing lighting, and adjusting transparencies. In addition, leveraging the use of the standardized PDF file format allows the final report to be cross-platform, dependent only on the installation of one of many readily available PDF viewers.

Where previous groups have looked at creating systems to generate multimedia reports [4], our system is a complete workflow for automatically generation of measurement with an output of PDF reports. A DICOM Structured Report (DICOM-SR) is attached to the PDF for quantitative data storage. DICOM-SR objects are created based on a custom-designed XML template. The XML template includes select DICOM headers (instance UIDs, study date/time, and other relevant metadata) from the original images, and the structured report content generated by the automated quantification modules. The report lists the details of the type of processing and post-processing methodologies that have been performed, the registration transform matrix, identification of source images, and the quantitative data itself. A sample of the structured report template is shown in the Figure 5.

The generated XML document is automatically converted to DICOM-SR via the C++-based DCMTK toolkit [5] and sent to a DICOM-based archive for data storage. In order to view the resulting structured reports, we have created a user interface that displays the DICOM-SR object in tabulated format. PDF and DICOM images are shown alongside the report content.

3. DISCUSSION

The human body is structured in three dimensions, but standard clinical reading of medical images is currently done in two dimensions at a time, generally in projections of orthonormal planes. This leads to an inherent bias where observations and measurements are

forced into three specific planes. To further confound the possible sources of error, measurements are currently determined subjectively, for example, in the case of tumors, by visually selecting the largest cross-section and then manually measuring its length. The user-dependent nature of measurement nearly guarantees the irreproducibility of the radiological read.

Our workflow, in addition to the 3D segmentation of the mass, will help standardize measurements by automating the measuring process. The user's responsibility will be on the segmentation of the mass, rather than the visual selection of the largest linear distance. The automated calculation of metrics will give referring physicians more information and data on which to base their treatment plans.

Issues will continue to exist with 3D segmentation, due to limitations of enhancement and resolution. Medical imaging, whether CT or MR, is dependent on differential enhancement of dissimilar tissues represented by gray-level encoded images. If the separation between the kidney and the renal mass is insufficient to discern one tissue from the other, no amount of post-processing will yield accurate results. Similarly, resolution plays a very significant role in measurement accuracy. Renal imaging can vary from submillimeter to centimeter thick slices. In general 3D processing is more accurate with thinner slices. We recommend performing all 3D segmentation with the thinnest possible images from the scanner.

Our report allows for the presentation of our calculated metrics in a clean and unambiguous manner. Impressions by the radiologists will still remain a key component of any report, but now there will be the addition of quantitative data that previously did not exist. Also, with the atlas based identification process for masses, physicians will be able to better track lesions in patients with multiple masses. The 3D scene included in the report allows for an interaction with the 3D model, and is completely portable.

Having all the data encoded in DICOM-SR opens numerous opportunities for research linking radiological reads to patient outcomes, and allows it to be completely data-driven. Often times in clinical studies, information is transcribed manually into some kind of research database. This process is effort intensive and leads to human entry errors. The structured nature of MIRRA allows for the quantitative data to be easily extracted for statistical analysis in a consistent manner, which will empower future retrospective studies.

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Figure 1.
Synapse 3D renal mass segmentation. The segmented region of interest is shown in green on the 2D views.

Figure 2.
Rendered tessellated renal mask. The surface consists of a 2D grid with triangular faces.

Figure 3.
Minimum bounding box of a renal mass.

Figure 4.

The left image shows the 3D models of a kidney (red) and its renal tumor (green). The right image is a rendering of the contact surface area (blue).

IMPRESSION:

1. Exophytic 5.2 cm prominently enhancing left renal upper pole mass invading the upper pole collecting system, suspicious for clear cell renal cell carcinoma. Delayed left nephrogram with mild left hydronephrosis and proximal hydroureter which tapers distally without a clear obstructing lesion.
2. A 1 cm low-attenuation lesion in the anterior interpolar right kidney appears to enhance on the portal venous phase, raising the possibility for a small renal cell carcinoma.
3. Lytic lesion in the left anterior acetabulum and left superior pubic ramus with areas of cortical erosion and thinning, suspicious for metastasis.
4. Two right renal arteries and single left renal artery. Single bilateral renal veins.
5. Atherosclerotic vascular disease and colonic diverticulosis.

VOLUMES:

Right kidney w/o lesions: 248.87 cc
Right renal lesion (purple): 261.53 cc
Left kidney w/o lesions: 251 cc

GFR = 110
Estimated GFR after surgery = 95

Figure 5.
Example of PDF report. The 3D scene can be interactive.

Figure 6. DICOM-SR schema for renal masses. The format allows the flexibility of adding new metrics as necessary.