Automated DICOM metadata and volumetric anatomical information extraction for radiation dosimetry

D Papamichail¹, A Ploussi², S Kordolaimi², E Karavasilis¹, P Papadimitroulas⁴, V Syrgiamiotis⁵, E Efstatopoulos²

¹1st Department of Radiology, Medical School, National and Kapodistrian University of Athens, Vas. Sofias 76, Athens 11528, Greece
²2nd Department of Radiology, Medical School, National and Kapodistrian University of Athens, Rimini 1, Athens 12462, Greece
³Radiology Research Unit, Medical Imaging Department, National and Kapodistrian University of Athens, Athens 11528, Greece
⁴Department of Medical Physics, Medical School, University of Patras, 15310, Rion, Greece
⁵MRI-CT Medical Imaging Department General Childrens’ Hospital of Athens Ag. Sophia
dimitris.papamihail@gmail.com

Abstract. Patient-specific dosimetry calculations based on simulation techniques have as a prerequisite the modeling of the modality system and the creation of voxelized phantoms. This procedure requires the knowledge of scanning parameters and patients’ information included in a DICOM file as well as image segmentation. However, the extraction of this information is complicated and time-consuming. The objective of this study was to develop a simple graphical user interface (GUI) to (i) automatically extract metadata from every slice image of a DICOM file in a single query and (ii) interactively specify the regions of interest (ROI) without explicit access to the radiology information system. The user-friendly application developed in Matlab environment. The user can select a series of DICOM files and manage their text and graphical data. The metadata are automatically formatted and presented to the user as a Microsoft Excel file. The volumetric maps are formed by interactively specifying the ROIs and by assigning a specific value in every ROI. The result is stored in DICOM format, for data and trend analysis. The developed GUI is easy, fast and and constitutes a very useful tool for individualized dosimetry. One of the future goals is to incorporate a remote access to a PACS server functionality.

1. Introduction

Patient-specific dosimetry gains considerable importance in medical field due to the increase use of ionizing radiation for diagnostic and therapeutic purposes and the radiation-associated risk cancer [1]. Nowadays, Monte Carlo (MC) simulations serve as a “gold standard” tool for patient-specific dosimetry.

In order to perform MC dose calculations, the first step is the modeling of the modality system with the exact definition of the ionizing radiation source (spectra, filtration, geometry) [2]. This step requires knowledge of the modality type and the acquisition parameters such as scan mode, pitch, rotation time and slice thickness. All necessary data for MC simulations are included in a DICOM (Digital Imaging and Communications in Medicine) file. Metadata in DICOM files contain
information regarding patients’ demographic characteristics, protocol settings, imaging parameters and a whole host of additional information essential for individualized dosimetry.

The second requirement for patient-specific dosimetry using MC simulation techniques is the creation of a voxelized anthropomorphic phantom [2]. Voxel-based phantoms are derived from patients’ anatomical images. Each image dataset is segmented in order to specify the regions of interest (ROIs) in every single slice.

Although several DICOM extraction metadata tools [3,4] and contour delineation methods [5,6] have been proposed in the literature, few of them are freely available and can meet the aforementioned requirements.

The aim of this study was to develop a simple graphical user interface (GUI) to automatically extract and store information from DICOM metadata in a single query, as well as interactively delineating the regions of interest on anatomical images without explicit access to the radiology information system.

2. Materials and Methods

The software tool was developed on MATLAB environment (version 7.14, MathWorks, Inc.) [7]. The structure of the GUI has been designed to extract the sought-after information in a user-friendly and time saving functionality (Figure 1).

Interactivity is the essence of the designed GUI [8]. In order to establish an interactive environment, two key components, the image display window and a series of buttons, form the GUI. Each button calls the corresponding computational module, developed in house. Images in DICOM format are processed as two-dimensional arrays (matrices). Each element of the matrix corresponds to a single pixel in the corresponding slice. All DICOM files should be retrieved from the PACS to a folder on a local hard-drive before the initialization of the program.

3. Results

3.1. Extracting metadata from multiple DICOM images

Starting the application, a dialog box enables the user to select multiple DICOM files from a folder. A computational module accesses and extracts automatically both metadata and image matrix of each file. By pushing the proper button, the application implements an algorithm gathering patient-,
dose- and scan-related data from all selected files. The resulting information is automatically formatted and presented to the end user as a Microsoft Excel file for post-processing (Figure 2).

![Figure 2. A sample of the output file containing the metadata.](image)

The data from the selected DICOM files are consolidated in the same worksheet for convenience. The accuracy of the results was tested by manual verification of contents seen on the DICOM metadata.

3.2. Specifying dosimetric regions of interest

In order to calculate radiation dose in Monte Carlo (MC) simulation, all regions of interest (ROIs) should be initially defined in each slice and subsequently be used as input for the simulations. Drawing contours in each slice is time consuming and requires a skilled user. A function to facilitate this process has been integrated in the developed application. The ROIs are defined interactively slice by slice, on the same image display window (Figure 3). The histogram of each image is automatically normalized, so that it is presented to the user in full-contrast range. If the boundaries of interest are not discrete, a desired range of intensity values (window level) can be specified, so that intensity is remapped to optimise the display of specific tissues.

![Figure 3. ROIs contouring in a CT slice of a PET/CT exam.](image)

The user can specify several ROI boundaries in each slice by using an interactive pointer on the image display window. A specific value can be assigned in every ROI, so that all ROIs of the same organ can be easily matched at the end of the process. Each ROI can be deleted and redefined in any slice. ROIs of the same organ can be filled with a unique intensity number, so that the MC software
can recognize each one as different tissue-equivalent material. Figure 4 depicts the flowchart of the algorithm developed.

![Image](image.png)

**Figure 4.** A graphical representation of the dosimetric map formation flowchart.

The interactive platform was successfully implemented in various computed tomography (CT) datasets like head, chest and abdomen-pelvis scans as well as for several modalities including angiography systems, γ-camera and positron emission tomography (PET).

4. **Discussion**

The proposed tool is designed to facilitate patient-specific dosimetry using MC simulations techniques. The application allows automated DICOM metadata extraction and manual contouring of ROIs. The performance of the application was evaluated by medical personnel for Radiology and Nuclear Medicine imaging modalities. The overall conclusion was that the software tool is effective, simple, fast and easy to use in clinical practice. The tool can be easily adapted for other modalities and examinations.

The use of the web-based platform is a step towards automatization of the pre-processing part of the data inserted in MC simulation codes saving time and effort in the whole process. The future goal of this study is the free disposal of the platform for use from a central server to any operating system.

**Acknowledgement**

The project was funded by the John S. Latsis Public Benefit Foundation. The sole responsibility for its content lies with its author.

**References**

[1] Mettler F, Huda W, Yoshizumi T and Mahesh M 2008 *Radiology* **248** 254–63
[2] De Marco J, Cagnon C, Cody D, Stevens D, McCollough C, O’ Daniel J, McNitt-Gray M 2005 *Phys. Med. Biol.* **50** 3989–4004
[3] Li X, Zhang D, Liu B 2011 *AJR* **196** 781-83
[4] Dave J, Gingold E 2013 *AJR* **200** 142-45
[5] Zhou W, Xie Y 2014 *J Appl Clin Med Phys.* **15** 4499
[6] De Bruijne M, Van Ginneken B, Viergever M and Niessen W 2004 *Med Image Anal.* **8** 127–38
[7] Sobie EA 2011 *Sci Signal* **4** tr7
[8] Marchand P, Holland T 2003 *Graphics and GUI's with MATLAB* (Florida CRC Press)