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ProstateAnalyzer: web-based medical application for the management of prostate cancer using multiparametric MR imaging

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Objectives: In this paper, we present ProstateAnalyzer, a new web-based medical tool for prostate cancer diagnosis. ProstateAnalyzer allows the visualization and analysis of magnetic resonance images (MRI) in a single framework.
Methods: ProstateAnalyzer recovers the data from a PACS server and displays all the associated MRI images in the same framework, usually consisting of 3D T2-weighted imaging for anatomy, dynamic contrast-enhanced MRI for perfusion, diffusion-weighted imaging in the form of an apparent diffusion coefficient (ADC) map and MR Spectroscopy. ProstateAnalyzer allows annotating regions of interest in a sequence and propagates them to the others.
Results: From a representative case, the results using the four visualization platforms are fully detailed, showing the interaction among them. The tool has been implemented as a Java-based applet application to facilitate the portability of the tool to the different computer architectures and software and allowing the possibility to work remotely via the web.
Conclusion: ProstateAnalyzer enables experts to manage prostate cancer patient data set more efficiently. The tool allows delineating annotations by experts and displays all the required information for use in diagnosis. According to the current European Society of Urogenital Radiology guidelines, it also includes the PI-RADS structured reporting scheme.

Keywords Applications, database management system, magnetic resonance imaging, magnetic resonance spectroscopy, medical informatics, prostate cancer

BACKGROUND

Prostate cancer (PCa) has become a significant health care burden (1). Early diagnosis and active follow-up allow improved prognosis and prevent life-threatening conditions. Once the decision of treatment is taken, having the most complete set of information for treatment and then for follow up is crucial. Among the techniques used to detect and diagnose PCa, magnetic

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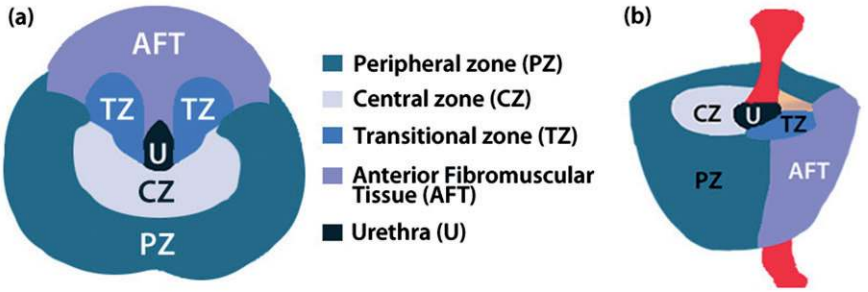

Figure 1. Anatomy of the prostate in (a) transversal and (b) sagittal planes.

resonance imaging (MRI) allows the non-invasive analysis of the anatomy and the metabolism in the entire prostate gland. The prostate is composed of peripheral (PZ), central (CZ), transition (TZ), and anterior fibromuscular tissue (AFT) zones (Figure 1). The PZ represents up to 70% of a normal prostate gland and around 75% of prostate cancers originate in this zone. The CZ represents about 25% of a normal healthy prostate gland in a young adult. Even if the frequency of cancers originating here is much lower, they tend to be of the more aggressive type (2).

MRI has been established as the best imaging modality for the detection, localization, and staging of PCa on account of its high resolution and excellent spontaneous contrast of soft tissues and the possibilities of multiplanar and multiparameter scanning (3). As such, three MRI techniques (anatomic 3D T2-weighted, diffusion-weighted, and perfusion-weighted imaging) and 3D MR spectroscopy will be illustrated in this paper. A 3D T2-weighted imaging (T2WI) sequence (4) yields good contrast between PZ and CZ tissues. Diffusion-weighted imaging (DWI) provides functional information of tissues such as cell organization, density and microstructure, and depends principally on the Brownian motion of water molecules (5). It can be displayed either as native diffusion-weighted images or as the ADC parametric map. The motion of water molecules is more restricted in tissues with a high cellular density and intact cell membranes and very low values are clearly indicative of cancer (6). Perfusion imaging is based on the dynamic contrast enhancement (DCE) of the signal during the first pass of the contrast agent. The theoretic underpinnings of this vascular technique are based on tumor angiogenesis. In fact, there is a relationship between abnormal perfusion and neoangiogenesis in tumors (7–9). Magnetic resonance spectroscopy (MRS) is a technique that allows the study of metabolite concentrations by means of a 3D chemical shift imaging protocol (10). This study is useful since healthy and cancer tissues show different concentration levels. Specifically, prostate cancer tissues show lower levels of citrate and higher levels of choline compared with healthy tissue (11–15) and metabolic data are often presented in the form of concentration ratios, e.g. [Choline + Creatine]/Citrate. The exact ratio can vary with equipment and settings. For example, ratios at 3 T differ slightly from those at 1.5 T because of differences in the shape of the citrate spectrum (16). However, it is generally accepted that PZ zone voxels, in which the ratio of choline and creatine to citrate is at least two SDs higher than the average ratio in healthy tissues, are considered to represent possible cancer (17). Voxels are considered

highly suggestive of cancer if the ratio of choline and creatine to citrate is more than three SDs higher than the average ratio (18).

The increasing amount of data available to analyze a study has not been accompanied with the development of a single standardized way to report it. Often the reports have been unstructured and in a narrative way (19). However, the European Society of Urogenital Radiology (ESUR) has recently proposed the Prostate Imaging-Reporting and Data System (PI-RADS) as the standard structured reporting scheme for prostate cancer (10). Although other schemes exist, such as the Likert score (20), the use of PI-RADS is rapidly extending (21–24). Therefore, we included in our tool the possibility to use this reporting scheme.

The medical support systems used to assist the diagnosis of prostate lesions are generally focused on prostate segmentation (25–28). They rely on computerized techniques for prostate cancer detection applied to ultrasound, magnetic resonance, and computed tomodensitometric images (29). For example, Vos et al. (30) used 3D-T2 imaging to define specific regions of interest (ROI), which were subsequently used on diffusion- and perfusion-weighted images to extract relevant features. The purpose was to train and classify the extracted set of features to calculate the likelihood of malignancy. Other related surveys have been focused on magnetic resonance spectroscopic data (31). The rapid growth of computer-based clinical exams has seen a significant increase in the number of online medical imaging systems (32,33), some of which being developed as web-based applications (34). The main challenge is the access and the interaction between the hospital database and the distant users. Thus, the aim of our work was to develop a new architecture system allowing including a web-based application connected to a prostate image database.

In the field of biomedical informatics, one of the long standing problems is finding a way to share medical data across a variety of media. Inherently, medical data are generated by a multitude of sources (35,36). eXtensible Markup Language (XML) has emerged as a leading facilitator. Although the XML is provided with predefined tags, one of its advantages is its extensible use. Over the last few years, a set of standards in the medical domain has been developed, called medical markup language (MML) to allow the exchange of medical data between different medical information providers (37,38). Therefore, the XML schema of tags can be defined for each individual case. Finally, the inclusion of the XML databases facilitates the management of XML files by storing them in an efficient way (39). Traditional object relational techniques, based on an XML model, are used to store XML files in an eXist-db database (40).

PRIMARY OBJECTIVES

In this paper, we propose a new medical tool in the form of an interactive JAVA applet application called Prostate-Analyzer. The purpose is to facilitate the inclusion of medical findings on existing prostate images using the combination of MRI techniques and MR Spectroscopy. The novelty of our proposed framework is that it includes the use of MRI and MRS in a compact application. Generally, users have different tools to evaluate prostate images

for MRI and MRS. However, it is necessary to compare regions of interest at the same time in order to determine pathologies or prostate lesions. For this reason, it is more efficient for each modality to provide a single tool that can easily manage all the data.

The main objective of the ProstateAnalyzer system is to develop a new tool that encompasses the visualization and analysis of prostate MR images, as well as a new storage system of clinical diagnoses in a single package. The tool is able to characterize the morphological (location, shape, and size) and the imaging features (mean and standard deviation of the signal, area, and center of mass) of a region within the image, defined and annotated by an expert.

Furthermore, it calculates the signal-time curve in perfusion studies and displays the LCModel signal spectrum for spectroscopic analysis (41). Besides, it allows the analysis of the same image by different experts, an essential feature in order to obtain a robust evaluation. The final outcome of the analysis is summarized in terms of the PI-RADS protocol.

With regard to the proposed architecture for storage of medical images, this should guarantee the connection and a secured access to the server, the DICOM database, and the system storage of clinical diagnoses (XML database).

RESEARCH DESIGN

Materials

Three-dimensional T2-weighted fast spin-echo (TR/TE/ETL: 3600 ms/143 ms/109, slice thickness: 1.25 mm) images (T2WI) were acquired with sub-millimetric pixel resolution in an oblique axial plane. DWI (TR/TE: 4200/101 ms) was performed using a pulsed gradient spin-echo technique with two b-values (100 and 800 s/mm^2). A parametric image, the ADC map, was directly generated (on the vendor's MRI consol) from the raw data on a pixel-by-pixel basis using the formula:

$$S = S_0 \exp(1 - bD)$$

where S_0 represents signal intensity when $b = 0$ and D is the ADC directly displayed as a gray scale number expressed in units of 10^{-6} mm^2/s.

The protocol was completed with DCE-MRI performed using a fat suppressed 3D T1 VIBE sequence (TR/TE/Flip angle: 3.25 ms/1.12 ms/100; temporal resolution: 6 s/slab over approximately 5 min). A bolus injection of Gd-DTPA (Dotarem, Guerbet, Roissy, France) was administered at a dose of 0.2 ml Gd-DTPA/kg of body weight. Finally, three-dimensional MR spectroscopic data were acquired using a water and lipid-suppressed sequence. Data sets were composed of $16 \times 16 \times 16$ phase-encoded spectral arrays giving nominal spectral resolution of 0.14 cm^3. Spectral data were processed using a modified version of LCModel (S. Provencher Inc., Asbestos, QC) for 1H spectroscopy of the prostate at 3T. Choline, creatine, and citrate were all quantified individually.

ProstateAnalyzer application

ProstateAnalyzer is a network-based database system whose aims are the management and processing of both MRI and MRS data sets in a single package.

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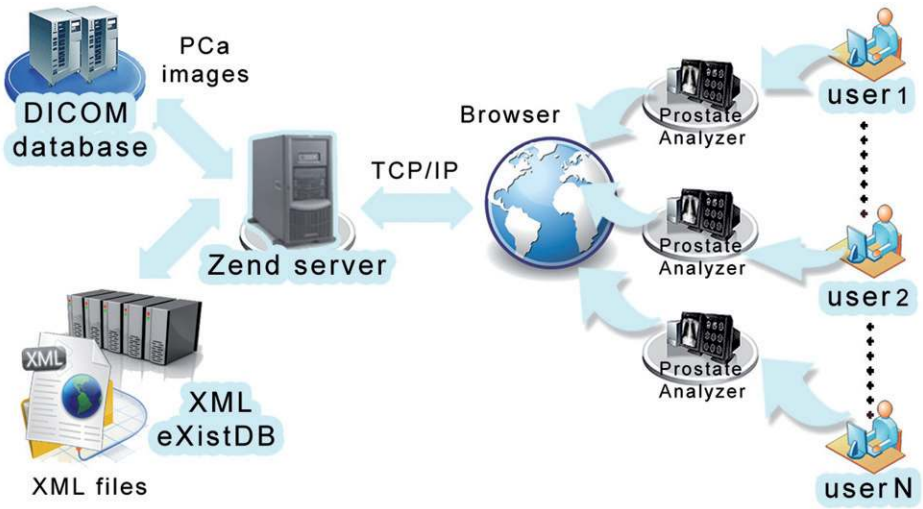

Figure 2. Network-based database system designed to implement the framework and the used hardware. The Zend server allows easy integration of the Apache server with database management tools.

This tool is implemented as a Java-based applet application to facilitate the inclusion of medical findings on existing prostate studies.

Architecture

A system has been designed in order to link the ProstateAnalyzer application to a database of DICOM images and a XML server, which stores the annotated files of the DICOM images. This architecture is supported by a Zend Server in order to allocate the ProstateAnalyzer application and a XML database provided by eXist-db (40). This type of architecture has been used in previous works for supporting other modalities of medical imaging databases such as PACS (42).

The ProstateAnalyzer application (Figure 2) communicates via socket TCP/IP with the Apache Server provided by Zend Server. This server is connected to a DICOM database, containing DICOM prostate images and with the eXist-db database, containing the XML files. We opted for the creation of the XML annotation files in the database in order to preserve the integrity of the original DICOM database (usually stored in a PACS system).

Furthermore, in order to avoid vulnerabilities during the transfer of information, internal security measures have been implemented. Besides using control User ID private keys, the algorithms have systems that protect and encrypt the information during its transmission. Currently, the secure socket layer (SSL) cryptographic protocol is used (43). Finally, the users can download the complete analysis performed by one user in a PDF file such a pre-medical report.

XML database

The ProstateAnalyzer application is related to the eXist-db manager, responsible for the XML database, incorporating its own server for access and management via web interface. We also opted for the creation of the XML

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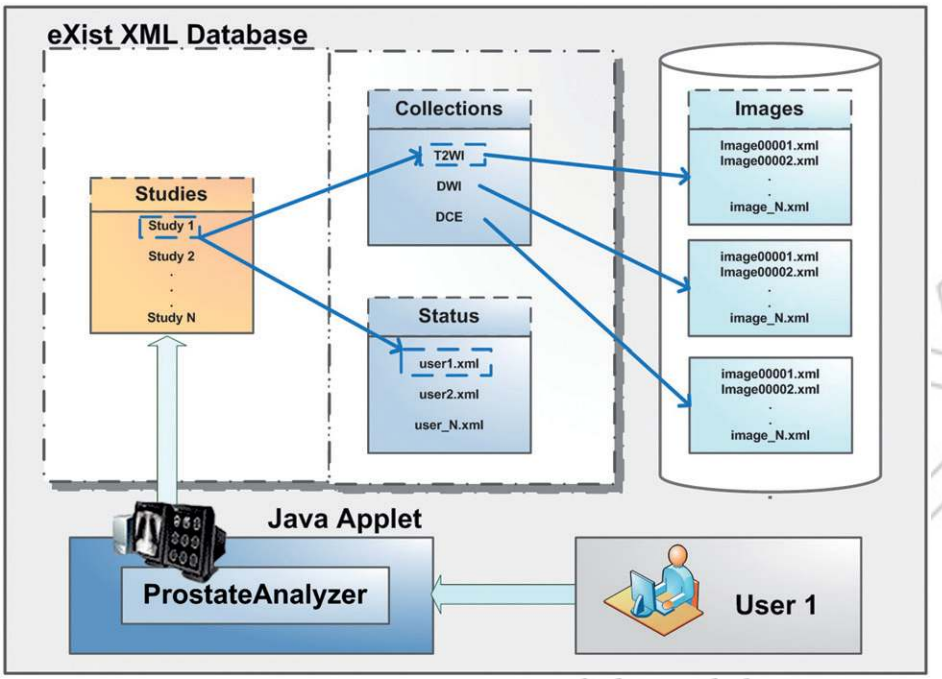

Figure 3. Connections to the eXist XML database within the ProstateAnalyzer and its interaction with the user.

annotation files in the database. Again, all XML files are related to their corresponding DICOM images and contain the records provided by experts.

Figure 3 shows a scenario of the use of the eXist-db XML database. The database is configured at different levels in order to store XML files associated with studies, collections, status and images. First, the ProstateAnalyzer application connects with the eXist-db to access a study, where each study contains a set of XML collections corresponding to 3DT2, DWI (as ADC map), and DCE techniques. Consequently, for each dataset, all the XML files concerning prostate images are allocated. It is important to note that each XML file contains the annotations provided by all the experts. In this way, the main structure of the XML file is the same for the images of the same study, thus enabling a faster access to the annotated information.

Moreover, at the status level, for each study, a XML file associated with each user is saved. Consequently, once the user is logged into the ProstateAnalyzer, the corresponding XML file is obtained.

Security and system access

ProstateAnalyzer is designed as a web application; hence the connection between the applet and the server can be both internal and external. The actual login process consists in an authentication measure with a unique username and password. One of the key elements in this application concerns the security of the data and the information across the network. In this sense, internal security measures to avoid vulnerabilities from the transfer of information are already included in the Zend Server.

HTTP was originally designed for the transmission and reproduction of multimedia documents, but these encodings are not part of the HTTP standard.

It is up to the applications themselves to break down and reassemble the information in order to transmit and receive it. Fortunately, Java applets are inherently based on the Internet Inter-ORB Protocol (IIOP). This protocol is based on the client/server computing model and a security algorithm is implemented as a security mechanism to ensure the integrity of the medical data being transferred. In the literature, several architectures use the IIOP in their security applications (19,44).

The most widely used regulations with respect to privacy and security are the Health Insurance Portability and Accountability Act (HIPAA) and the European Data Protection Directive 95/46/EC. Both regulations mandate health institutions to protect health information against unauthorized use or disclosure (45). In ProstateAnalyzer, the login/password signature allows knowledge of who is dealing with the individual data. Therefore, an audit-log for each study is produced identifying the user who has read the data and thereby allowing one to generate audit trails on data access activities for any specific patient (46).

ProstateAnalyzer engine

The search engine is the front-end for users once ProstateAnalyzer is accessed. There are two types of patient searches: search for all the patients and an advanced search. In the first option, the search engine returns a list with all the patients recorded in the database. In the second case, the system returns just the patients who share the same regular expression used as a query. To perform a search, it is necessary to create a data set that contains information concerning the four MR modalities described before. For each item, the tool shows different attributes (patient name, comments, and status) and the number of images provided by the concerned modality (anatomy, diffusion, perfusion, and spectroscopy). Moreover, each case is represented by a different color depending on the status of the study. When a state is color-coded as yellow, it means that the study has been analyzed partially; a green color-coding indicates that the study has been completely analyzed and validated. Finally, white represents a study that has not yet been analyzed.

Anatomy 3D-T2WI

ProstateAnalyzer offers a new visualization platform to provide annotations for different kinds of tissues (tumor number 1, tumor number 2, PZ, CZ, TZ, or others) obtained from T2WI studies. This visualization capability is combined with basic post-processing tasks such as zooming, gamma correction, user-specific ROI, surface, and volumetric measurements. In addition, the viewer provides information from the DICOM header, the status of the anatomical study (validated, partial, or empty) and the list of the annotations added by different users.

Figure 4(a) shows an example of visualization of the T2WI in prostate cancer analysis. When an overlay is manually drawn, a label is automatically defined with the user's specified color. This label is defined using the first letter of the user's first name and surname followed by the number of annotations (in the figure, the first region of interest is identified by letters "AL0" in green). A table shows a list of color-coded overlays, specifying the username and the tissue type (indicated by the user). It also allows us to

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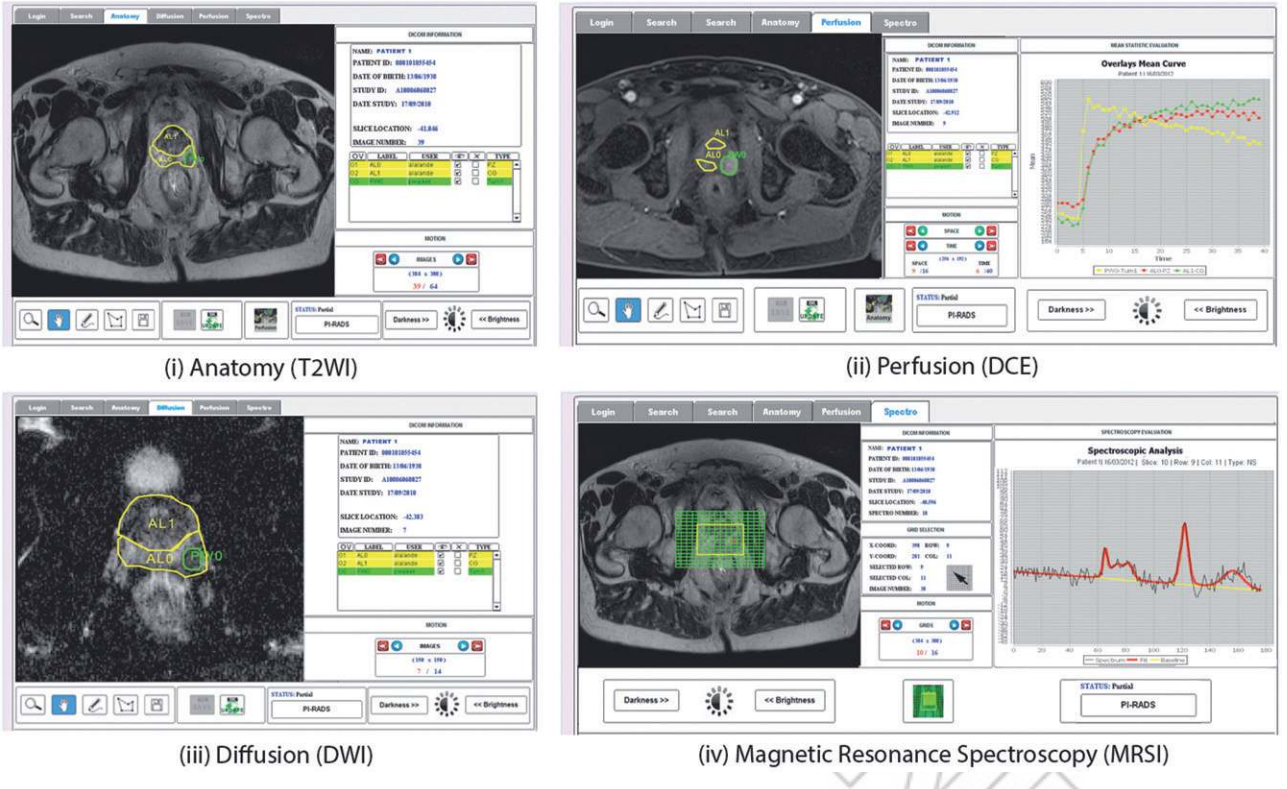

Figure 4. The four visualization screens of ProstateAnalyzer. Notice that all of them follow the same structure, with the corresponding image in the left part, the information of the image or related with the specific modality in the right part, and the imaging tools in the bottom part of the image. (a) T2WI, (b) DWI, (c) DCE with corresponding signal-time curves, and (d) MRS with a LCModel-processed signal spectrum.

visualize or to delete each overlay, although this latter option is only available to the expert who created it. Selecting an overlay of the table allows displaying its related information (the annotations filled in a pop-up window). Finally, after pressing the confirmation button of the pop-up window, the overlay is added to the table, displayed on the image and stored in the XML database.

DWI

ProstateAnalyzer also provides a support tool for the DWI studies with similar basic post-processing tasks as presented previously for T2WI. Figure 4(b) shows an example of an ADC map with annotations provided by different users. In the example, a multiple user-specific region of interest (ROI) study is presented.

Perfusion imaging analysis (DCE)

Dynamic contrast enhanced (DCE) MRI is also catered for in the ProstateAnalyzer. The tool also contains basic post-processing tasks using the same features applied in T2WI and DWI. The most important difference with respect to the other techniques is that the perfusion images are displayed in time–space partitions.

Furthermore, this viewer uses a mean signal–time curve to display the signal enhancement during the arrival of the contrast agent into the tissue. Figure 4(c) shows an example of the ROI analysis in perfusion MR images. For each overlay, the mean signal from each ROI is calculated and displayed as the corresponding signal-time curve: the mean–curve is denoted with a different color according to its associated area.

MRS

ProstateAnalyzer offers individual spectrum visualization from a 3D spectroscopic grid. Figure 4(d) presents an example of a MRS study with a LC Model-processed signal spectrum. This viewer displays a set of 3D-T2 images allowing the spatial location of the spectroscopy study. For each spectroscopic grid, there is a corresponding image. In order to obtain a specific spectrum, the user must click on the corresponding voxel (highlighted in red) within the grid. The LC model is widely used for processing clinical single and multi-voxel spectroscopic data (47). It allows individual and batch analyses of the main metabolites within the spectra of the prostate: citrate, choline, creatine, and spermine.

Interaction between spectroscopy and anatomy

One of the most important features of ProstateAnalyzer is the interaction of the imaging modalities among themselves. Figure 5 shows an example of the interaction between MRS and T2WI. The aim is to display the annotations, obtained from the T2WI study panel, on the spectrum illustrated within the graphical window. The way to link the processing is provided by the slice location (it is shown in the DICOM information panel of the MRS image, and boarded in yellow). In the MRS study panel, when the expert selects a voxel within the spectroscopic grid, the spectrum is displayed. The next step is to determine whether the selected voxel contains any annotations from the anatomical 3D-T2 panel. If the information exists, it is displayed in the

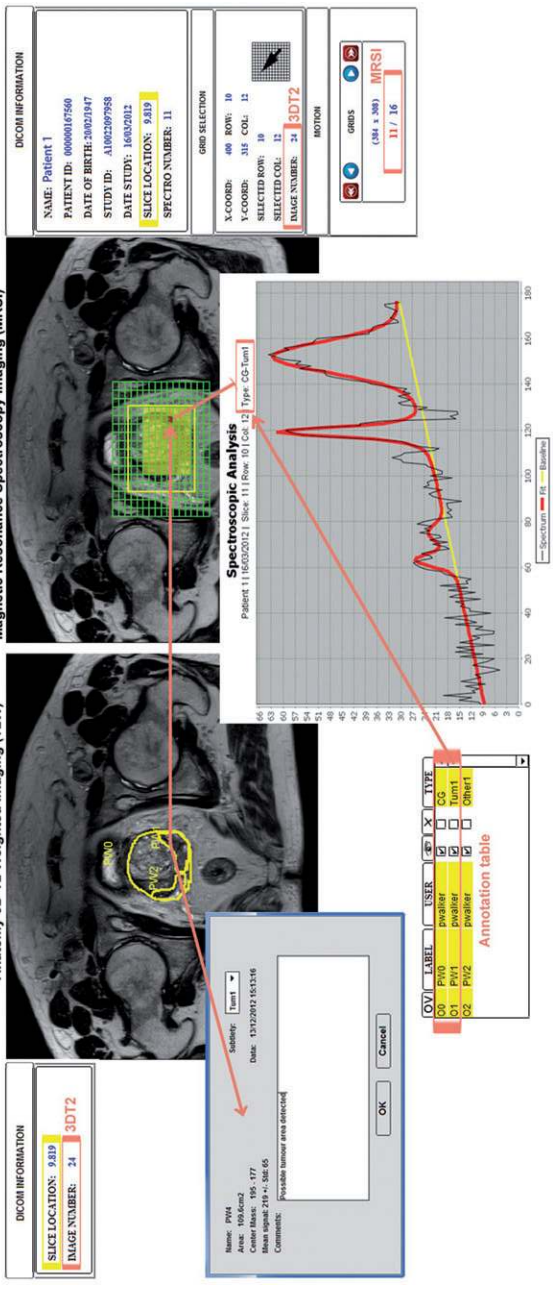

Figure 5. Example of the interaction between a 3D spectroscopic imaging study with T2W imaging.

spectroscopic graphical area along with the spectrum. The example shows the selected voxel corresponding to an area (in the anatomic analysis) with two denominations for one tissue (named as Tum1 and CG in the figure), and is also represented on the annotation table. This interaction is very important, because one can visualize the information of both techniques in only one representation.

Interaction between anatomy and perfusion

In this case, the anatomic and perfusion studies are not using the same reference image due to the differences in spatial resolution. Consequently, the solution is to locate the image from a set of corresponding perfusion DCE-MRI images, as close as possible, to the slice location of the anatomical 3D-T2 image.

Figure 6 shows an example of the analysis on a perfusion-weighted study using the ROI drawn on the corresponding 3D-T2 image. On the interface of the perfusion image analysis, when the "anatomy" button is pressed all the annotations concerning the anatomy study are displayed. ProstateAnalyzer adapts the annotated regions into the correct position in the perfusion image, according to the spatial resolution and the pixel spacing. In order to distinguish the overlays between perfusion and anatomy, the viewer displays all the anatomy overlays and adds the prefix "A" before the label name.

Reporting

Once the study is analyzed, the findings need to be reported, if possible in a standardized way. ProstateAnalyzer includes the PI-RADS structured reporting scheme, according to ESUR prostate MR guidelines in 2012 (10), which is being established as the common protocol in European countries (21,22). The use of a standardized graphic reporting scheme facilitates the communication with referring colleagues, and it increases the quality and diagnostic value of prostate analyses.

The inclusion of the PI-RADS is carried out using a form with a drop-down list that includes the different answers of the PI-RADS question. Selecting the option, the corresponding number is assigned. The report is saved in an independent XML file and loaded into the XML database. The use of an independent XML file allows a faster search when looking just for similar cases in terms of PI-RADS scores. Besides, there is the option of downloading a PDF file with that information.

MAIN OUTCOME

In this section, a complete example of use of the ProstateAnalyzer application is presented. In order to display the environment of the application, the obtained results using the four visualizations platform (T2WI, DCE, DWI, and MRS) are fully detailed. The main purpose is to demonstrate the usability of the ProstateAnalyzer application in the localization and the analysis of a tumor, if present.

Clinical diagnosis

The upper image of Figure 7 shows an example of a localized tumor displayed on T2WI. Prostate cancer usually shows low signal intensity on T2WI that is

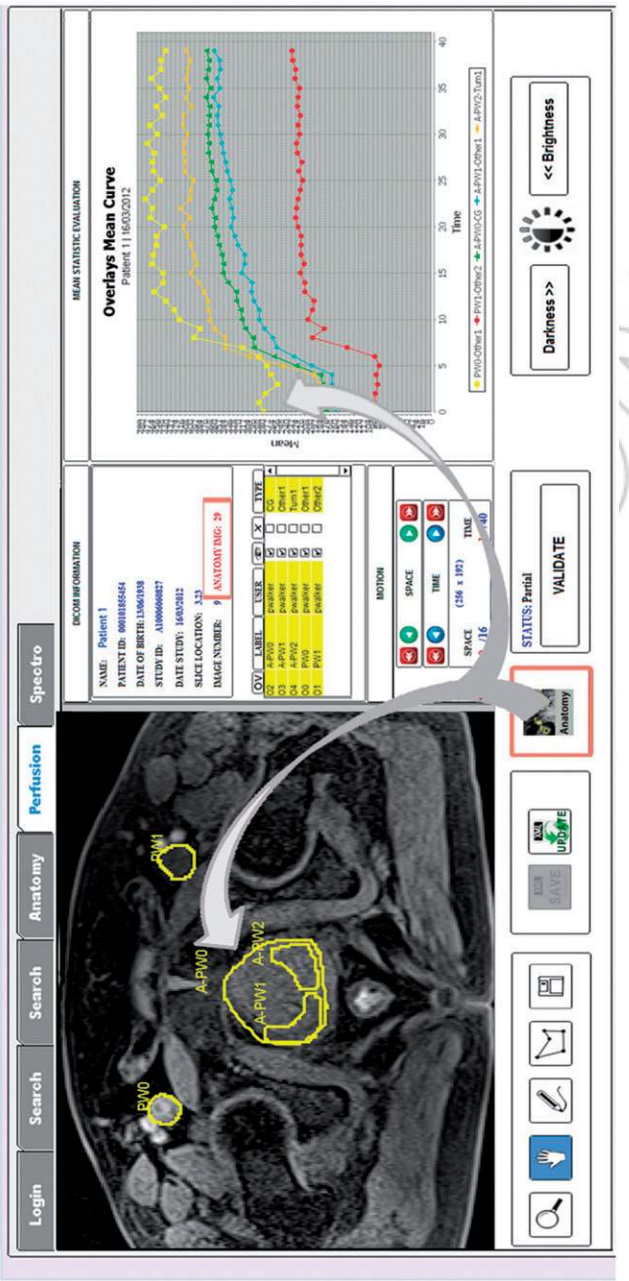

Figure 6. Example of the interaction between a perfusion slice with a 3DT2 image.

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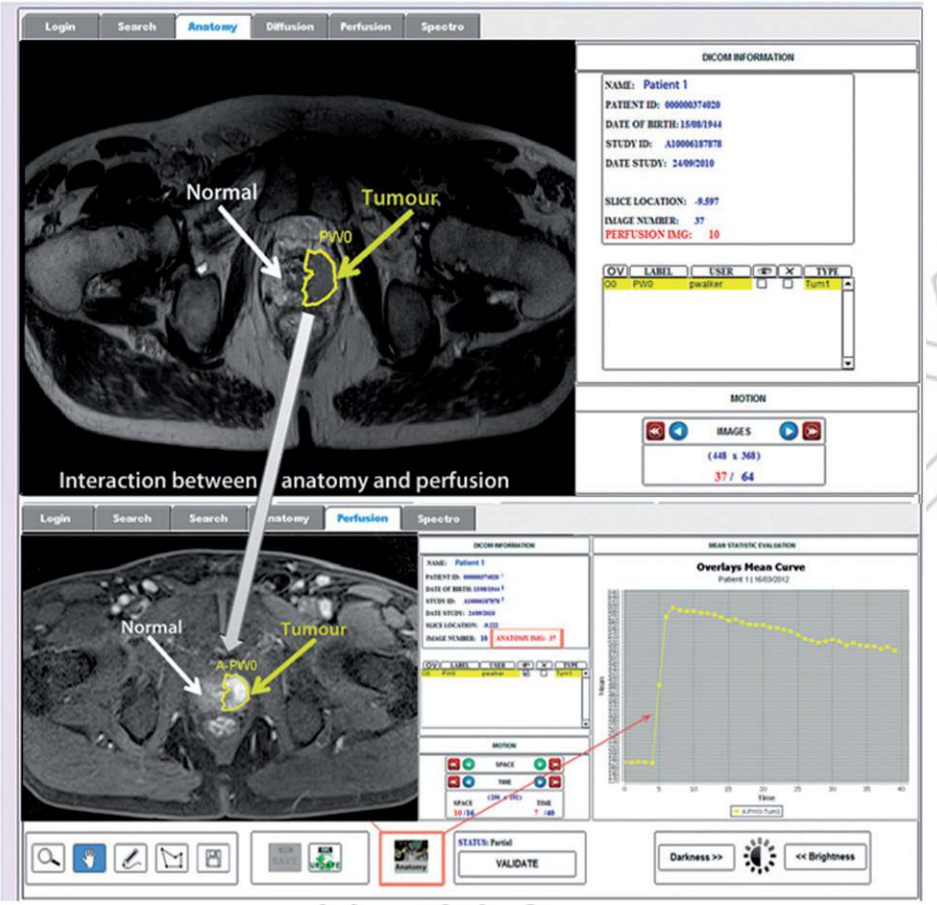

Figure 7. Interaction between T2WI and DCE.

well defined with respect to normal PZ zone tissue. However, it is not always easy to localize a pathologic area. One of the advantages of the ProstateAnalyzer application is to analyze the same study using other techniques. Once a sequence of the T2WI is analyzed, the application offers an efficient solution to compare the same ROI in DCE, DWI, and MRS. On the DCE, the peak of the curve corresponds to the first pass of the contrast agent and indicates the rapid uptake of the contrast agent, typically observed in cancer tissue.

We compare the mean curve of a representative tumor tissue with that of healthy tissue in Figure 8. The first curve (in yellow) is from tumor tissue and the second from healthy tissue (in red). In this case, the first annotation corresponds to a tumor region labeled as “PW0” which is made in the perfusion panel. The second, which represents healthy tissue, is annotated in the anatomical panel and displayed in the perfusion panel labeled as “A-PWO”. In the diffusion panel, the analysis also demonstrates the presence of a tumor (Figure 9). It is important to notice that the user draw a different ROI as the one in Figure 7. Indeed, the tumor will correspond to low signal (therefore, low diffusion coefficient) on the ACD map.

On the MRS panel (Figure 10), the example shows a selected voxel corresponding to an area of cancer tissue (Tum1). The LC Model-processed

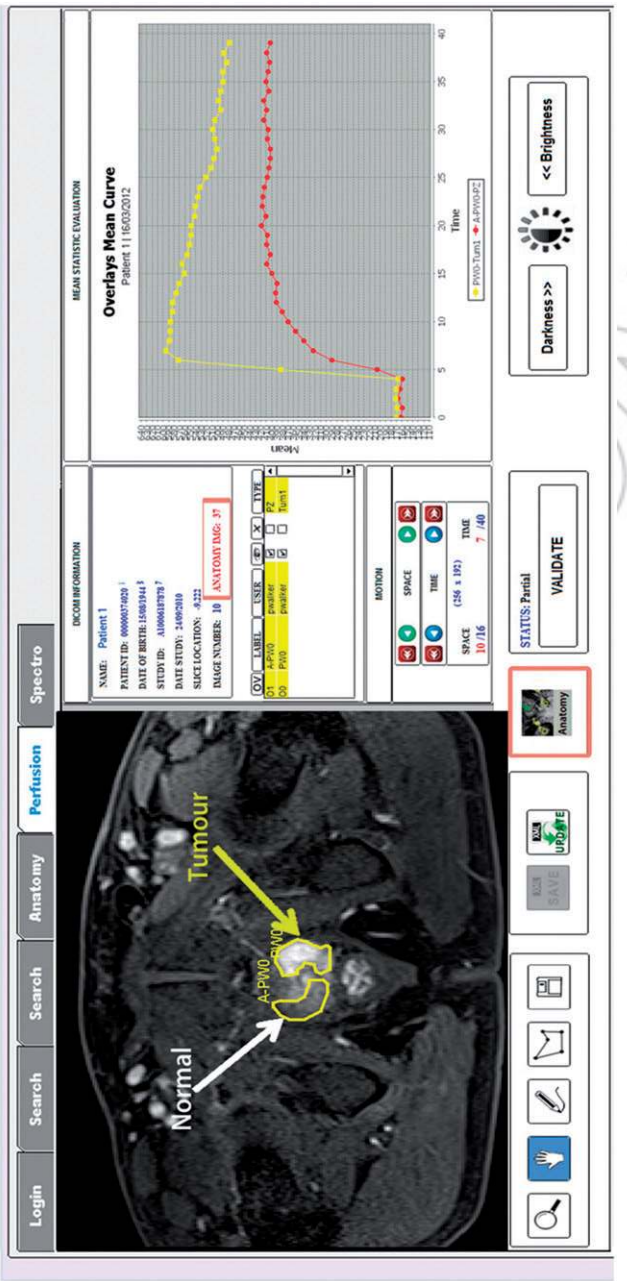

Figure 8. Example of two annotated regions (tumor and healthy) represented in perfusion analysis. A schematic illustration of time-mean curve for DCE is also depicted in both cases (tumor in yellow, healthy area in red).

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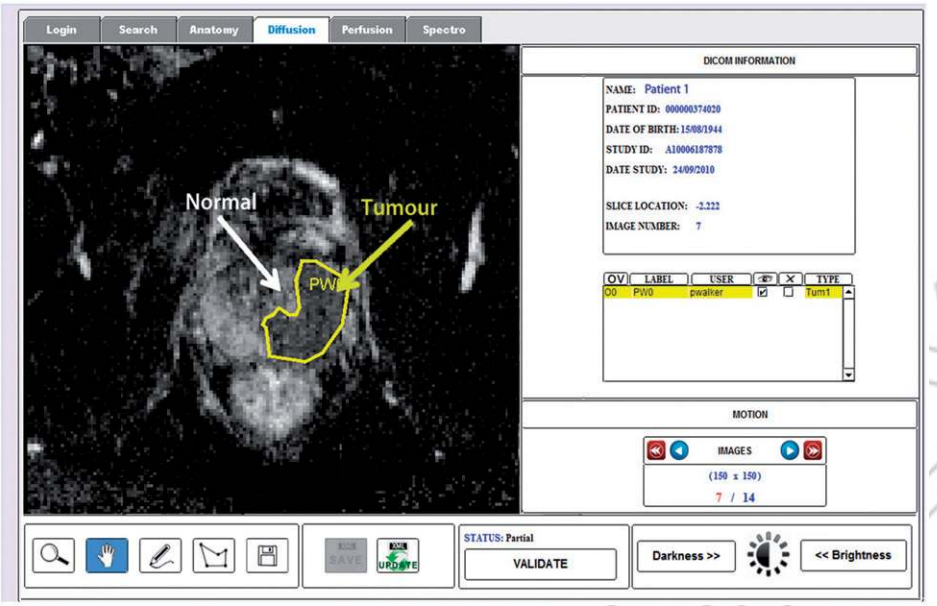

Figure 9. Example of a localized tumor is represented using diffusion-weighted imaging of the same prostate study.

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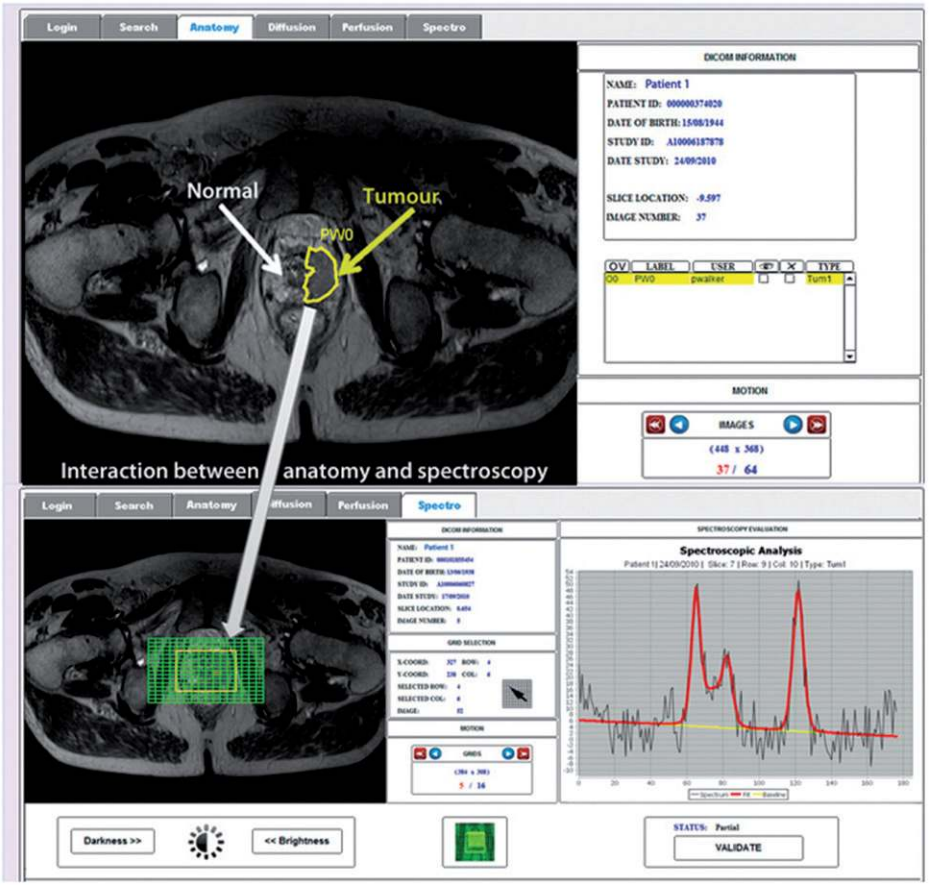

Figure 10. Example of the interaction between T2WI and MRS studies showing the spectra of the cancer Voxel.

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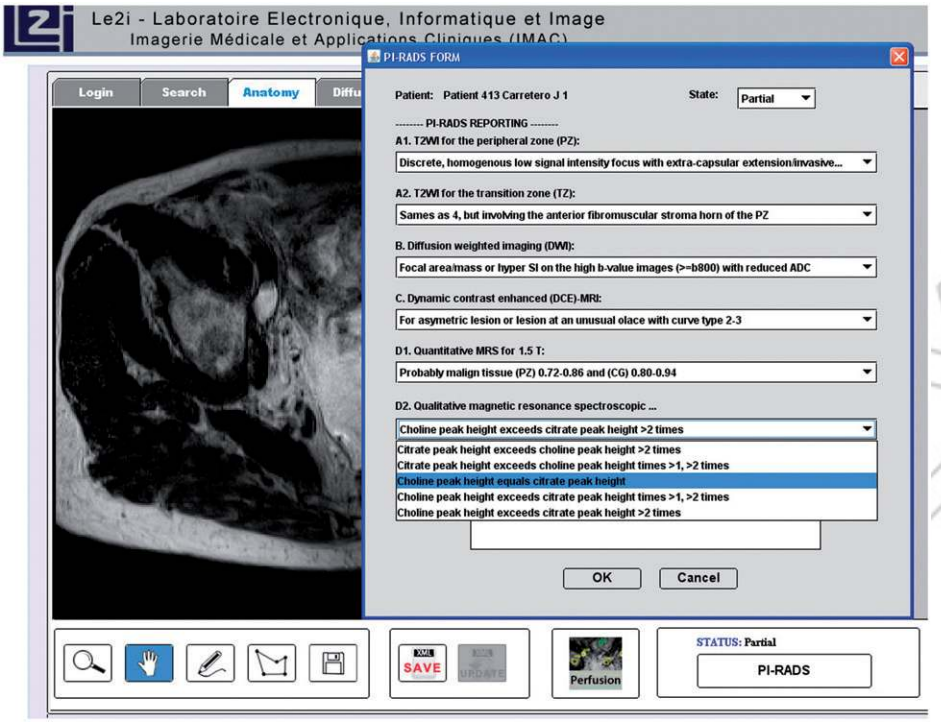

Figure 11. A window pop-up allows to report the case according to the PI-RADS protocol.

signal spectrum demonstrates how the signal is modeled in red from the noisy signal in black. Hence the different peaks of the spectrum are easily extractable. Illustrating graphically the levels of these metabolites is very important, since cancerous tissue is characterized within the spectrum as reduced citrate and elevated choline peaks. In the figure, the first two consecutive peaks correspond to choline and creatine, while the third one corresponds to citrate. It is clear that the relative levels of choline and creatine are very different to those observed in normal healthy tissue (Figure 4d), where higher levels of citrate and lower levels choline are observed.

Once the clinical diagnosis has been performed, users have the option to create a MR reporting, as depicted in Figure 11. For each MR technique, a "PI-RADS" button is available in the option panel. When it is pressed, a window pop-up appears where the user can report the findings for each technique according to the PI-RADS protocol.

Design effort benchmarks

ProstateAnalyzer is currently being used in the MR department of the University Hospital of Dijon (France). The present working database is composed of more than 1600 patient datasets. The time to access to the Java Applet application (ProstateAnalyzer) by users is around 2–3 s in an intranet environment. It has been tested with the following common internet web browsers: Mozilla Firefox, Internet Explorer, Google Chrome, and Opera. It is preferable to use the Java Deployment Toolkit 6.0.160.1.1 or superior and to use the JavaTMPlatform SE 6 U16 6.0.160.1. The most time-consuming part corresponds to loading a prostate study. A typical study consists of a set of

64 anatomical images, 14 ADC images, 640 perfusion images, and a set of spectroscopic data containing up to 1000 files. It is important to note that the number of spectroscopic data files is very variable and depends on the prostate size. The average of the time consuming is around 60–70 s to load and display a typical prostate study with the data presented previously.

The search engine provided by ProstateAnalyzer is tested in order to obtain the complete study. The timing response to retrieve a prostate study was around 1 min including the corresponding XML-associated files. The time necessary to record annotations on the database is around 3–5 s for anatomical and diffusion images and around 12 s for perfusion images. The computational cost is higher for the latter because of the need to calculate the signal-time curve. In order to obtain a spectrum, the cost is around 5 s to display it in the graphical window. Once the analysis is finished by the user, ProstateAnalyzer takes around 4 s to save the XML file into the database.

With the new architecture, ProstateAnalyzer can also be accessed using regular external network connections outside the intranet connection of the hospital. We tested the connection from Girona in Spain (several hundreds of kilometers from Dijon). Experiments were carried out by loading a large study consisting of a set of 64 anatomical images, 15 ADC images, 720 perfusion images, and a set of spectroscopic data containing up to 1200 files (corresponding to around 150 MB of transferred data). We loaded the case several times during a week, and the total elapsed time response varied between 100 and 130 s. When comparing the times provided by the internal and external connections using the same study, the difference was found to be around 40–70 s. The difference was due to two main reasons. On one hand, it depends on the instantaneous network load and on the other hand to the number of users being connected to the ProstateAnalizer server. The main conflict, when multiple users are connected, is in the downloading of the cases, since the server must split the downloading process between the connected users. However, once the study is loaded, the usability, visualization, and annotation times are independent with respect to the number of users – they just depend on their own machine, not on the server).

DISCUSSION

ProstateAnalyzer is a web-based application for the analysis of prostate images using four MR modalities: T2WI, DWI, DCE, and MRS. One of the most evident advantages of ProstateAnalyzer is that it allows simultaneous analysis of a prostate study using the different modalities. It also provides an interaction among them and MR spectroscopy. Since the application has been designed to work with DICOM files, any equipment that operates under such image standard can potentially be used with ProstateAnalyzer.

The principal problem encountered in the diagnosis of a prostate study is the localization of a ROI-containing tumor tissue. Normally, experts use different tools to validate the diagnoses using different software and make many annotations in different files. This is not a practical solution to managing abundant medical data. ProstateAnalyzer offers the solution, because it allows experts to analyze prostate ROI on T2WI, DWI, DCE, and MRS panels within the same application.

The development of the proposed interface has been made in such a way that it is simple and intuitive to use for the users. The interface is divided in four panels with the purpose of visualizing a patient study, simultaneously, for the different techniques. The main objective was to provide useful tools for experts to manage examinations with different types of images and data. ProstateAnalyzer allows the annotation of findings provided by different experts in the prostate. All annotations are saved in XML files associated with the prostate images. Although a prostate study can be shared among all the users, they can still validate or modify their own diagnosis in individual cases.

Finally, our tool offers the possibility to work remotely via the web and represents an improvement in the data management. The access to the ProstateAnalyzer should be provided to multiple users in order to make easier both local and external connections. In order to facilitate this task, the application is implemented as a JAVA applet tool. Thus, it is not necessary to install any program on computers to run our interface unless users have a browser that supports Java technology. Moreover, applets can be executed from any operating system (Windows, Linux, and MAC) because they are running in a Web browser. ProstateAnalyzer can be integrated in a server to manage medical images stored in a prostate database.

ProstateAnalyzer still presents some limitations which will be addressed in order to enrich the tool. For instance, in perfusion analysis, the tool uses a mean DCE signal–time curve to display the signal enhancement during the arrival of the contrast agent into the tissue. However, providing quantitative values related to microvascular permeability, K^{trans} or the diffusion space, υ_{e} could also be helpful. With regard to the spectroscopy section, the possibility of displaying 2D and 3D metabolite maps will be addressed. For this task, specialized spatial and spectral data processing methods, for which sources are not commonly available, are needed (e.g. morphological analysis and spectral characteristics of the observed metabolites). We are also trying to improve the efficiency of the computational cost. One solution could be to load single frames only, on the basis of their spatial correspondence, instead of the whole dataset. This would also allow the possibility of automatically displaying the four sequences simultaneously. Thus, when scrolling the slices, the information will change simultaneously on the T2WI, DWI, DCE, and MRSI displays.

Taking into account how rapidly clinical databases are growing, ProstateAnalyzer should be an important contribution to the management of large databases. Indeed, the implementation of ProstateAnalyzer offers the possibility to extend and adapt to other MR modalities. As a proof of concept, this project is an adaptation from previous work based on mammography (42) and it demonstrates that our approach is easily portable to other sources of medical images. Finally, as ProstateAnalyzer allows downloading reports in PDF format containing the annotations and graphical results (mean signal–time curve and signal spectra), it should also be useful as a pre-report.

CONCLUSION

In this paper, we have presented ProstateAnalyzer, a new medical tool that allows the evaluation of the prostate cancer in an effective way. ProstateAnalyzer visualizes the different MRI techniques

(anatomy, diffusion, and perfusion) together with MR spectroscopy, and automatically places annotations, made in one of the images, onto the others. In addition, ProstateAnalyzer also includes the PI-RADS reporting protocol, thereby offering the possibility to fully report the prostate study in a standardized way.

It has been implemented as an interactive JAVA applet application with the purpose of facilitating the inclusion of medical findings on existing prostate images, using the combination of MRI techniques and MR spectroscopic analysis. Furthermore, a new architecture is presented to store the medical records in a XML database which stores a set of annotated files.

DECLARATION OF INTEREST

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