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Implementation of a Semi-automated Post-processing System for Parametric MRI Mapping of Human Breast Cancer

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Magnetic resonance imaging (MRI) investigations of breast cancer incorporate computationally intense techniques to develop parametric maps of pathophysiological tissue characteristics. Common approaches employ, for example, quantitative measurements of T_1, the apparent diffusion coefficient, and kinetic modeling based on dynamic contrast-enhanced MRI (DCE-MRI). In this paper, an integrated medical image post-processing and archive system (MIPAS) is presented. MIPAS demonstrates how image post-processing and user interface programs, written in the interactive data language (IDL) programming language with data storage provided by a Microsoft Access database, and the file system can reduce turnaround time for creating MRI parametric maps and provide additional organization for clinical trials. The results of developing the MIPAS are discussed including potential limitations of the use of IDL for the application framework and how the MIPAS design supports extension to other programming languages and imaging modalities. We also show that network storage of images and metadata has a significant ($p<0.05$) increase in data retrieval time compared to collocated storage. The system shows promise for becoming both a robust research picture archival and communications system working with the standard hospital PACS and an image post-processing environment that extends to other medical image modalities.

KEY WORDS: Magnetic resonance imaging, digital image management, digital image processing, digital imaging, Digital Imaging and Communications in Medicine (DICOM), digital libraries, image analysis, image database, image processing, imaging informatics, MR imaging, PACS, workflow, workflow reengineering, user–computer interface

INTRODUCTION

Cancer imaging of the breast using magnetic resonance imaging (MRI) has been evolving to incorporate computationally complex techniques that provide measures that can discriminate between normal, benign, and malignant tissues[1,2] as well as monitor treatment response[3,4]. This change has brought about imaging protocols that can be used to create parametric maps that represent calculated parameter values at each voxel level. The values are derived from parametric models of underlying pathophysiological changes that can enhance contrast between healthy and diseased tissue[5,6].

Investigators at our institution, the Vanderbilt University Institute of Imaging Science (VUIIS), are studying the use of quantitative MRI to characterize breast tumor status before, during, and after neoadjuvant chemotherapy. Several types

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of parametric maps are derived from the MR images: T_1 maps that report the longitudinal relaxation time of a tissue, apparent diffusion coefficient (ADC) maps that measure the diffusion of H_2O within tissue, and dynamic contrast-enhanced (DCE) maps that can measure K^{trans} (the volume transfer constant), v_e, (the extravascular extracellular volume fraction), and τ_i (the average intracellular lifetime of a water molecule)[8,9]. These parameters are extracted from multiple MR measurements by curve fitting of each voxel in the relevant time series. The techniques require approximately 13,000 nonlinear curve fits per image, based on a typical region of interest (ROI) selected from the image.

Motivated by the encouraging results[2–4,6–9] that quantitative MR imaging has shown, new approaches are being developed to improve the protocols to acquire the data[13,14], the quality of the parameter estimation process[10–12], and the post-processing techniques and systems[15–22]. Newer approaches to the problem include the use of linear programming techniques utilizing linear functions maximized within constraints[23,24], Bayesian estimation approaches[25,26], techniques that present additional computational costs that result in longer post-processing times, and new approaches to registration that incorporate kinetic models to better describe the time series being fit[27].

In a research setting, the images may be acquired from dedicated research and/or clinical imaging devices. Research devices may not be integrated with the hospital PACS, while clinical MRI scanners typically use the digital imaging and communication in medicine (DICOM) standards to send patient imaging data to the PACS. Investigators often prefer vendor-specific proprietary image data file formats that conveniently contain the information required for image analysis. These proprietary formats are a subset of the data that can be transmitted by the DICOM standard but retain information that the PACS system may discard because it resides in private DICOM tags that are not normally used in a clinical setting and thus may not be part of the clinical information dataset. This latter problem may be characterized by the needs that led to the adoption of the DICOM 2003 CT/MR objects where a number of attributes and terms increased significantly, removing the need for many private tags and increasing the likelihood that the data needed by investigators may be in PACS systems[28].

Early approaches to solving these problems included Image Engine[17], which linked images in multiple formats to a metadata database, medical record information, and utilized the unified medical language system to improve query capabilities. Work at the University of California, San Francisco[18], established a three-part system in which the hospital PACS was linked to a database supporting image processing and a knowledge base.

Recent efforts responding to the storage and processing challenges include systems like the Bio-Image Warehouse System[19]. The Bio-Image Warehouse System incorporates a PACS interface, DICOM compliance, an image storage system supporting DICOM and non-DICOM image types, a metadata database, image processing, and validation tools. Extension of these systems to deliver services over networks by web-based services with full integration into the PACS and radiology information systems demonstrates how these research needs are being met outside of traditional clinically oriented software systems[20,21].

The National Cancer Institute is supporting efforts to organize image datasets through projects like the CT Image Library for the Lung Screening Study[22] and the National Cancer Imaging archive[29]. By establishing national repositories of images and the ability to provide post-processing and image retrieval of qualified datasets through disk media or internet transmission services, these libraries provide a programming toolset, computing resources, and image datasets to standardize and extend investigator techniques and data sources. The Center for Information Technology (CIT) at the National Institutes of Health is developing the medical image processing, analysis, and visualization (MIPAV) application[16] to facilitate research collaboration through standardized tools and solutions to give investigators common environments that interoperate. This is accomplished by basing MIPAV on the Java programming platform for cross-platform support, an application programming interface that permits custom programs to access MIPAV functions, and the development of a new medical image format (MIPAV XML) based on the extensible markup language (XML) to facilitate a broader open data exchange standard.

In response to the demands of the specific research at our institute to automate DCE-MRI and ADC analysis[8] and archiving, we have developed an integrated software system to analyze and organize MR breast images. A review of the existing image management and post-processing

procedures and software led to key decisions to develop the new system on a new workstation, in a single programming language (interactive data language, IDL) with DICOM network services, and to store all metadata in a Microsoft Access database. These choices simplified software and database development, and utilized the expertise of the project members to develop this specific application.

The database for the system serves as a research PACS management tool for all images in raw, intermediate and final format by managing the archival and retrieval of all images within the file system. It also acts as a post-processing controller, providing the necessary configuration and run-time information to support a post-processing menu system plus all of the image attributes that are used in the post-processing algorithms. The final key role of the database is the DICOM dictionary services that support the creation of updated code for the DICOM import/export functions.

Constructing the new system has simplified the original image post-processing effort. The original process required up to 20 h over a period of days, while the new implementation has reduced processing to 2–5 h dependent upon the extent of image segmentation and post-processing required for a given parametric map.

This system design has shown promise to expand to other modalities and serve as a more generic medical research imaging post-processing and image archive solution. This extensibility offers a means to reduce the time and effort spent by an investigator to manage large datasets within multiple studies. The increased efficiency allows more time to explore alternative hypotheses or techniques with the available data. This system also provides a means to self-document the process of investigation, increasing the ability to audit results and identify points where post-processing may fail.

METHODS

MR Image Acquisition

All imaging studies were performed on a clinic or research Philips 3.0 T Achieva MR scanner. A clinically approved transmit–receive double-breast coil covering both breasts was used for all imaging. Data for a T_1 map was acquired employing a 3D gradient echo multi-flip angle approach with a TR\TE of 7.9:1.3 ms and ten flip angles of 2°, 4°, and 20° (in 2° increments). The acquisition matrix was $192\times192\times25$ (full breast) over a FOV of 22 cm^2 with slice thickness of 5 mm, two acquisitions, and sensitivity encoding (SENSE) = 2. A catheter placed within an antecubital vein delivered 0.1 mmol/kg of the clinically approved contrast agent Magnevist over 20 s (followed by a saline flush) for the DCE study. The dynamic scan used identical parameters and a flip angle of 20°. By setting the SENSE factor = 2, each 20-slice set was collected in 16.5 s, yielding 25 time points in just under 7 min. A diffusion-weighted (in three orthogonal directions) single-shot echo planar imaging (EPI) sequence was employed for full-breast ADC mapping; TR\TE=2,500\44 ms, b values of 0 and 500 s/mm^2, and a 128×128 matrix over the same FOV as above. The number of acquisitions is 16, yielding data for a (relatively) high signal-to-noise ADC map in less than 6 min.

MR Image Post-processing

As this type of analysis is complicated and time-intensive, we have invested a significant effort in automating the process so that such analyses can be completed within 2 h of the examination. The automated post-processing steps begin by automatically importing studies performed on either the clinical or research 3.0 T scanners into a central database that was created to manage the entire analyses process and storage issues. The analysis begins by converting the native 16-bit signal intensity files into 32-bit real data, followed by registration of T_1, DCE-MRI, and diffusion-weighted MRI data to the first dynamic image volume. Then, the T_1 map is created from the T_1-weighted multi-flip angle data and combined with the dynamic data to develop the K^{trans}, v_e, and τ_i maps. The ADC map is then created. As each parametric map is constructed from data that was initially registered to the first dynamic image volume, all parametric maps are inherently registered. Both interactive graphical interfaces and automated code modules exist in each step of the post-processing mentioned above. The automation of this process has the potential to bring a high order of organization to this study and presents an entire process (from data acquisition to analysis) that is transportable to other imaging sites. This could potentially

help to facilitate multi-institutional studies of MRI of human breast cancer response to treatment.

Examination Protocol

The examination protocol is a dedicated (IRB-approved) research exam that includes fast field echo (FFE) scout and reference scans, a multi-flip sequence (to generate the T_1 map), T_1-weighted FFE dynamic scans before and after contrast administration (for the DCE analysis), diffusion-weighted single-shot EPI scans (for production of ADC maps), and a post-contrast high-resolution fat-sat T1-weighted FFE for anatomical definition. Women 18 years of age or older with biopsy-proven infiltrating breast cancer, stages IIA to IIIB, and Eastern Cooperative Oncology Group performance status 0 to 1, are enrolled in our ongoing study. Patients signed a protocol-specific consent that was approved by the ethics committee of our Cancer Center.

User Requirements

The existing programs and processes for this research study were evaluated and documented to establish the initial functional requirements for the new system. This is necessary to establish a benchmark of functionality with which to compare the new system, to provide a basis for the transition planning, and to establish if previous work can be retained or adapted for use in the new system. Systems engineering methods are utilized to gather stakeholder inputs (for example, investigators, collaborators, and other interested or affected parties), define operational objectives, develop the requirements of the system, design the functional, physical, and operational architectures of the system, and create the plan for validating and verifying the system's ability to perform as specified.

System Design

Workstation and Software. A Dell Precision 470 workstation (2 GHz dual-core dual processor, 2-GB memory, 80-GB SCSI Raid 0, 100-MB Ethernet, dual DVD-RW, 19-in. Monitor, Dell Inc., Round Rock, TX, USA) with Windows XP SP2 (Microsoft Corp., Redmond, WA, USA) was installed and connected to the research network. A dual-core dual-processor system provides the capability to extend the post-processing programming to include multi-threaded parallel implementations to further improve run-times. The programming languages used were IDL 6.3 with DICOM network services and Dataminer (ITT, Boulder, CO, USA) for the core application services, with Matlab 2006a with the Database Toolbox (Mathworks, Natick, MA, USA) to test multi-language implementations. The database was implemented with Access 2003 (Microsoft) to provide fast prototyping, small user environment use, and an upgradeable basis to more functional SQL database solutions. MR images were transferred from the Philips MRI scanners either in the Philips PARREC format to a server location and then downloaded to the workstation using the SSH Secured Shell 3.2 (SSH Communications Security, Helsinki, Finland) or transmitted to the workstation by DICOM push services. Windows XP remote desktop services were enabled to allow remote access to the workstation to facilitate multiple users accessing image post-processing services without physically being at the workstation. Windows XP allows the transfer of files by the mapped network drive function to the user's workstation.

Main System Functions. Figure 1 is a representation of the MIPAS core structure and interaction. The MIPAS system is composed of five primary functions: (1) *database*—stores all metadata for image datasets and post-processing controls; (2) *import image dataset*—provides the addition of specific image datasets into the database and file storage

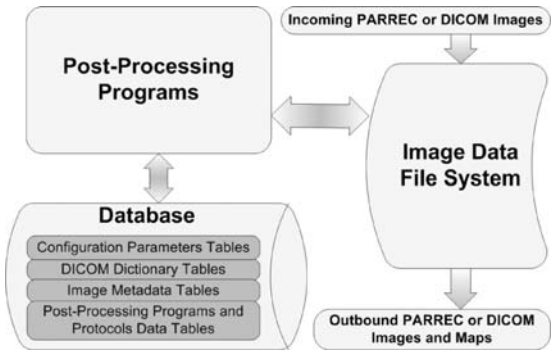

Fig 1. MIPAS relies on the database to store and track all metadata and post-processing states for all incoming and temporary images. Post-processing programs, which include user interfaces to MIPAS and individual programs, use the database to determine how and where to access images and other data stored in the operating systems file system.

system; (3) *file system*—this provides the storage location for all acquired image data in its original form and all image dataset binary files created during post-processing; (4) *post-processing*—this is the library of post-processing routines utilized by the system that includes master menu of post-processing functions (the user interface to select and invoke post-processing protocols), inbound DICOM and PARREC image processing, image registration, T_1 mapping, ADC mapping, and DCE-MRI mapping; and (5) *export image dataset*—provides for the extraction of selected image datasets for use outside of this system.

The system is event-driven, responding to selected processing requests. Generation of each parametric map follows a sequence of post-processing steps (Fig. 2) that develops the information required to calculate each parameter from the acquired images. Each branch of this process represents points where the post-processing requirement for a specific map type differentiates from another and requires a specific code module to be processed.

Following the integrated definition (IDEF) modeling method, the IDEF0 diagram (Fig. 3) documents each function's three primary elements (inputs, outputs, and triggering events) through which it interacts with other functions in the system.

File Storage. All image datasets are stored in the Windows file system in structured file directories, Figure 4. Incoming DICOM and PARREC files are placed in their respective directories to facilitate selection for post-processing. The original image datasets are retained to facilitate complete reprocessing with new protocols and for audit and verification purposes. Image datasets that result from post-processing are automatically stored in designated directory locations with file names that link them to the original image acquisition accession (DICOM) or session ID (PARREC) by way of an anonymous HeaderID assigned to each dataset. Investigators can access image datasets throughout the post-processing cycle using these identification numbers. The number of distinct file locations is defined by the protocol retention requirements, the computational cost (processing time, amount of computing resources, and investigator time) to recreate a dataset, and the post-processing program requirements for intermediate storage.

Image Dataset Metadata. The PARREC metadata serves as the master template for the MR image metadata stored in the database. The PARREC format is a specific subset of the DICOM information that is available for an image dataset, but it does include all information required to support the currently implemented post-processing programs. Metadata for the MR modality is stored in a unique set of tables to preserve the unique parameters for that modality; other modalities can be added in similar fashion. Common information that links a modality to a subject and study are stored in shared master tables. Normalization of the metadata reduces the total storage space requirements and the effort to maintain metadata integrity.

Post-Processing Management. All post-processing programs are organized by the post-processing protocol in which they are used. Each program has a brief description of its purpose and requirements and is identified by its file name, the language in which it is written, and its position in the post-processing sequence. This information is presented to the user through the main menu of the system,

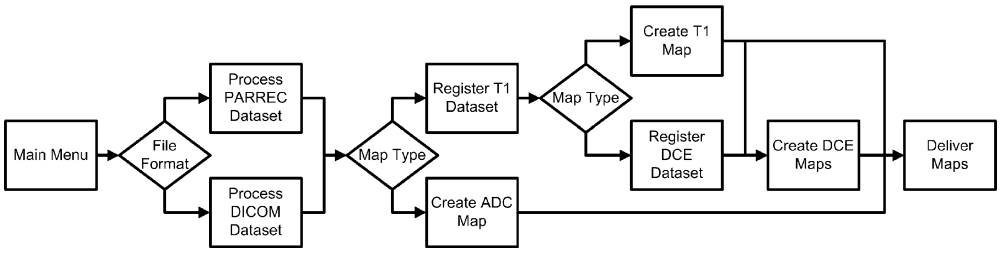

Fig 2. Each research protocol requires certain tasks to be performed in a specific order to properly create the parametric maps for this research project. The main menu is the starting point where the user selects the initial image dataset load program, which is followed by appropriate branches in the processing cycle based on the MR image protocol and finishes with the final map stored in the file system and made available for pick-up or delivery to the investigator.

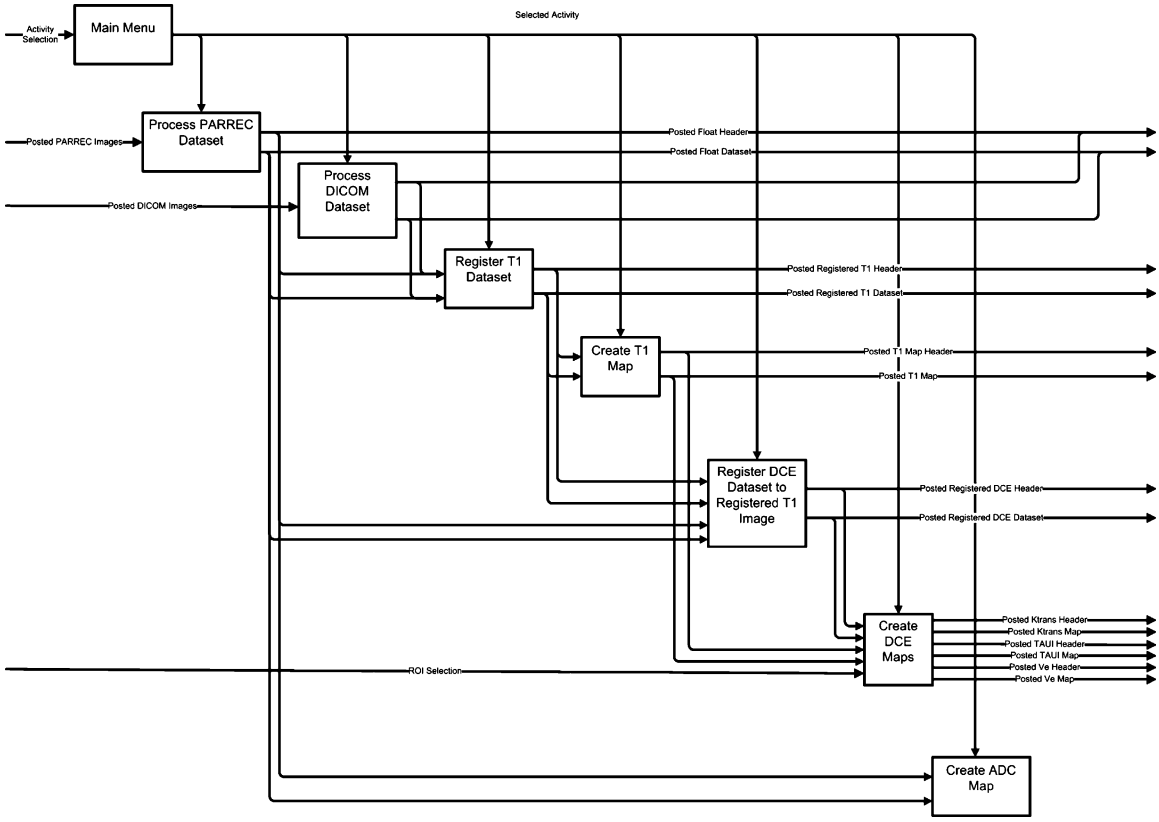

Fig 3. The IDEF0 diagram documents the inputs, outputs, and triggering event(s) for each interactive or image processing function of the system. User selections, newly acquired image datasets, or retrieved image datasets output from previous post-processing steps are inputs, while image datasets and metadata or process control information are outputs. Event triggers (new images or a post-processing request) are external system events that can evoke automated or interactive responses from the MIPAS system.

permitting the user to locate protocols by modality, protocol, and specific function.

Post-Processing Programs. All programs in this system implementation are written in IDL. A C++ image registration program used in previous work was incorporated into the system through an IDL program, and a Matlab program was coded to interact with the system to test Matlab integration. The general structure of the program is a database

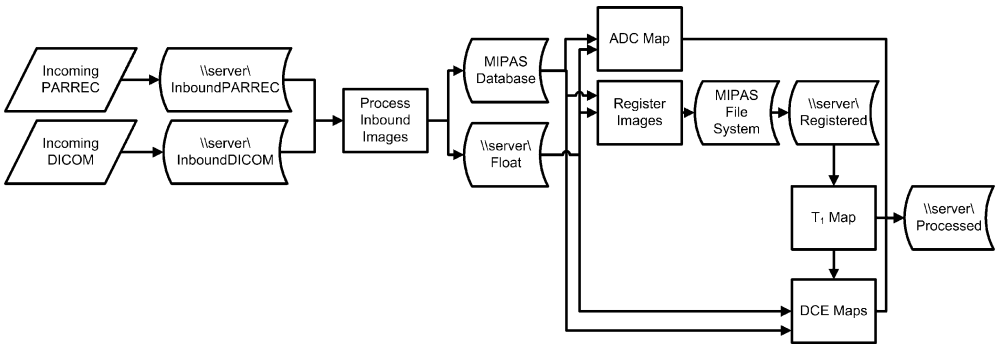

Fig 4. Image datasets follow a flow through the file system storage structure to facilitate easy access to image types and external verification of processing status. This structure also provides a means to access datasets in an intermediate form for reuse.

access function, a core processing function, and file system read and write functions. Programs may include command line interfaces and graphical user interfaces (GUI), plus calls to compiled external programs.

DICOM Support. IDL provides a DICOM network services function that enables the workstation to exist as a node in our medical center DICOM network. This enables MR image acquisition on clinic and research scanners to be transmitted directly to the MIPAS server. The database includes a DICOM 1.2 dictionary to facilitate accurate IDL code generation to support the DICOM processing module. Only those DICOM tags (image metadata) that contain the equivalent PARREC information are extracted and stored in the database by the DICOM processing module. For future use, all other DICOM information is retained only in the original DICOM files.

Database Design

The database design is centered on four core table sets (Fig. 5), the *image metadata* tables, the *post-processing programs and protocols data* tables, the *DICOM dictionary* tables, and the *configuration parameters* tables. The incoming image dataset contents and structures were analyzed to determine the appropriate elements to archive in the database for use by the post-processing programs and later reuse by the investigators in the analysis process. The metadata is organized into table types (master, index, and detail) with identification of the relationships between each table type. Normalization of the metadata minimizes its replication between tables and facilitates the establishment of master and detail tables in the database. Unique indexed record identification numbers are automatically assigned to each entry in master and detail datasets, providing uniqueness to every entry, while user-

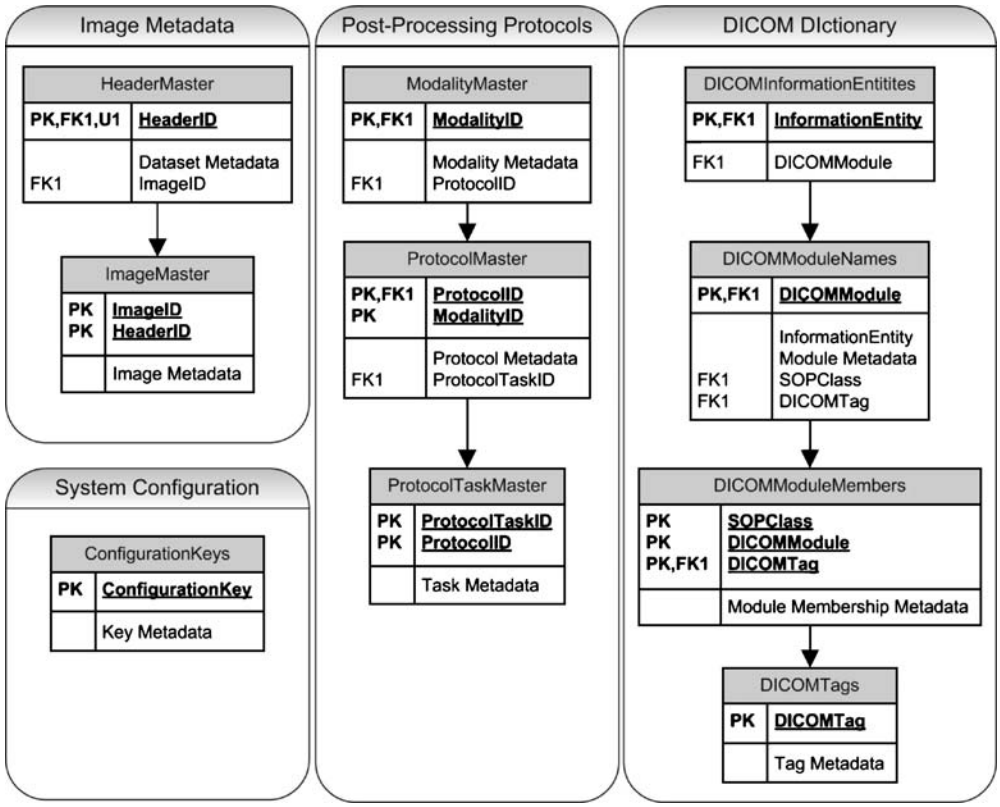

Fig 5. The MIPAS database structure is based on four distinct types of metadata and function: image metadata, post-processing protocols, DICOM standards, and system configuration. Each table is composed of primary keys (PK), foreign keys linking tables (FK), and the metadata within that table. These keys enable fast access to specific records needed throughout the post-processing cycle. The metadata for each table is described further in the text.

defined unique identifiers are incorporated to support identification of record sets based on subject, study, imaging session, and other selected identifiers or study parameters.

Image Metadata Tables. The MR image metadata is contained in two tables, the HeaderMaster and the ImageMaster. A single header record exists for each inbound imaging dataset's (corresponding to a single PARREC file or equivalent DICOM record set) metadata and is identified by a unique HeaderID. The unique individual image metadata is stored in the image record with unique ImageID. This structure preserves the unique acquisition information for every image acquired. Image records are linked to the header record by the automatically assigned HeaderID. This record set is created during the inbound processing of new data sets and updated during post-processing.

Post-Processing Programs and Protocols Data Tables. Post-processing programs are organized into specific protocols that are fully described by in the tables shown in Figure 5. They are organized by imaging modality, processing protocol, and specific protocol tasks. This design allows for the creation of any number of unique post-processing scenarios, which are self-documenting and guide the user through the specific sequence of tasks required for a particular post-processing sequence. The ProtocolMaster contains a user-assigned unique ID (ProtocolID) to specifically identify the protocol to the user. This unique ID supports versioning of post-processing protocols, allowing for variation of the individual post-processing tasks, algorithms, or parameters on a given dataset. The ProtocolTaskMaster table identifies the specific language of the program to be called, the program name, its position in the sequence, and a brief explanation of the sequence purpose and attributes. Tasks may be automatic and/or interactive, written in IDL, Matlab, or C++ programming languages and be script and/or GUI-based.

DICOM Dictionary Tables. To meet DICOM standards compliance, the Philips DICOM 1.2 standards conformance statement for the MR modality are encoded into a DICOM dictionary. The DICOM tags are fully described in the DICOMTags table. DICOM tags are also linked to the necessary DICOM structure elements in the DICOMModuleMembers, DICOMModulesNames, and DICOMInformationEntities tables to create specific code segments to read or write DICOM tags. Microsoft Access database reports were created to use the DICOM dictionary to properly construct IDL code segments that can read, parse, or post DICOM information within the image metadata tables, like the example in Figure 6.

Configuration Parameters Tables. Current dynamic parameters that affect the entire system are stored

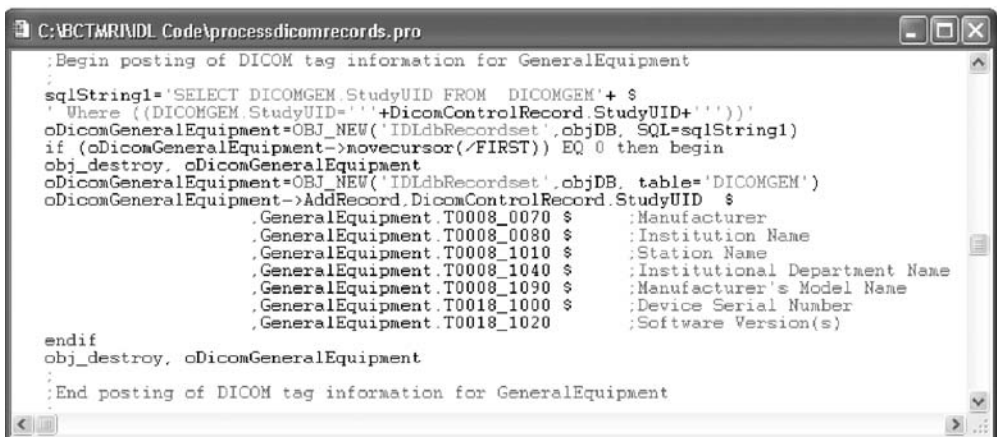

Fig 6. In this DICOM IDL code module, you can see how a set of DICOM tags (Txxxx_xxxx) are composed and placed into the appropriate program statements and function calls to access the database. The DICOM dictionary facilitates the creation of these consistent, well-defined code modules that match the DICOM standard. Hundreds of these code modules are required to process DICOM images.

in the configuration keys table. Each parameter is assigned a unique configuration key, a data type, and value. Each key can be retrieved by a program for use in directing program operation.

Software Code Modules

Main Menu. The user interface (Fig. 7) performs a query of the protocol tables in the MIPAS database, extracting all tasks ordered by imaging modality, protocol name, and then the sequence of the protocol tasks. Maintaining this structure in the database allows for changes over time to individual protocols without any recoding of the menu program. Organization of the menu tree is controlled by the structure of this design encoded in the main menu program.

PARREC Processor. This module is the entry point for all incoming PARREC image datasets into the MIPAS system. The program posts the PARREC information into the header and image master tables of the database and writes an integer-to-floating-point-converted-image binary REC file in the "/images/floats/" directory. The user can override parameters as necessary before the execution of the conversion and loading into the MIPAS system.

Post-Processing Programs. All post-processing programs follow the same basic structure and functional flow, regardless of where within a post-processing protocol the program occurs. This sequence involves opening a user interface, such as the DCE-MRI interface shown in Figure 8. All programs access the configuration table to get specific information about file directory locations and other processing parameters. Then the selected image dataset metadata is retrieved from the database as well as specific protocol task information that are required for this analysis. The program then responds to the user and produces the output images, which are logged into the database and made available for download to the investigator.

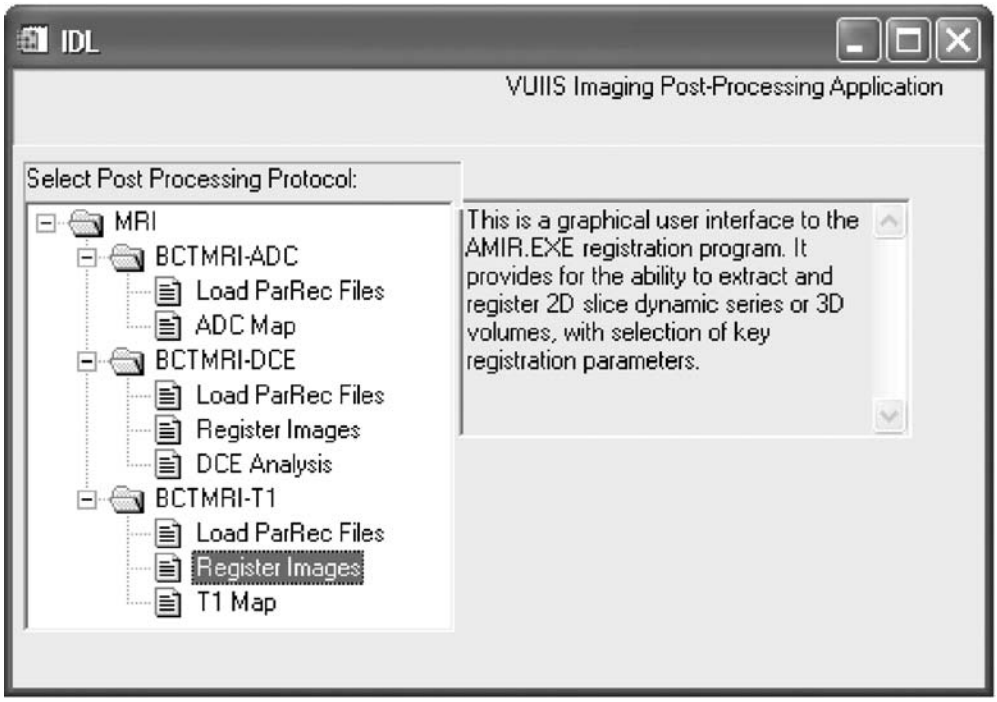

Fig 7. Main menu user interface where post-processing protocol tasks are loaded from the database into a hierarchical structure organized by imaging modality, protocol name, and sequence. Selections can be expanded through the "+" preceding each folder icon. Information about a protocol task can be viewed by single-click selection of the task. Double-click selection of the task executes that task by way of a *task-load* function in this program.

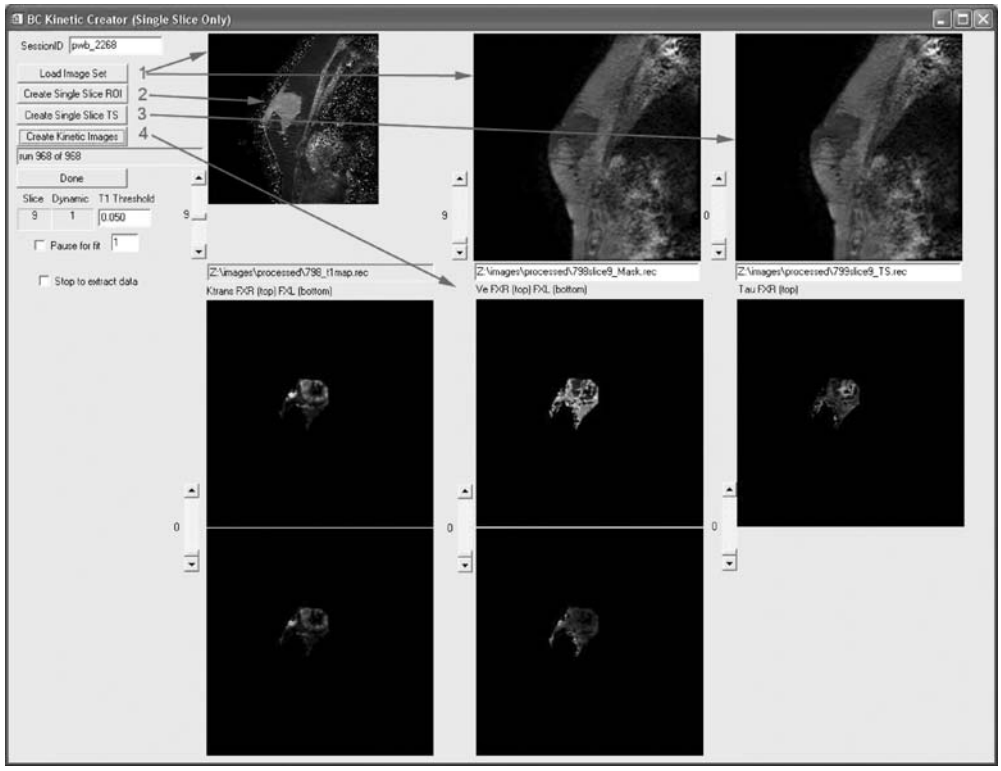

Fig 8. In this DCE-MRI user interface, the way the database supports processing can be illustrated. In step 1, the program takes the SessionID and uses it to retrieve the image metadata to locate and load the appropriate T_1-registered images for this DCE-MRI analysis, loading them into the *top left window*. At the same time, the registered DCE-MRI images are loaded into the *top center window*. For step 2, the ROI is extracted from the T_1 image and stored for later use. Step 3 creates the single-slice time series from the 3D DCE-MRI image volume seen in the *top right window* and step 4 runs the actual analysis producing the K^{trans}, v_e, and τ_i maps.

Validation and Verification

Over the course of the system development, the requirements, system design, and program development were periodically reviewed with the project owners to ensure that the implemented functionality was meeting requirements and expectations. To verify program compliance to the requirements and previous work, data post-processing scenarios were used for which there were known outcomes. To verify correct implementation of the analysis functions, MIPAS output image datasets were subtracted from the output image datasets created by other methods previously used and then evaluated by study investigators for quality and accuracy. This approach was acceptable because the MIPAS system has no direct impact on the data, just the storage and post-processing management of that data. Performance of the system distributed across the network was measured using a 500-image PARREC dataset located on the local hard drive and on the server. The PARREC processing program was modified to capture timing of the read and write operations for the directory listing, the input file processing, the database access, and the output file processing.

RESULTS

The primary objective of this project, to automate this series of MR image post-processing tasks, has been substantially accomplished, evidenced by a processing time reduction from 15–20 h for a complete parametric map set to 2–5 h, dependent on the size of the image dataset and the complexity of the regions of interest. The primary system modules are contained in six program modules and a single database, located on a dedicated workstation and a single server. The system is located within the secured network, but it is accessible to authorized individuals from around the globe and can receive and transmit DICOM

images within the research and clinical network of our institute.

More than 90 code modules were constructed or converted to create the MIPAS system. Fifty MRI data sets were used to test the functionality of the system. The extensive process of changing scripted languages like IDL and Matlab to process multiple data sets has been significantly simplified through the parameterization of the variables in six primary program modules and a single database. Extension of the system to support post-processing programs written in other languages was verified with the successful testing of a Matlab program configured in a post-processing protocol and the incorporation of a C++ program within the registration IDL program.

Network implementation of the file storage system and the database has resulted in an increase to the post-processing time. A performance analysis of the PARREC Processing program was performed using a single image dataset composed of 500 images 192× 192 in size. With the MIPAS database and the image dataset located on the remote server, processing time over ten trials was 18.42±0.96 s versus 8.31±0.59 s (F test and Student's t test, two-tailed, unequal variances, $p<0.05$) when these files are located on the MIPAS server. Analyzing each access to the network files revealed that all steps suffer the delay but some are very close (3.62±0.46 s versus 3.23± 0.31 s, F test and Student's t test, two-tailed, unequal variances, $p<0.05$), and others differ by a magnitude or more (3.72±0.09 s versus 0.15±0.23 s, F test and Student's t test, two-tailed, unequal variances, $P<$ 0.0001). These delays have not been sufficient to warrant moving storage to the local workstation but are sufficient to consider further study into the source of the delays (network congestion, network connection speed, server response, etc).

The MIPAS system serves as a research PACS system allowing for rapid location of specific image datasets. Changes to code modules can be introduced at will and used to post-process any appropriate image dataset in the system. Consistent code structure facilitates faster development of new programs that are compliant with the MIPAS architecture and capable of using the MIPAS PACS features.

DISCUSSION

Though we have demonstrated MIPAS utility in breast imaging, one could envision similar formulations in, for example, functional MRI, brain segmentation, or any task where a large number of computational steps need to be automated. The MIPAS architecture could provide the means to manage very large studies with hundreds of thousands of images undergoing extensive post-processing protocols with dozens of steps, numerous intermediate image, and analytic data files across multiple modalities.

The MIPAS workstation and services were placed within the institute network and added as an available DICOM node on the research and clinical MR scanners. This configuration facilitated the transfer of acquired research images from all MR scanners in our institution and makes possible the potential to return the calculated MRI maps back to the original image PACS datasets. Images are currently transferred in the Philips proprietary PARREC format as that data format is closest to the internal storage format of the intermediate image files and is the preferred output format of the investigators.

Once a subject has been scanned, the images are transferred to the workstation and put through each appropriate post-processing protocol. Final output files are then placed on a central server for retrieval by the investigator. Complete automation of this process has not yet been possible due to data inconsistencies that require review and correction preceding key post-processing steps. These interventions have been simplified to data entry screens or mouse-click choices to minimize operator intervention. Reprocessing of raw image datasets using new algorithms is readily done through the inclusion of database-aware software functions in the new algorithm software module. This has allowed investigation of alternative approaches with minimal input from the investigator to select and process the datasets.

The development of program functions that provide an interface to the database and image datasets in PARREC and DICOM formats allows other projects to modify their post-processing programs to take advantage of the system's features. The network capability of the workstation provides the toolset to post-process other MR imaging studies as a server within the VUIIS and can readily incorporate other imaging modalities with the addition of functions to read/write their file formats. All of the system functions are agnostic to the data type and source, and the database is easily adapted

to handle non-MR image parameters not currently configured. Returning clinically relevant MRI maps requires preservation of clinically acquired patient information, such as an accession number to which the maps are designated a derivative image properly linked to the original source images. At present, MIPAS solution provides for the preservation of the original DICOM data files to create all DICOM tags in the derivative maps. Future work should include a more robust DICOM function to interface this system into a clinical PACS environment.

Implementation of any structured program or data management solution imposes a certain amount of rigidity upon the users of such a system. The largest challenge in this project derived from that rigidity where users felt constrained from their usual coding and processing practices. The approach used in this project to overcome that challenge involved creating a flexible coding structure, moving many of the variables of previous programs into parameters retained or selected from the database, and having the database serve as a state management tool that supports higher variation in program execution. A final level of flexibility is possible where functions, such as different curve-fit techniques, are coded as choices in the program and selected and tracked within the MIPAS system. This type of approach provides an investigator the means to evaluate multiple approaches to a problem in a single post-processing run with the ability to trace out the performance and quality of the results of the various approaches.

This system does not represent a final set of tools for use in this research effort. It is designed as a foundational platform where current and new tools can be readily added for use, such as an automated published literature search based on image metadata and derived parameter information or a reporting tool that submits maps to the PACS system for review by clinicians. The structure of the open-ended process management architecture allows an unlimited number of programs to be incorporated into the system and sequenced into specific post-processing protocols. The ability of IDL to call programs written in other languages coupled with the database storing program and post-processing states allows the MIPAS system to act as a communications conduit between these various languages, expanding the ability to develop new programs in any language without compromising the integrity of data analysis and management. However, other languages, such as Java or C++, contain features to create nested graphical interfaces or effective text-based screens that could serve as a robust user interface across multiple platforms through a web-centric client-server approach.

The results of the network performance testing indicated a need to examine what configuration of data storage is optimum. The test configurations should be (1) all files and the MIPAS database located on the local hard drive, (2) the files and the database on the network server, or (3) a mixed storage arrangement to locate optimal files and database placement. This determination should be done for a large number of datasets and under multiple-user test scenarios before deployment. Consideration should be given to collocate storage and analysis servers on the same high-speed network segment to improve performance in a distributed implementation.

CONCLUSIONS

The MIPAS system has shown promise as a solution to improve MR image post-processing turnaround and multiple protocols processing of image datasets. Adding post-processing tasks that are capable of automatic ROI and/or parameter selection would increase both efficiency and effectiveness of the post-processing programs. Incorporating multi-threaded program structures would increase performance by distributing the CPU load across all available processors on the server.

Adapting the MIPAS research picture archival and communications system and post-processing control functionality to integrate with new analytic environments like MIPAV or the Cancer Biomedical Informatics Grid (caBIG) could extend their functionality while introducing emerging research models into the local research toolset. Another potential extension includes a post-processing service environment where collaborative research efforts use this architecture to service multi-institutional trials or industry/academia initiatives.

This system has the potential to be extended to other MR and non-MR imaging projects, incorporating post-processing programs written in languages other than IDL. Such an expansion would increase demands on the system and would extend the MIPAS database beyond the capacities of the database used to develop this project, but it is well

within the scope of a range of enterprise level SQL servers available today on which a future MIPAS could be based.

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