코바기반 협업지원 의료영상 분석 및 가시화 시스템

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요   약

본 논문에서는 분산환경에서 사용자들에게 효과적인 접근성과 사용성을 제공하는 코바기반 협업 지원 의료영상 분석 및 가시화 시스템을 소개한다. 개발된 시스템은 분산환경에서 의료영상 분할 및 모델링과 같은 의료영상 분석 및 처리 기능을 제공하며 아울러 의료영상 데이터의 효율적 관리 기능을 제공한다. 영상의 분류 및 특정 세포조직의 추출은 베이지안 방법과 활성 윤곽선 모델등 적용하여 수행되며, 획득된 영상의 특성정보는 의료영상의 실시간 3차원 모델링에 사용된다. 개발된 시스템은 브로드 케스팅과 동기화 메커니즘에 기반하여 시스템을 사용하는 다중 사용자들간의 협동작업을 지원한다. 본 시스템은 분산 프로그램을 지원하는 자바 및 코바에 의해 개발되었으며, 따라서 클라이언트는 분산 객체의 위치나 분산객체가 수행되는 운영체제에 관한 정보가 없이도 메소드 호출방법에 의해 서버 객체에 접근할 수 있다.

A CORBA-Based Collaborative Work Supported Medical Image Analysis and Visualization System

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ABSTRACT

In this paper, a CORBA-based collaborative medical image analysis and visualization system, which provides high accessibility and usability of the system for the users on distributed environment is introduced. The system allows us to manage datasets and manipulates medical images such as segmentation and volume visualization of computed geometry from biomedical images in distributed environments. Using Bayesian classification technique and an active contour model the system provides classification results of medical images or boundary information of specific tissue. Based on such information, the system can create real time 3D volume model from medical imagery. Moreover, the developed system supports collaborative work among multiple users using broadcasting and synchronization mechanisms. Since the system is developed using Java and CORBA, which provide distributed programming, the remote clients can access server objects via method invocation, without knowing where the distributed objects reside or what operating system it executes on.

1. Introduction

Medical image analysis and modeling involves the determination of selected geometric features from the system or structures within the medical imagery and three dimensional visualization of neuroantomical structure if necessary [1, 2]. Recently, there has been a great deal of interest and progress in developing medical image analysis and visualization systems based on the internet environments [3, 4]. The major issues for WWW-based medical systems are how to make the analysis and 3D visualization faster and how to make group work feasible. Meanwhile, the collaborative computing technology has become a major factor to develop collaborative medicine systems [5-7].

The work described here is directed toward a design and implementation of a platform independent telemedicine system that provides various image analysis and real time three dimensional visualization of computed geometry from a region of interest (ROI) and supporting three types of group work, such as a single, a view and sharing mode. The proposed collaborative medicine system, which is web-based and has client-server architecture, can provide flexibility, extensibility and location transparency of the medical data. The analysis of medical images and visualization of the volume data on the internet using CORBA and the JAVA

programming language offers new perspectives for distribu-ted and platform independent applications [8, 9]. For the development of the system we adopt the DICOM (Digital Image and Communications in Medicine) standard for a method of transferring images and associated information device.

In the following sections, we explain the overview of the system and its design and implementation issues. The theoretical background for image analysis and volume rendering is briefly discussed and the collaborative components are introduced. We also illustrate some experimental results of the system with concluding remarks.

2. System overview

The system allows us to analyze medical images using image segmentation and volume visualization of medical images and manage medical image database in distributed environments. In order to support platform independency of the system in distributed environments, we adopt CORBA and Java technologies for the system development.

2.1 System architecture

The developed system consists of 3 major components : a client component, an application server component, and DBMS server as illustrated in (Figure 1). A client component consists of graphical user interface to access the system and CORBA component object. The client can be distributed for several nodes. An application server component can be processed for manipulating medical images and communicating to one or more DBMS via JDBC (Java Database Connectivity). When a client asks a service from an application server, the application server provides a CORBA object. The ORB (Object Request Broker) accepts the request of the client application and selects the proper server implementation. The data management component encompasses the mechanisms, which import data from external sources into the visualization system and manage the data internally. The system uses MySQL and JDBC to store and retrieve medical images, which are stored in an information table by BLOBs (Binary Large Objects).

The major advantage of the proposed 3 tier architecture is that the overhead on the client system site can be reduced on the internet environments since the client has only initial code and user interface.
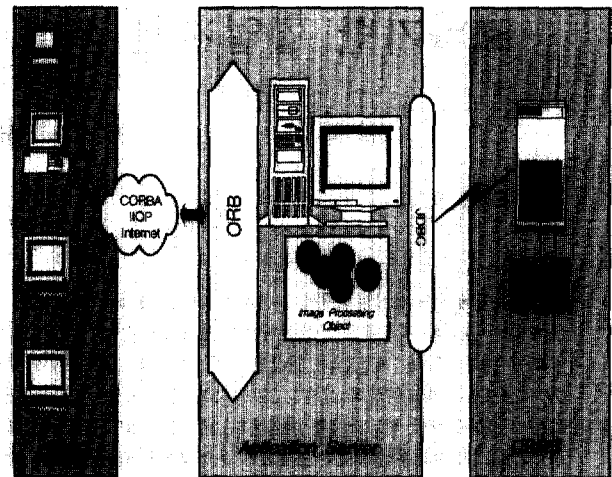
(Figure 1) System architecture

2.2 System implementation

The proposed system can work on any system with COR BA/Java since the system is implemented by using COR BA/Java on the internet. In order to use CORBA objects, IDL (Interface Definition Language) must be defined. Following code is IDL definition for medical image processing and 3D rendering processing.

```
Module ImageFunc {

    sturct img {
            unsigned short height ;
            unsigned short width ;
            sequence < unsignd short > image ;
    }

    interface scaleOp {
            void scaleOp ( in struct img ) ;
            void getImage ( out struct img ) ;
            void setParameter ( in param ) ;
    }

    interface rotateOp {
            void rotateOp ( in struct img ) ;
            void getImage ( out struct img ) ;
            void setParameter ( in param ) ;
    }

    interface 3DRenderingOp {
            void 3DRenderingOp ( in struct img ) ;
            void getImage ( out struct img ) ;
    }
    ......

    }
```

Java IDL includes CORBA/IIOP ORB with Java platform 2. Using the Java IDL compiler, a server application code and client application code can be generated as shown in

(Figure 2). A client code calls for a CORBA object within an application server and consists of a graphical user interface parts, CORBA initialization part. Application server code consists of an image processing object, volume rendering object, and database management object.
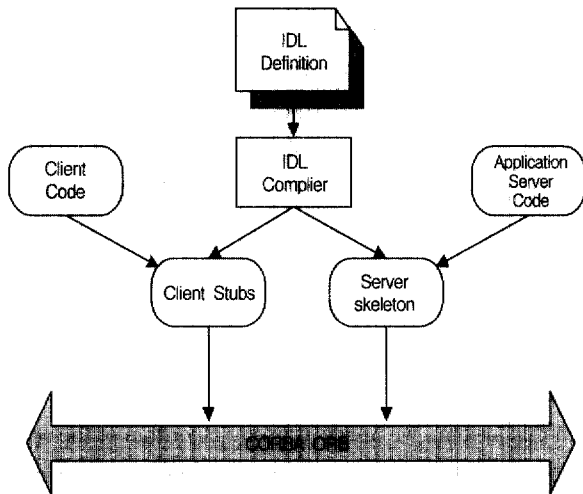
(Figure 2) Code generation using IDL

As described, the system is designed and implemented for working in the distributed environments using CORBA and Java. Following are adopted characteristics of Java and CORBA for developing the system. Java, which simplifies code distribution in the network supporting CORBA, deals with code transparency, while CORBA supports network transparency. The Java Advanced Imaging (JAI) API, which allows sophisticated and high-performance image processing, is utilized for the image analysis and volume visualization. CORBA is designed to allow object components to discover each other and to interoperate on an object bus. CORBA objects are packaged as binary components, and resided anywhere on a network. Since CORBA supports a transparent object reference among distributed objects through object interfaces, the remote clients can access server objects via the method invocation, without knowing where the distributed object resides or what operating system it executes on. In order to develop the system, we have used the CORBA 2.0 specification.

The developed system, which is platform independent, provides various medical image formats, methods for image analysis, real time 3D visualization, medical image retrieval, and collaborative work. The medical image processing components are developed using plug-in classes and those classes are working on the application by the class loader. Fol-

lowing is an example of image processing plug-in.

```
Static Object runPlugIn ( String commandName, String className,
                         String arg ) {
    if (!className.startsWith ( "mipas" ))
        return mipas.runUserPlugIn ( commandName, className, arg,
                                      false ) ;
    Object thePlugIn = null ;
    try {
        Class c = Class.forName ( className ) ;
        thePlugIn = c.newInstance ( ) ;
        if ( thePlugIn instanceof PlugIn )
            (( PlugIn ) thePlugIn ) .run ( arg ) ;
        else
            mipas.runFilterPlugIn ( thePlugIn, commandName, arg ) ;
    }
    catch ( ClassNotFoundException e ) { write ( "Plugin not found : "
                                                 + className ) ; }
    catch ( InstantiationException e ) { write ( "Unable to load plugin
                                                 ( ins )" ) ; }
    catch ( IllegalAccessException e ) { write ( "Unable to load plugin
                                                 (acc)") ; }
        return thePlugIn ;
}
```

3. Medical image analysis and visualization

For the visualization or quantitative analysis of normal or abnormal tissue in biomedical images the proper segmentation of soft tissues is necessary. The proposed system can produce segmentation of ROI using region-based model and edge-based boundary detection using active contour model. The region-based model involves an unsupervised classification of the image by exploiting the statistical properties of medical images. Agglomerative clustering and Bayesian methods are well adapted for this purpose. For edge-based segmentation, an active contour model [10] is applied to the specific tissue of the image and it produces tissue boundary. Subsequently, the segmentation results of a certain tissue type from the consecutive slices of a volume image can be used for the volume visualization. For the volume visualization, the additive re-projection method, which is a ray casting method [11], can quickly render a 3D image regardless of the user's view direction.

3.1 Image Segmentation

The correct image classification/segmentation [12-15] provides clinically important information to analyze the tissue for physicians as well as to reconstruct 3D volume visualization based on the segmentation results. The developed system supports both region and edge based image segmentation for this purpose. The region based image segmen-

tation uses Bayesian framework, which has been successfully adopted in a number of image analysis and computer vision problems. The classification problem can be sated as : "given a set of observed features, **y**, from an image **x**, classify **x** into one of the classes in Ω". In the Bayesian framework, all inferences are based on the *a posteriori* probability function, which is obtained by combining the class-conditional models with the *a priori* class probabilities. The Bayesian classification technique we adopt is an example of an unsupervised method. Unlike traditional clustering techniques, the Bayesian approach does not just partition the cases but rather attempts to find the *best* class descriptions in an image space. The best classification result satisfies the log posterior probability that the feature **x** belongs to the subjective class using the following Bayesian formulation [16] :

$$g_i(x) = \ln P(\omega_i \mid x) \propto \ln p(x \mid \omega_i) + \ln P(\omega_i)$$

If the image I is assumed to be partitioned into k classes $\Omega = \{\omega_1, \omega_2, \wedge, \omega_n\}$, these classes are exhaustive and mutually exclusive, i.e., any image **x** from I belongs to one and only one class. In order to use Bayesian approach, the intrinsic numbers of class k and the probability density function of the random variable can be derived by using agglomerative clustering approach. The agglomerative clustering algorithm proceeds as follows :

① Image is subdivided by $n \times n$ blocks, such as 3×3 and each block is assumed be homogeneous in its nature.

② Homogeneous blocks are merged based on the mean and variance of each block. Recalculate mean and variance of merged blocks.

③ Repeat 2 until the values of mean and variance of each block are converged.

The goal of the clustering phase is to identify these clusters and estimate their parameters. Our hypothesis is that these clusters are normal random process with parameters, mean vector and covariance matrix since Bayesian approach is optimal when the distribution of the cluster is normally distributed. As the hypothesis test the chi-squared test for goodness fit to a distribution is used. Our approach is novel in which the classifier attempts to identify these regions for itself. In our case, the stage of clustering and classification proceed in tandem, and are based on a spatially localized

approach to cluster/classification that embodies statistical hypothesis validation as it proceeds.

The system also provides edge-based segmentation approach based on the active contour, which is widely used for optimal contour detection in the fields of computer vision, such as segmentation and object tracking. The active contour is a computer vision model commonly used to fit closed curves around image contours of interest. In general, it is a set of points initially placed near the ROI that are gradually brought closer to the exact shape of the desired region in the image. This is accomplished through iterative minimization of an energy function with elements of internal energy, and external energy. Using the optimization procedure of the active contour model, the system extracts the boundary information of specific tissue and utilizes the segmentation results for 3D volume visualization.

In this system, we utilize a greedy algorithm of the active contour model proposed by Kass et al to detect boundaries of specific tissue type. Let the contour be represented by $v_s = (x(s), y(s))$. The active contour model involves minimizing energy function defined by

$$E_{snake} = \int (\alpha E_{con} + \beta E_{curv} + \gamma E_{image}) ds$$

for the active contour to move onto the tissue boundary. The continuity energy enforces the shape of the contour and is expressed by

$$E_{con} = d - \mid v_i - v_{i-1} \mid$$

where d is the average distance between two points. The curvature energy, which presents the smoothness of the contour, can be expressed by

$$E_{curv} = \mid v_{i-1} - 2v_i + v_{i+1} \mid^2$$

The image energy attracts the deformable contour to object boundaries and is defined by

$$E_{image} = (G_{min} - G_i)/(G_{max} - G_{min})$$

When the active contour model is applied to boundary detection, the initial boundary condition is critical to determine the final boundary of the object. The developed system provides an interactive graphical user interface to assign the initial boundary location of a specific region effectively. (Figure 3) (a) and (Figure 3) (b) illustrate an example of

initial boundary condition assigned by a user and the final result of active contour model, respectively.
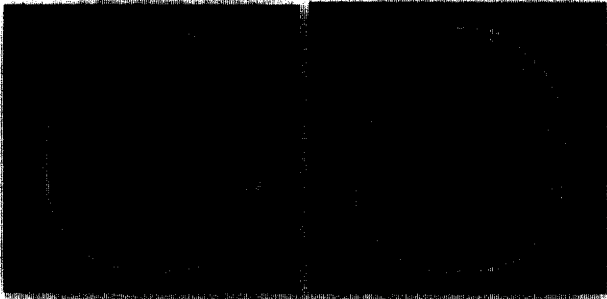
(Figure 3) The initial boundary (left) and the final result of active contour (right)

3.2 Volume Rendering

Feature data resulting from the analysis of the sequential 2D images provides clinically important information of the tissues and can be used for volume rendering. Recently introduced web-based rendering technique which uses scene graph for creating and manipulating 3D needs much time for rendering images [17]. The use of 3D texture mapping hardware for volume rendering [18] has become a powerful visualization option for direct volume rendering but it needs specialized graphics hardware. Thus, in this work, for the volume visualization, we adopt a ray casting method so called additive re-projection, which uses a combination of reflected and transmitted light from the voxel. As illustrated in the (Figure 4), it projects voxel along a certain view direction and intensities of voxels along parallel viewing rays are projected to provide an intensity in the viewing plane. Voxels of a specified depth can be assigned a maximum opacity, so that the depth that the volume is visualized to be controlled. The major advantage of using this method is the volume can be visualized from any direction and the hidden surface removal can be easily implemented.
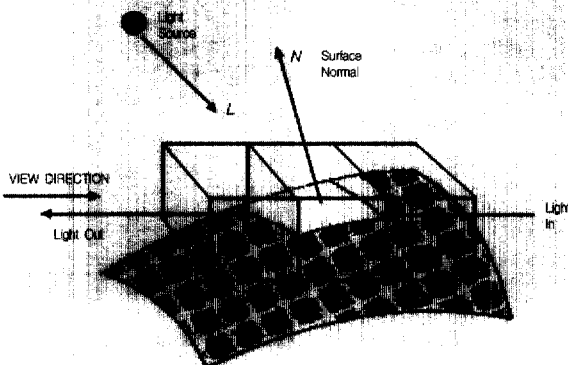
(Figure 4) A model of additive reprojection

4. Collaborative work components

As described, the system can provide collaborative modes for the users. For this, the clients can broadcast events to the application server so the application server and the screen of the local clients should be synchronized.
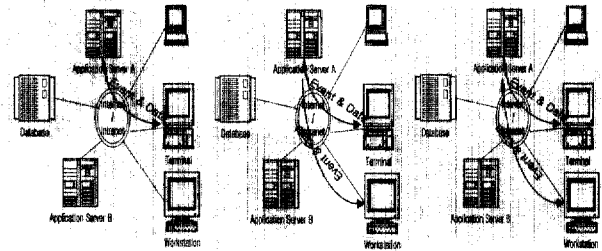
(Figure 5) Collaborative work (single, view, sharing mode from left to right)

The system provides three collaborative modes which are *single*, *view*, and *sharing mode*. (Figure 5) illustrates schematic description of collaborative modes provided in this system. Especially in the view or sharing mode, an application server shows the various imaging information processed the multiple users. When the users broadcast events to server site, the server and local screens of each user are synchronized. Thus, multiple users can share the same screen. For the collaborative work, the system provides a method to communicate each other by allowing a communication window for each user.

The major functions of each mode are as follows :

- The *single mode* activates single user work by locking current data and event.
- The *view mode* allows for clients share the screens of other clients while only an authorized client can modify the data.
- The *sharing mode* allows a group of multiple users can share and change the current events and data. While modifying any sharing data by a client, the system temporally locks the other client's trial to change the data and broadcasts an event to each client after the modification is finished. As illustrated in (Figure 3) multiple clients and a server can broadcast data and event both directions.

5. Experimental results

Some experimental results from the system are illustrated

in (Figure 6)~(Figure 8). Classification results of MRI in the single mode work and a result of 3D rendering using the active contour model and ray casting method are illustrated in (Figure 6). The sytem is working on window, solaris or Linux etc..
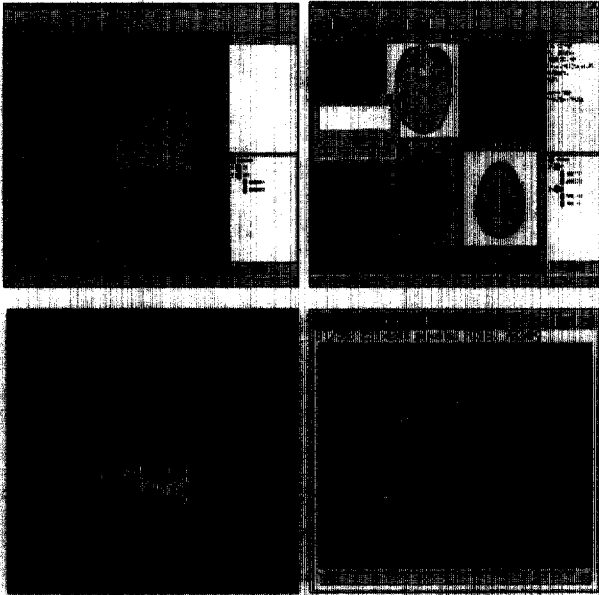

(Figure 6) Segmentation result (up) and volume rendering result (down)

(Figure 7) (a) is an example of the single mode. In this mode, only one client works its own work and the co-work signal is off. (Figure 7) (b) illustrates two examples of the view mode where an authorized client can modify the data and does not allow the other clients modify the data. The other clients can only share the screen of the authorized client. Meanwhile, it is possible to share and modify current data and events for collaborative work using the sharing mode as illustrated in (Figure 7) (c).
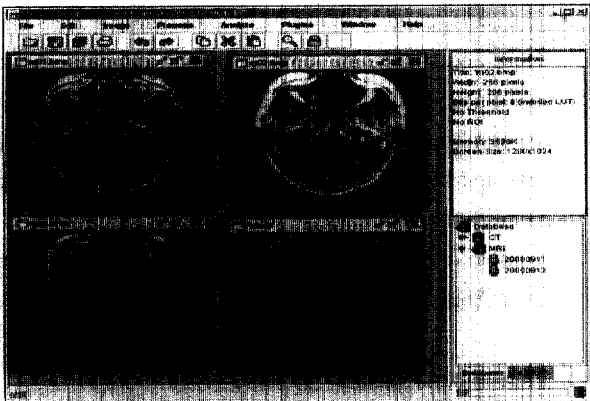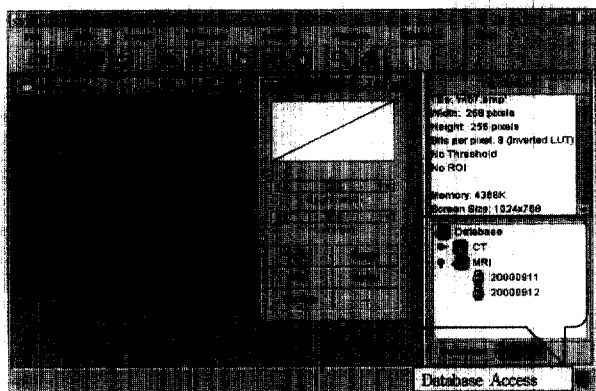

(a) A Screen example of single mode
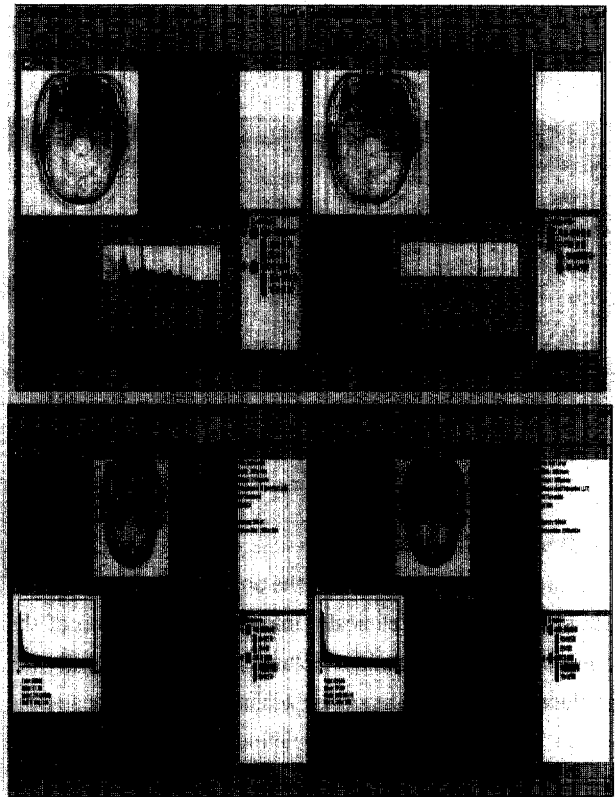
(b) Two screen examples of view mode
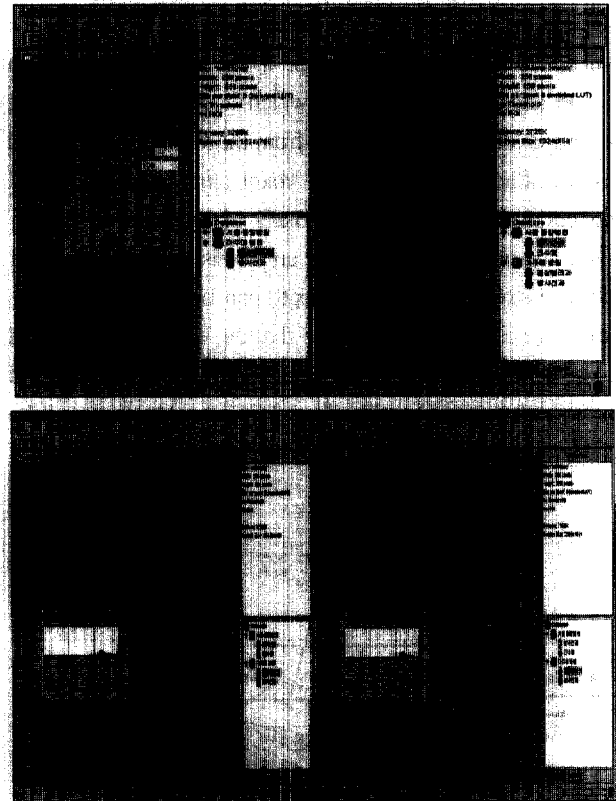
(c) Two screen examples of sharing mode

(Figure 7) Collaborative work using (a) single (b) view and (c) sharing mode (from top to bottom)

(Figure 8) is a screen example of the medical data management. Using MySQL and JDBC the system can store and retrieve medical image in a rapid and convenient fashion.

(Figure 8) A screen example of data management

6. Concluding remarks

In this paper, a platform independent telemedicine system for medical image analysis and 3D visualization was presented. Reliable results from the medical image analysis and volume visualization provide clinically important information for people in biomedical and biophysical areas. In that sense, the developed system has reliability and usability. An important characteristic of the system is that it is designed and implemented based on CORBA and Java and thus it provides high usability and accessibility for users at remotely located sites. In addition, the system supports interactive collaborative work for the group of users.

As for the further work, the security assurance problem in collaborative work will be studied even though CORBA supports high security in the system. The enhancement and optimization of the system functions will be considered as future works.

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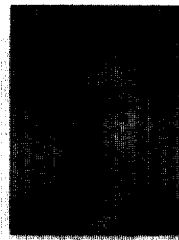 공학과 대학원 석사
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