17 CONTENT-BASED RETRIEVAL FOR MEDICAL DATA

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The recent information explosion has led to massively increased demand for multimedia data storage in integrated database systems. Content-based retrieval is an important alternative and complement to traditional keyword-based searching for multimedia data, and can greatly enhance information management. However, current content-based image retrieval techniques have some deficiencies when applied in the medical imaging domain. Many of the proposed techniques for content-based retrieval of medical data use features or patterns specific to medical images. In this chapter, we address content-based retrieval techniques for the following types of medical data: one-dimensional ECG signals (Section 17.2); two-dimensional X-ray projection images (Section 17.3); three-dimensional CT / MRI volume images (Section 17.4); and four-dimensional PET / SPECT dynamic images (Section 17.5). Finally, a summary is given in Section 17.6.

17.1 Introduction

The increasing use of information and telecommunications technologies, including Internet technologies, has laid the foundation for a revolution in traditional healthcare, and resulted in the development of Electronic Health (e-health), to improve the efficiency and effectiveness of current healthcare systems [1-2]. Ehealth includes the use of digital multimedia medical data transmitted electronically - for clinical, educational and administrative applications - both locally and at a distance. Healthcare services today rely heavily on digital multimedia medical data, including one-dimensional electrocardiogram (ECG) signals, two-dimensional X-ray projection images, three-dimensional computed tomography (CT) and magnetic resonance imaging (MRI) volume images, and four-dimensional positron emission tomography (PET) and single photon emission computed tomography (SPECT) dynamic images. The volume of medical data generated in the clinical environment has been rapidly growing due to an increase in both the usage and the range of digital medical diagnostic modalities. To illustrate the amount of data generated in a typical examination consider the example of a dynamic PET study of the brain which involves the reconstruction of 30 or more cross-sectional images, each of 128×128 pixels, at 22 time points. The resulting four-dimensional data set requires upwards of 22 megabytes of storage. Dynamic whole body PET studies generate even more data

due to the need to scan at several positions to cover the axial length of the body. The amount of data has not only made clinical interpretation and examination more difficult, but also hinders classification and management. Most medical multimedia databases can retrieve data based on textual or numerical fields (e.g. image file name, patient hospital identification number, examination date, or pathological description). However, purely text-based methods pose significant limitations on multimedia data retrieval. Some visual properties or features of images, such as shape and texture, are extremely difficult to describe in text. The description limits the scope of the search to that predetermined by the author of the system or the current application, and leaves no means for using the data beyond that scope. Description can be subjective, and different people may give quite different descriptions for the same image. Since descriptive text is entered manually, the indexing process is slow.

In contrast to traditional text-based methods, content-based image retrieval usually uses color [3-7], texture [8-10] and shape [11-13]. In addition to these three major visual features, some other features such as icons [14], and geometrical (Radon) features [15] may also be included. Color is one of the most widely used visual features. It is relatively unaffected by the background and independent of image size and orientation. As one of the major visual features, texture plays an important role in human perception. It involves visual patterns with homogeneity properties that cannot be provided by color and intensity alone. Shape includes boundary-based and region-based shape representations, such as the Fourier Descriptor and Moment Invariants. All of the above visual features are extracted automatically in the indexing process when images are entered into a multimedia database. Queries and retrievals can be based directly on the visual properties of the images and return results ranked by the degree of content matching. In recent years, various contentbased image retrieval systems have been developed in research prototypes and commercial systems [16-24]. Obviously, content-based data retrieval has become a major technique for overcoming the drawbacks of existing retrieval methods. Content-based retrieval of medical data could potentially open up interesting new avenues for research. However, existing content-based image retrieval approaches may not be applicable to medical images due to their unique characteristics. For example, color is not normally captured in the medical imaging process and medical images are usually acquired and displayed in grayscale, or pseudo-color. Therefore, the color index is likely to be of lesser importance in medical images. Texture may be confounded by the noise in many medical images, especially in nuclear medicine. There is a need for efficient techniques for multimedia medical data browsing. searching, and retrieval. Previous work in this area based on features and patterns specific to medical images is described in the following sections.

17.2 Content-based Retrieval of One-dimensional Medical Data

The electrocardiogram (ECG) is a one-dimensional recording of cardiac electrical potentials [25-26]. The electrical signal originates in the cardiac muscle fibers. The ECG may roughly be divided into the phases of depolarization and repolarization. The depolarization phases correspond to the P-wave (atrial depolarization) and QRS-

wave (ventricular depolarization). The repolarization phase signifies the T-wave (ventricular repolarization). Figure 17-1 shows a typical ECG waveform. The ECG is measured by placing ten electrodes on selected spots on the human body surface. Six electrodes are placed on the chest, and four electrodes are placed on the extremities. For regular ECG recordings, the variations in electrical potentials in 12 different directions out of the ten electrodes are measured.

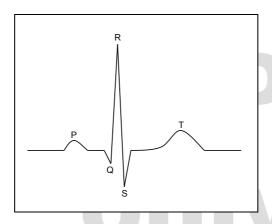


Figure 17-1. A typical ECG waveform. The points P, Q, R, S and T are known as the P-wave, Q-wave, R-wave, S-wave and T-wave respectively.

The ECG is used to identify cardiac abnormalities, such as abnormal rhythms (arrhythmias) [27], sleep apnea [28-29] and myocardial infarction [30-31]. Large amounts of ECG data are generated in the primary care, home and hospital environments which often need to be processed, evaluated and shared among clinicians. The classification of ECG data into different physiological disease categories is a complex pattern recognition task. Computer based classification of the ECG can achieve high accuracy and offers the potential of affordable mass screening for cardiac abnormalities. Successful classification is achieved by finding patterns in the ECG data that discriminate effectively between the required diagnostic categories. Conventionally, a typical heart beat is identified from the ECG data, and the QRS-, T- and possibly P- waves are characterized using measurements such as magnitude, duration and area. The ECG classification is then performed on the basis of these measurements. The content-based search for ECG data can then be worked out based on such a classification.

Several classification algorithms with alternative representations of the diagnostic content of the ECG have been investigated [27-35]. Chazal et al. [32] derived a standard cardiology feature set from standard QRS features. For each QRS detection, the associated QRS onset and offset was determined. The features were derived from the scalar lead parameters abstracted from the P-waves, QRS complexes and T waves; vector loops; and 3D loop e.g. planarity of the QRS plane. Bousseljot et al. [33] presented a technique which was not based on the measurement and extraction

of individual features of the ECG data. With comparison of the signal patterns of 12channel ECG of unknown diagnosis with signal waveforms of an ECG database, those ECGs whose waveforms were most similar to those of the unknown ECG are identified. The result of each reference ECG comparison was a 12-dimensional vector whose elements give the correlation values for the respective lead. Chazal et al. [34] later showed that it is possible to classify with features extracted from the wavelet transform (WT) of ECG data and achieve comparable diagnostic accuracy to the standard cardiology features. The advantage of this representation is that the approximate QRS detection point is the only characteristic point required. By eliminating the need to find other characteristic points a significant amount of computation is saved. Bozzola et al. [30] presented an approach for the automated ECG classification and searching based on a hybrid Neuro-Fuzzy model. In this approach the classification power of the connectionist paradigm has been coupled with the ability of the Fuzzy Set formalism to treat natural language in a quantitative way, which allows clinicians to build up a system capable of both a good classification accuracy and to give meaningful explanations of the diagnoses for cardiac abnormalities, such as myocardial infarction. Recently, Bousseljot et al. [35] proposed a method for the interpretation and comparison of 12-lead ECG data without feature extraction, using a modified algorithm of cross correlation for normalized multi-lead waveforms described in [33], and demonstrated this ECG multi-lead waveform recognition with 10,000 ECGs. Reference cases are selected from the ECG database which best match the signal patterns of the unknown ECG.

17.3 Content-based Retrieval of Two-dimensional Medical Data

Traditional X-ray projection imaging provides a map of tissue density that reflects the composition of the human body in two-dimensional domain. The radiograph is classically a negative image on photographic film made by exposure to X-rays that have passed through the body. Radiographically the breast mainly consists of two component tissues: fibroglandular tissue and fat. Fibroglandular tissue is a mixture of fibrous connective tissue (the stroma) and the functional (or glandular) epithelial cells that line the ducts of the breast (the parenchyma). The remainder of the breast is fat. In terms of X-ray attenuation, fat is more radiolucent than fibroglandular tissue; thus, regions of fat appear darker on a radiograph of the breast. Regions of brightness associated with fibroglandular tissue are referred to as mammographic density.

The detection of mass lesions on mammograms can be a difficult task for clinicians or machines. The potential variability and heterogeneity of normal breast tissue often produces localized findings that may simulate mass lesions or create distractions during the search process. Several multi-scale methods based on the wavelet have been introduced [36-40]. In [38], tumour detection is directly accomplished within the transformation domain, relying on a thresholding of the wavelet coefficients to produce a detection or no-detection result. Karsseme [41] proposed a method to incorporate a priori knowledge within the analysis phase and to exploit structural geometric knowledge which mainly relies upon Bayesian techniques. Recently Balestrieri et al. [42] developed a retrieval method based on a hierarchical entropy-based representation (HER) [43], which transforms two-

dimensional visual signals such as contour and texture into a one-dimensional representation with a number of invariance properties: rotation, reflection, translation, contrast, luminosity, and optical zoom.



Figure 17-2. An example of hand-bone X-ray image

A number of techniques have also been developed to handle content-based retrieval for other types of X-ray images, such as dental and hand-bone X-rays. Figure 17-2 shows an example of hand-bone X-ray image. Zhang et al. [44] developed a prototype clinical dental radiograph image database to be indexed by image content. The underlying content-based search engine is based on an efficient modal shape description method, embodying two main techniques -- the finite element method (FEM) and eigen-decomposition, for characterizing the shape of a two-dimensional image region. Pietka et al. [45-46] developed content indices for hand-bone X-ray image retrieval. Since the X-ray images of the phalanges have very well-defined edges and lend themselves to automatic image processing routines, this method assesses and estimates bone age using the following steps. It first separates the third finger image from the image, then measures the lengths of the distal, middle and proximal phalanxes. After converting the measurement into an age estimate using the standard phalangeal length table, it finally compares the estimated age with the patient's age. This method has been used as a feature extraction tool in KMeD, a knowledge-based multimedia medical distributed database system [47].

17.4 Content-based Retrieval of Three-dimensional Medical Data

The most widely used three-dimensional medical imaging techniques are magnetic resonance imaging (MRI) and computed tomography (CT). MRI and CT provide

more detailed, comprehensive information on skeletal structures than traditional Xrays, and also image soft tissue more effectively. Magnetic resonance is a phenomenon that relies on the "magnetic moment" present in a wide variety of organic and inorganic materials [48]. The most important source of magnetic moment is hydrogen nucleus. Thus, the gradient differences in magnetic resonance signals rely mainly on the amount of hydrogen in various tissue types. For example, as shown in Figure 17-3(a), in magnetic resonance signals, bone and air, which contain minimum amounts of hydrogen, produce dark pixels, while fat and water, which contain large amounts of hydrogen, produce bright pixels. MRI can be used to obtain exquisitely detailed images of anatomical and pathological structures. A typical MRI is 256 × 256 pixels per slice, and the number of slices can vary between 16 and 124 on a standard clinical protocol. Like MRI, CT is capable of producing three-dimensional images. CT images are based on density within the imaged object. The denser the tissue is the brighter the pixel. For example, bone produces very bright pixels in CT, whereas air produces very dark pixels, as shown in Figure 17-3(b). CT images typically consist of 512×512 pixels per slice, and the total number of slices can vary between 44 and 64.

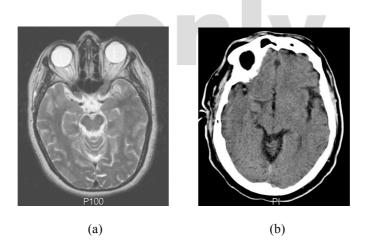


Figure 17-3 (a) a brain MRI; (b) a CT brain image

Content-based retrieval for MRI and CT images has been investigated previously [43, 49-56]. The capacity to retrieve images containing objects with shapes similar to a query shape is desirable in medical image databases. Robinson et al. [49] proposed a similarity measure and an indexing mechanism for non-rigid comparison of shape which added this capability to an MRI database. The similarity measure is based on the following observations. Firstly, the geometry of the same organ in different subjects is not related by a strictly rigid transformation. Secondly, the orientation of the organ plays a key role in comparing shape. A KD-tree was constructed for indexing shapes and an algorithm for using the similarity measure along with the KD-tree for efficient retrieval was proposed. The indexing strategy changes with

similarity measure and as such does not require recomputation of the indexing tree? (This sentence doesn't make sense) Hou et al. [50] proposed a content-based medical image indexing technique based on spatial features derived from the relative spatial relationships among internal image entities. The similarity measurement is based on causality (probability) that indicates the degree of similarity between a user's query and images. The technique was demonstrated on MRI chest images. Orphanoudakis et al. [51-52] developed a network of servers which provided content-based similarity search for medical images. The representation of image content consists of geometric properties and texture descriptors of selected ROIs. Such features, differentiated with respect to their relative clinical significance, play an important role in comparisons of medical images routinely carried out by clinicians. For each physiological ROI extracted from images, the following set of features was computed: location, shape, size and a set of texture descriptors. Shape and size properties include roundness, compactness, area, and orientation. Chu et al. [47, 53] developed a knowledge-based approach to retrieve medical images by feature and content with spatial and temporal constructs. Selected objects of interest in a medical image are segmented, and contours are generated from these objects. A knowledgebased semantic image model is proposed that consists of four layers (raw data layer, feature and content layer, schema layer and knowledge layer) to represent the various aspects of an image object's characteristics. Such a four-layered integrated spatial and temporal data model characterizes low-level image features (such as raw image data, and contours), abstract semantic image representations (including image objects and streams), and generic domain knowledge. This approach also supports automatic feature analysis and classification for knowledge-based query answering. Recently, Liu et al. [54] proposed a content-based approach for volumetric pathological CT neuroimage retrieval. A set of novel image features were computed to quantify the statistical distributions of approximate bilateral asymmetry of normal and pathological human brains. They applied a memory-based learning method to find the most-discriminative feature subset through image classification according to predefined semantic categories. This selected feature subset is used as indexing features to retrieve medically similar images under a semantic-based image retrieval framework.

17.5 Content-based Retrieval of Four-dimensional Medical Data

Biomedical functional images obtained from positron emission tomography (PET), single photon emission computed tomography (SPECT) and other nuclear medicine imaging modalities play an important role in modern biomedical research and clinical diagnosis. Unlike X-ray, CT and MRI imaging, which primarily provide structural information, PET and SPECT are dynamic functional imaging techniques that allow the in vivo study of physiological processes. Physiological function can be estimated by observing the behaviour of a small quantity of an administered substance 'tagged' with radioactive atoms. Images are formed by the external detection of gamma rays emitted from the patient when the radioactive atoms decay. Because they allow observation of the effects of physiological processes, functional imaging techniques can provide unique diagnostic information [56-57]. Figure 17-4

illustrates the classical approach to processing and analysis of functional images, and subsequent generation of brain parametric images using PET with the glucose tracer 18F-fluoro-deoxyglucose (FDG).

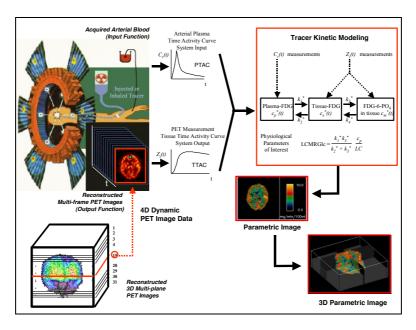


Figure 17-4. Quantitative estimation of regional glucose metabolic rate with PET

After intra-venous injection of the radiotracer (FDG) the time course of the regional radio-tracer concentration in the brain is obtained by acquiring a series of images. At the same time the input function is obtained from a series of blood samples. The physiological parameter of interest, in this case the local cerebral metabolic rate of glucose, is estimated by fitting a compartmental model to the data. Four-dimensional dynamic data (three dimensions in space and one in time) are required to construct the three-dimensional parametric image, which depicts regional glucose metabolism quantitatively in quantitative units of mg/100g/min. To estimate physiological parameters and form parametric images, the PET scanner acquires a series of scans at a pre-determined rate (not necessarily constant), typically for 20–60 minutes. Each scan, when reconstructed, represents the 3-D radiotracer distribution at a particular point in time during the study. From these data a tissue time-activity curve (TTAC) can be plotted for each voxel, and the physiological parameter value for that voxel calculated by the application of a tracer kinetic model to the TTAC. The parametric image is obtained by displaying the parameter estimates for each voxel. In dynamic functional imaging many different physiological parametric images can be obtained. Glucose metabolism, oxygen utilisation, and blood flow in the brain and heart can be measured with compounds labelled with carbon (11C), fluorine (¹⁸F), nitrogen (¹³N), and oxygen (¹⁵O), which are the major elemental constituents of the body.

Existing content-based medical image retrieval approaches may not be suitable when applied to functional images since quantitative physiological information in the functional image is unlikely to be recognized by common image retrieval techniques based on color, texture and shape index. Indeed function is likely to result in changes in apparent shape during acquisition as the tracer redistributes. A new approach for content-based functional image retrieval, which could support indexing and retrieval based on specific physiological kinetic features, seems to be required. Furthermore, in current content-based image retrieval database systems, the textual annotations that describe the content of the images are usually stored in a standard database. The images themselves are only referenced and linked by text strings or pointers, rather than part of the database. Such image archival techniques are only suited to small, slow growing, or static image databases. When applied to large functional image databases, such content-based retrieval techniques would severely tax the most advanced computer systems, and impede efficient archival, transmission, and network-based retrieval of the stored images. Therefore, it would appear highly desirable to incorporate image data compression techniques in the functional image content-based retrieval system.

Recently, Cai et al. [58] described a prototype design for a content-based functional image retrieval database system (FICBDS) for dynamic PET images based on a previously described 3-step functional image data compression technique that can achieve very high compression ratios without degrading image quality [59-60]. Pixel kinetics are encoded during image data compression to achieve image indexing and compression simultaneously. The proposed functional image retrieval system not only supports efficient content-based retrieval based on physiological kinetic features of the stored functional images, but also greatly reduces image storage requirements.

TRACER KINETIC FEATURE EXTRACTION AND DATA COMPRESSION

Tracer kinetic modeling techniques are widely applied in PET to extract physiological information about dynamic processes in the human body. Generally, this information is defined in terms of a mathematical model $\mu(t|p)$ (where t=1,2,...,T are discrete sampling times of the measurements and p is a set of the model parameters), whose parameters describe the delivery, transport and biochemical transformation of the tracer. The input function for the model is the plasma time activity curve (PTAC) obtained from serial blood samples. Reconstructed PET images provide the output function in the form of a tissue time-activity curve (TTAC), denoted by Zi(t), and i=1,2,...,I corresponds to the i-th pixel in the imaging region. Application of the model on a pixel-by-pixel basis to measured PTAC and TTAC data using certain rapid parameter estimation algorithms [59-62], yields physiological parametric images.

TTAC curves extracted pixel-by-pixel can be used to build a content-based functional image retrieval system. However, there are some potential problems. Firstly, since pixel TTACs are obtained from a sequence of twenty or more image frames acquired with a conventional sampling schedule (CSS), the high dimensional TTAC feature vectors (twenty or more dimensions) need to be indexed for the

retrieval system, making similarity measurement much more complex and inefficient. Secondly, due to the high level of statistical noise in dynamic PET image data, TTACs are inherently noisy. Thirdly, when large numbers of extracted TTACs are stored in the database, content-based image retrieval and network-based retrieval may be inefficient. Fortunately, these problems can be overcome by applying a three -step dynamic image data compression technique [59-60], as illustrated in Figure 17-5.

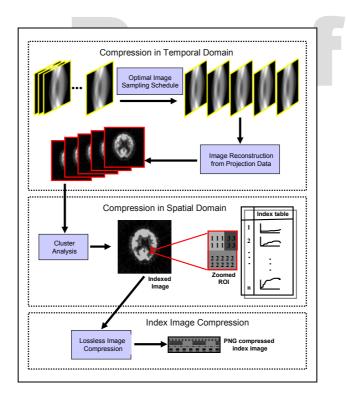


Figure 17-5. The three-step dynamic data compression method which supports fast content-based retrieval

In conventional PET image-wide parameter estimation, TTACs are obtained from a sequence of twenty or more image frames acquired with sampling schedules that have been largely empirically developed and may not be optimal for the extraction of accurate physiological parameters. Recently, Feng et al. [63] have developed an optimal image sampling schedule (OISS) which greatly reduces image storage requirements, as well as improving the signal-to-noise ratio for individual frames. For a five-parameter FDG model, only five image frames are needed [64]. The first step of the data compression technique is to apply OISS to the acquired images which removes temporal redundancies and minimizes the number of temporal frames while preserving data quality and fidelity. OISS can also be used to reduce the

number of TTAC feature dimensions. Since only five image frames are needed, the number of extracted TTAC feature dimensions can be reduced to five, considerably reducing the computation required for similarity measurement. The OISS design has been integrated into a prototype image retrieval database system as a pre-processing routine for dimension reduction of physiological TTAC feature vectors.

In the second step, compression in the spatial domain exploits spatial redundancies in the image data. Using a knowledge-based cluster analysis (KCA) technique [59], the reduced set of temporal frames can be further compressed to a single indexed image. In this step, the physiological TTAC feature extraction from functional image contents can be implemented using KCA. In dynamic PET a physiological tissue time-activity curve (TTAC) can be extracted for each pixel from the sequence of image frames. Pixels in physiologically similar regions should have similar kinetics. The KCA method automatically classifies image-wide TTACs into a certain number of typical TTAC types corresponding to different physiological kinetic patterns. The clustering algorithm classifies the image-wide TTACs, Zi(t) (where i=1, 2, ..., R, R is the total number of image pixels and t=1, 2, ..., 5), into S cluster groups Cj (where S<<R, and j=1, 2, ..., S) based on the magnitude of natural association (a similarity measure) [59]. The mean TTAC values for each identified cluster group are stored in an index table, indexed by cluster group. The averaging yields a set of highly smoothed TTAC features. The average TTACs represent j distinct physiological behaviours.

The KCA algorithm has been integrated into a prototype database and image retrieval system [58] as a pre-processing routine to facilitate storage and physiological kinetic feature extraction. In the final compression step, the indexed image obtained from cluster analysis is compressed using the portable network graphics (PNG) format which is a standard lossless compression file format. A detailed description of the theory and implementation of this three-step dynamic image data compression technique can be found in [59]. It has been shown that this technique can reduce storage requirements by more than 95% [59-60], providing much faster access to the data, particularly in a networked environment.

Raw dynamic PET images and parametric images can be rapidly recovered from the compressed data [59]. Firstly the indexed image can be decompressed. The perfectly reconstructed index image can then be used to recover the dynamic PET image sequence and generate the parametric image. Using the cluster TTAC's defined in the index table, parameter estimates for the tracer kinetic model are obtained by fitting the model parameters to the cluster TTACs. Finally, the parameter estimates and calculated physiological parameters for each cluster TTAC to their respective pixel locations are mapped by reference to the indexed image to obtain parametric images.

FOUR-DIMENSIONAL FUNCTIONAL IMAGE RETRIEVAL SYSTEM

A prototype content-based functional image retrieval database system (FICBDS) has been developed on a SUN Ultra-2 workstation running Solaris 2.5, using IDL and the C programming language. Figure 17-6 shows the overall architecture of the prototype retrieval system. Key components are: (1) the functional image processing

engine; (2) the image database engine; (3) the dynamic image archival system; and (4) the graphical user interface.

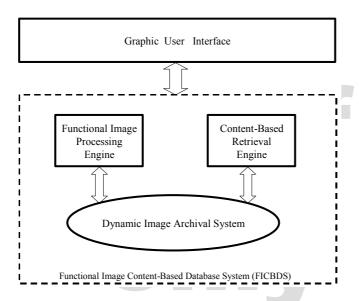


Figure 17-6. The prototype database system for four-dimensional functional image retrieval

Functional Image Processing Engine

The role of the functional image processing engine, which is based on the functional image processing system (FIPS) [65] with a set of special image processing tools, is to manipulate and process dynamic image data. It includes several special image processing routines: (1) A routine to resample CSS data to conform to the optimal PET image sampling schedule (OISS) [66]; (2) a knowledge-based cluster analysis (KCA) tool, which identifies specific physiological kinetic features within the functional image content; (3) a number of fast algorithms for the generation of functional images, such as the Patlak graphic approach (PGA) [67], the linear least squares method (LLS), and the generalized linear least squares algorithm (GLLS) [68], which can rapidly calculate functional parameters from the database; (4) tools for the statistical analysis of dynamic image, such as a tissue time activity curve (TTAC) and plasma time activity curve (PTAC) viewer, dynamic image player, profile, histogram, and surface plotting routines, and (5) image display functions, including a 3D parametric image rendering routine.

Image Database Engine

The FICBDS database engine manages functional image data with a two-level data model and supports information retrieval by image content.

Image data modeling

The image data model includes two levels: (i) physiological features or attributes, such as the tissue time activity curve (TTAC); and (ii) textual patient attributes, e.g., patient ID, study number, name, sex, age and so on. Based on the two-level data model, the engine supports some query models, such as query by TTAC feature and query by textual attribute.

Content-based retrieval

The FICBDS database system provides for content-based functional image retrieval on TTAC characteristics. The user defines a TTAC feature vector or selects a querying example from a set of pre-defined TTAC samples. Images containing similar TTAC feature vectors are then retrieved from the database. Let TTAC $_{\rm EX}$ be the example TTAC feature vector and TTAC $_{\rm DB}$ be the all extracted TTAC feature vectors stored in the database. The measure of similarity can be computed by $D_{\rm E}({\rm TTAC}_{\rm EX}, {\rm TTAC}_{\rm DB}),$ the Euclidean distance between TTAC $_{\rm EX}$ and TTAC $_{\rm DB}$. All TTAC $_{\rm DB}$ satisfying { $D_{\rm E}({\rm TTAC}_{\rm EX}, {\rm TTAC}_{\rm DB}) \leq M$ } are retrieved, where M is a user-defined TTAC matched degree.

Dynamic Image Archival System

Dynamic functional images are stored for each plane using the three-step technique for dynamic image data compression. There are three tables in the database: (1) Image TTAC Feature Vector Index Table which contains the study number, patient ID, plane number, cluster number and TTAC vector (activity concentration in different time points); (2) TTAC Index-Map Table which stores the TTAC cluster index map of each image plane. A conventional approach would store the entire image data set prefixed with a header in the image table and would require a large amount of storage space. However, in this functional retrieval system, the use of the three-step functional image data compression means that only a cluster index table needs to be stored for each image plane; (3) Patient Information Table, which includes textual information about the patient, such as patient ID, name, sex, age, height, weight, study number, PTAC input function, injected dose, physician name, physical examination date, medical history, pathological results and so on.

Graphical User Interface

Figure 17-7 shows the graphical user interface of the FICBDS system. There are three individual query entry windows. With the "Query by TTAC Feature" option, the user can use a slider control to define a TTAC sample curve for querying. Weighting parameters can be added to different time points. The sample curve is plotted in the "TTAC Sample" window. The "Query by Activity Concentration" entry window allows the user to retrieve TTAC, associated with a certain activity range of measurement. The "Query by Textual Attribute" allows the user to enter textual information, such as patient ID, patient name, sex, age range, etc. The system also supports combinations of these different query methods using the "Query Model Select" option. Studies containing planes that match the search criteria are listed, together with their matching planes. The numbers of matched planes for a highlighted list are shown in the "Matched Plane List" window. Some utilities, such as matched plane viewing and frame viewing are also available.

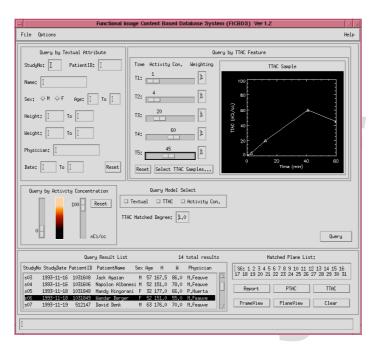


Figure 17-7. The graphical user interface of the database system with different query methods

CASE STUDIES

To assess the feasibility and practicality of this content-based functional image retrieval database design, a set of 15 dynamic clinical FDG PET studies was used to create a prototype database. The studies were acquired by a SIEMENS ECAT 951R PET scanner, at the PET and Nuclear Medicine Department, Royal Prince Alfred Hospital, Sydney. The number of cross-sectional image planes was 31. A typical conventional sampling schedule (CSS) consisting of 22 temporal frames was used to acquire the PET projection data. The PET scanning schedule was 6×10.0 second scans, 4×30.0 second scans, 1×120.0 second scans, and 11×300 second scans. The dynamic PET data were corrected for attenuation, decay-corrected to the time of injection and then reconstructed using filtered back-projection with a Hanning filter. The reconstructed images were 128×128 with a pixel size of 2mm×2mm. The 22frame CSS-format image data were re-sampled into a 5-frame OISS-format, using the dynamic image re-sampling tool of the functional image processing engine. The OISS consisted of the following five scanning intervals: 1×41 , 1×136 , 1×567 , 1×1711, and 1×1145 seconds. The prototype database contained 465 images (15 studies, 31 planes for each study).

Figure 17-8 shows a user-defined TTAC query. The sample TTAC associated with a high metabolic rate is shown in Figure 17-8(a). The results are shown in Figure 17-

8(b). Images in the first row are tissue regions with similar TTAC features to the sample TTAC. Their cluster index images and original temporal images are shown in the second and third rows, respectively. The results show the query successfully identified brain regions with a relatively high metabolic rate. It is possible to identify and retrieve images containing tissue regions which exhibit physiological behaviour similar to a pre-defined pattern. Such a content-based functional image database system could facilitate the identification of patients with particular disease states, and potentially increase the understanding of underlying disease processes and improve specificity in diagnosing disease.

The content-based functional image database retrieves index images corresponding to specific physiological kinetic features. A dynamic image sequence representing the original kinetic information and image data are then reconstructed from the index image. Kinetic feature indexing allows our database to avoid the need to store the raw image data but still enables rapid access to the dynamic functional image data. In contrast, conventional image retrieval techniques based on features such as color, texture and shape require the entire image to be stored in the database. Also, since dynamic images are compressed and indexed simultaneously, the complexity of database design and implementation is significantly reduced. The reduction in database size speeds network-based access to dynamic data for interpretation by the physician.

17.6 Conclusion

Current content-based image retrieval techniques may not be applicable in the medical imaging domain. In this chapter, we have summarized the major content-based retrieval techniques for medical data which include: one-dimensional ECG signals; two-dimensional X-ray projection images; three-dimensional CT / MRI volume images; and four-dimensional PET / SPECT dynamic images. These content-based medical data retrieval techniques may offer potential advantages in clinical decision making, retrospective studies, surgical planning, radiation therapy and telemedicine.

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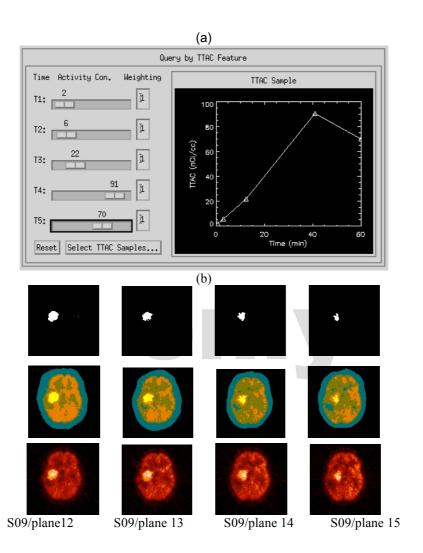


Figure 17-8. Some query results by using an user-defined TTAC sample

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