

Knowledge-based client-server approach to structural information retrieval: the Digital Anatomist Browser

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Abstract

Structural information can be defined as data and knowledge about biological objects ranging in size from molecules to the whole body. A framework is described for organizing structural information around a well-defined set of terminology and semantic relationships, and for disseminating multimedia structural information by means of a wide-area information server that is accessible over the internet. A Macintosh-based client of this server, called the Digital Anatomist Browser, has been used to teach neuroanatomy for the last 2 years. The client-server approach provides each student unlimited access to a rapidly growing knowledge base of structural biology that, while immediately useful for anatomy teaching, has the potential to be an organizing framework for other kinds of medical knowledge as well.

Key words: Medical informatics; Structural informatics; Anatomy; Client-server; Knowledge-based systems

1. Introduction

One of the most important kinds of medical information is structural information about physical objects ranging in size from molecules to the entire body [1,2]. The traditional media for organizing and disseminating this information are books, journals and films, and these media are likely to remain important because of their convenience. However, recent advances in computer technology have allowed the development of newer hypermedia systems that combine sound, images and text, to present the information in a more flexible and dynamic fashion than is possible with printed media alone [3]. Images and graphics are particularly important for structural information because so much of the information is visual (or spatial) in nature. The hope is that these sys-

tems, by providing better access to relevant structural information, will allow both professionals and students to cope more effectively with the information explosion.

Several such hypermedia systems have been developed for anatomy teaching [4-7]. The supporting computer programs, usually written by anatomy or clinical faculty members, often run on a personal computer such as a Macintosh or PC, and are developed via a commercial package such as Apple's Hypercard. Because the programs are developed by people knowledgeable in the subject they are often useful adjuncts to the more traditional teaching approaches. However, there are at least two difficulties with these efforts.

First, although the programs are often distributed to others at nominal cost, it can be difficult to adapt them to other applications, because the information contained within them is not organized according to any commonly agreed-upon

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framework. For this reason, duplicate information resources are often developed at several institutions.

The National Library of Medicine, in recognition of this problem, has initiated the Unified Medical Language System project as an attempt to develop uniform representation schemes for medical information [8]. Successful completion of this long-term project will provide the basis for applications that can be shared among many groups, including knowledge-based systems that are able to utilize intelligently structural information developed at disparate sites. Two of the first products of the UMLS are a Metathesaurus of commonly used medical terms [9], and a semantic network that encodes the semantic type and relationships among many of these terms [10]. It is expected that the scope of these products will be expanded over the years, as new specialty areas such as structural information are added.

A second problem with current stand-alone multi-media systems is obsolescence as new information is generated. This problem of currency is common to all branches of informatics, and has led to the recent emergence of wide area information systems, that is, systems that use the worldwide computer network to connect local client computers with information servers located throughout the world [11,12]. Most of these systems only provide access to textual information, but as high speed networks become a reality, multimedia information will become increasingly available.

In this paper we describe a multimedia Digital Anatomist Browser that addresses these two problems. The browser appears to the student as a drill and practice module for reviewing anatomy on 2-D and 3-D images. However, unlike most current systems, the anatomical knowledge displayed to the student is stored on a separate server that may be located far from the browser client. The knowledge on the server is organized around a semantic network of structural terms and relationships that is a superset of the structural terms contained in the current UMLS Metathesaurus. The information in the server is maintained and updated by expert anatomists, and the client-server architecture insures that this in-

formation is made available to the clients as soon as it is entered, thereby greatly alleviating the problem of obsolescence.

This approach is similar to the Brain Database proposed by Wertheim for sharing neuroscience information [13], although the Brain Database was initially targeted more towards research than education.

The advantages of the knowledge-based client-server approach are: (1) essentially an unlimited amount of information is potentially available to each client; (2) there is no lag between information generated at the source and information delivered to the user, so information can only become obsolete if the information at the source becomes obsolete; (3) the information is organized in a meaningful way that permits intelligent use and retrieval; and (4) new kinds of information may be easily added.

2. System design

2.1. *The Digital Anatomist framework*

The Digital Anatomist Browser is one component of a larger structural information framework that we are developing as part of the University of Washington Digital Anatomist Program [14]. Fig. 1 is a conceptual view of this framework. The framework is a client-server architecture in which various modules communicate with each other over the network. The primary motivations for this design are: (1) a structural information resource is too large for any one group to develop, so different portions will need to be developed in different locations; (2) a single computer could never hold all the information since the amount of generated information is increasing faster than individual storage capacity; and (3) some computer architectures are better suited to certain tasks than others. For example, one of the computers we use is optimized for fast graphics but has poor interface design tools, while another has the opposite features. The figure will be described from the bottom up. The modules relevant to this paper are shaded.

The bottom portion of Fig. 1 shows the four basic structural information resources we are cur-

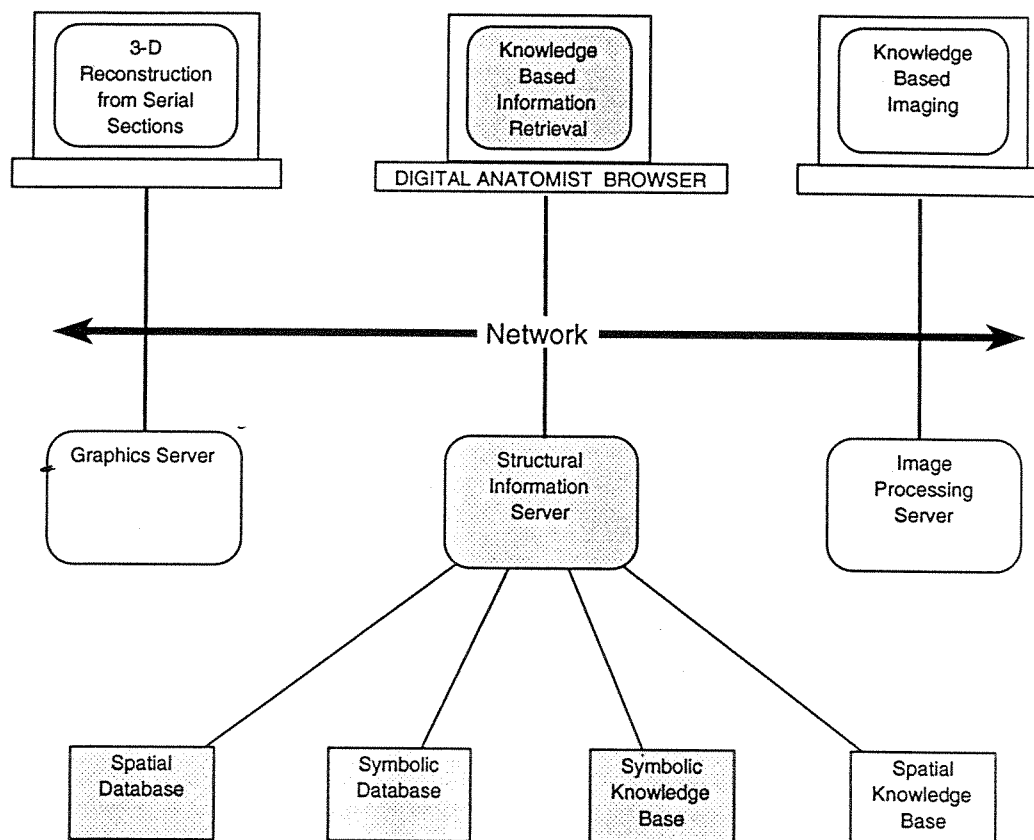


Fig. 1. Digital Anatomist framework. Shaded areas are the subject of this paper.

currently developing: a spatial database, a symbolic database, a symbolic knowledge base and a spatial knowledge base. These four resources arise from our classification of structural information along two dimensions: structural information that represents data versus structural information that represents knowledge, and structural information that is spatial in nature versus structural information that is symbolic in nature.

We define structural data as information about individual structures: a single medical image or a single 3-D reconstruction. Structural knowledge, on the other hand, is information about classes of structures: for example, a model of the shape and range of variation of all normal kidneys.

Spatial structural information is geometrical information about 3-D space occupying objects, or

information (such as charge distribution) that is expressed in relation to a coordinate system. This kind of information requires the most bits to represent, and includes images, 3-D reconstructions of organs or molecules, shape models, etc. Symbolic information, on the other hand, refers to all the rest of the structural information: anatomic names, symbolic relationships among names, textual descriptions, and other attributes. Spatial structural information roughly corresponds to the pictures in an anatomy textbook, whereas symbolic structural information corresponds to the accompanying text.

According to these classifications, we are developing the four basic components of the structural information resource shown in the bottom portion of Fig. 1.

(1) A spatial database of images, 3-D reconstructions, and graphics renderings. Examples include a series of 2-D image slices through the lateral ventricle (a fluid-filled cavity in the brain), xyz coordinates defining a 3-D reconstruction of the lateral ventricle from these slices, and a digitized movie showing the ventricles rotating in space.

(2) A symbolic database containing information necessary for retrieving the objects in the spatial database, as well as other non-spatial information about specific structural objects. Examples are the image and reconstruction file names of the lateral ventricles in the spatial database, the name or identifier of the specimen from which the ventricles were obtained, the dates when the images and reconstructions were obtained, and the name of the person who did the reconstruction.

(3) A symbolic knowledge base consisting of a well-defined nomenclature including synonyms, symbolic relationships among structural names and other attributes of anatomic objects. Examples include the names *ventricle*, *lateral ventricle*, *Ventriculus lateralis*, *telencephalon*, and *anterior horn of lateral ventricle*, and the relationships *lateral ventricle* IS-A *ventricle*, *Ventricularis lateralis* is a SYNONYM of *lateral ventricle*, *lateral ventricle* is a SUBDIVISION of *telencephalon* and *anterior horn of lateral ventricle* is a SUBDIVISION of *lateral ventricle*. Other information includes textual attributes of these terms that are not necessarily computer readable.

(4) A spatial knowledge base describing the shape and range of variation of structural objects, as well as the spatial relationships among objects. Examples include a model that encodes the average shape and range of variation of the lateral ventricles as seen in many patients, and a model that describes the geometric relationships between the lateral ventricles and other brain parts.

These information resources are accessed by an increasingly 'intelligent' structural information server that provides a high level protocol for accessing the resources from anywhere on the net, thus hiding the actual implementations from network clients and allowing us to change the underlying representations with only minimal changes in the access protocol. The structural in-

formation server is in turn accessed over the network by the Digital Anatomist Browser client shown in the top portion of Fig. 1.

The non-shaded modules in Fig. 1 are also part of the Digital Anatomist framework, but are being developed as part of separate projects [14-16]. The client-server approach is leading to synergistic interaction between these modules since programs within each problem area are able to take advantage of solutions developed for the others.

The following sections describe the modules relevant to the Digital Anatomist Browser in more detail. Figs. 2 and 3 expand the server portion of Fig. 1 (the shaded modules below the line labelled 'Network'), whereas Figs. 4 and 5 expand the client portion (the shaded module above the line labelled 'Network').

2.2. The structural information resources

The current implementation of the structural information resources is shown as the three shaded boxes in the bottom portion of Fig. 2. These boxes are more detailed depictions of the corresponding boxes in the bottom portion of Fig. 1. The spatial knowledge base is not shown in this diagram because it has not yet been incorporated into the browser, although portions of it have been developed as part of the knowledge based image project [17]. This implementation is subject to change as we develop new methods for representing structural information, but the conceptual organization shown in Fig. 1 remains the same.

The structural information is currently stored on a NeXT computer, and is organized as an extended relational model [18], in which most of the information is stored in standard relational tables that are part of a database file, whereas images and other large data structures are stored as separate files that are pointed to by names in the relational database. We currently use Sybase as our relational database. The database file is accessed by the Sybase database server, whereas the other files are accessed directly by the structural information server after their names are found in the database.

The symbolic and spatial databases are currently organized around the needs of the browser. The browser data is organized into subjects, each

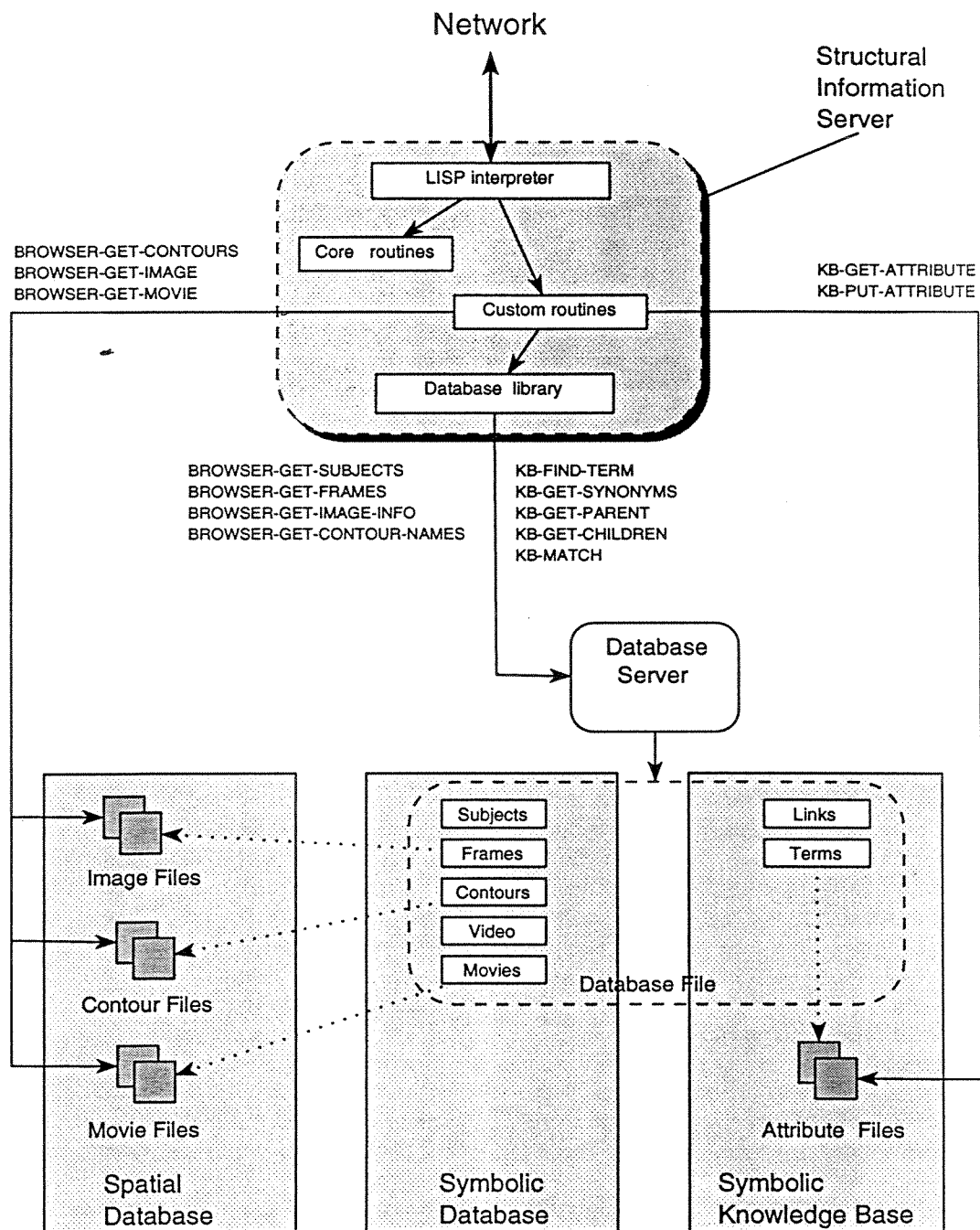


Fig. 2. Structural information resources and server. Actual implementation. Shaded areas are more detailed depictions of the corresponding shaded areas in Fig. 1.

which is a collection of image frames. Each image frame in turn contains a series of contours (lists of xy coordinates) which delimit the structure on the image. The frame and contour tables in the database file point to image and contour files stored in the spatial database, by means of the image and contour file pathnames. The relational tables also point to video sequences that depict 3-D animations of brain structures on an associated video disc produced by our group [19], as well as Apple Quicktime movies of 3-D animations: The Quicktime movies are stored as movie files in the spatial database.

The symbolic knowledge base is also stored using the extended relational model. The knowledge base is object-oriented, in which the objects are anatomic terms that were obtained either from the UMLS Metathesaurus [9] or from an augmented set of neuroanatomic terms developed in the UW Primate Center [20]. The terms are arranged in a semantic network that is stored in the Links and Terms tables of the relational database. Different link types allow the terms to be arranged in multiple hierarchies reflecting different points of view. Attributes of each term include items such as 'Glossary' and 'Definition' and are stored in textual attribute files. This approach was chosen because we recognize that symbolic knowledge representation is difficult and we wanted to develop a system of immediate practical use. As we learn how to represent the attributes in computer-readable form we will gradually transfer the files to the representation that we develop. A similar approach for organizing hypertext around a semantic network of concepts was proposed by Cimino et al. [21].

We chose not to use a commercial frame-based expert system shell because most of the systems that we were aware of were not designed for the large persistent knowledge structures we expect to need. However, our approach allows us to incorporate these kinds of systems as they become available.

Fig. 3 shows a portion of the symbolic knowledge base for the lateral ventricle. The top portion shows a semantic network diagram, with two link types, the IS-A link and the SUBDIVISION link. The bottom portion of the figure shows the sections of the Terms and Links tables that encode

this network, although in the actual implementation the entries in the Links table are the numeric identifiers shown in the first column of the Terms table.

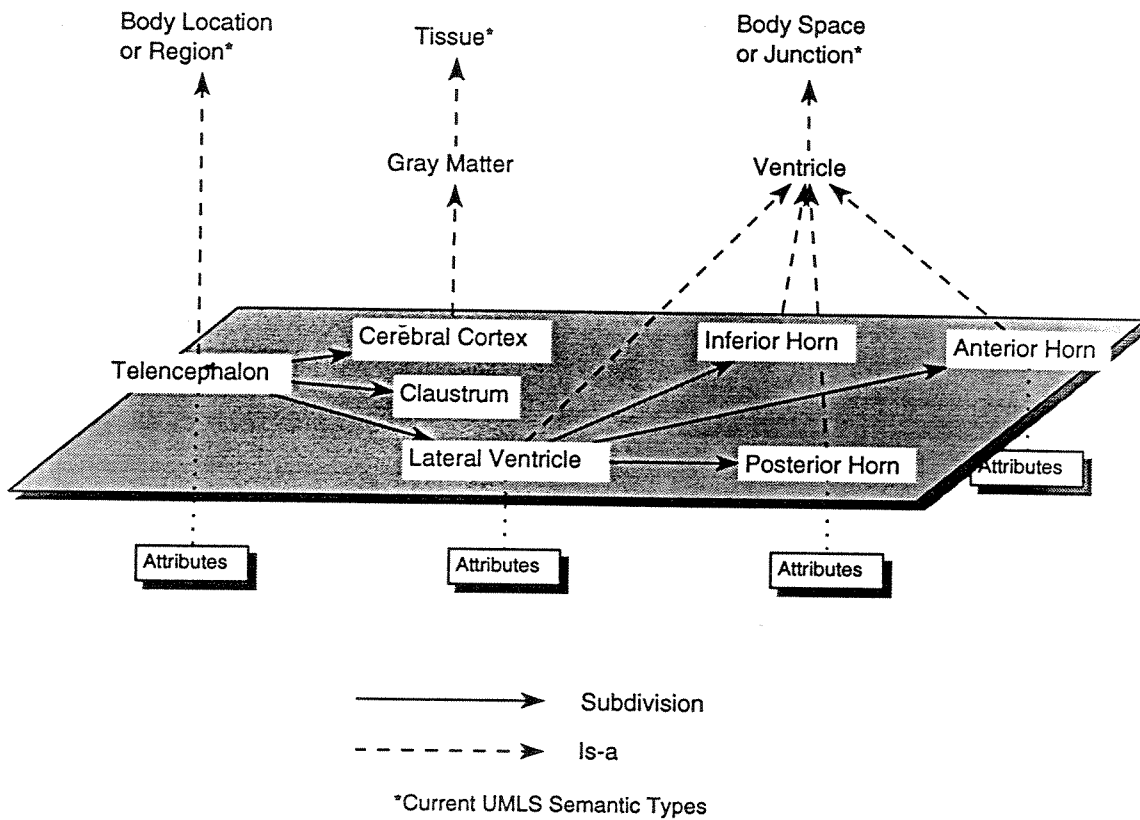
The Terms table allows a single identifier to represent a concept that can be referred to by multiple names. One of the term names is considered the 'master' name, and is the name that is printed by default whenever the identifier is looked up in the Terms table. Other names with the same identifier are synonyms. For example the same identifier 10000444 refers both to the Lateral Ventricle and the *Ventriculus lateralis*, but the *Ventriculus lateralis* is specified to be a synonym. As long as all tables and files in the knowledge base use either the identifier or one of the synonyms of a given concept, it is always possible to find the master term. It is also simple to change which term is the master term by changing the usage field in the terms table.

This approach of using identifiers to represent concepts rather than individual names is taken from the UMLS Metathesaurus [9], and is an example of our attempts to be compatible with the current state of the UMLS. Another example of compatibility is that the identifiers in the Terms table are the same as those used in Meta-1, except where we needed to add new terms, in which case a systematic approach was used. In addition the IS-A hierarchy is designed to fit into the UMLS semantic network, since the IS-A links form a semantic type hierarchy whose highest level nodes are current UMLS semantic types. For example 'Body Location or Region', 'Tissue', and 'Body Space or Junction' are UMLS semantic types whereas 'Gray Matter' and 'Ventricle' are subclasses of these types that are currently not in the UMLS semantic network.

We believe, as does the UMLS project, that correct naming conventions are crucial to a knowledge base of structural biology, since they provide the 'glue' that binds all the disparate information resources together. Therefore, we are attempting to be very careful in our use of names, and in our ability to incorporate expanded versions of the UMLS as they are developed.

2.3. The structural information server

Structural information is accessed over the net



Terms Table

Id	Name	Usage
200039452	Telencephalon	Term
20007776	Cerebral Cortex	Term
20018220	Gray Matter	Term
10000444	Lateral Ventricle	Term
10000444	Ventriculus lateralis	Synonym
10001073	Inferior Horn	Term
10000996	Anterior Horn	Term
10001194	Posterior Horn	Term
30032400	Ventricle	Term
10004614	Body Location	Term
10004609	Tissue	Term
10004615	Body Space	Term
20008910	Claustrum	Term
10001821	Is-a	Link
10001822	Subdivision	Link

Links Table

Node	Link	Target
Telencephalon	Is-a	Body Location or Region
Cerebral Cortex	Is-a	Gray Matter
Gray Matter	Is-a	Tissue
Lateral Ventricle	Is-a	Ventricle
Inferior Horn	Is-a	Ventricle
Anterior Horn	Is-a	Ventricle
Posterior Horn	Is-a	Ventricle
Ventricle	Is-a	Body Space or Junction
Telencephalon	Subdivision	Cerebral Cortex
Telencephalon	Subdivision	Claustrum
Telencephalon	Subdivision	Lateral Ventricle
Lateral Ventricle	Subdivision	Inferior Horn
Lateral Ventricle	Subdivision	Anterior Horn
Lateral Ventricle	Subdivision	Posterior Horn

Fig. 3. Symbolic knowledge base.

work by means of a structural information server, shown in the top portion of Fig. 2. This server is run by a Unix daemon *inetd* (described in the Unix online documentation) whenever a TCP connection is made over a specified port on the server machine. The server program always reads and writes to the standard input and output streams, but once the remote connection has been made these streams are redirected to the network.

The structural information server is based on Xlisp, a free subset of Commonlisp that is written in C and is designed to be small, fast and portable [22]. Xlisp has the advantage that computationally intensive routines can be compiled in C, while not throwing away the interactive Lisp environment. Xlisp basically consists of a LISP interpreter that parses a lisp expression, looks up the name of the lisp function referred to in the expression, then transfers control to a C routine that executes the function. The standard Xlisp distribution includes a set of core routines that implement the standard LISP primitives. For our structural information server we have added a series of custom routines that access the structural information resource files. We have also included the Sybase database library routines, thereby allowing the structural information server to access the Sybase database server, and through it, the database file. The Xlisp architecture is also the basis for the image processing and graphics servers that we are developing (J.S. Prothero et al., in preparation).

These features allow the client to specify all queries and commands as LISP functions which are then translated into the required low level C, SQL or Ftp routines. This approach means that we can specify a high level LISP-based protocol for the information server, and can change the underlying database storage mechanisms without changing the clients. We can also gradually increase the 'intelligence' of the server by adding inference functions to the LISP interface.

Some of the LISP functions that are available to the client are also shown in Fig. 2. The routines BROWSER-GET-SUBJECTS, BROWSER-GET-FRAMES, BROWSER-GET-IMAGE-INFO and BROWSER-GET-CONTOUR-NAMES formulate SQL commands that return information from the symbolic database.

The routines KB-FIND-TERM, KB-GSYNONYMS, KB-GET-PARENT, KB-GCHILDREN and KB-MATCH formulate SQL commands that access the relational portion of symbolic knowledge base, and KB-GATTRIBUTE and KB-PUT-ATTRIBUTE access the attribute files in the symbolic knowledge base.

The routines BROWSER-GET-CONTOUR, BROWSER-GET-IMAGE and BROWSER-GET-MOVIE retrieve the corresponding information from the spatial database, given the file name returned by a query into the symbolic database. BROWSER-GET-IMAGE and BROWSER-GET-MOVIE use unix ftp routines to establish a data connection on a separate port in order to transfer the files to the client.

2.4. The Digital Anatomist Browser client.

The current browser client is written in SuperCard running on a Macintosh [23]. The client runs on any Macintosh with a color monitor, at least 1 mb RAM, and at least 2 mb available hard disk space. If a TCP/IP connection is available the client can access the structural information server from any Macintosh in the world that is connected to the Internet. If not, the client can run in stand-alone mode, in which case portions of the structural information are downloaded as local Macintosh hard disk files. How much can be downloaded depends on the available Macintosh hard disk space. This feature allows versions of the browser to be exported as ordinary stand-alone Macintosh programs, which can be used to teach different subjects, depending on which part of the structural information resource is downloaded. In this case text files encode the information in the symbolic database, and only the textual attribute files of the symbolic knowledge base are available. If the semantic network is not available, so any inference methods that use the semantic network are not present.

Fig. 4 shows most of the windows that appear on the Macintosh client. This screen was captured from a 21-inch monitor. For smaller screens the image in the upper left will fit, and the other windows can be superimposed over this window as needed. The various windows provide views of the knowledge and data that are accessed by

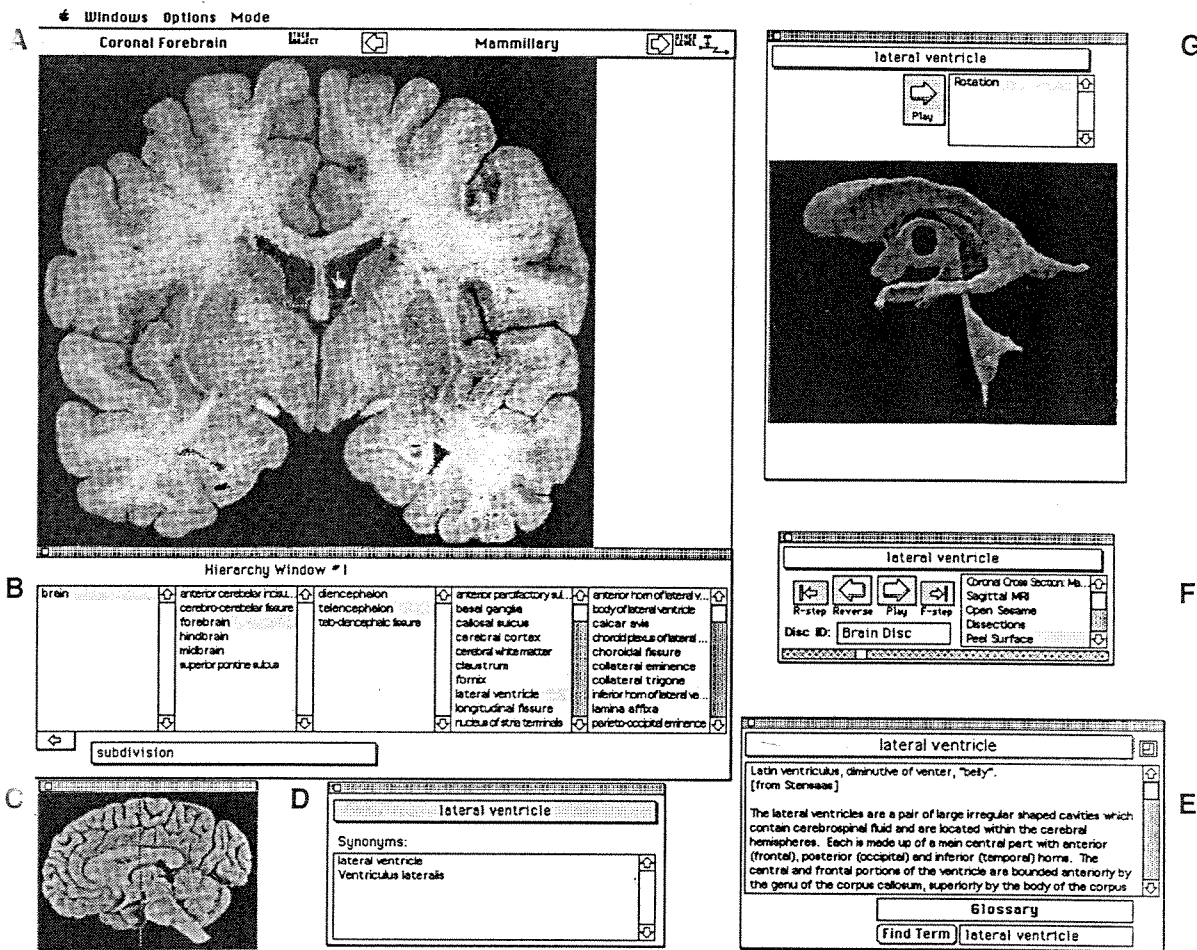


Fig. 4. Screen dump of Macintosh client windows. A. Image, showing a cadaver slice through the mammillary level of the coronal forebrain, with the lateral ventricle outlined and selected with the mouse. B. Hierarchy window, showing the subdivision link in the semantic network. C. Orientation view, with vertical line showing the slice level. D. Synonyms of the selected structure. E. Textual attributes window, showing the Glossary attribute. F. Video disc controls with list of relevant 3-D video sequences that can be played if the video disc is available. G. Quicktime movie, showing 3-D reconstruction of the lateral ventricles.

structural information server. Window A is the image window, window B shows one of the hierarchies encoded in the semantic network (in this case the SUBDIVISION hierarchy), window C is an orthogonal view that is useful for orientation, window D shows the master term and synonyms of a selected structure, window E shows textual attributes for the selected term (in this case the Glossary attribute), window F shows the video sequences that are available if a video disc is attached, and window G shows any Quicktime movies

that may be available. The visibility of these and other windows are controlled by a pop-up menu which appears when the 'Windows' text is clicked at the top of the screen.

A student usually interacts with the browser by choosing a particular subject from an initial subject window (not shown) which is loaded at start-up from the corresponding table in the relational database (via the server routine BROWSER-GET-SUBJECTS shown in Fig. 2). Each subject consists of a series of frames, which are usually named 2-D

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image slices through the region of interest, but they can be any other type of image as well. In Fig. 4 the student has chosen the 'Coronal Forebrain' subject, which loads a frames window (also not shown) with the names of all frames associated with the subject (BROWSER-GET-FRAMES). The frame shown in the figure is called 'Mammillary', and is a coronal slice through the mammillary bodies in the forebrain. The current subject and frame are shown along the top of window A.

Once the subject and frame have been chosen the server accesses the name of the image file through the Frames table in the database (BROWSER-GET-IMAGE-INFO), sends a copy of the image file to the Macintosh client (BROWSER-GET-IMAGE) loads the image into Supercard, determines the names of all the structures that have been outlined on that image (BROWSER-GET-CONTOUR-NAMES), sends the contour files to the client (BROWSER-GET-CONTOURS), and loads them into Supercard. The contours are loaded as mouse-sensitive but-

tons, each of which is given the name of the corresponding structure.

The student can then interact with the image in various ways, depending on the setting of the 'Mode' menu. In 'Browse' mode (the default) the student clicks the mouse on various parts of the image. If the mouse is clicked over an outlined structure the outline is blinked, and a request is sent to the server to retrieve any attribute files (KB-GET-ATTRIBUTE). The name and attributes appear in the textual attributes window. In Fig. 4 the student has pointed to the lateral ventricle (window A), whose glossary definition appears in the textual attributes window (window E). If the Movie or Video disc windows are opened (via the Windows menu in the client) the relevant video sequences are accessed from the relational database and can be played by pointing to the appropriate controls (windows G,F).

Window G in Fig. 4 shows a frame from a Quicktime movie of the lateral ventricle, and Fig. 5 shows one frame from the attached video disk.

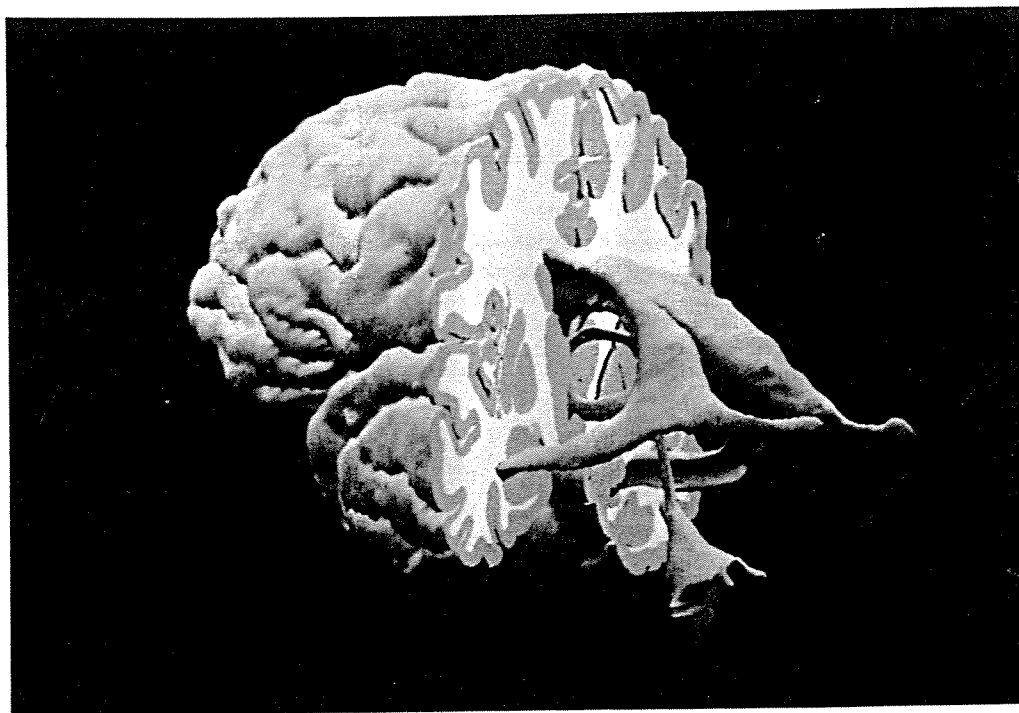


Fig. 5. Example video disc frame showing the lateral ventricles in relation to a cutaway section of the brain.

A video disk is still the most cost-effective way to display complex 3-D animated renderings, but as hardware and image compression technology improve we expect all-digital methods such as Quicktime to replace the video disk. Our framework will allow us to incorporate these new technologies easily as they develop.

The student can also interact with the browser in various quiz modes which are set using the Mode menu. For example, the computer can ask the student to point to various named structures, to pick the name of a highlighted structure from a list, or to type the name of a highlighted structure.

The latter test is the most similar to the classroom situation, and also demonstrates our first use of the semantic network for rudimentary inferencing. When the student types the name, the server is asked to (KB-MATCH) the typed term with the correct answer. If the name is not an exact match the server will first perform a simple spell check, then look for known synonyms, then check to see if the term is too general within the SUBDIVISION hierarchy, in which case it will ask the student to be more specific. This algorithm is implemented as a LISP function in the server which calls the custom routines KB-GET-PARENT and KB-GET-CHILDREN, which in turn issue SQL commands to traverse the semantic net.

3. Current status

3.1. Usage

The browser has been used in more than 6 neuroanatomy courses over the last 2 years. Between 2 and 5 networked clients are available to students in the Health Sciences library (depending on the academic quarter), and additional stand-alone versions are used in the neuroanatomy lab courses. At least one of the library stations is connected to a video disc player which controls a video disc of brain animations produced by our group [19].

Experimental versions of the Macintosh client have also accessed our server from the Radiation Oncology department here, as well as from the University of North Carolina. The program was very slow in the latter case, but it worked. The

department of Radiation Oncology is designing a different X-windows client that will integrate with their radiation treatment planning software, so that a clinician can review the anatomy relevant to a specific tumor site [24]. In addition the Health Sciences library is planning to integrate a client into their 'Willow' interface that is being developed as part of the Integrated Academic Information Management Systems (IAIMS) project here [25].

The current browser contents are mostly confined to neuroanatomy, with some material on the heart and mediastinum. The information resources contain 11 subjects (Topography, Dissections, Coronal Forebrain, Horizontal Forebrain, Brain Stem, Fetal, Pathology, Mediastinum, Coronal Forebrain MRI, Horizontal Forebrain MRI, Spinal Cord), comprising 206 images stored in Tiff format on the server, 4443 contours, one video disc containing about 54 000 images, and 2 Quicktime movies. The knowledge base has all UMLS terms that were deemed relevant for structural biology (2117 terms), 3770 additional terms provided by the UW primate center [20] which are due to be incorporated in the next version of the UMLS, 197 SNOMED terms, 543 from the Hyperbrain brain glossary produced by Suzanne Stensas [4], and 139 local terms. The primary link types are the IS-A link (1085 links) and the SUBDIVISION link (647 links). The SUBDIVISION links were obtained from the Neuronames Hypercard stack [20]. There are 1553 attribute text files associated with the terms, many of which were obtained from the Hyperbrain stack [4]. These numbers are continually changing as new information is added; the programs themselves need not change.

Each client has associated with it a log file that allows us to track system usage. Students are invited to input their student ID (but they are not required to do so). The log files track time-stamped individual events (such as pointing to structures) as well as performance on quizzes. Partial analysis of these files for Winter Quarter 1992 showed that the browser was used for a total of 495 sessions, with an average of 48 min per session. Sixty-eight separate students entered their ID, and of these the average number of sessions per student was 4.3, with a range between 1 and 24 sessions.

Users are also allowed to enter comments (which may be anonymous), and most of the comments have been highly favorable. A more detailed analysis of the log file data will be published elsewhere (Eno et al., in preparation).

3.2. Retrieval performance

A potential problem with the client-server model is retrieval time for the large data sizes that comprise structural information. However, the fact that students have been able to use the browser within the local area network of the Health Sciences complex at the UW shows that this approach is feasible. But image retrieval time is slow, and students have noted this problem. In order to alleviate this deficiency we are developing methods, such as caching, to speed up information retrieval, and the High Performance Computing and Communication Initiative [26] should lead to much faster access over the network.

In order to get a feel for the bottlenecks in structural information retrieval we developed a script that automatically emulates the sequence of operations that resulted in the windows in Fig. 4. The operations are shown as the first column in Table 1 and include Choose-Subject (Coronal Fore-brain), Choose-Frame (Mamillary), and Point-to-Structure with the mouse (Lateral Ventricle). For Point-to-Structure the primary operation was retrieving and displaying the attributes file. The time to complete each of these operations was measured and recorded in a log file. In addition, the completion times for important components of

the Choose-Frame operation were measured and recorded. The Choose-Frame time is comprised mainly of the time to transfer an image over network (when not in local mode), the time to port an image from the local Macintosh hard disk into Supercard, and the time to transfer and port all the contours for a given frame (contour retrieval). The sum of these individual times is roughly but not exactly equal to the overall Choose-Frame time, since some other processes are done besides these operations.

TOTAL time is equal to the sum of the Choose-Subject, Choose-Frame and Point-to-Structure times. Movie transfer time is shown separately because movies are not yet available to the Health Sciences students, and the transfer times are long that they would overshadow the other times.

The measurements shown in the next three columns of Table 1 are means and standard deviations of measured times for 5 runs of the script in each of three configurations (*local, same subnet and other subnet*).

Measurements were for the average case that has been in use in the Health Sciences library for the last 2 years. In this situation, images are cached in the local memory, and images are stored on the server in uncompressed TIFF format which is considerably slower than the compressed PICT files that the Macintosh is able to process more efficiently. The single Quicktime movie we tested comprised 1.8 megabytes of 122 frames compressed by a factor of 5 (which involved some information loss but no discernible loss in im-

Table 1
Timing tests^a

Operation	Local (s)	Same subnet (s)	Other subnet (s)
Choose subject	3.9 (0.29)	1.0 (0.15)	1.2 (0.18)
Choose frame	22.3 (0.99)	28.4 (1.16)	27.4 (0.98)
Image transfer	n/a	4.8 (0.07)	6.15 (1.04)
Image import	6.49 (1.2)	6.8 (0.43)	6.29 (0.44)
Contour retrieval	15.9 (0.24)	13.0 (1.21)	11.9 (0.37)
Point to structure	0.82 (0.17)	2.3 (0.1)	2.3 (0.1)
Total	27.9 (1.97)	31.7 (1.37)	30.98 (1.12)
Movie transfer	n/a	29.8 (1.07)	32.9 (2.18)

^aMeans and standard deviations (in parentheses) for 5 runs of each operation in each of three network configurations.

quality). Students do not yet have access to Quicktime movies.

All tests were run on the same Macintosh client between 10:15 and 11:20 h. In the local configuration the client was disconnected from the network, and all retrieved information was stored as local Macintosh hard disk files. Thus, in this case Image-Transfer time is not applicable. In the same subnet configuration the client and server were on the same subnet in the Department of Biological Structure at the University of Washington Medical Center, and in the other subnet configuration the client was moved to the Department of Radiation Oncology in the University of Washington Medical Center, which is separated from Biological Structure subnet by at least one router. The actual distance between client and server was about 0.25 mile, which is nearly the maximum distance in the large UW medical center. No timing tests were done outside the University of Washington Medical Center.

The results of these tests show that, at least within the University of Washington, there is no significant difference between the two network configurations, so if the client-server approach works anywhere within the local medical center it will work everywhere in the local medical center.

The main component of the processing times for all three configurations is the local Macintosh client, as evidenced by the fact that there is not much difference between the local and networked TOTAL times. The relatively long times are due to our use of Supercard, which works in an interpreted mode. We are currently developing improved teaching mechanisms and other image storage formats (such as compressed PICT) that considerably speed up the Macintosh processing. As we develop faster clients, either as custom Macintosh programs or on different machines, we expect that the client processing times should be greatly reduced.

The fact that there is not much difference between the local and network times implies that with faster clients, local area versions of this approach within a medical center will be quite feasible. As network distances become longer, the delays due to image transfer times will increase, and the long movie transfer times show that interactive transfer of large amounts of structural infor-

mation is not feasible with the current networking infrastructure. However, the High Speed Computing and Communication Initiative promises that very high speed networks will be developed in the relatively near future [26], and when these networks become available, our structural information resources will be interactively accessible without any changes to the programs.

4. Discussion

In this paper we have presented a client-server approach to structural information retrieval, and have described an implementation of this approach that has been used to teach neuroanatomy for the last 2 years.

Although the browser client that the user sees is similar to many of the stand-alone Hypercard teaching modules that are available, the client server approach that we have taken is very different, and offers several advantages over the stand-alone systems. These advantages include: (1) the client has access to an essentially unlimited amount of structural knowledge and data, since the server can be distributed over multiple machines in multiple locations; (2) there is no lag between information generated at the source and information delivered to the user, so information can only become obsolete if the information at the source becomes obsolete; (3) the knowledge base and information server can become much 'smarter' without changing the interface, so that the system will be able to selectively present information to the user, depending on his or her background and interests, without the user necessarily being aware of the increasing sophistication of the underlying programs; (4) different clients can be written for different machines, while accessing the same underlying knowledge base; and (5) new kinds of information may be easily added.

These advantages will allow us to rapidly add new knowledge and data to our existing structural information resource, so that we will be able to gradually include most of the anatomy and histology course material, and make this material available not only to the students taking these classes,

but also to anyone in the world who has a network connection and the necessary client software.

The client-server approach will also allow us to rapidly incorporate and disseminate new advances in knowledge representation and visual databases. The semantic network representation that we have developed is useful for classification of structural information, but newer techniques from artificial intelligence will be necessary in order to allow more intelligent reasoning about anatomic information. As these techniques become implemented our belief is that the high level LISP interface will not have to change appreciably.

Similarly, there is currently much work in the development of visual database systems, and some of this work could be incorporated without changing the server interface. For example, several database systems (including Sybase) allow images to be stored directly in the database, and various object-oriented database systems are also being used for multimedia information. By maintaining a high level LISP based access protocol it should be possible to change the underlying database system without appreciably changing the server interface.

A more difficult research problem is the development of content-based visual query methods such as that alluded to by Garber and Grunes in their study of image search techniques of artistic directors in advertising agencies [27]. It is possible in our system to retrieve images along paths other than subjects and frames, although we have not yet implemented these in our current interface. For example, since each contour is identified by the name of the structure in the knowledge base as well as the image with which the contour is associated, it is possible to retrieve all images that contain a given previously-contoured structure (i.e. all images, regardless of subject, that show the lateral ventricle), or all images that contain a class of structures in the symbolic knowledge base (i.e. all images that show any structure that is a SUB-DIVISION of the brain).

However, our system cannot perform retrieval by finding images that look visually similar to a given image, which is a desirable capability not only for art directors but also for students or clinicians who want to compare an image with images

that were previously seen. Such a capability would require that the computer automatically or semi-automatically extract features from the image that would be useful for indexing. We are working on that problem as part of our knowledge-based imaging project, but the general problem of computer-based image understanding is far from solved. An important advantage of our distributed framework is that program modules that represent even partial solutions to the problem of image understanding will potentially be reusable for content-based image retrieval as well.

These potential synergistic interactions between program modules are one of the major long term benefits we expect to see as a result of the knowledge-based client-server approach. The other major benefit is the potential for organizing medical information. Since our structural information resources are based on a well-defined set of anatomic terms and relationships, and since anatomy and structural biology is a foundation for most medical information, the structural knowledge base that we are developing should become useful as an organizing framework for other kinds of medical knowledge, and the client-server approach should allow this framework to be made available not only to many other people, but also to many other computer programs.

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