

Construction of a Human Topological Model from Medical Data

Nadia Magnenat-Thalmann and Frédéric Cordier

Abstract—Medical imaging can provide data for useful views of the interior details of human anatomy. In addition to visualization, which in general has been the primary reason for obtaining these data, many other uses are possible. These include modeling of different elements and their inter-relationships—topological modeling, simulation of physical processes, analysis of movements, and validation of models. Here, we describe some of the modeling issues from medical imaging. The issues are particularly related to topological modeling of different anatomical elements: bones, muscles, articulations, etc. A three-dimensional topological modeler is presented with which anatomists and other users can build a topological database containing structural, topological, and mechanical information of anatomical elements.

Index Terms—Deformable model, organ reconstruction, topological model.

I. INTRODUCTION

THE CHALLENGE of imaging science is to provide advanced capabilities and techniques for acquisition, processing, visualization, and analysis of biomedical images to enable faithful extraction of scientific and clinical information. This is a difficult task. However, there have been considerable efforts in this direction in the last decade [3], [4]. These efforts have been primarily directed toward the display and visualization of the contained information. Now clinicians can have a complete three-dimensional (3-D) view of the volume of a human organ. It is also possible to reconstruct or extract 3-D surface of elements from those images [9]. However, these efforts concentrate on 3-D visualization of volumes or surfaces. There is also a need for modeling and analysis of the relevant information coming from images, which can be used for other purposes.

Computationally, modeling is the representation of a collection of data in a coherent way [5]. The related data items may be associated semantically, physically, or in some other useful form. Modeling with medical images and data in our context provides both structural and topological information of different elements [6]. In addition to displaying these elements, our interest is in using them for physically based simulations of deformations, motion generation and analysis, and model validation.

The simulation of body deformations [14], [15] during motion requires taking into account the articulations of the skeletal structure as well as the mechanical properties of soft tissues.

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Once the components of the model are connected with their mechanical characteristics defined, a dynamical process is used for simulation. The forces estimated for muscles are fitted to the centroid line of action and applied to the skeleton, and the articulated structures deform. The incremental dynamic process of simulation accounts for the finite element computation of deformation and interaction of all the soft tissues.

In this module, we are not only concerned with providing the facilities of 3-D display and reconstruction of shapes of the anatomical elements but also in integrating useful additional information of elements which will be used in other modules such as simulation of deformation and movements. A comprehensive database consisting of the structural as well as topological description of a body part is built, which can be used for several applications. Such a database can be treated as a generic description of a canonical specimen, out of which a specific specimen can be derived or matched. This gives a large scope to the use of the topological modeler.

This paper is organized as follows. First, in Section II, we give an overview of the main tasks involved. Surface modeling of elements is presented in Section III. In Section IV, issues related to topological modeling are discussed: we define the topology in our context and present the data structure for the topology, features of the library, and the interactive tool for building the database. The potential uses of the topological database for different applications are presented in Section V. Finally, we conclude and outline related future work.

II. OVERVIEW

An overview of the main tasks involved in building a topological model based on medical data is illustrated in Fig. 1. It demonstrates the pipeline from the acquisition of images to the construction of the topological model. The human specimen images acquired from sources like magnetic resonance imaging (MRI) or computed tomography (CT) are first converted to readable form, which may then be preprocessed and filtered. Next, these images are interpreted and labeled to identify the useful regions of the image. The interpretation involves definition of contours of the elements of interest (bone, muscle) on the image slice. These contours may be refined by a matching tool to obtain finer contours. The 2-D contours are then connected to give a 3-D representation of the element [8]. The 3-D surface model of parts like bone is used in the topological modeler [2] to establish the inter-relationships between different elements for a specific body part. A data structure representing the structural and topological information is provided to build the topological model for the given body part. Supplementary information for

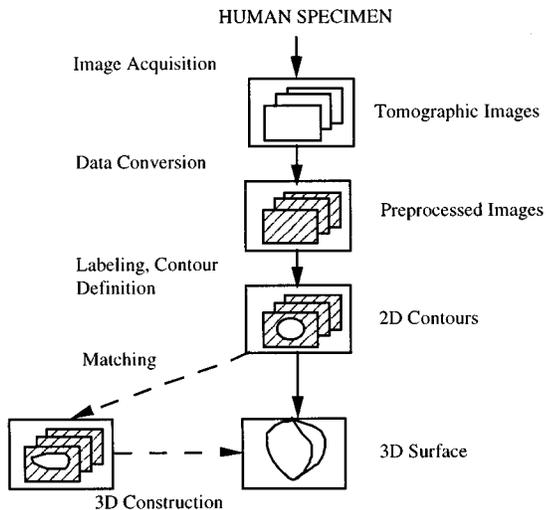


Fig. 1. Overview of construction using the “snake” technique.

mechanical and physical attributes for an element can also be imparted.

III. SURFACE MODELING

A number of complementary diagnostic tools exist, such as X-ray, CT, MRI, or positron emission tomography (PET). In general, the resulting images are interpreted visually and qualitatively by a radiologist or other medical experts. Voxel-display representation, while providing useful sophisticated visualization, offers little capability for treatment of the data in a manner consistent with their physical properties. This is due to the lack of geometry. Surface models are capable of representing the geometric structure of the elements. These structures facilitate the use of models for various tasks such as fabricating prostheses, facsimiles, inspecting occluded joints, preoperative simulation, postoperative analysis, etc. [7]. In the two following sections, we will give a description of two techniques for organ reconstruction.

A. Reconstruction Using Snakes

The process of surface reconstruction with the “snake” technique [17], [12] is divided into many steps: preprocessing, labeling, and postprocessing. A single tool, “label,” performs most of these steps. The steps for surface reconstruction are given briefly in the next sections. Fig. 1 gives an overview of the method.

1) *Preprocessing:* In data preprocessing, the images are first converted to a single image format with 8 bit per channel per voxel. Due to limitation of the memory size, the images of slices are then both scaled and cropped around the region of interest.

2) *Labeling:* Labeling involves identifying and delineating each organ of interest in the cross-sectional images. For the exact fitting of the contour of the organ on a slice, we use discrete snakes. This allows the fitting of the contour to points of maximum contrast close to the already-defined rough contour. Once the element has been interpreted and labeled on the different cross sections as contour, 3-D reconstruction is performed by joining the contour of all the pertinent slices. This yields a 3-D surface of the anatomical object of interest.

3) *Postprocessing:* Some postprocessing operations for matching are employed in order to assemble all reconstructed elements. Reconstruction from different modalities needs to be assembled in the same space [1].

For this technique, we have used the Visible Man Dataset [13], [16].¹ There are primarily three types of anatomical elements (organs) reconstructed: bones, muscles, and skin. The organs are those from the shoulder to the wrist for the left arm. Organ reconstruction causes problems specific to each type of organ. Delineation of the bones on the anatomical cross section is easy where they are surrounded by muscle, as the white color of the compact bone contrasts well with the red of the skeletal muscular tissue. The segmentation of the skin surface does not impose problems due to the fact that the embedding medium (blue) is in clear contrast to the white color of the skin. For muscles, it is illusory to believe that the contour of every individual organ can be clearly and easily identified. Muscle reconstruction requires specialized anatomical knowledge. In conclusion, this technique is useful if we have to reconstruct organs from scratch. On the other hand, this method is time-consuming and identification of some organs as muscles requires the help of an anatomist. In order to reduce these two disadvantages, we have developed a second technique that uses deformable surfaces.

B. Reconstruction Using Shape Constrained Deformable Model

As described early, the reconstruction process with “snakes” can be slow because the user has to define the cross-sectional contour on each slice. As organ boundaries do not appear clearly in some cases, reconstruction with a snake also requires anatomical knowledge. Therefore, another technique has been developed. This technique uses the shape constrained deformable model [10], [11]. In the next section, we will give a description of our method, its implementation, and the results. In this method, we use an initial model that is placed approximately to the position of the organ we want to reconstruct. This model is modified using a generic model and the information from the medical images of the patient. The segmentation process is formulated as the minimization of a cost function associated to each point of the shape:

- 1) a shape memory force that keeps the shape of the generic model;
- 2) image interest force that tends toward vertices to move into high edge density.

In the next sections, we first present the generic model, then describe different types of forces, and finally, the energy minimization process followed by the results.

1) *Initial Shape and Generic Shape:* As described earlier, our method uses two shapes: the initial shape and the generic shape. The initial shape is the shape at the first iteration in the computing process. We can use an initial shape which is different from the generic shape. The only restriction is that the initial shape and the generic shape must have the same topology. In most cases, the initial shape is identical to the generic shape. Sometimes, for specific images such as CT images, it is helpful

¹Visible Human Project. Available: <http://www.nlm.nih.gov/research/visible/index.html>

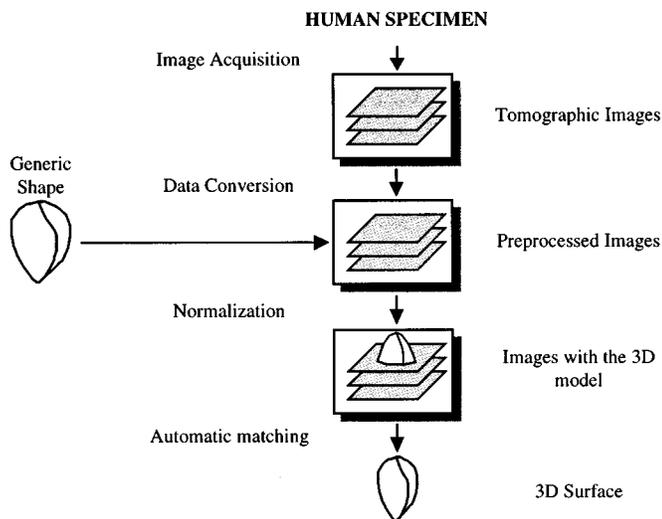


Fig. 2. Overview of construction using the shape constrained deformable model.

to define an initial shape. On these images, bones appear with two contours very close to each other. During the reconstruction process, some vertices move to the internal contour and some other to the external contour. In that case, we define an initial shape big enough to contain the entire organ to be reconstructed. In this way, vertices only move to the external contour. A generic shape is used to compute the shape memory force which will be described later. Fig. 2 gives an overview of the method.

2) *The Deformable Model*: Our model is represented by points that define the object contours. The surface of the object is defined by a triangular mesh where each vertex knows its neighboring vertices. Thus, reconstruction algorithms such as the labeling tool described earlier can directly be used in a first step to build the generic model. The vertices of the mesh triangles correspond with voxels in the volume being segmented.

3) *Cost Functions*: These cost functions can be defined as a set of forces applied to each vertex. As described earlier, there are two types of force: shape memory force and image interest force applied on each particle X_i . The resultant force in each particle can be calculated as:

$$f_{\text{result}}(X_i) = f_{\text{ShapeForce}}(X_i) + f_{\text{ImageForce}}(X_i)$$

All these forces are explained in the next two sections.

a) *Shape memory force*: The elastic properties of an object can be defined as its ability to return to its original shape once deformed. It corresponds to a force called shape memory force that is deduced from the generic shape and the current shape. It is different from the elastic model that uses spring to link each neighboring point and it offers better convergence. A triangular mesh defines the surface of the object and each vertex knows its neighborhoods. For each vertex, we use an approximate coordinate system calculated with neighboring vertices. The computation of the shape memory force consists of two steps described as follows. During initialization, we calculate for each vertex the local coordinate system with the generic

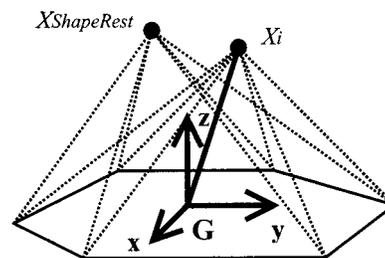


Fig. 3. Local coordinate system.

model. In this local coordinate system, we compute the coordinates of the vertex. This is the position of the local null deformation of the vertex relative to its neighbors.

For each iteration, we calculate for each vertex the local coordinate system relative to its neighbors. This local coordinate system changes at each iteration because the shape is modified during the fitting process. In this local coordinate system, we know the current position of the vertex and position of the local null deformation. This position has been computed in the initialization step. Between these two positions, we apply a force that will move the current position to the position of the local null deformation. The local shape tends to be similar to the local shape of the generic model.

For Fig. 3, we define:

- G : isobarycenter of the neighbors of point P .
- Z : unit vector normal to the approximate neighbor plane. X and Y are two vectors normal to Z . (X, Y, Z) is an orthonormal coordinate system.
- X_i : current position of the vertex. This position is defined by three values x_c , y_c , and z_c .
- $X_{\text{ShapeRest}}$: position of the local null deformation. It corresponds to the rest position.

With these two positions, the value of the shape memory force applied to each vertex i is:

$$f_{\text{ShapeForce}}(X_i) = K \cdot (X_{\text{ShapeRest}} - X_i)$$

b) *Image interest force*: External forces attract the deformable contour to interesting features, such as object boundaries, in an image. Any force expression that accomplishes this attraction can be considered for use. In our case, the computation of external forces is defined in two steps.

- 1) At the initialization, we apply a 3-D Sobel operator on the entire voxmap. The gradient map is then stored in a cache. Using a memory cache is a good strategy because we intensively use the value of the gradient for each vertex in the next process. The input voxmap can be represented as gray-level data as well as color.
- 2) During the process, the algorithm finds the closest position of the gradient value which is greater than or equal to the threshold parameter. This position is considered an ideal position. The threshold parameter is controlled by the user. In order to limit time, the research for the ideal position is restricted along the normal of the surface around the vertex. This normal of the surface has already been computed during the computation of the internal

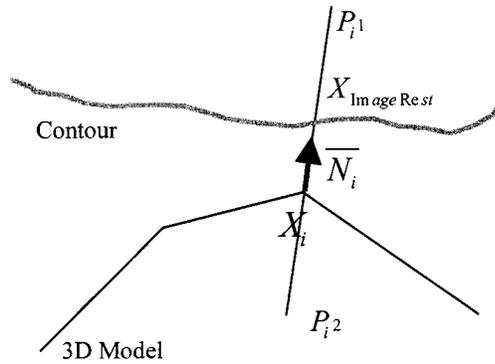


Fig. 4. Computation of the ideal position.

force. This normal is the Z vector in the local coordinate system described earlier. A parameter defines the size of the neighbor, and this parameter can be edited by the user. A force has been defined to move the vertex to this ideal position.

For Fig. 4, we define the following:

- P_i1P_i2 : segment on which the search of the ideal position is done.
- N_i : normal to the surface.
- X_i : vertex of the mesh.
- $X_{ImageRest}$: ideal position.

The expression of the external force is similar to internal force. The value of this force applied to a vertex i is

$$f_{ImageForce}(X_i) = K \cdot (X_{ImageRest} - X_i)$$

C. Results and Problems

Deformable surfaces have been tested with the Visible Woman Dataset [1]. Model-based reconstruction is well suited for the extraction of anatomical structures from 3-D medical images. In most cases, organs have similar shapes between patients. That is why using a prior shape for reconstruction is a good strategy. Reconstruction of bones has given good results. Only CT images have caused some problems. In these images, bones appear with two contours very close to each other. During the reconstruction process, some vertices move to the external contour and some others to the internal contour. To solve this problem, we use an initial shape that includes the entire organ. Reconstruction of muscles has also given good results. In places where the image has a very low contrast, the deformable model takes the shape of the generic model which has the more satisfactory shape. Figs. 5 and 6 show examples of reconstruction using deformable models.

Fig. 5 shows surface models of bones and muscles of the shoulder constructed with MRI images. MRI images render better details for soft tissues like muscles; however, for bones these are less effective.

Fig. 6 shows reconstructed bones of the knee from MRI data of the Visible Human Project. These models have been used in

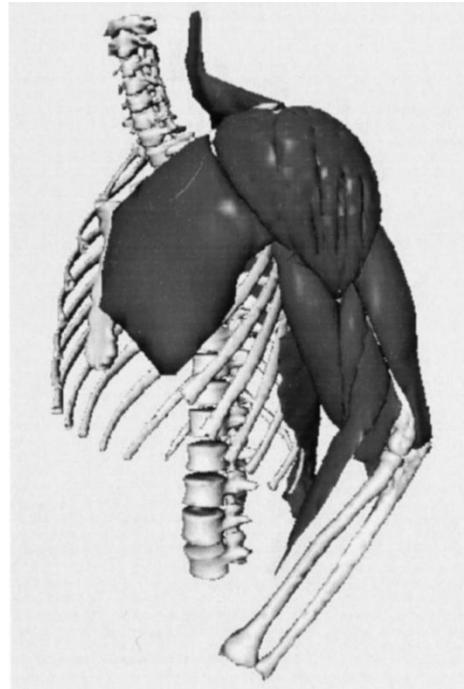


Fig. 5. Bones and muscles of the shoulder reconstructed from Visible Human Data [8].

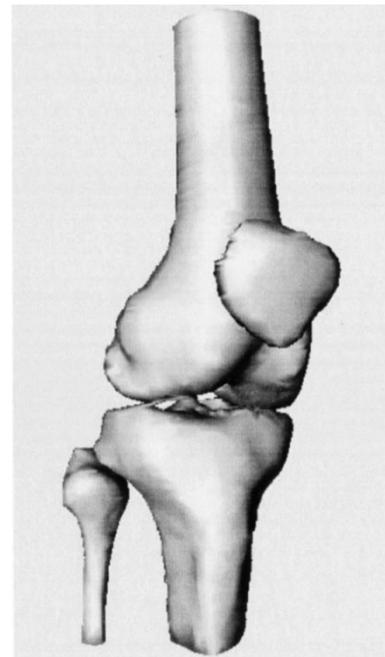


Fig. 6. Bone reconstruction using MRI images.

the frame of the MIAS project² for virtual endoscopy of the knee.

IV. TOPOLOGICAL MODELING

Topology in our context is defined as a 3-D connectivity graph of anatomical elements for a given body part (e.g., arm). The topological relation in terms of connectivity of the elements can

²MIAS Biomed Project BMH4-CT96-0865. [Online]. Available: <http://www.miralab.unige.ch/Mias.html>

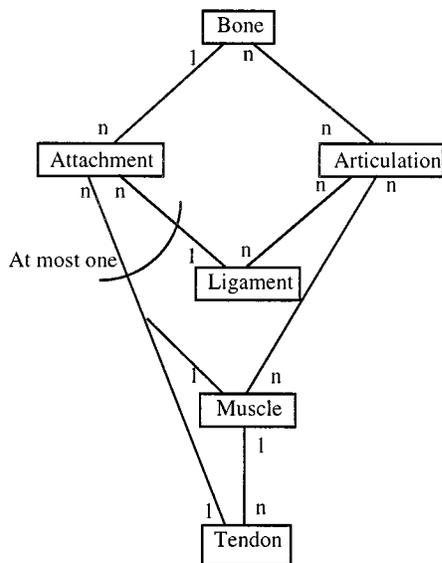


Fig. 7. Connectivity graph.

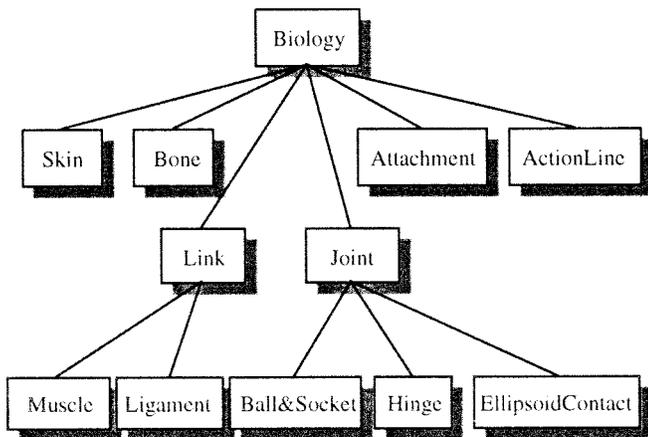


Fig. 8. Class inheritance.

be drawn as shown in Fig. 7. The number shown on the arc connecting two different elements indicates the cardinality of the relationship, i.e., the manner in which the two elements are related. For example, between bone and attachment, there are several (*n*) possible references for the bone whereas for an attachment there is a single reference for the bone.

For the data structure, object-oriented methodology is used where each element is considered like a class, encapsulating the necessary information about its geometry and physical attributes.

A library is built for manipulation and access of different elements and thus provides means for creating, editing, and saving the database for the topology of different elements. There is a base class *Biology* which includes general functions for accessing and manipulating the element of the class type. All the specific elements like bone and muscle, etc., are the derived classes of the class *Biology*. Fig. 8 shows the inheritance of the class *Biology*.

The class *Biology* is considered to define a generic part of the body, such as a limb (leg, arm), which would be modeled. For a body part, there are two components: the topology of the

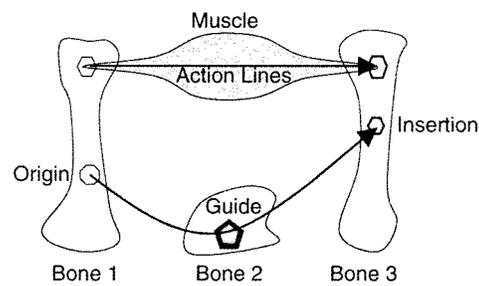


Fig. 9. Attachments.

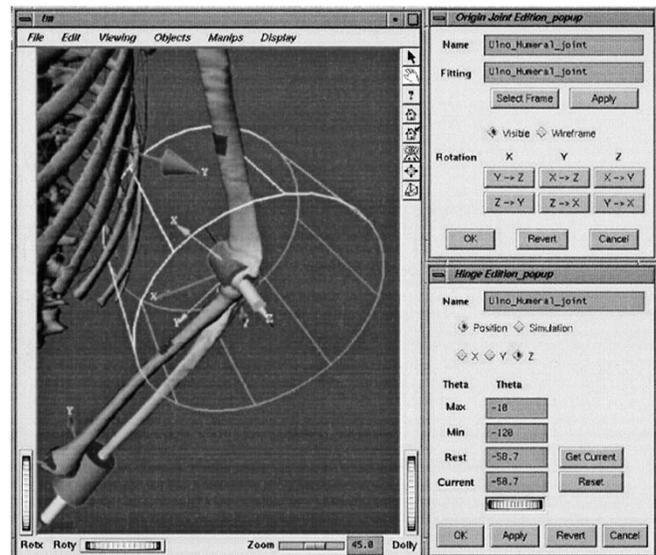


Fig. 10. Topological modeling in *tm*.

biological elements and the hierarchy. The topology contains the reference for all the topological elements and their relations between each other, and the hierarchy helps define hierarchical information of biological elements. Hierarchical relations for elements like bones may provide the necessary constraints for the movements of the elements in a body part. For example, in the case of an arm, when the shoulder moves, the other bones lower in the hierarchy (humerus, radio-ulna) follow the movement.

The following information presents brief descriptions of the various elements considered.

A. Bone

Bones are represented as 3-D geometry acquired from image slices. The 3-D geometry consists of a triangular mesh to represent the shape. Bones are considered as rigid and “undeformable” parts. These are used in many instances as the “referential” elements to associate the other elements.

B. Articulation

An articulation contains information about its connectivity with one or more bones, one or more muscles, or one or more ligaments. Implicitly, it is represented as an “axis frame” with three orthogonal axes and a center. Articulation plays an extremely important role for the motion of the skeleton. The reference bone used for the articulation is called the “master.”

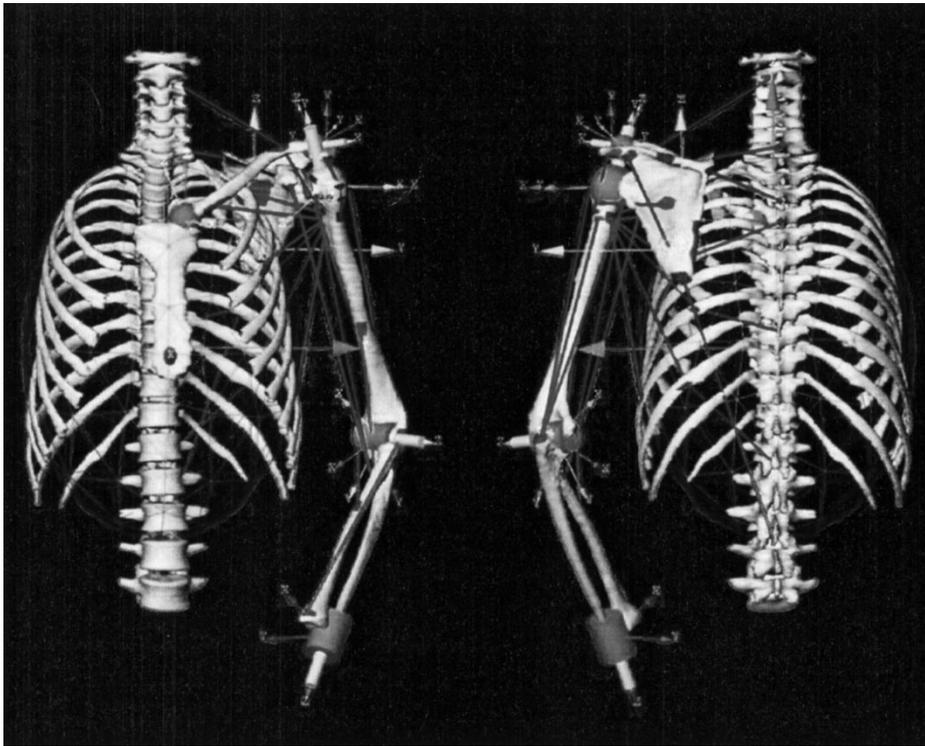


Fig. 11. Topological model of the shoulder.

C. Attachment

An attachment provides the information for “what” link is connected to the bone and “where.” Thus, it contains information about the bone, the muscle, the tendon, and/or the ligament. The attachment is defined as a collection of triangles/polygons of the bone where the link is attached. It also contains the point of attachment and its type (ORIGIN, INSERT, GUIDE, NONE). ORIGIN pertains to where the link initiates and INSERT to where it terminates. The option of GUIDE is meant for the constraints imposed by the intermediate bone attachment(s). Fig. 9 shows attachments for the two bones. The geometrical reference for the attachment is the bone with which the attachment is constituted.

D. Link

A link is defined as the generic element which is connected to the bones through the “attachment.” A link can be a muscle, ligament, or tendon. A muscle, in fact, gives the power and control for the motion, a ligament provides a control for the limit of the joint movement (articulation), and a tendon is the transmission network of the muscle and the bone. Each link type may have its own characteristics. For example, a muscle is defined as a set of arcs consisting of a set of points and a direction defined on the attachment point indicating the force direction (see Fig. 9). The true geometry of shape can also be obtained with surface modeling like that of bones.

E. Interactive Manipulation

Obtaining a static model is generally considered a major task of modeling. However, refining, modifying, and supplementing it with other information is also a critical aspect. A model with no notion of constraints, no perception of dynamics, and no

knowledge of muscle attachments would restrict its utility to only visualization. In our topological model database, we provide these properties and the functional relationships of different elements. The intention is to build the working models with capabilities for a medically acquired and biomedically valid musculo-skeletal system [2].

In order to create such a database, we provide a convivial interface for user interaction and manipulation. The tool developed for this purpose is called a topological modeler (*tm*). It provides extensive 3-D visualization and direct interaction and manipulation. The main task of *tm* is to create and modify the information contained in a topological database (see Fig. 10). The OpenInventor [18] toolkit is used to realize the interface of *tm*. The OpenInventor (or Inventor 2.0) toolkit provides a library of objects for describing 3-D scenes and methods for interacting with them. A scene built with such objects (called nodes) may be saved and loaded from a file and may also be easily rendered, with no low-level graphics programming. Furthermore, OpenInventor includes many other features such as triangulated meshes, NURBS, light sources of different types, draggers, and manipulators for direct 3-D interaction, engines for animation, automatic update of object dependencies, and more. It also provides a simple event model for 3-D interaction, efficient picking and rendering, defines a standard file format for 3-D data interchange, and is independent of platform and window systems. Tasks such as scene traversal, interactivity, picking, bounding box calculations, and other object space tasks are relatively easy to handle. The usage and layout of *tm* conform mainly to the mainstream look and feel.

Each class of the database may correspond to a new class of Inventor nodes encapsulating all the features and behavior needed for user interaction and for database interfacing. These new nodes are more precisely nodes [18] encapsulating different

nodes together. The 2-D user interface is realized through the use of the Motif widget library.

F. Example

Fig. 11 shows topological modeling of some elements in the shoulder part of an arm using *tm*. The muscular links are shown as straight-line arcs between bones. The surface of attachments (origins and inserts) for links are defined by the reference surface of the bones. The articulations are shown as frames at the joints.

V. USES

The utility required for interactive model manipulation can serve a variety of purposes. In our context, 3-D tools can be used to specify tissue composition and relationships; muscles and attachments could be created and connected to specific bone sides and given properties that will characterize their behavior.

Most of the applications using medical imaging can use these tools to facilitate investigations and experimentation with the data. These may be diagnosis of abnormality (structural or movement), interactive surgical investigation, examination for orthopedics, therapy, and prostheses design and simulation. In addition, the topological database can be used for other potential applications such as sports, education, and entertainment.

VI. CONCLUSIONS

Volume display of medical images provides good information for clinical evaluation; however, more advanced capabilities such as structural manipulation of the data, and simulation and analysis of dynamic function and behavior, require different formalisms of modeling and design of tools. We have employed surface-based models comprising 2-D and 3-D representation of the data and developed interactive 3-D tools for their investigation, analysis, and manipulation. These tools may help medical experts in their investigation and analysis. In addition to the medical applications, topological modeling of human anatomy has a wide scope in other applications such as sports, education, and entertainment.

The contents of the modeler may evolve in many ways. Improvement of tools will occur both for their interface and their functionalities from the feedback of the users. For certain functionalities, like segmentation and 3-D matching, it may be necessary to seek more generality and offer better automation. A class "skin" is to be added to the database, allowing for simulation of biological processes such as aging and wrinkle formation [19].

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