DEVELOPMENT OF A COMPUTATIONAL TOOLKIT FOR BIOMECHANICAL ANALYSIS AND SIMULATION: *THE VERTEBRATE ANALYZER*

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Abstract

This paper discusses the development of a computational modeling and analysis toolkit to construct, animate, and biomechanically analyze sophisticated models of vertebrates. Users will be able to create virtual musculoskeletal models of almost any vertebrate, extinct or extant, and run biomechanical analyses on one element or more of those models during simulated activities. By imposing selectable mechanical and physiologic constraints on each anatomical component comprising the virtual models (e.g., bone, tendon, muscle), resulting models will be variably limited in the behaviors that they can be programmed to emulate. The purpose is to both visualize and "experiment" with these biomechanically constrained models under known or estimated conditions and thereby test hypotheses relating to form, function, and/or behavior. The system is designed to be open-source and expandable, so that users can add their own functions and/or modify existing features.

Keywords: Biomechanical systems, Virtual Reality, Computer Graphics and Animation, Computer Modeling and Simulation

1 INTRODUCTION

The advent of Computer Aided Design and Engineering (CAD/CAE) has enabled engineers and designers to build, test, and analyze simulated structures and devices well before they are physically manufactured. As much as these technologies have advanced in the engineering domain, there are countless other research domains that have yet to employ them. Areas that have traditionally been slow to adopt these technologies, either because of lack of exposure, or disciplinary skepticism of their true utility, could benefit tremendously from their successful implementation.

One such area is anatomical/biomechanical modeling. To date, CAD technologies have not been employed ubiquitously in this field primarily because of the lack of sufficient domain-tailored tools. Numerous researchers have investigated modeling and animating animals and humans in a virtual, simulation-based environment. For instance, the Fauna Group [7,10] participates in the modeling and animation of articulated creatures such as humans and other animals. They attempt to achieve realistic joint motion through the use of studio motion capture for "simpler" models, and are exploring the extraction of 3D motion from monocular digitized video sequences for more complicated objects. Terzopoulos et al. [8] have created a virtual marine world inhabited by realistic artificial fishes. Their algorithms emulate the appearance, movement, and behavior of individual animals and groups. Furthermore, their models deform and displace in accordance with published biomechanic and hydrodynamic principles. The eSkeletons Project [4] is an on-line database that enables users to view and gather information about bones of a human, gorilla, and baboon. *Despite these and other innovative efforts, our research team has yet to identify any existing work that allows for user-interactive and parameterized vertebrate modeling, mechanical articulation of these reconstructed models, fleshing of those models with anatomically and physiologically constrained "tissues", and real time biomechanical analyses of models engaged in "behaviors".*

We are attempting to build a toolkit for constructing, articulating, and visualizing physically accurate and physiologically constrained biomechanical models, which can be programmed to emulate known or hypothesized behaviors. This graphical toolkit, called *The Vertebrate Analyzer*, will allow a user to assemble a skeleton, add muscles, tendons, and ligaments, all with specified characteristics, and determine the feasibility or efficiency of a movement or activity. To develop the preliminary tools and to test the feasibility of the project, virtual models of jaws and skulls of a lion, tiger, and an extinct saber-toothed cat (*Smilodon*) have been assembled from CT images. We envision the capacity for real-time biomechanical analysis (e.g., torque, position, velocity, acceleration, etc.) during simulated biting. These models will hopefully allow testing of hypotheses about how these vertebrates use, or once used, their jaws and teeth.

2 THE VERTEBRATE ANALYZER: Image-to-model reconstruction

Figure 1: *Smilodon* skull and mandible
(www.ucmp.berkeley.edu/mammal/carnivora/smilside.gif)

To test hypotheses involving biomechanical form and function, particularly of extinct forms, we need accurate, 3-D digital depictions of our subjects. Figure 1 shows the mandible and skull of a Smilodon that was CT scanned at 1.5 mm intervals. The output is a series of 2D segments or "slices". One slice is shown in Figures 2 and 3, before and after editing. To convert these 2D slices into a useful 3D format, we had to follow a number of steps using a variety of commercial and in-house software. The result is a 3D *isosurface* [9], depicted in Figure 4. Because the VA toolkit is programmed in ANSI C [5] and OpenGL [11] - *our desired final format of the 3D data is a sequence of model vertices and outward surface normals.*

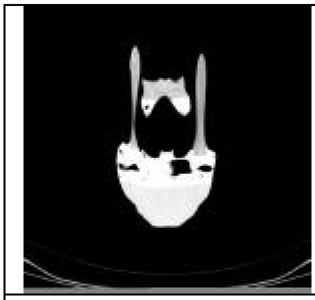

Figure 2: unedited CT scan

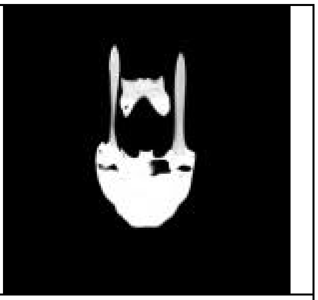

Figure 3: same slice, artifacts removed

3 THE VERTEBRATE ANALYZER: Features and operability

Once the physical model has been converted to a usable 3-D digital format, the data can be parsed into the "Vertebrate Analyzer" (VA) software module for biomechanical modeling and visualization. Though the development of the VA is still very much a "work in progress", the existing tool presently contains a number of useful features that will be outlined in this section. Future features and plans for the development of the VA will be discussed later in the paper.

Figure 4: Reconstructed 3-D Isosurface

3.1 Navigation and display

The VA toolkit allows for basic navigation about the model – rotation (using the mouse) and translation (using the keyboard) in 3-dimensions. The orientation of the model (roll/pitch yaw, and X/Y/Z translation) with respect to the global reference frame is tracked in the top left corner of the display window. Textual information pertaining to model fidelity, jaw angle, collision properties, and attached muscle characteristics can also be viewed on the perimeter display window, which can be toggled on/off at any time.

Figure 5: VA sabretooth (shaded)

3.2 Multi-model investigation

Locations of muscles, tendons, and ligaments on an extinct cat will never be known for certain, but can be intelligently speculated from existing tiger anatomy. Hence, the VA incorporates an interactive "multi-model" feature that allows the user to change to a different model on the fly. At present, the VA toolkit contains models of the sabretooth cat, a tiger, a lion, and a human skull. These models can be displayed using either full shading or vertex-only plotting mechanisms. Figure 5 depicts a "shaded" model. Figures 6 and 7 (forthcoming) represent vertex-based models.

3.3 Model Fidelity

A highly accurate digital depiction of an animal may contain thousands or millions of vertices. While the detail is visually desirable, it is often detrimental to performance speed, and the user may wish to alter this level of detail interactively, depending on available computational resources. Hence, the "model fidelity" option allows the user to display the model in vertex mode, plotting only 1/n vertices, where "n" is an integer fidelity parameter. Clearly, a smaller "n" represents a higher fidelity model, but one that will likely exhibit slower performance throughout any of a variety of pertinent graphics operations.

3.4 Anatomical component connectivity

One of the primary features of the VA toolkit is the ability to attach virtual muscles and other anatomical components to the vertices that comprise the model. Each of these components will modify characteristics of the model (e.g., alter weight and/or center of gravity) and impose limits on what the model can be programmed to do (e.g., limit range of motion at a joint). At present, virtual muscles are applied by requesting the user to click on two vertices that represent "endpoints" of a muscle bundle. Graphically, the endpoints are represented by 2 color-coded spheres, which are connected by a cylinder that represents the muscle bundle. Virtual tendons are represented by darkened cylinders that are interposed between endpoints and muscle bundles. These remain fixed in length even as the muscle stretches or contracts. The endpoints are color-coded for identification,, and the muscle bundle has "traffic light" color coding to indicate its condition relative to its resting length (i.e. position of maximal contractile strength). In other words, when at resting length the muscle bundle is colored green. As the virtual muscle is stretched or contracts beyond resting length, the color gradually changes through yellow ("caution") and towards red ("stop"). A secondary visual cue that has been incorporated involves the *thickness* of the bundle. A sense of "stretch" is conveyed by thinning the bundle as it elongates beyond resting length, and contraction is conveyed by thickening the bundle. Color and thickness cues are seen in Figures 6 and 7. In Figure 6, the muscle is greatly shortened, and is nearing its lower limit, so it is depicted as thick and red. In Figure 7, the muscle is stretching, but still lies close to its resting length, within the "intermediate" safe zone, so it is depicted as thin and green.

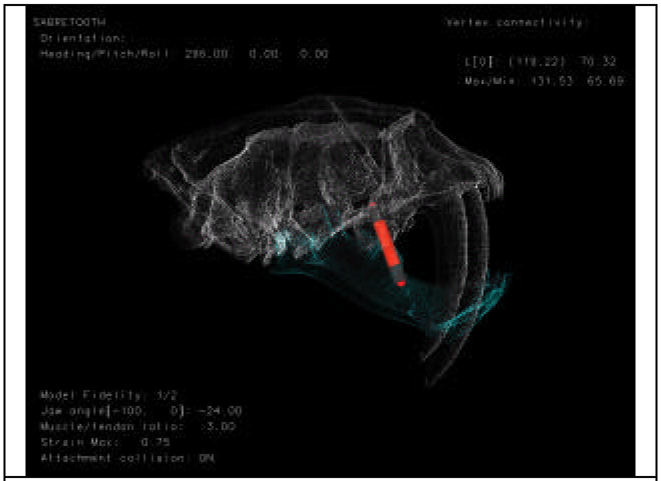
Figure 6: Muscle attachment - closing

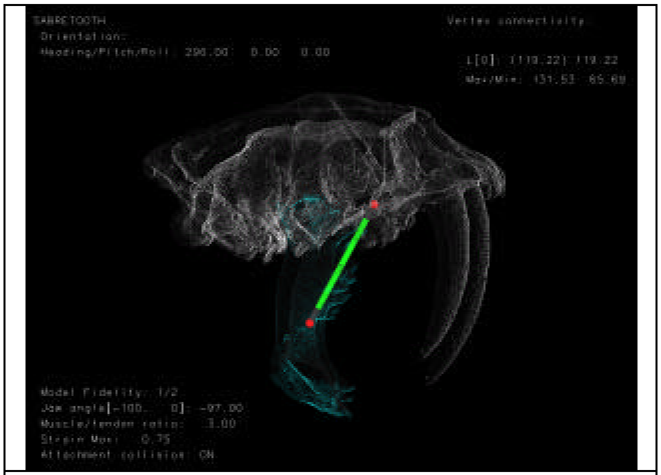
Figure 7: Muscle attachment - open

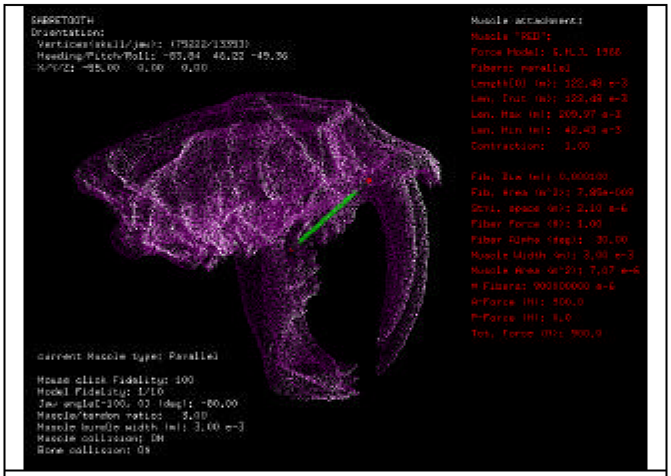
Figure 8: Selected muscle bundle within the VA toolkit

To attain more detailed geometric and structural information about each of the muscles on the model, the user can utilize a mouse menu option to click on the object. This will subsequently display detailed and user-definable information about the muscle, such as: fiber type (parallel or pinnate – each of which has distinct structural characteristics), initial and current length of the muscle bundle, the maximum and minimum allowable length of the bundle, based on the force model that is being utilized, muscle fiber diameter and area, resting tension within a muscle fiber, and active, passive and total force within the muscle bundle. Figure 8 is a depiction of a selected muscle bundle with relevant information shown on the right side of the window.

3.5 Animation

The VA toolkit allows the user to animate movement of one bony element on another. At present, this complicated spatial motion is simulated by assuming 2-D (planar) motion of the mandible about a pivot point on the skull. Essentially, the skull remains rigid (fixed) as the mandible moves, and the user has control over various aspects of this motion. The user can stop/start a continuous animation by way of a mouse menu option, or can step through the animation (forward or backward) by a user-defined angular increment via keyboard keystrokes.

3.6 Collision detection

A potentially useful display option involves model collision detection, involving both the virtual bones and muscles. At present, the *bone collision* feature lacks sophistication, and does not (yet) incorporate true graphics-based collision detection. Currently, this option simply constrains motion of the jaw between the "fully closed" (theta = 0) position, and a "fully open" (theta = *user defined*) position. The *muscle collision* option is substantially more elaborate. When a user selects vertices for muscle end points, the muscle is defined with published tension/compression limits [1,3,6], which will be briefly discussed in the next sub-section. If an animation is attempted that would open or close the mandible beyond the stretch/contraction capacities of an attached muscle, the motion is prohibited. The user can toggle either of these options on and off.

3.7 Stereoscopic viewing

Finally, to provide the user with some sense of depth and immersion, the VA toolkit contains a "stereo" option that allows a user to view the model in anaglyphic "2-color" stereo [2]. The popular stereo pairs of Red-Blue, Red-Cyan, and Red-Green are available in the VA toolkit. Anaglyphic stereo glasses are readily available and inexpensive, and attaining the stereo effect, which is highly effective, requires no additional auxiliary hardware.

4 THE VERTEBRATE ANALYZER: Mechanical modeling

The purpose of this section is to discuss the mathematics and algorithms that underlie the computer graphics produced by the VA. The code is open and modular so users have the option of using default algorithms, selecting alternates, or constructing their own. Our current defaults are described next.

4.1 Muscle fiber arrangement

Currently we offer two arrangements of muscle fibers, parallel and pinnate. In *Parallel* fibered muscles, the fibers run (in series) for the whole length of the muscle (Figure 9a), and attach to bones via tendons. Here, "x" and "y" represent the cross-sectional dimensions of the muscle, A represents the cross-sectional area of the muscle, F_n represents the force of a muscle fiber at a fraction "n" of its original length, "l" is the length of the muscle, and α is the angle of inclination of fibers to tendon (pinnate only). Fibers of *pinnate* muscles are typically shorter than the overall length of the muscle, and are inclined relative to the longitudinal axis of the muscle (Figure 9b) [1]. The respective forces that these muscle fibers can develop are shown in the following equations:

$$F_{\mathbf{par}} = (x\ y\ F_n)/\ A \tag{1}$$

$$F_{\mathbf{pin}} = (2\ x\ l\ F_n \sin\alpha\ (n^2 - \sin^2\alpha)^{1/2})\ /\ nA \tag{2}$$

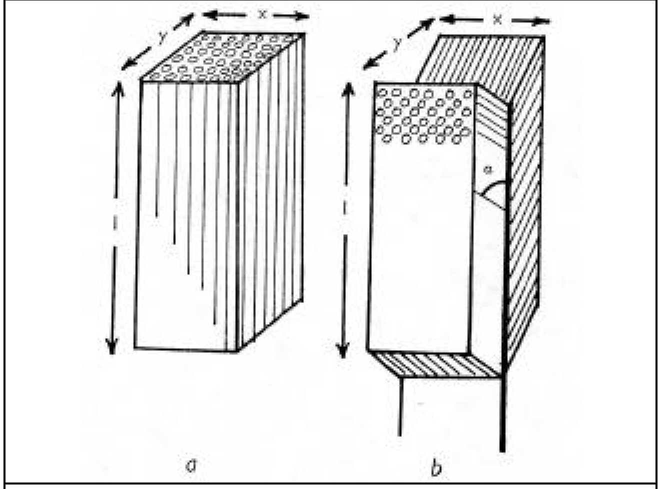

Figure 9: Parallel vs. Pinnate fibered muscles

4.2 Active fiber force

The force (tension) that a muscle exerts varies with the length at which it is held when stimulated [3]. Maximal tension is produced when the muscle fiber is approximately at its "slack" (resting) length. When the muscle fiber is contracted beyond resting length, the fiber tension declines slowly at first, and then rapidly. As fiber length increases beyond resting length, tension progressively decreases [6]. These relationships (shown in Figure 10) can be simulated during dynamic muscle force calculations with the VA, provided that various geometric and structural properties of the muscle (fiber diameter, number of fibers per bundle, angle of inclination for pinnate fibers, etc.), and the individual fibers that it contains, are known, or can be estimated and parameterized.

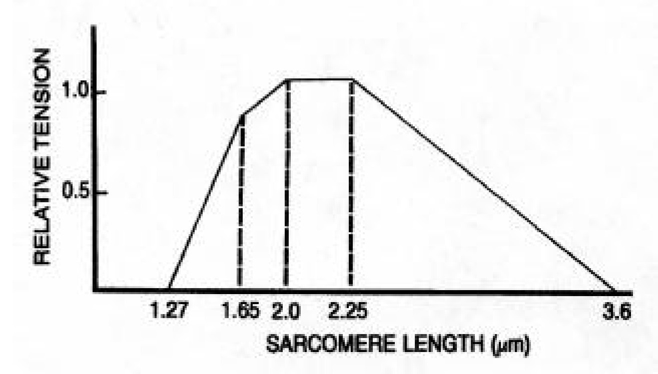

Figure 10: Active fiber force

4.3 Passive and total muscle force

To compute the total force in a bundle of muscle, one must consider more than the just-discussed active fiber force. Active tension in the muscle represents the tension developed by the contractile elements of the muscle, and its curve (Figure 11) resembles the curve for an individual fiber (Figure 10) [3]. Passive tension is present only when the muscle surpasses its resting length. The total tension present within a muscle, therefore, is the net sum of this active and passive tension. Clearly, just as with active fiber force, passive force is represented in the VA toolkit and can be fully user-parameterized.

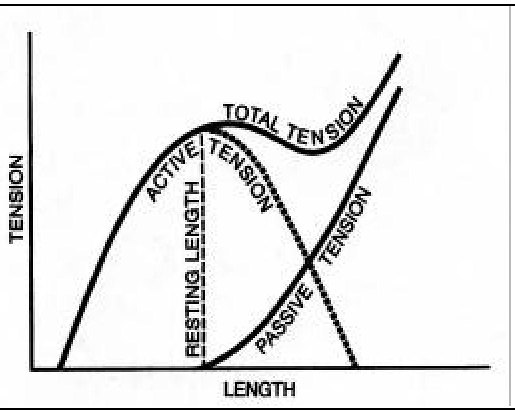

Figure 11: Active/Passive/Total muscle force

With an understanding of the VA toolkit, its features, functionality, intended utility, and a sampling of its underlying science, we can now briefly discuss methods by which we can calibrate, verify, and validate all of our digital models.

5 VERIFICATION PROTOCOL

Several verification methods are designed into this toolkit, one intrinsic and the other extrinsic to the program. The intrinsic method depends on simultaneous or serial analysis of mechanical/physiologic properties of component tissues (e.g., bone, muscle, tendon, ligament) under various conditions. Overloading of any one tissue (shown graphically and numerically) during a particular motion or simulated activity would indicate that the motion/activity is not possible, the tissue configuration on the model is incorrect, or that the mechanical/physiologic properties used in the program are not correct. All three sources can be investigated when working with extant vertebrates. In theory at least, a motion or activity of the animal of interest could be captured and compared to the motion or activity predicted or programmed using the VA. Again, in theory, the tissue configuration of the animal of interest could literally be dissected and used to model the virtual beast. Similarly, the mechanical/physiologic properties of the animal of interest could be more fully determined by physical experiments, and the new values then loaded into the VA. These then, are the extrinsic methods of verifying the protocol.

When new parameters (derived from extrinsic examinations) are plugged into the VA, the motion or simulated activity can be re-executed, at which time the “intrinsic” inter-component mechanical/physiologic comparison is reinitiated. When working with extant vertebrates at least, infinite adjustments in parameters are a potential. When a virtual motion or activity emulates with great fidelity that of the real vertebrate, then a user can program the VA to emulate another motion or activity. When the VA successfully emulates a number of related motions/activities without adjustments to parameters of underlying component tissues, then the user should have some confidence that the model is reasonably well “tuned”. Once tuned, a user can use the model to test hypotheses regarding how a component might function under a number of conditions, and hence gain understanding of how that component evolved.

6 CONCLUSIONS

The *Vertebrate Analyzer* aims to empower scientists to model, simulate and analyze biomechanical motion and constraints in an intuitive, 3D virtual environment. No tools currently exist that allow scientists to model skeletons, add muscle and other parameterized connective tissues, and “simulate” behaviors to assess the biomechanics of extant and extinct vertebrates.

The preliminary effort described in this paper is a natural extension of mature CAD technologies into domains that have yet to adopt them It is the aim of the authors to facilitate the incorporation of these mature technologies into new domains to empower users to model and validate hypotheses, designs, and reconstructions of vertebrates. The goal is to build the toolkit in stages, using the comparison of living and extinct big cats to test and validate the individual tools.

7 FUTURE WORK

There are three broad areas of future development of the toolkit that we currently envision: a) ease of use, b) breadth of modeling, and c) fidelity of calculations.

a) The toolkit is currently lacking rapid skeleton construction capabilities. The ability to quickly import and reconstruct basic skeletal structures from various sources - CT scans, VRML models, CAD models, etc., will be incorporated. Additionally, a more robust interface, including more detailed menus, more user-customizable parameters, and "wizard" type step-by-step guide will be added.

b) We intend to incorporate a far greater breadth of modeling constituents into the dynamic and mechanic calculations. In addition to basic bone, muscle, tendon, and lgament modeling, we will incorporate complex hinges, structural surfaces (such as fat and skin), and other higher detail physical structures to allow for greater flexibility and accuracy in the model.

c) Currently, the toolkit can handle fundamental primitive models of biomechanics. We intend to incorporate complex joints and hinges, deflection in hard material (such as bone), non-linear behavior in connective tissue, as well as a wide range of muscle types and behaviors. Additionally, the current constructs will be re-parameterized to allow for more complex models. Furthermore, finite element analysis techniques will be applied to the skull/mandible models to determine compression, tensile and shear stresses of these bony elements under different loading scenarios. Using observations of extant animal tissues, we expect to predict viability of different loadings, and hence evaluate hypotheses relating to function. Conversely, given incomplete fossils, but good knowledge of function, we should be able to predict reasonable forms using optimal design techniques.

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