Anatomy-based Kinematical Joint Model with Soft Connective Tissues*

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1. Introduction

The bodies of humans and other animals are articulated structures, usually supported by a more or less rigid skeleton. Such articulated structures are based on a hierarchical setup of joints, the elements where most of the movements take place or are constrained. Then, modeling joints is a key issue in human body modeling.

However, in human body animation, joint models are often poor simplifications of real joints. They are usually based on classical works in Robotics, where joints are rather idealized and not conceived to deal with many important biological issues. It is not crucial for Animation because the details of joint motion have little influence on global motion, and other animation techniques are able to mask imperfections. Other science domains, like Biomechanics, addressed the problem differently. Because of their specific interests, they have created models that describe better the lower level details of joint motion. But, in turn, they usually neglect visual and interactive aspects.

In this context, and to make clinical applications viable, a need arises of a joint model dealing with issues on both sides of the problem.

2. Approach

Our approach divides the problem into two parts to better treat its complexity. First, we define a kinematical joint model for the skeleton which parameters are estimated from motion analysis on optical motion capture and dynamic MRI data. Second, connective tissues (cartilage and ligament) are represented by a soft tissues model, which deforms following basic skeleton constraints.

2.1. Kinematical joint model

Computer Graphics literature on joint modeling presents various works. However, they either choose to simulate a specific type of joint, like shoulder or hand, or propose simplifications in joint representation. Schemes like H3D [1] or APJ [2] were presented in order to provide a mechanism to keep topological structure. Wilhelms [3] presents a simplified articulated skeleton that also support muscles and flexible skin surface of animals' bodies. Some other works are particularly focused on simulating specific, complex articulated parts of the body. Monheit and Badler [4] presented a spine and torso model applied in the Jack System. In a work very close to human anatomy, but focused on the human shoulder, Maurel and Thalmann [5] presented a model based on constraints of scapula movement relative to the thorax.

In our approach, the skeleton model represents the human body articulated system as a tree where joints correspond to the nodes of the tree. Organs like bones and cartilage caps are instantiated onto these nodes to give anatomical appearance to a human body part. Any generic joint of the model is able to describe any kind of relative motion between two or more adjacent segments of the body. Such motion can be given by: a) a rotation around one axis; b) a composed rotation

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around two or three axis; c) a translation in one to three Cartesian directions; d) rotations associated to translations; and e) an axis sliding on a parametric curve during rotation. One particularity of our model – (e) above – is an approach to solve the problem of a joint center or axis that presents a displacement during motion. As the sliding axis move along a *curved path*, we chose to represent it by a standard parametric curve in 3D space. To constrain the axis to slide on the curve, the angular parameter (normalized within the range of motion) is mapped into the curve equations to determine its respective point on it. More details in [6].

2.2. Soft tissues model

Existent methods applied to bio-tissues deformation are time consuming – like Finite Elements Method (FEM), or not sufficiently faithful to reality – like classical mass-spring and particle systems. Others, less known, are purely conceptual models proposed by biomechanics researchers; they do not aim at visual or interactive applications. Nevertheless, some interesting results can be found that are based on hybrid and adaptive methods [7, 8]. They present improvements on visual appearance and execution time. However, the price for such improvement is the simplification of the complex properties of biomaterials by means of assumptions that decrease the results precision to levels not acceptable for a number of applications. Still, some of these methods work well when applied to one kind of deformation, but present important drawbacks when the deformation happens differently. One example is the method proposed by Debunne et al. [9] to compute real-time FEM by adaptively refining the resolution of the set of elements in the regions where the degree of deformation increases. This works fine for objects that present much localized deformations, but not for the ones that present deformations of large extent, like muscles and ligaments.

Our approach to fulfill the mentioned limitations is based on a discrete method [10] inspired on subsystems of the real tissue (cellular, molecular, etc.). We exploit a generalized mass-spring model, where mass points are, in fact, spherical mass regions called molecules. Elastic forces are then established between molecules by a spring-like connection.

Our main contribution to this model is in the integration of properties of real biological materials to define the stiffness of its spring-like connections. The rheological standard to define the elasticity of a material is Young's modulus. Young's modulus is a property of a material, not of an object. So, it is independent of the object's shape. However, when one discretizes an object by a set of springs, the stiffness k of every spring must be proportional to the fraction of the volume of the object it represents. It means that if a cube of side l_0 is compressed by a force F, it should shorten in the direction of the force, of the same elongation variation Δl both if it is represented by only one spring and if it is discretized by n springs. Eq. 1 establishes the Young's modulus E from: the knowledge of the elongation variation Δl; an applied force F; the length of the object in rest conditions l_0; the cross-sectional area of the object A. Applying Eq.3 iteratively in the simulation loop we minimize the difference between the obtained and the aimed E increasing or reducing the value of k's accordingly. See more details in [11]. The multiphase feature is being added to the method, with which we expect to obtain a viscoelastic behavior.

$$E = \frac{F \cdot l_0}{\Delta l \cdot A} \tag{1}$$

3. Hip Joint: a Case Study

3D boundary models of organs (meshes) are reconstructed from segmented MRI data in a parallel work [12]. The 3D meshes representing bones are considered rigid bodies and are used as is. Cartilage meshes have their volume discretized into a number of spherical regions representing the molecules of the deformation model (Fig. 1). The vertices on the surfaces of the cartilage caps

are then linked to the neighborhood of underlying molecules with weights according to distances, and follow the model deformations. Surface molecules are used to generate contact avoidance forces. These forces, that are calculated using a penalty method, are consequently used by the soft tissues model to produce deformation. Global motion is generated using the kinematical model. Finally, stress is calculated relating internal forces with their area of actuation. The last step is using color mapping for effective visualization of these values (fig. 2). Interactive visualization techniques allow free exploration of the simulation setup.

4. Summary

We have presented the combination of a deformable model for biological soft tissues with an anatomy-based kinematical model of human joints, which we used to simulate motion on the hip joint and evaluate stress on cartilage surfaces. The model demonstrated its ability to handle the stress computation for two coupled surfaces with interactive user control. Associated to a palette of visualization tools, the user interaction permits easily highlighting regions subject to high stress, hence to pathologies.

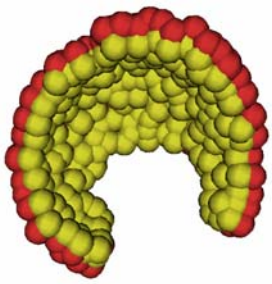

Fig. 1 – discretized cartilage cap.

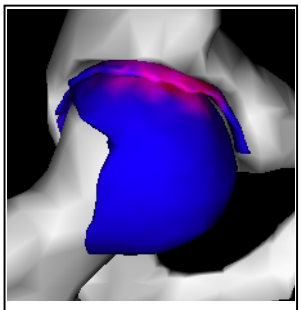

Fig. 2 – stress on cartilage surface.

At this moment, the deformation model is linear elastic and isotropic. We are working to improve it by adding viscous components and considering fibers orientation in the tissue. We aim at making it a viscoelastic, anisotropic and heterogeneous model, which is closer to the nature of the real biological tissues. It is crucial to support the envisaged medical applications.

5. References

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