

FAST 3D MUSCLE SIMULATIONS USING A NEW QUASISTATIC INVERTIBLE FINITE-ELEMENT ALGORITHM

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INTRODUCTION

Computer models of the musculoskeletal system generally represent muscle geometry using a series of line segments [e.g., 2]. This simplification limits the ability of models to accurately represent the paths of muscles with complex geometry and assumes that moment arms are equivalent for all fibers within a muscle (or muscle compartment). Recently Blemker and Delp [1] demonstrated that three-dimensional (3D) finite-element models of muscle can improve representations of muscles with complex geometry, like the gluteus maximus, which has broad attachments and wraps around underlying structures.

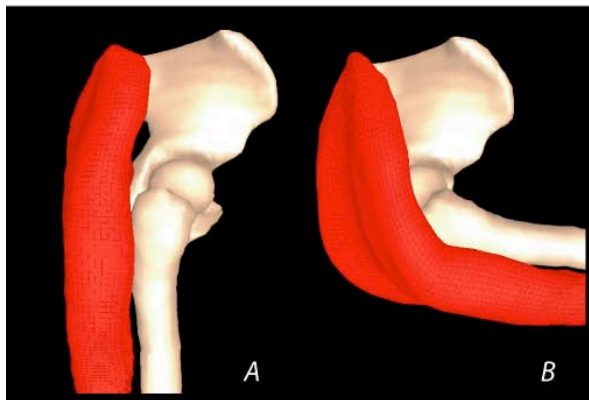
3D muscle modeling has the potential to improve our ability to represent complex musculoskeletal structures, including the shoulder and neck. However, the applicability of 3D muscle modeling to these problems is limited due to computational expense. Solutions take over three hours for one or two muscles using a standard nonlinear finite-element formulation. Recently, Teran et al [5] introduced a new quasi-static invertible finite-element algorithm that allows for major improvements in simulation times over traditional techniques. The goal of the present work is to evaluate the accuracy of this new finite-element solution strategy for representing skeletal muscle behavior. To do this, we created a 3D model of the gluteus maximus (a complex muscle that has broad attachments and wraps around underlying structures), simulated the motion of the muscle through hip flexion-extension using new the formulation as well as the standard formulation, and compared the results from the two methods.

METHODS

A solid finite-element mesh representing the gluteus maximus muscle and triangulated surface meshes representing the pelvis and femur bones were created from magnetic resonance images. The muscle's underlying fiber geometry was modeled by fitting a pennate fiber geometry template to the 3D model (see [1] for details). A transversely-isotropic, incompressible, hyperelastic constitutive model was used to describe the stress-strain relationship in the muscle tissue. Flexion motion about the medial-lateral axis of the hip joint was prescribed as the boundary conditions, and penalty-based formulations were used to resolve muscle-bone contact. We ran simulations using the new quasi-static invertible algorithm (described below) as well as in NIKE3D, a nonlinear implicit finite-element program [4].

The new finite-element algorithm provides two significant improvements over the existing techniques. First, elements are allowed to invert by computing robust finite-element forces with the invertible framework described by Irving et al [3]. Typically inverted elements are not allowed during a simulation process, which greatly hinders the generation of a solution. This method relaxes this constraint, while still enforcing the final solution to have all non-inverted elements. Secondly, a fast conjugate-gradient solver is used for each iteration by ensuring that the stiffness matrix is positive semi-definite. This is accomplished by analyzing the eigenstructure of the element elasticity tensor and modifying the negative values that correspond to spurious local directions of the decrease in hyperelastic potential. Full details of the algorithm can be found in [5].

Quasistatic Invertible Results



NIKE3D Results

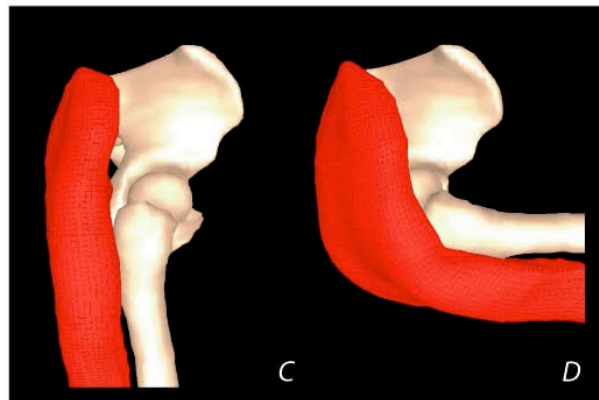


Figure 1. Results from the new quasistatic invertible formulation (A,B) compare well with NIKE3D results (C,D) for simulations of the gluteus maximus through hip flexion-extension. The NIKE3D simulation required 4 hours of computation time on an SGI Octane; in contrast, with the new algorithm, the solution was achieved in 50 minutes on a Dell PC.

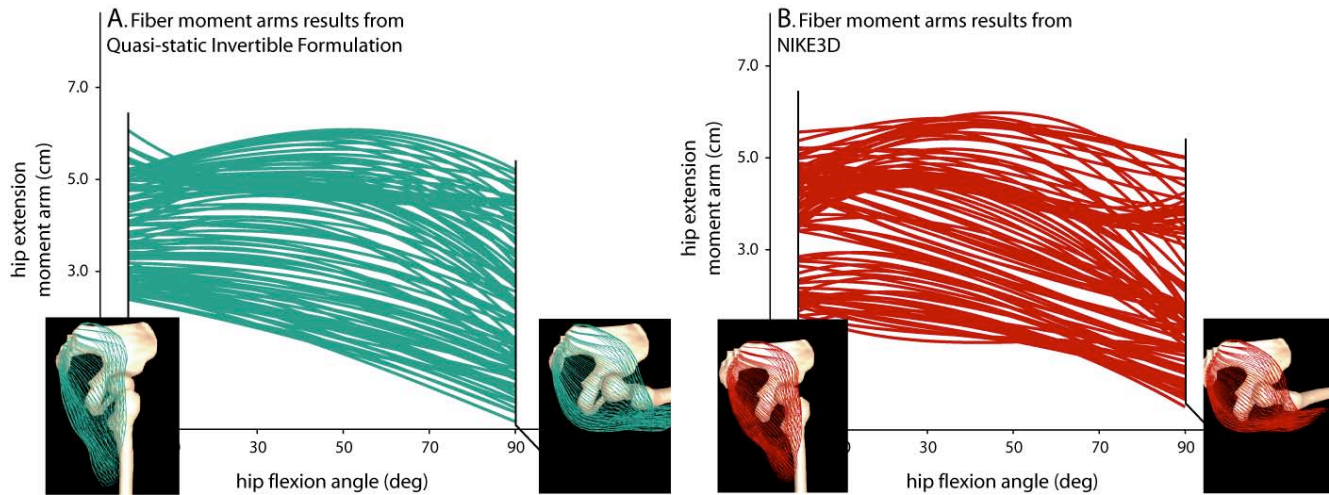


Figure 2. Gluteus maximus fiber moment arm results from the quasi-static invertible solution (A) compare well with the fiber moment arms from NIKE3D (B). These models allow us to characterize the geometry of complex muscles and explore the variation in moment arms across fibers within a single muscle.

METHODS continued

We characterized the difference in overall shape change predictions of the two solutions by calculating the distance between the surfaces in the flexed position. We also calculated individual fiber lengths as a function of joint angle, and the resulting fiber moment arms for both solutions.

RESULTS

The NIKE3D simulation required 4 hours of computation time on an SGI Octane (Dual MIPS R12000 Processors). In contrast, with the new algorithm, the solution was achieved in 50 minutes on a Dell PC (2.79Ghz Xeon Processor).

The new algorithm predicted similar changes in shape (Fig. 1), fiber lengths, and moment arms (Fig. 2) to those predicted by the standard finite-element method. The average, minimum, and maximum difference between the two muscle surfaces in the flexed position were 3, 0, and 6 mm, respectively. Comparatively, we previously reported NIKE3D muscle simulations to be within 5mm of image data [1]. The average moment arm was 4.7cm for the new formulation and 4.8cm for NIKE3D. These results indicate that the new method robustly predicts muscle geometry – both methods capture the variation in fiber excursions and moment arms across the muscle.

CONCLUSIONS

Three-dimensional muscle models offer the potential to improve our ability to represent complex muscle geometry and architecture and enhance the accuracy of models of the musculoskeletal system for a wide variety of applications.

The results presented in this paper suggest that the new, quasi-static invertible finite-element formulation can dramatically speed up 3D muscle simulation times, while providing reasonably accurate results. We expect that the improvements in speed will be more dramatic for simulations for many (five or more) muscles, as once there are many muscles with a lot of contact, element inversion becomes a major issue.

Once rigorously validated, this method will allow for 3D simulation of many muscles together and provide a new paradigm for exploring normal and abnormal muscle function in complex musculoskeletal structures.

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