EFFICIENT, ACCURATE, AND CUSTOM MODELING OF BIOMECHANICAL JOINTS

Ajay Seth, Michael Sherman and Scott Delp

Bioengineering Department, Stanford University, California, USA

email: : aseth@stanford.edu, web: www.stanford.edu/group/nmbl/

INTRODUCTION

Biomechanisms rarely exhibit simple motion characteristics of mechanical joints such as sliders, pins, and ball–and-sockets. Current multibody-dynamics formulations [1] exploit the simplicity of mechanical joints in their assembly of system equations of motion. Consequently, the modeling of a biomechanical joint first employs a mechanical joint with more degrees-of-freedom (dofs) to enable the full biomechanical motion and then requires constraints to keep the movement on a biomechanical path. For the purposes of simulation of biomechanisms, this approach is: 1) inefficient, because it does not yield the minimum number of system equations, 2) prone to inaccuracies, since constraints cannot be satisfied exactly, and 3) difficult to customize, when general (complex) constraints require custom code. To address these difficulties, we present a new formulation to reduce the number of system equations, exactly capture permissible motion between two bodies, and make it possible and easy for the user to define.

METHODS

A novel multibody-dynamics formalism– called a mobilizer– was developed to strictly grant motion to a body and to map from internal coordinates (a minimum set of dofs) to a permissible motion-space in the 6-dimensional (6-d) space between one body and another. For example, the permissible motion of a slider joint is a single axis (1-dof) in the motion-space between two rigid bodies. A mobilizer, however, also maps coordinates along non-axial paths, such that motion across multiple axes are governed by one or more mobilizer coordinates. The mobilizer mapping, that dictates how the body moves in 6-d, requires functions to be twice differentiable with respect to the mobilizer coordinates. A recursive Newton-Euler method [1] was formulated in terms of the mobilizer coordinates and their derivatives to provide a minimum set of system equations of motion.

Two types of custom biomechanical joints were tested. First, analytical functions of point motion on an ellipsoid surface were used to create an ellipsoid mobilizer, which was applied to model scapular motion on the surface of the thorax [2] (Figure 1). Second, splines of tibial translations as functions of knee flexion [3] were used to couple knee translations in a 1-dof knee joint (Figure 2). Mobilizers were implemented in the Simbody™ dynamics solver. Motion and performance were compared to a conventional approach of employing extra dofs and enforcing kinematic constraints.

RESULTS AND DISCUSSION

Table 1: Performance of mobilizers vs. constrained joints.

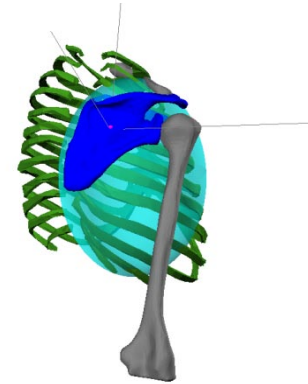| Method	Normalized Simulation Time		Tolerance
	Shoulder	**Knee**	
Mobilizer	1.01	1.98	< 1.0e-14
Constraints	10.37	7.17	< 1.0 e-4
Speedup ($\times$)	**10.3**	**3.6**	

Figure 1: A 3-dof scapulo-thoracic joint enabled by an ellipsoid mobilizer approximating the surface of the thorax.
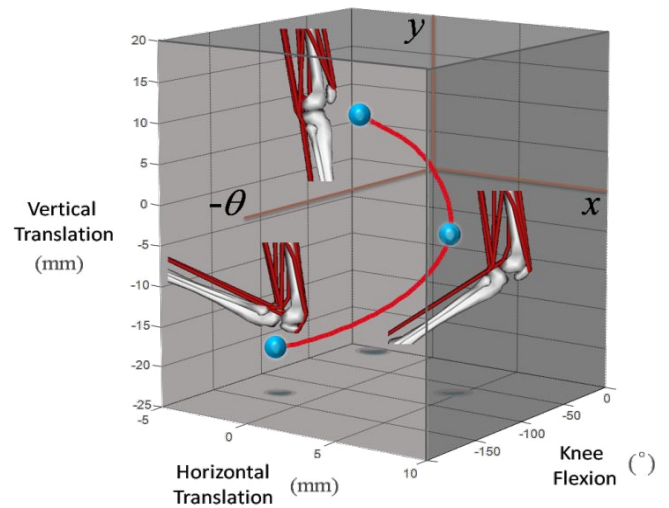

Figure 2: A 1-dof knee joint model where translations (x, y) are specified by user-defined functions of knee-angle (θ).

CONCLUSIONS

Mobilizers are a powerful new way of modeling biomechanical joints because they efficiently map from convenient model coordinates (e.g. knee angle) to spatial movement. These mappings are mathematically equivalent to conventional constraints but require fewer coordinates and satisfy the biomechanical motion-space exactly. Therefore, mobilizers simultaneously reduce computational costs and bolster simulation accuracy compared to mechanical joints. Furthermore, mobilizers can be specified by user-supplied functions such as splines, which provides a direct means of defining joint behavior from experimental data. Custom joints are included in OpenSim [4] available at www.simtk.org.

REFERENCES
1. Jain A, et al. *J Comp Phys.* **106**:258-268, 1993.
2. Van der Helm FCT. *J Biomech.* **27**:527-55, 1994.
3. Delp SL, et al. *IEEE Trans Biomed Eng.* **37**:757-67, 1990.
4. Delp SL, et al. *IEEE Trans Biomed Eng.* **54**:1940-50, 2007.