

BIOMEX 2 - an environment for complex biomechanical simulations

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1 Introduction

Dynamical simulations of biomechanical models within a rigid body framework are becoming more and more important. In addition with increasing computer power the models themselves become more complex, i.e. they include many segments, muscles, sensors and numerically costly control schemes. With BIOMEX2 we present a software package, specifically designed for efficient simulations of such complex biomechanical systems. BIOMEX2 is written entirely in C and is tested under Linux on Intel and Dec-Alpha architectures. Fig. 1 shows its modules.

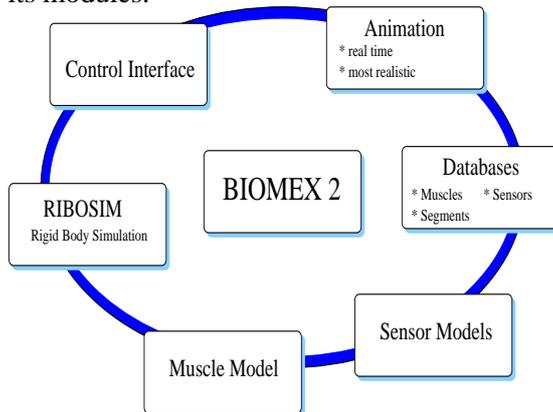


Fig. 1: Modules of the BIOMEX2 software package

joint in these coordinate systems, and the type of joint between two articulating bones (see Fig. 2). In addition the data of human muscles with 608 individual muscle paths are stored in the muscle database (see Fig. 3). For simulation purposes the number of the segments, the composition of the segments, and the number of muscles can be individually chosen according to the movements, thereby adapting the processing load to the complexity of the task.

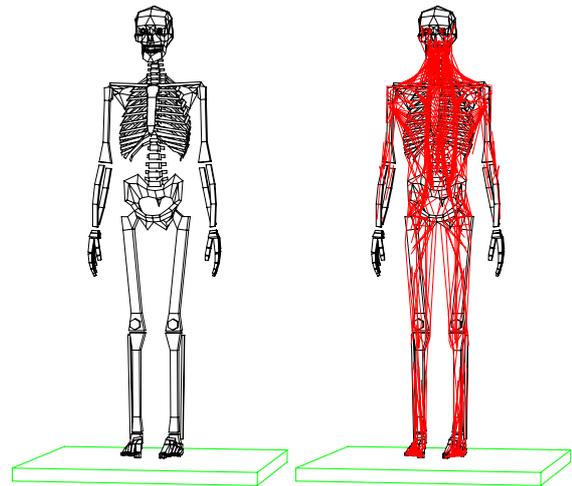


Fig. 2: Human skeleton, Fig. 3: Human muscle-comprising 220 differentculo-skeletal system with 608 individual muscle paths.

2 Description of the BIOMEX2 package

2.1 Databases

Databases are available for both human muscles and segments. The local coordinate systems of 220 bones is defined as is the localisation of the

2.2 Sensor models

A variety of biological and technical sensors can be accessed from a library, including tendon forces, reaction forces, segmental and angular accelerations and a model of the human vestibular organ.

2.3 The muscle model

For a realistic description the muscle geometry must be complemented by a model of the non-linear muscle dynamics. In our simulations we use a two stage SISO-model [1] of the Hill type, which includes a prediction of muscle forces for positive velocities, i.e. when the muscle is actually lengthening during activation.

2.4 RIBOSIM, a rigid body simulation tool

2.4.1 The general equations of motion

The rigid body system is internally represented in natural coordinates [2], resulting in the descriptor form of the differential algebraic equations

$$\begin{aligned} M\ddot{q} + G^T\lambda &= f & \text{Dynamic eq.} \\ g(q) &= 0 & \text{Constraint eq.} \end{aligned} \quad (1)$$

M is the systems mass matrix, G is the Jacobi matrix of the constraints, q are the systems' coordinates, λ are the Lagrange parameters and f are the external forces. Two differentiations of the constraint equations with respect to time lead to

$$\begin{aligned} M\ddot{q} + G^T\lambda &= f \\ G\ddot{q} &= \gamma \end{aligned} \quad (2)$$

with $G = g_q = \frac{\partial g}{\partial q}$ and $\gamma := -\dot{q}g_{qq}\dot{q}$.

2.4.2 The structure of the rigid body system

Rigid body systems are represented in form of a tree. Each node of the tree can be a normal segment or a closed loop (see above), resulting in a hierarchical ordered system (see Fig. 4).

Intersegmental connections are established by additional constraint equations, resulting in differential equations of the i -th segment in a tree [3] of

$$\begin{aligned} M_i\ddot{q}_i + G_i^T\lambda_i &= f_i - \sum_{\text{succ. } j} C_{n_j}\lambda_{n_j} \\ G_i\ddot{q}_i &= \gamma_i + C_i\ddot{q}_{\text{pre.}} \end{aligned} \quad (3)$$

The sum is over all successors of the i -th segment. C_{n_j} is the part of the Jacobi matrix of the intersegmental constraints that contains the partial derivations concerning the coordinates of the more proximal segment.

The usage of natural coordinates in connection with a description of the bodies in the coordinate system of the base of their inertial tensor results in 12-dimensional, diagonal mass matrices of the single bodies.

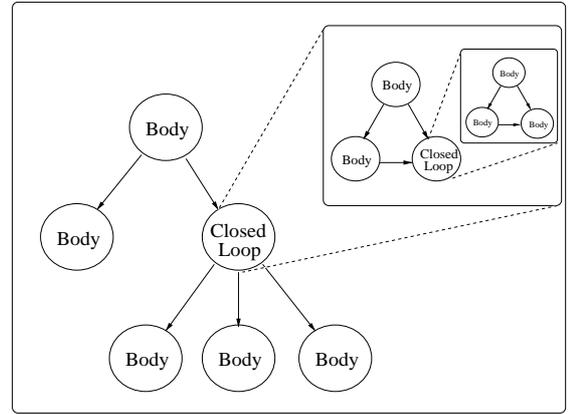


Fig. 4 Hierarchical tree-structure of multi body systems.

The algorithm to solve for the left hand side of the system (3) makes use of the special topology of the tree-structure, resulting in a $O(\text{number of nodes})$ -class.

2.4.3 Closed loops

Closed kinematic loops have to be opened at an arbitrary intersegmental connection. The constraints g_{loop} , responsible for closing the loop have to be taken into account separately. I.e. denoting by T the (sub)system matrix with chain configuration, by $y := \begin{pmatrix} \ddot{q} \\ \lambda_{\text{loc}} \end{pmatrix}$ the accelerations and local multipliers and by $h := \begin{pmatrix} f \\ \gamma_{\text{loc}} \end{pmatrix}$ the local exter-

nal forces and local curvature information, the system may be written in the same form as (3)

$$\begin{aligned} T\ddot{q} + G_{\text{loop}}^T \lambda_{\text{loop}} &= h - \sum_{\text{succ. } j} C_{n_j} \lambda_{n_j} \\ G_{\text{loop}} \ddot{q} &= \gamma_{\text{loop}} + C \ddot{q}_{\text{pre.}} \end{aligned} \quad (4)$$

allowing for a recursive algorithm to efficiently solve the complete system of equations for all levels of the tree hierarchy.

2.4.4 Integration

The user can choose from a library of integrators, which comprises currently a Runge-Kutta-Fehlberg 4/5 method with variable stepsize and an Adams-Bashford-Moulton method with variable stepsize and order.

The equations of motion are integrated either directly or by inverse dynamical integration [4] with the result of less factorizations of the system matrix.

Due to the algebraic constraints that were differentiated twice, integrating the system (3) leads to a drift of the numerical solution from the constraint manifold. This is remedied by projection technique using Moore-Penrose Iteration [5], resulting in an even more accurate solution.

2.4.5 Contact points - discontinuities in the constraints

Each segment can be assigned an arbitrary number of contact points. Off the ground, their contact conditions have to be monitored. Each new contact of a segment, that was without contact before, results formally in a closed loop with its more proximal node in the graph. During contact the respective constraint forces decide about the break-up of the contact point.

The change in the number of points contacting the ground results in a change - or discontinuity - in the number of constraints.

These discontinuities are detected by localizing the zeros of respective switching functions

by an integrator with interpolation capabilities. After each integration step it is checked, whether the sign of any switching function has changed. If this is the case, the integration process is restarted with the new set of constraints just after the switching point.

2.4.6 Animation

There exist two interfaces for animation. One for realtime purposes and one for a most realistic output. The realtime interface allows for a visual supervision of the simulations in the X-Windows System. The realistic output is achieved using the external raytracer POV-Ray.

2.4.7 Control Interface

For programming a controller, the BIOMEX2 package provides an interface that gives as output the sensor data and expects as inputs either joint torques or muscle activations.

3 Examples and Tests

The software package is currently (Feb. 1999) tested with standing/walking paradigms for different models. Among others are simulations of a simple walking machine with 2 inner degrees of freedoms and one point contact on either foot and simulation experiments of the stance/gait-control of a paraplegic patient with an artificial controller for the lower limbs. Both will be demonstrated at the conference.

Literatur

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