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APPLICATIONS OF EFFICIENT FORWARD DYNAMICS SIMULATION IN BIOMECHANICS

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Abstract: Optimizing and analyzing human motion is a very complex task. We here present results for the efficient forward dynamics simulation which is prior to inverse dynamics simulation in terms of general merit functions and its flexibility with respect to different tasks such as analysis of measured human motion or prediction of free goal oriented human motion. Efficient multibody system dynamics calculation methods as well as efficient numerical optimal control techniques are used and lead to a forward dynamics optimization approach being two orders of magnitude more efficient than existing approaches. Results are presented for a kicking motion. Currently, jumping and control of a bio-inspired muscle driven humanoid robot are investigated.

Introduction

Biomechanical systems are very complex due to the absence of a unique assignment of actuation and resulting motion: one joint is driven by more than one muscle (even often more than only two antagonistic muscles) and there are muscles that span and influence more than one joint. Furthermore, a certain motion goal like reaching a certain position may be realized by an infinite number of joint motions. The subject of this paper is how to overcome these two redundancy problems and calculate muscle activations for measured or free (goal oriented) human motions efficiently using general biodynamical human models, where the latter in fact means prediction of human motion.

Biodynamical Model

The human body is modelled as multibody system in two or three dimensions including mass, center of mass and inertia of all limbs, position and orientation of the joints and boundary constraints for the joint angle range. This leads to the well-known differential equations of motion of general multibody systems:

$$\mathbf{M}\ddot{\mathbf{q}} = \boldsymbol{\tau} - C(\mathbf{q},\dot{\mathbf{q}}) - G(\mathbf{q}) + \mathbf{J}_c^T \mathbf{f}_c,$$

where $\mathbf{q},\dot{\mathbf{q}}$ are the joint angles and velocities, τ are the total torques, $\mathbf{M}$ is the mass matrix, $C(\mathbf{q},\dot{\mathbf{q}})$ are the Coriolis and centrifugal forces, $G(\mathbf{q})$ are the gravitational forces, and $\mathbf{J}_c^T \mathbf{f}_c$ are the contact forces.

The calcium ion concentration γ (which directly leads to force generation in the muscle) lacks behind muscle activation u. Differential equations are used to describe this relation:

$$\dot{\gamma} = c_1(c_2 u - \gamma),$$

with appropriate parameters c_1 and c_2. The relation between calcium ion concentration and muscle force is algebraic. Figure 1 shows the relation between activation, calcium ion concentration and muscle force for some example parameter values.

The muscles are modelled in a Hill-type way; force-velocity-(FV) and tension-length-(TL)-relations describe the functional capabilities of the muscles, cf. Figure 2. Those relations are given by parameterized algebraic equations.

Muscle paths are modelled to get the right working range of the FV- and TL-relation and to get the right line of action and point of actuation of the muscles. Properties of tendons and ligaments are taken into account by passive torques.

Several general merit functions Φ for distribution of the total joint torque to the muscle forces are of interest, e.g. minimization of the sum of all muscle forces, where each of the forces may be scaled by diameter of the muscle or by the torque to be applied to the joint, see [10]:

- $\Phi = \sum_{i=1}^{N} F_i^m$ (minimum sum of muscle forces),
- $\Phi = \sum_{i=1}^{N} (F_i^m / q_i)^3$ (muscles that have higher cross-sectional area and thus can exert higher forces must exert higher forces),
- $\Phi = \sum_{i=1}^{N} (F_i^m / M_{\max})^3$ (muscles that are attached to joints where high torque is needed must exert higher forces),

where F_i^m is the muscle force of the i-th muscle, q_i its cross-sectional area, $M_{\max}$ is the maximum torque required at the respective joint and N is the number of muscles. With our approach any general merit function may be investigated.

The models are validated by comparing the optimization results with data of real human data such as EMG measurements or joint angle trajectories. Once having validated the model and having found which merit function applies in human motion, it is possible to predict motions.

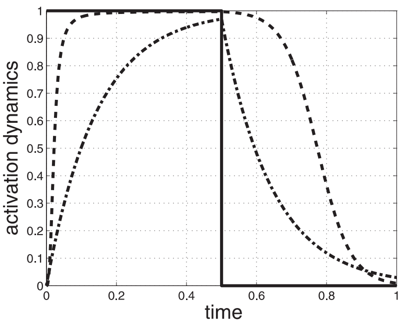

Figure 1: Calcium ion concentration (dotted line) lacks behind muscle activation (solid line) and directly leads to force generation (dashed line).

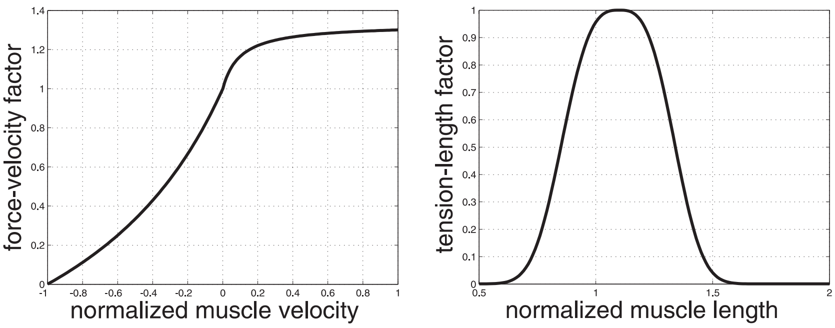

Figure 2: Hill-type muscle characteristics: Force velocity relation (left) and tension-length-relation (right). Both relations give a factor that is to be multiplied with the maximum isometric force and the muscle activation to get the actual muscle force.

Forward vs. Inverse Dynamics Simulation

The problem to be solved may be stated as: minimize a suitable merit subject to the multibody system and muscle activation system of differential equations and nonlinear and boundary constraints. Two generally different approaches exist for solving it: inverse and forward dynamics calculations. While inverse dynamics calculation directly concludes from the joint motion to the muscle activations by some specific assumptions on the model only [6], forward dynamics approaches solve the optimization problem of adjusting the muscle activations so that the resulting motion (here the forward dynamics calculations are involved) best fit the given (measured) motion.

More precisely, the target is to find control vectors $\mathbf{u}(t)$ (and thus also state vectors $\mathbf{x}(t)$) that minimize some objective function

$$J = \varphi(\mathbf{x}(t_f), \mathbf{x}, t_f) + \int_0^{t_f} L(\mathbf{x}(t), \mathbf{u}(t), t)\,dt,$$

which consists of a scalar part (which may involve the state at final time t_f, all states and the final time) and an integral part (which may involve all states and controls). This objective function is minimized subject to constraint, which may consist of a system of nonlinear ordinary differential equations

$$\dot{\mathbf{x}}(t) = \mathbf{f}(\mathbf{x}(t), \mathbf{u}(t), t),$$

initial and final values

$$\mathbf{r}(\mathbf{x}(0), \mathbf{x}(t_f), t_f) = \mathbf{0},$$

and nonlinear state and control constraints

$$\mathbf{g}(\mathbf{x}(t), \mathbf{u}(t), t) = \mathbf{0},$$

where a special case of the latter are box constraints (simple lower and upper bounds for the states and controls).

Inverse dynamics approaches currently are the most efficient numerical methods but they have the drawback that they are directly applicable only to the problem of analyzing a given motion; forward dynamics approaches also can handle the problem of optimizing goal oriented motions (i.e. predicting human motion) for validated models. The assumption of specific merit functions in inverse dynamics approaches does not allow considering general merit function of interest as it is the case with forward dynamics simulation.

Currently, forward dynamics approaches are based on control parameterization where only the controls are discretized; the states are obtained by numerical integration of the differential equations of motion. Repeated evaluations are needed to obtain gradients for optimization which leads to high computational effort. Our approach is based on discretizing both the controls and the states and thus solving the differential equations of motion simultaneously to the optimization [7], which is more efficient.

Dynamics Algorithms and Optimal Control Techniques

The two main numerical tasks with the forward dynamics approach are computing of the forward dynamics and solving the optimal control problem.

For only few degrees of freedom, the systems of differential equations of motion may be stated in closed form. For larger systems, numerical methods are used. We use the Articulated Body Algorithm (ABA) [1], which is a recursive algorithm of linear order w.r.t. the number of joints and shows high modularity for different components of the model which allows an efficient object oriented implementation [3]. The contact case may be handled and gradient information that may be useful for optimization may be calculated at low computational cost.

The optimal control problem is solved using the direct collocation method DIRCOL [8]. The states and the controls are discretized by piecewise polynomials and thus the optimal control problem is transformed into a nonlinear constrained optimization problem (NLP), where the parameters to be optimized in the NLP are the coefficients of the piecewise polynomials of the state and control approximation. The NLP is solved using efficient SQP method SNOPT [2]. By this descretization of both the states and the controls, the system of differential equations is solved simultaneously to the optimization. DIRCOL allows treatment of any kind of constraints and successive grid refinement.

Applications

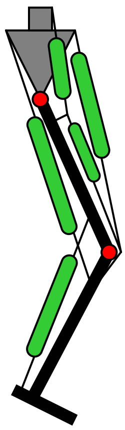

Figure 3: Leg model [9]

As a first application of the method, the kicking motion from [9] was chosen. The task is to find a kicking motion, i.e. the motion of the leg from a given initial posture to a final posture in minimum time. The objective function is thus chosen to be:

$$J = t_f .$$

The planar leg model consists of two joints and five muscle groups, cf. Figure 3. The resulting optimal control problem comprises two states for each of the joint angles, two states for the joint angle velocities and five states for the calcium ion concentration in the muscles. The muscle activations of the five muscle groups are the controls. The complete state vector is thus given by

$$x = \begin{pmatrix} q_1 \\ q_2 \\ \dot{q}_1 \\ \dot{q}_2 \\ \gamma_1 \\ \vdots \\ \gamma_5 \end{pmatrix} = \begin{pmatrix} \text{hip angle} \\ \text{knee angle} \\ \text{hip velocity} \\ \text{knee velocity} \\ \text{ca ion concentration muscle 1} \\ \vdots \\ \text{ca ion concentration muscle 5} \end{pmatrix}$$

and the control vector is given by

$$u = \begin{pmatrix} u_1 \\ u_2 \\ u_3 \\ u_4 \\ u_5 \end{pmatrix} = \begin{pmatrix} \text{activation of muscle 1} \\ \text{activation of muscle 2} \\ \text{activation of muscle 3} \\ \text{activation of muscle 4} \\ \text{activation of muscle 5} \end{pmatrix} .$$

To make the model perform a kicking motion, the initial and the final values of the hip and knee angles are enforced as boundary conditions for the starting time t_0

$$q_1(t_0) = 0.1,$$
$$q_2(t_0) = 0.15$$
$$\dot{q}_1(t_0) = \dot{q}_2(t_0) = 0$$
$$\gamma_1(t_0) = \ldots = \gamma_5(t_0) = 0$$

and for final time t_f

$$q_1(t_f) = 0.8$$
$$q_2(t_f) = -0.05$$
$$\dot{q}_2(t_f) = 0.$$

The velocity on the knee angle is constrained to zero to avoid to high extension of the knee. Inequality constraints are imposed to the states and controls to model geometric constraints and the box constraints on the activation rates and calcium ion concentrations:

$$0 \le q_1 \le 1.5$$
$$-0.05 \le q_2 \le 1.5$$
$$0 \le u_i, \gamma_i \le 1, i = 1, \cdots, 5.$$

As a starting solution, linear interpolation of initial and final values are used if known and 0 otherwise. More details may be found in [7].

Discretization of the states and controls on a grid of 60 grid points leads to a NLP with 531 variables and 829 nonlinear constraints which is solved in about 6 sec on a 1700 MHz+ Athlon computer, which is two orders of magnitudes faster than current methods for forward dynamics optimization for exactly the same problem. The resulting joint motions match those observed in real human kicking very well (cf. Figure 4). The activations may be found in Figure 5. Although there is no measurement data available, the activations seem reasonable. Consider e.g. muscle group 4 (Hamstring group) which is responsible for flexion of the knee. It is not activated because the knee mainly is extended.

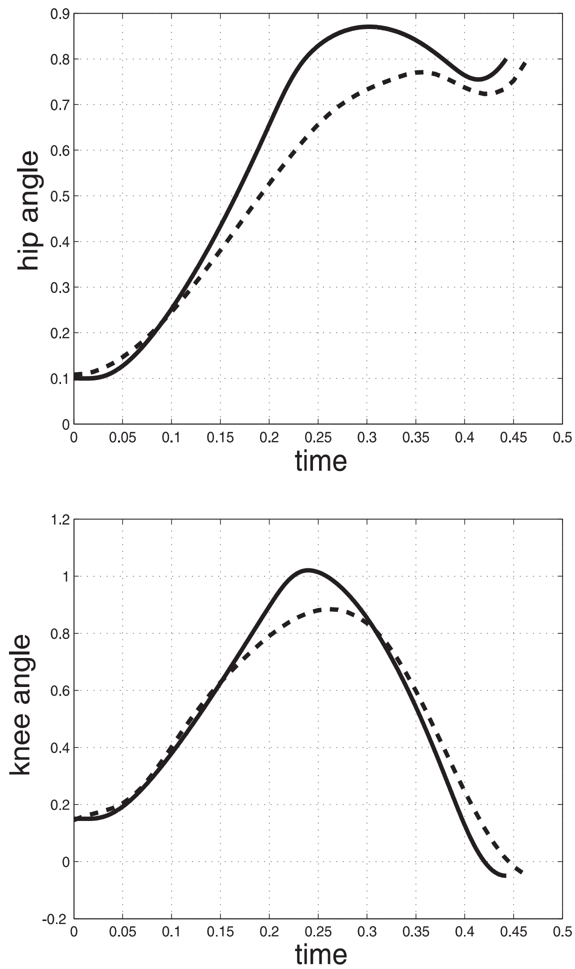

Figure 4: Joint motion of the hip (left) and the knee (right). Solid line is obtained from optimization, dashed line a measurement of real human kicking.

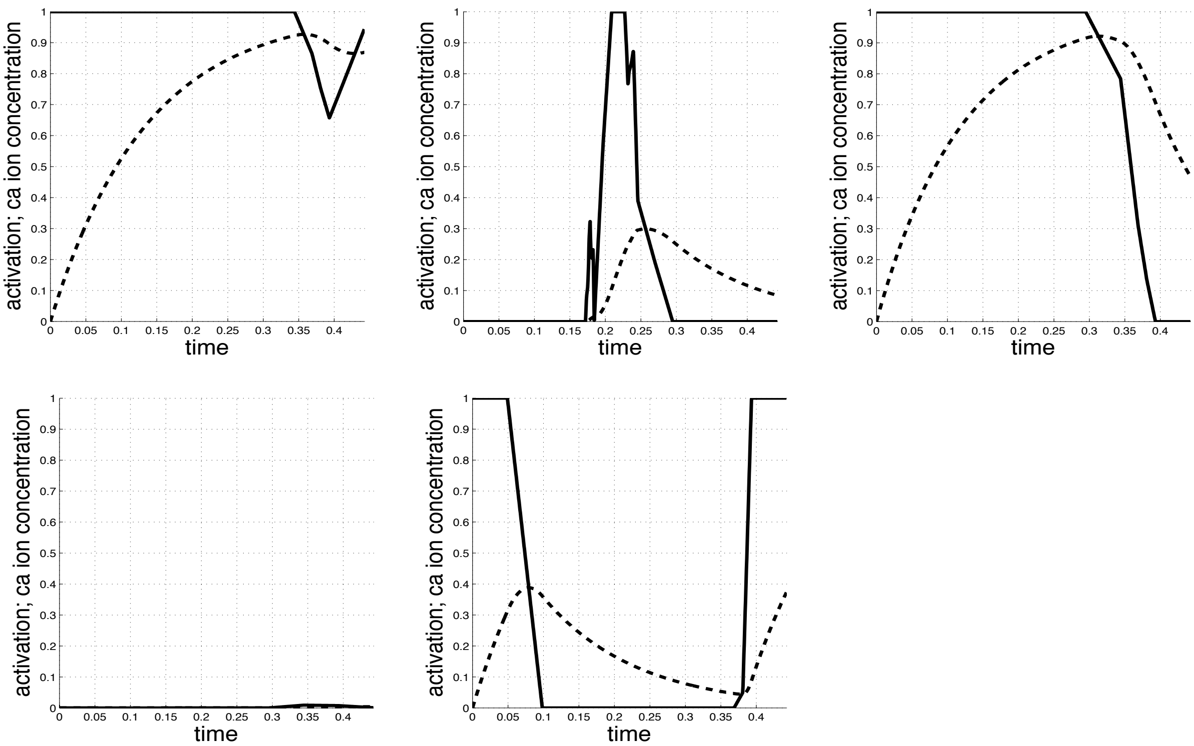

Figure 5: Computed muscle activations (solid line) and computed calcium ion concentrations (dashed line) for the five muscle groups (time optimal kicking)

Conclusions and Outlook

Our approach for forward dynamics simulation and optimization can reduce the computational effort by two orders of magnitude. We verified our approach and validated the model by a simple example. Current work includes the extension to more complex models such as for jumping, where, if human motion shall be predicted, contact models of the foot are need. Furthermore, the methods shall be applied to a humanoid robot driven by artificial muscles [4], where similar problems of redundancy and questions of optimality arise.

Acknowledgements

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