# Muscle interaction in the context of muscle deformation modelling by a Position Based Dynamics method

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## Introduction

Various musculoskeletal diseases, such as osteoporosis, can cause serious degeneration of bone tissue. A computer musculoskeletal model can support the decision of a medical professional whether to perform an invasive surgery to prevent dire medical consequences. Musculoskeletal computer models come in varying complexities, usually using straight or bone-wrapped line segments representing the muscles. But these approximations may not always suffice the inference precision, hence a more realistic model is wanted.

One of these more realistic models [1] represents the muscles as triangular surface meshes, which are deformed using a Position-Based Dynamics (**PBD**) method by the bone movement. The model exhibits a problem, particularly in the hip area, where the *iliacus* muscle unnaturally bends during hip flexion, being passively dragged behind the *femur* bone in a rag-doll manner. Such an observation motivates the development of a model better reflecting muscular physiological mechanisms, such as the contraction and the relaxation of the muscles in a synergistic manner (active interaction). Moreover, the new model should address the penetration of these elastic muscles (passive interaction) by developing a collision-handling method.

## Methods

The PBD method [1] works with each muscle vertex as a particle with associated position and mass. The velocities of the particles are approximated by differences in consequent positions. Their displacements are calculated using the Störmer-Verlet step. If the particle is not fixed to the bone attachment site, its movement is (softly) constrained to preserve the **distances** to neighbour particles, the **dihedral angles** between adjacent triangles, and the **volume** of each muscle. The penetration of the particles with the bones has also been solved (hard constraints) using signed distance fields already in the former model [1], which works well and is therefore adopted here.

PBD has a problem where the stiffness of the constraints is dependent on the simulation step [2], causing non-consistent behaviour. Therefore, this thesis employs the Extended PBD (**XPBD**) method [2], which solves the PBD drawback by incorporating a "well-defined concept of elastic potential energy" [2]. The XPBD basic control flow graph is in Figure 1.

To overcome muscle penetration, the so-called **virtual edges Zig-Zag** method is proposed as the means of passive interaction. This method exploits the muscles' presumable anatomical closeness by finding a few true closest pairs of vertices (in parallel) every few steps and in between these update steps, lets each virtual edge scout its topological neighbourhood to try and minimize its length by possibly changing vertex on both sides repeatedly. Once a Contact Proximity Distance is reached, a collision can be expected and avoided by e.g. pushing the vertices away. Local optima are usually resolved by a change in geometry and accumulation of the edges for one global optimum is usually beneficial for collision resolution.

A method to make the muscles actively and synergistically contract is proposed. To know which muscles should contract (activate) under a specific position of the bone (e.g. 30° of flexion), the **OpenSim Static Optimization Tool** (opensim.stanford.edu) was used. These activations for groups of muscles have been collected for various bone rotations. If the user moves the bone to a position for which no activations are available, a **K-means** search in the bone orientation space is performed and out of these neighbours, the activations are interpolated using a Gaussian radial basis function. To project these activations onto the particular muscles, the distance-preserving XPBD constraints have been repurposed. The main idea is to **change the constraint** desirable **distance dynamically** according to the activation level of the whole muscle and put these constraints onto the muscle surface. These dynamic constraints on the surface have been made to follow the approximation of internal (parallel) muscle fibres in the muscle rest-pose, just by snapping these internal fibre polylines to the nearest surface vertices of the particular muscle.

The solution is implemented in modern **C++** with the use of *static polymorphism* and the *Eigen* library. Many areas are parallelized using the **Parallel Standard Template Library** to achieve maximal execution time effectiveness. The soft constraints are divided into exclusive groups of influence by a graph colouring method to be able to run in parallel, whereas synergistic contraction of muscles is parallelized trivially per muscle.

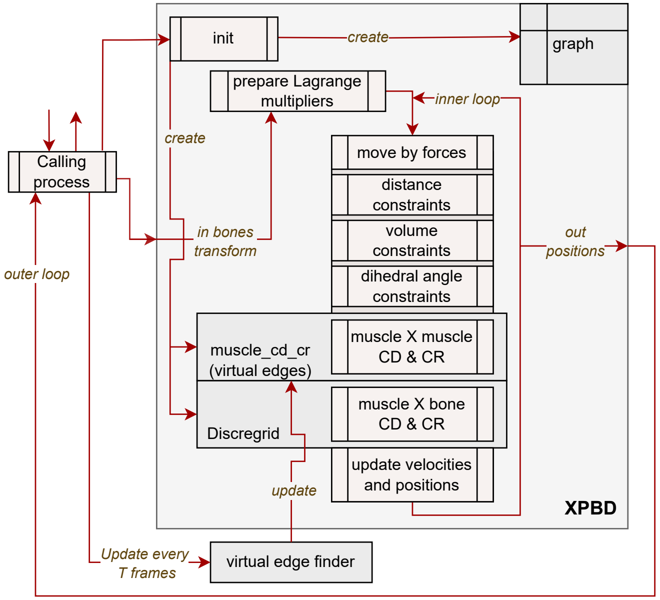

Figure 1. Basic control flow graph of the XPBD algorithm

## Results & Discussion

The results were verified for visual plausibility, adherence to the physiology of muscle interaction, correspondence to the results of the former method, and the preservation of muscle shapes and volumes. The quality of the proposed muscle penetration avoidance method was also assessed. In Figure 2, results for *iliacus* during hip flexion can be seen, whereas in Figure 3, more muscles can be seen during abduction. Moreover, internal muscle fibres were inscribed for each method for the *musculus iliacus* during hip flexion. The lengths of these fibres are depicted in Figure 2 in the chart on the right side of the image in red for the results of this thesis and in blue for the results of method [1].

The result in Figure 2 for the *iliacus* muscle shows an immense improvement in comparison with the other model in terms of visual quality - **the muscle no longer unnaturally bends**. This success is further highlighted by the change of the inscribed fibre lengths for this muscle during the same movement. This result is important since, at the end of the day, the inscribed fibres serve to compute the biomechanical properties. Hence, seeing the red fibres decrease steadily all at once indicates that all internal fibres are deformed more uniformly (this muscle exerts a lot of force during flexion, therefore this is expected behaviour) compared to the results in blue for the model presented by [1], which perhaps even lengthens the fibres.

The abduction progression (3) shows clear signs of synergistic muscle behaviour with no visible muscle intersections. Thanks to the time-efficient implementation and the consistency of the XPBD solver, it is possible to explore the results interactively, where each frame of the simulation takes approx. a few hundred milliseconds (maximally 2-3 seconds when great displacements take place) to compute. The speed of computation also allowed for more solver steps each frame. This often helps the convergence of the constraints solver, providing a better global optimum of the deformation, leading to more pronounced model behaviour.

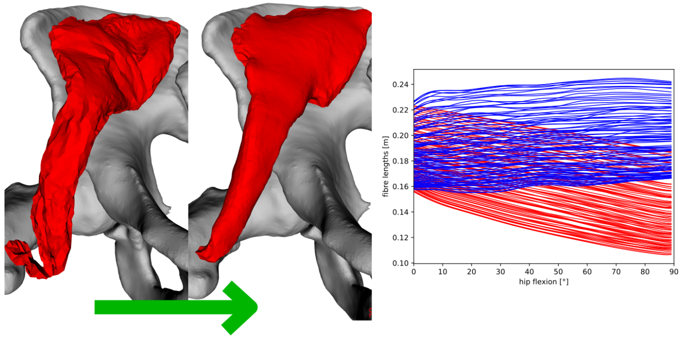

Figure 2. Comparison of hip flexion for the *musculus iliacus* with internal fibres lengths; left: model [1], fibre lengths in blue, right: this thesis result, fibre lengths in red

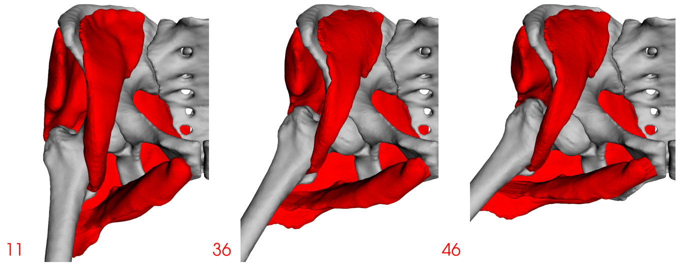

Figure 3. Progression of hip abduction for more (4) muscles

Unfortunately, advances in one problem gave a chance for other problems to arise, such as a possibly over-constrained system and related oscillations, as described in detail in the thesis text. One explanation could be the naive method of acquiring surface fibres.

This novel approach of incorporating passive and active muscular interactions into complex musculoskeletal models, the majority of which seem to neglect these interactions, can provide more realistic decision support to medical experts on-site in a feasible time.

## References

[1] Josef Kohout, Martin Červenka. Muscle Deformation Using Position Based Dynamics. Biomedical Engineering Systems and Technologies, Springer International Publishing, 2021, 486-509. DOI:10.1007/978-3-030-72379-8_24.

[2] Miles Macklin, Matthias Müller, and Nuttapong Chentanez. Xpbd: Position-based simulation of compliant constrained dynamics. In Proceedings of the 9th International Conference on Motion in Games, MIG '16, New York, NY, USA, Association for Computing Machinery, 2016, 49–54.