Skeletal muscles have a wide range of anatomical architectures. They often form a heterogenous curvature, while the tendon and bone attachments vary in their morphology. Each muscle consists of multiple muscle fibers which can contract via Myosin motors \cite{Jiangcheng2015} and thus create a force pulling on the bones. These fibers are not long enough to spread across the whole muscle, so they are grouped in paralleled bundles called fascicles.

According to \cite{Etemadi.et.Al.} the biceps of an athletic individuals has around 300.000 muscle fibers, which are single cells approximately 50μm in diameter and several centimetres long \cite{Cooper2000}. Each fiber has a thick myosin filament and a thin actin filament, which surrounds the myosin. During the process of muscle contraction, the actin and myosin filaments slide past each other resulting in shortening of the fiber.

Since the mechanical force is transmitted along the muscle fibers, it is important for biomechanical simulations to obtain an adequate representation of their trajectories. This way we can get much more realistic geometries e.g. of a contracted biceps. However, this is not a simple task because of the complexity and diversity of the various muscles. To simplify the problem by a small degree, we can simulate the fascicles instead of every single fiber.

To simulate the contraction of a muscle we need an approximation of the fascicles, that stretch across the muscle. Although we can see them with our bare eyes, it is not possible to determine their pathway using an ordinary CT-scan.

Therefore, we need a method to calculate the stream of these fascicles. Muscles are often modelled using a lumped-parameter approach that assumes a simplified arrangement of fascicles. However, as Choi and Blemker stated, these models are not able to cover three-dimensional deformations.

One of the more promising approach was using a Laplacian vector field as presented in \cite{Choi2013}.

The goal of our work is the approximation of Muscle fascicles based on the 3D-model of a muscle, primarily the musculus biceps brachii, with an approach using a Laplacian vector field. Gmsh ~\cite{Geuzaine2009} is a tool for generating 3-D finite element meshes with built in pre- and post processing. We use it for multiple reasons as it is free software that features it's own scripting language, which uses code similar to C++ with loops, conditionals and user-defined macros. We use these features, because they match our needs for Meshing, Simulation and analysis of the Model. It can be compiled without the GUI, directly from the command line. For other manipulations and computations we use Python.