

Universität Stuttgart

Generating and Visualizing Muscular Fascicle Arrangements

Simulation großer Systeme – SGS

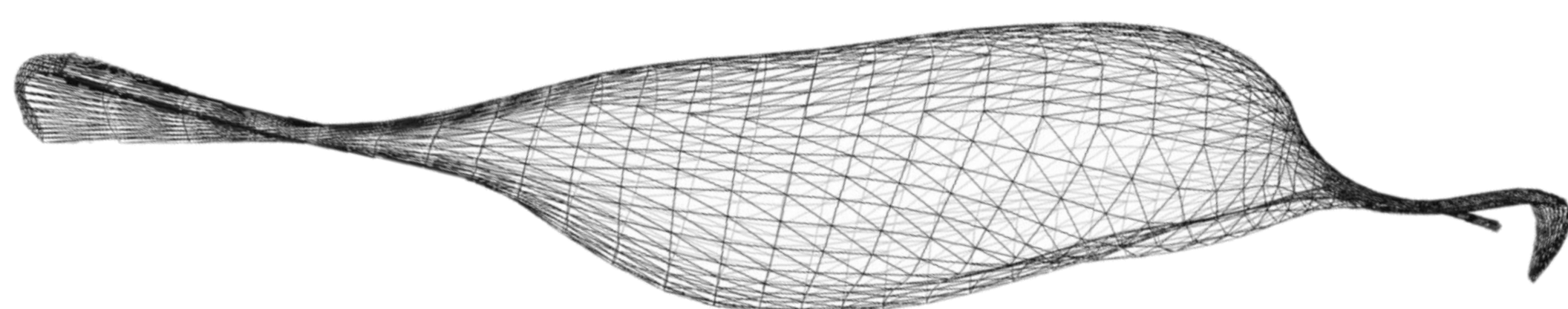


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- Calculating Arrangement of muscular fascicles using Laplacian vector field simulation and Dirichlet + Neumann boundary condition
- Creating a reliable, semi-autonomous procedure
- 3D-meshing and Simulation using Gmsh
- Visualization of generated fascicles
- Variable amount of generated fascicles

Introduction

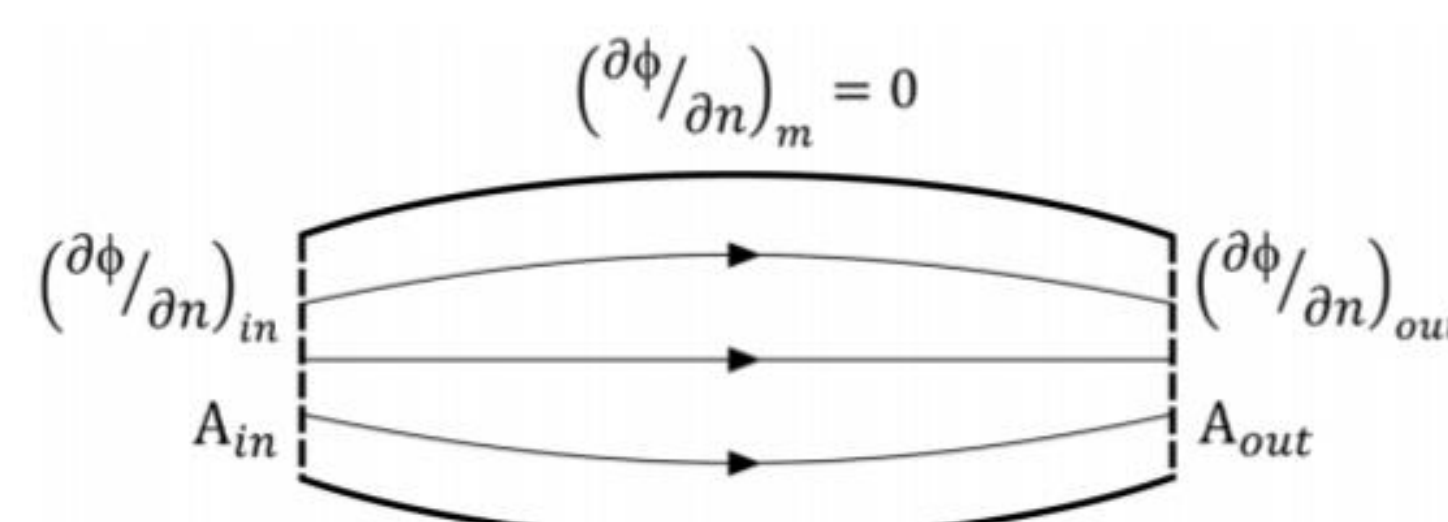
In biomechanical simulations it is important to acquire an adequate representation of the muscle fibers. It's impossible to obtain these fibers from a simple CT-scan and in order to simplify the problem we calculate the trajectories of the fascicles instead of the muscle fibers. This can be achieved by using a Laplacian vector field with Dirichlet and Neumann boundary conditions.



CT-scan of the musculus biceps brachii

Laplacian Vector Field

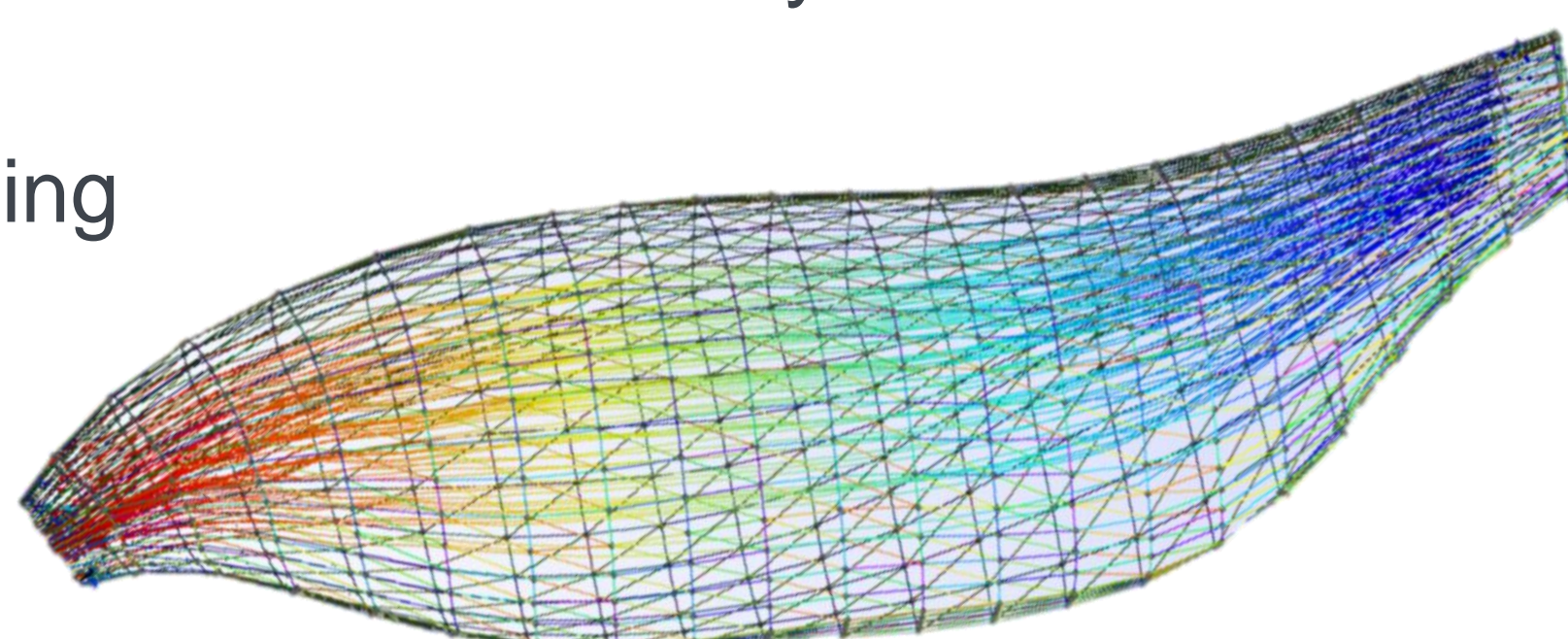
- Dirichlet boundary
- Neumann boundary
- Calculates stream, given an inflow and outflow



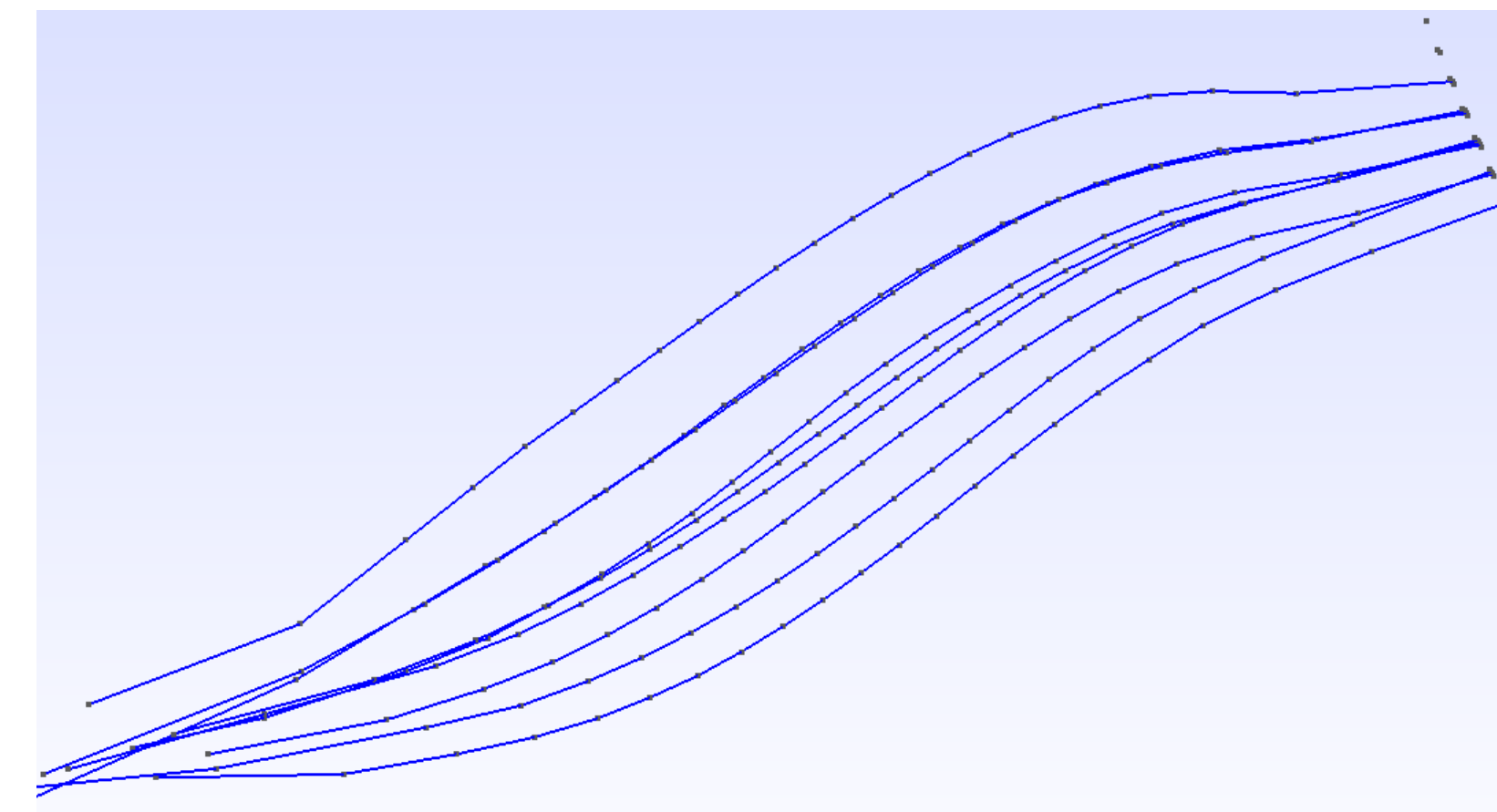
Choi and Blemker already showed 2013 that the muscle fascicles can be reconstructed using a Laplacian vector field simulation. After solving the Laplacian potential flow ($\Delta\Phi=0$), the fibers are obtained by tracing streamlines through the volume. Because of that, we use the meshing program Gmsh and its build-in solver GetDP. It is a three-dimensional finite-element mesh generator. The simulation of electric potential in a dielectric volume implements the Laplace equation and the two boundaries and thus is a perfect fit for our conditions.

Gmsh features

- GUI, own scripting language
- Automation: loops conditionals, user-defined macros and external system calls
- Compiling without the GUI and use directly from the command line
- Pre- and postprocessing
- Built-in solver
- Free software

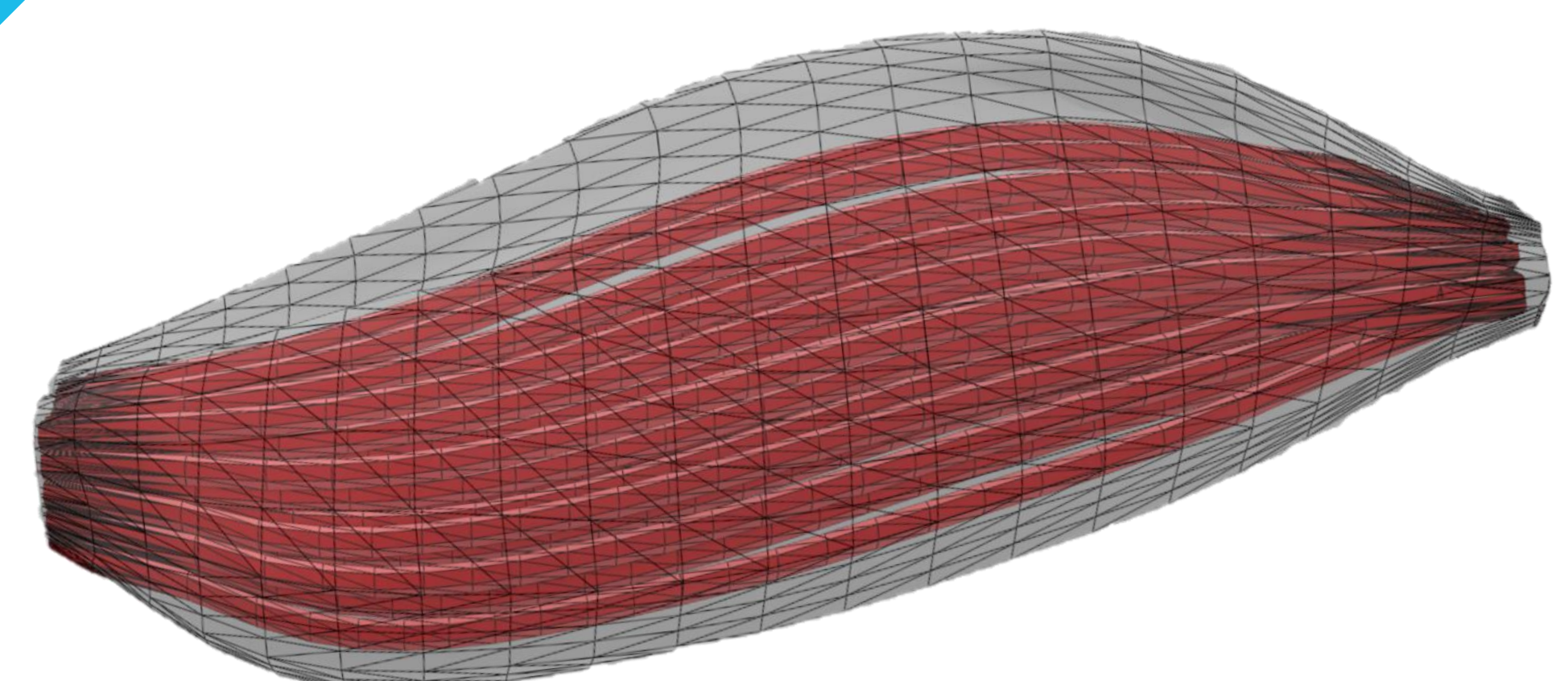
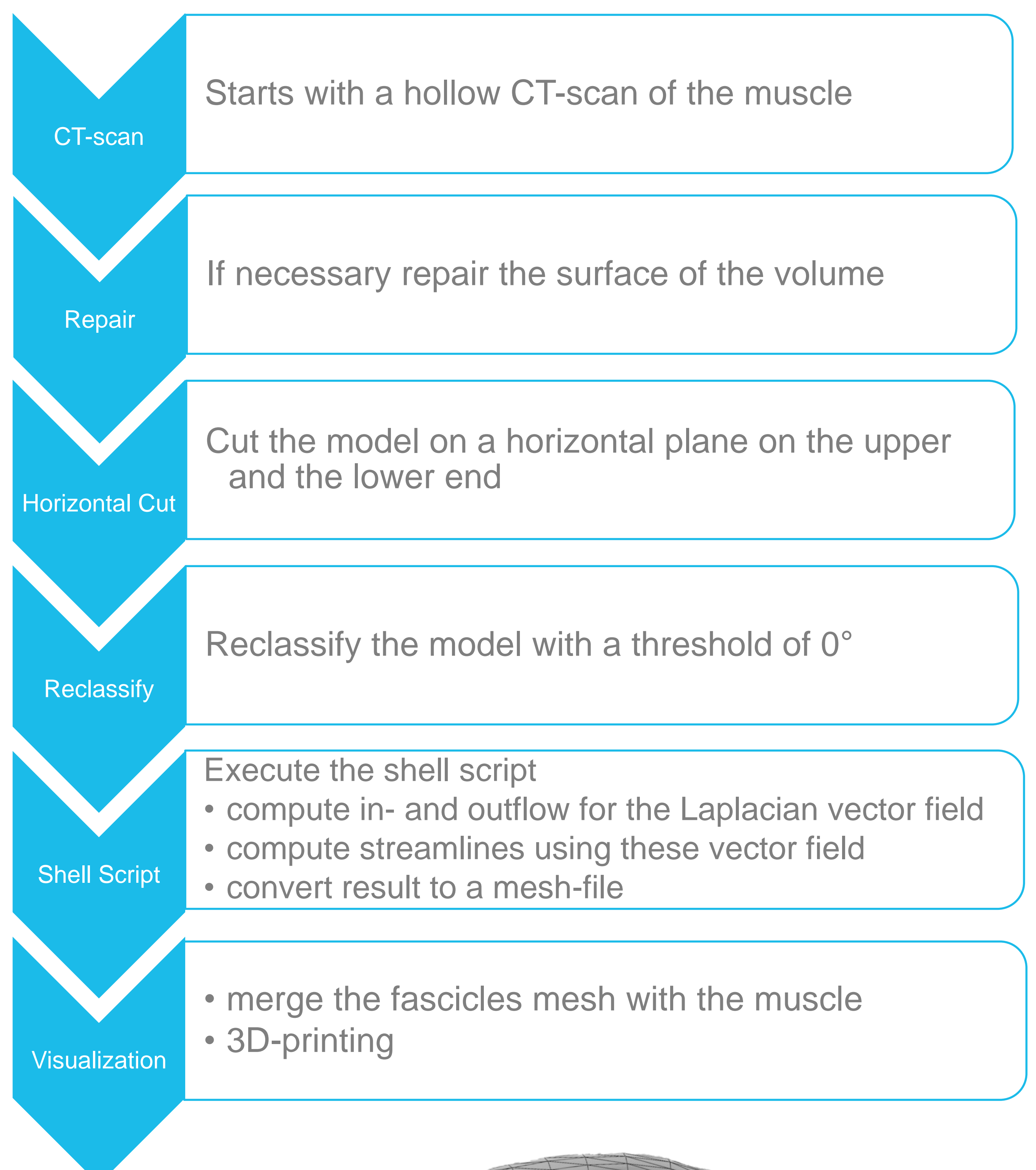


Postprocessed streamlines (fascicles) in Gmsh



Generated fascicles without the muscle volume

After the postprocessing we get the trajectories of the fascicles. These however aren't in a suitable file-format and thus we have to process the data with our python-script. The resulting fascicles are set for presentation as shown in our pictures (e.g. 3D-visualization).



Completed generation of the muscle including volumes for the fascicles