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Computational workflow to build a data-driven model of a „Virtual Parasite"

In this project, we will build "virtual parasites"from high-resolution image data as basis for a precise data-driven mechanical understanding of parasite biophysics in the context of the DFG priority programme "Physics of Parasitism".

The parasitic life cycle involves a multitude of physical interactions with the host microenvironment during stages of motility and adhesion. The shape and elasticity of unicellular parasites are largely defined by their cytoskeleton. In parasitic kinetoplastids such as Trypanosoma brucei, the cytoskeleton includes a subpellicular array of microtubule filaments that forms a corset around the entire cell. How exactly the interaction between the beat of the flagellum, which is attached to the cytoskeleton and winds around the cell, and the mechanical response of the cell body, gives rise to the intricate rotational motility patterns of T. brucei is not known.

To answer this question, a detailed structural and mechanical model of the microtubule cytoskeleton and the interior of the cell, which together define its elasticity, is needed. We will first perform a complete semantic segmentation (pixel-level annotation) of electron tomography image volumes of different developmental stages of T. brucei using a deep learning workflow. We will then apply automated tracing of microtubule filaments and semi-supervised instance segmentation of the cell interior to arrive at a complete 3D structural model of the cell. This model will be converted to an annotated volume mesh amenable for finite element analysis
and subjected to in-silico deformation test to validate the model against experimental data. By adapting the workflow to other image data, similar mechanobiological phenomena in other model parasites can be studied. Our data-driven approach will enable new ways of understanding the physics of parasitism by connecting imaging with computer simulations.

The complete workflow as well as the image data and model will be made available to collaborators within the DFG Priority Programme "Physics of Parasitism". A web-based collaboration platform for visualizing and exploring the image and model data will be developed and hosted alongside the data. All code and accompanying interactive Jupyter notebooks for image analysis and neural network training will be under version control and accessible from a gitlab instance. Pre-trained networks will be available for download, as well container definition files to run the workflows in different computational environments. Image analysis code that could be relevant for other researchers within the Physics of Parasitism priority programme will be documented and made available on the same platform. We will ensure publication of code and data under the FAIR principles in all collaborating projects by working closely with the research data management units and libraries.

Slot length

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