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Title of your talk: Semi-automated segmentation in 3D electron microscopy imaging

Brief (one paragraph) description/abstract:

As image acquisition hardware evolves rapidly, larger amounts of data sets become easier to retrieve. In particular, state-of-the-art high throughput resolution microscopy devices offer a plethora of opportunities in research areas such as biotechnology, medicine, micro- and nanotechnology. The problem in these thriving industries does not lie in the acquisition, but in the fact that data processing research cannot keep up with the increasing data stream. For example, in recent research at the Max Planck Institute of Neurobiology, a team of 224 people manually annotated 950 neurons in a 1 million mm^3 electron microscopy (EM) data set at nanometer resolution, leading to more than 20,000 annotator hours. As a result, microscopy image analysis typically is a tedious and time-consuming process.

A second issue arises as a consequence of the big data problem: many researchers rely on (typically low-quality) image restoration and analysis algorithms that require low computational cost. Therefore, the processed data will require a substantial amount of manual post-processing and even consists of unwanted artifacts that might influence the conclusions.

In our research project, we aim to develop high quality segmentation algorithms as this is currently one of the most time-consuming processes within the timeline of a microscopic imaging experiment. More specifically, we focus on two use-cases: segmentation of mitochondria and endoplasmic reticula (ER). These organelles are responsible for cell energy maintenance. Biological experts believe they have a crucial role in diseases such as lung cancer, where lung cells have too much energy and divide too quickly, or Alzheimer, where – vice versa – brain cells have a shorter lifespan.

In order to tackle the big data problem, we propose a micro-segmentation pre-processing step where so called superpixels (homogeneous connected regions that cluster similar pixels together) will be generated. Given an input of much less superpixels, compared to the original large amount of pixels, subsequent (macro-)segmentation algorithms are expected to have a cheaper computational cost. Secondly, we will implement our techniques within a GPU framework, allowing for massive parallelization. As for the second problem that was mentioned above, we have performed a statistical noise and blur analysis specifically for 3D EM imaging, which – combined with state-of-the-art joint denoising and deconvolution

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algorithms – allows for more accurate image representation. It is our goal to implement these techniques in an interactive user-friendly interface, such that biological users can, for example, decide to what extent the image restoration step should be performed, which features or structures are relevant for the segmentation, etc. In the long term, the system should be self-learning such that interaction with the user becomes less necessary in order to improve parameter modelling.