Tutorial 2: Computational Modeling of the Dividing Human Cell

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Abstract: Cell division/mitosis is a fundamental process of life where a mother cell undergoes profound morphological transformations to divide into two daughter cells. This process is driven by tight coordination of a large number of essential proteins in space and time. Recent publication from our group (Cai Y. and Hossain MJ et al., Nature 2018) utilized four-dimensional (3D+time) image data to construct a canonical model of the morphological change of human cells during the cell division in order to quantify spatio-temporal dynamics of essential mitotic proteins. We also constructed a dynamic protein atlas containing 28 mitotic proteins where user can visualize distributions of mitotic proteins during cell division within the cell model and obtain various parameters such absolute number proteins and average concentration inside different cellular compartments.

During this tutorial, I will first introduce the project and the computation framework briefly. Then with a simpler version of source code, mostly developed in MATLAB, I will demonstrate various steps needed such as segmentation, parameters extraction, registration, cylindrical axis based representation and averaging in order to construct a canonical model of mitosis using a small set of data. The model will be used to integrate proteins of interest from different cells to obtain average distributions. I will also demonstrate the functionality of the protein atlas.

Preparation: Prospective participants can go through our manuscript (Cai Y. and Hossain MJ. et. al., Nature 2018), specially the parts related to construction of canonical model and computation of average protein distributions. It would be helpful to visit our project webpage for source code, data, results and the protein atlas, where one can interactively play with different proteins.
http://www.mitocheck.org/mitotic_cell_atlas/
Instruction to use the package is available at
https://git.embl.de/grp-ellenberg/mitotic_cell_atlas/blob/master/README.md

Participants willing to run the package in their own notebook should have access to MATLAB with the following toolboxes:
- Statistics and Machine Learning Toolbox
- Image Processing Toolbox
- Curve Fitting Toolbox
- Computer Vision System Toolbox

Reference: Yin Cai, M. Julius Hossain, Jean-Karim Hériché, Antonio Z. Politi, Nike Walther, Birgit Koch, Malte Wachsmuth, Bianca Nijmeijer, Moritz Kueblbeck, Marina Martinic-Kavur, Rene Ladurner, Stephanie Alexander, Jan-Michael Peters & Jan Ellenberg, "Experimental and computational framework for a dynamic protein atlas of human cell division", Nature 561, pages 411–415 (2018) doi: 10.1038/s41586-018-0518-z