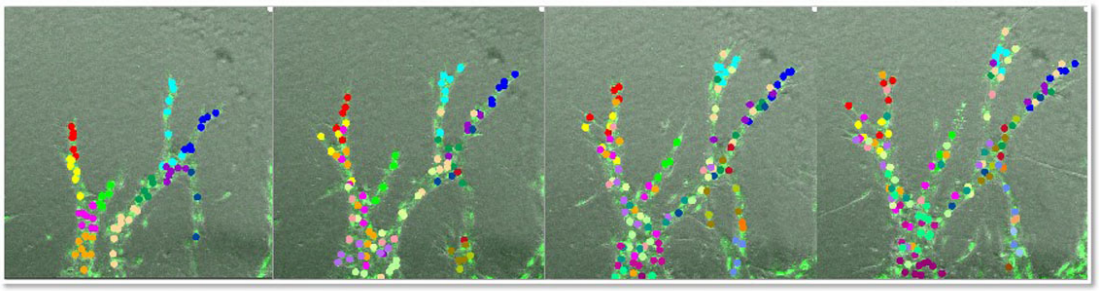
Guest Seminars



IMB Guest Lecture

Speaker
Koichi Nishiyama, MD and PhD
http://kumamoto-ircms-nishiyama.jp/en/
International Research Center for Medical Sciences
Kumamoto University

Time and Place
Thursday 5, 11:00-12:00
Domus Medica, room LU-035

Title
On chip reconstitution of the roles of pericyte and intraluminal pressure in angiogenesis

Abstract
Angiogenesis is a multicellular morphogenesis process that expands vascular networks in tissue. Various biological components concertedly contribute to angiogenic morphogenesis. The most important cellular component is endothelial cells, which we use to reconstruct 3D angiogenic process in a extracellular matrix in response to angiogenic growth factors. In addition, perivascular pericytes, blood flow and extravascular tissue importantly serve as (sub)components that allow constructing more sophisticated vascular networks. However, a mechanistic understanding of how the individual components contribute to various angiogenic processes is largely missing. In this seminar, I will introduce a reconstitution angiogenesis assay system with a microfluidic device that allows dissecting the phenomenon in a bottom-up way by adding individual components to the essential one. I will discuss the roles of pericyte and intraluminal pressure on angiogenic morphogenesis based on recent unpublished data obtained using this technology.

Biostatistics Seminar

Speaker
Walter de Back, PhD
http://walter.deback.net/
Institute for Medical Informatics and Biometry
Faculty of Medicine, TU Dresden (Germany)

Time and Place
Friday 6, 11:30-12:00
Domus Medica, new meeting room at the Biostatistics department

Title
Dynamics of endothelial cell shape: deep learning, shape analysis and multi-scale modeling

Abstract
Endothelial cells, a main component of our blood vessels, exhibit rich dynamics in cell motility and shape changes. Exactly how these dynamics affect the growth of new blood vessels, however, remains unclear. In this talk, I will outline the analysis pipeline we established to quantify and model single-cell shape and motility. Obtaining faithful cell shape information from time-lapse confocal microscopy images is complicated due to an inhomogeneous distribution of fluorescence. We therefore employed a deep learning approach based on convolutional neural networks to segment cells using both the fluorescence and bright-field channels. Subsequently, we analyzed the extracted 2D shapes in an unbiased fashion using principle component analysis and compared the results with a common feature-based shape analysis. Finally, we constructed a preliminary multi-scale model combining an intracellular reaction-diffusion model with a cellular Potts model using the Morpheus simulation platform and are now looking to infer model parameters to fit our experimental data. Several components of this pipeline may be of interest to other domains in quantitative biology.