Lecture topics

Cell mechanics and motility analysis
Keywords: active contours, mechano-imaging, shape

This lecture will address the analysis of cell motility and shape. Cell motility is governed by a complex molecular machinery that converts physico-chemical cues into whole-cell movement. Understanding the underlying biophysical mechanisms requires the ability to measure physical quantities inside the cell in a simple, reproducible and preferably non-invasive manner. The goal is to extract quantitative analyses of motion and/or shape changes of biological objects from image time series. This requires the ability to compute the positions and/or boundaries of these objects automatically (detection and/or segmentation) and linking these in time (tracking). We will present BioFlow, a computational mechano-imaging method and associated software able to extract intracellular measurements including pressure, forces and velocity everywhere inside freely moving cells in two and three dimensions with high spatial resolution in a non-invasive manner. This is achieved by extracting the motion of intracellular material observed using fluorescence microscopy, while simultaneously inferring the parameters of a given theoretical model of the cell interior.

Statistical spatial statistics
Keywords: colocalization, Statistical Object Distance Analysis (SODA), Marked-point process

This lecture will address the analysis of the spatial organization of objects, which is essential in many scientific areas to provide information about objects' interactions and their interplay with their environment. Objects' organization can be studied at different scales, ranging from country size in epidemiology to atomic structures in physics, through proteins distribution in biology. In all spatial organization studies, objects (disease cases, trees, molecules) are represented as points in a delimited field of view (country, forest, cell) and quantitative methods are used to extract features about spatial point distributions. Biological processes rely on the coordinated action of multiple players such as (macro-) molecules in cellular processes and host-pathogen interactions, or individual cells such as neurons. Elucidating protein functions and molecular organisation requires to localise precisely single or aggregated molecules and analyse their spatial distributions. We will present the new methods that we have developed to extract new information and parameters in a robust and fast analytical manner, and surpass classical methods.

Artificial intelligence for image segmentation
Keywords: multicell segmentation, domain adaptation,

Image segmentation has become one of the most important applications of Machine and Deep Learning in bioimage analysis. Machine learning and computer vision are indeed propelling a revolution in image data analysis, whereby many segmentation and classification tasks considered unfeasible a few years ago, can be approached today efficiently with neural networks. This lecture will address some of our latest developments for image analysis based on Deep Learning, trained on annotated images, to tackle multicell segmentation problems.