Post-doc position offer

Multi-scale matching of dynamic content and structure in correlative microscopy

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In many domains now, multiple imaging modalities are available delivering images of different types and at different scales of the same scene. In particular, we are interested in settings where one modality acquires temporal (or time-lapse) image sequences and the other one supplies high-resolution static images of the same scene. Dynamic information can be extracted from the former while fine structure can be recovered from the latter. The challenge is then to properly match and combine these two sources of information for a better analysis and understanding of the observed scene.

More specifically, we are concerned with the correlative fluorescence light microscopy-electron microscopy approach. Fluorescence light microscopy enables to visualize tagged proteins or vesicles moving within the live cell with a resolution of about 100nm. Electronic microscopy can image the fine complete structure of the cell at a few nanometers scale but the cell must be first frozen. We aim at developing multi-scale and multimodal image registration methods to get a unified view of molecular complexes. High resolution of protein structures is extremely important for accurate interpretations of biological functions at the molecular level. Correlative microscopy provides unique multi-scale and multi-modal information on protein localization and interactions by combining the advantages of the live fluorescence microscopy with the high resolving power and ultra-structural information of electron microscopy.

The goal of this postdoctoral research is to define a method for co-localizing the moving proteins extracted from the fluorescence image sequences and the corresponding structure parts in the electron microscope image. Statistical approaches will be investigated. For example, Bregman distances could be exploited along with CRF models. The work could also draw from techniques developed in image retrieval and in image super-resolution. Methods for proteins detection and motion estimation previously developed in the team will be available. The designed matching method will be experimentally evaluated on a set of microscope image data acquired at Institut Curie in Paris. We have a long-term and tight collaboration with Jean Salamero’s team at Institut Curie.

Team bibliography:


