

Accurate quantification of spatial-temporal patterns from high resolution microscopy

Many important processes in biology follow spatial or spatial-temporal patterns. Whether a gene is expressed or not might depend on its spatial location at a particular time, and spatial clustering of proteins has a key role in gene expression, cell signaling, etc. These are inherently multi-scale processes: a protein that is clustered in the microscale might not be clustered in the nanoscale, or might be clustered in both scales but differently. With advanced high-resolution microscopy¹ (Nobel prize in 2014), it is possible to study these processes with the required spatial and temporal resolution. Yet, quantitative analysis tools have lagged behind^{2,3} in accurately processing the large quantities of noisy data ('big data'), though several recent attempts have been made (e.g., Stone et al, Nature Communications 2015⁴; Rubin-Delanchy et al, Nature Methods 2015⁵, Baumgart et al Nature Methods 2016⁶). We propose a project that, depending on the candidate's skills and interests, can combine both programming (preferably Matlab, but open to other languages like Java or Python), and quantitative method development. The candidate will have the possibility to perform experiments to validate the tools developed. The starting point of the project will be the fast, scalable, efficient implementation of existing key spatial/spatial-temporal correlation & cluster analysis methods^{3,4,7}. The tools developed will immediately be used by several researchers and groups to study various systems including nuclear organization and epigenetics and also in cell biology in general. We expect the results of the project to be published in high quality journals and open-source software to be released publicly.

The project will be conducted at the LOCCO group, UMR 168, Institut Curie. We are a highly inter-disciplinary group, with a high level of collaboration between physicists, biologists and computer scientists and have a history in publishing software works in high-impact journals such as Nature Methods^{8,9}.

Skills required: basic mathematics and programming. **Recommended skills:** signal & image processing, probability & statistics, algorithms, quantitative biophysics

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References and suggested reading

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