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STATISTICAL AND COMPUTATIONAL METHODS FOR INTRACELLULAR TRAJECTORY ANALYSIS IN FLUORESCENCE MICROSCOPY

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The characterization of molecule dynamics in living cells is essential to decipher biological mechanisms and processes. This topic is usually addressed in fluorescent video-microscopy from particle trajectories computed by object tracking algorithms. However, classifying individual trajectories into predefined diffusion classes (e.g. sub-diffusion, free diffusion (or Brownian motion), super-diffusion), estimating diffusion model parameters, or detecting diffusion regime changes, is a difficult task in most cases. To address this challenging issue, we propose a computational framework based on statistical tests (with the Brownian motion as the null hypothesis) to analyze short and long trajectories, and derive spatial diffusion maps. The methodological approach is well-grounded in statistics and is more robust than previous techniques, including the Mean Square Displacement (MSD) method and variants.

In this talk, I will present the concepts and methods and focus on dynamics of biomolecules involved in exocytosis and endocytosis mechanisms, observed in total internal reflection fluorescence (TIRF) and lattice light sheet microscopy. The algorithms, dedicated to short or long trajectories, are flexible in most cases, with a minimal number of control parameters to be tuned (p-values). They can be applied to a large range of problems in cell imaging and can be integrated in generic image-based workflows, including for high content screening applications.

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