Motion switching along cells receptors trajectories

Internship Position
Biological Image Analysis Unit, Institut Pasteur, Paris, France

Motion classification for cells receptors. Nowadays, fluorescence microscopy coupled with tracking algorithms allows the detection of objects at the cell membrane level and the reconstruction of their trajectories. In a recent paper [1], these techniques are used to describe the trajectories of specific receptors (CCR5) in human cells. These are involved in several inflammatory processes and are involved in HIV infection. Dynamical characterization enables the identification of several populations of receptors and the investigation of their behavior in the presence of drugs.

The paper [1] establishes a statistical method to distinguish standard classes of movement for CCR5 receptors (sub-diffusive, Brownian, directed). The method uses a decision test for motion characterization [2] based on the maximum distance from the initial position.

This method has been improved by a recent internship work, defining a machine learning method to classify a more prominent family of motions. This work is based on the geometric characteristics of the trajectories [3] allowing different subdiffusive behaviors to be distinguished (Continuous Time Random Walk, Ornstein-Uhlenbeck, Fractional Brownian Motion).

Project. The methods presented above enable the classification of trajectories of a given length. Then, the windowing approach allows the study of motion variability along longer trajectories. This approach is very sensitive to the chosen length. Moreover, different dynamical behaviors can correspond to sub-trajectories of different lengths. Few works exist on the detection of points of movement change. Moreover, existing approaches develop statistical methods based on Brownian motion properties [4].

The internship aims to develop a novel method to analyze motion switching along long trajectories. The main goal consists of defining suitable parameters whose variation in time corresponds to a change of motion. In particular, the method should distinguish several sub-diffusive processes corresponding to the natural states of the CCR5 dynamic.

Expected work. A good knowledge in mathematics and machine learning theory is need for this topic. After a review of the literature on stochastic process and relative features for motion classification, a new method of motion switching will be developed. The method validation will be performed on simulated trajectories and on real data (HIV receptors).

Contacts :
Giacomo Nardi et Thibault Lagache, Biological Image Analysis Unit, Institut Pasteur
Emails : giacomo.nardi@pasteur.fr, thibault.lagache@pasteur.fr

References

[1] F. Momboisse, G. Nardi, P. Colin, M. Hery, N. Cordeiro, S. Blachier, O. Schwartz, F. Arenzana-Seisdedos, N. Sauvonnet, J.-C. Olivo-Marin, *et al.*, "Tracking receptor motions at the plasma membrane reveals distinct effects of ligands on ccr5 dynamics depending on its dimerization status," *Elife*, vol. 11, p. e76281, 2022.

[2] V. Briane, C. Kervrann, and M. Vimond, "Statistical analysis of particle trajectories in living cells," *Physical Review E*, vol. 97, no. 6, p. 062121, 2018.

[3] Y. Meroz and I. Sokolov, "A toolbox for determining subdiffusive mechanisms," *Physics Reports*, vol. 573, pp. 1–29, 2015.

[4] V. Briane, M. Vimond, C. Valades-Cruz, A. Salomon, C. Wunder, and C. Kervrann, "A sequential algorithm to detect diffusion switching along intracellular particle trajectories," *Bioinformatics*, vol. 36, no. 1, pp. 317–329, 2020.