Precise mapping of intracellular diffusion and drift from SPT data analysis

Antoine Salomon, Charles Kervrann

Precise mapping of intracellular diffusion and drift from SPT data analysis

Antoine Salomon[1], **Charles Kervrann**[1]
[1]Inria, Centre Rennes - Bretagne Atlantique, Campus Universitaire de Beaulieu, 35042 Rennes Cedex, France

Email: antoine.salomon@inria.fr

Keywords: Diffusion, drift, mapping, classification, single-particle tracking.

It is of primary interest for biologists to be able to visualize diffusion and drift inside a cell. These two notions are used to characterize particle motion in the Langevin equation:

$$\boldsymbol{dX} = \boldsymbol{b}(\boldsymbol{X})dt + \sigma(\boldsymbol{X})\boldsymbol{dw}$$

where **X** designates the (2D or 3D) spatial coordinates of the particle, **b** the drift vector, σ the diffusion coefficient, and **w** standard gaussian white noise.

We propose a new mapping method inspired from the method of N. Hozé [1], providing results in the form of bitmap images for the diffusion and vector field matrices for the drift by scanning SPT data by spatial blocks, and from the work of V. Briane [2-3], who developed two methods to classify SPT data by particle motion types and detect switches in-between them.

To obtain satisfying sharpness - i.e. to avoid the blurring effect due to calculation of both diffusion and drift in cell coordinates where no data is available - we replace the scanning movement of an averaging window by a trajectory-following movement of a product of spatial and temporal gaussian weights. Each diffusion point and each drift vector are calculated at coordinates corresponding exactly to the coordinates given by the preliminary particle tracking, which gives us more detailed results in the form of point clouds and vector fields.

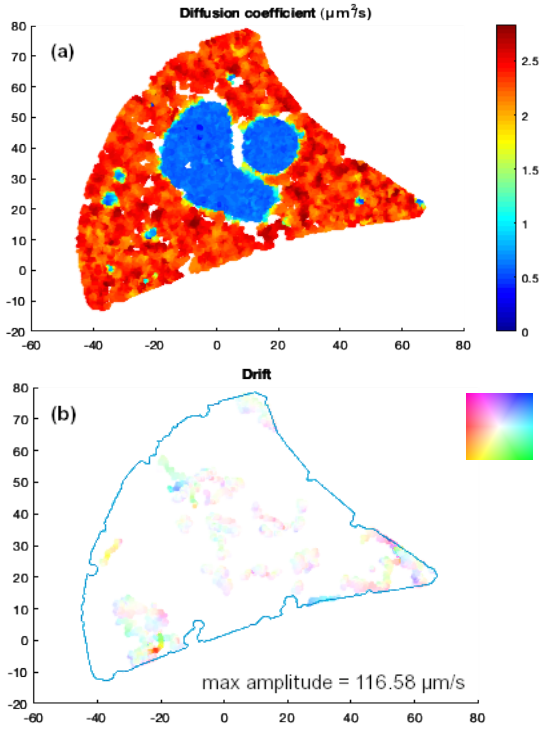

Figure 1. (a) *Intracellular diffusion and* ***(b)*** *drift maps processed from SPT data generated with FluoSIM cell simulator. In* ***(b)****, the hue represents the orientation of the vectors while the saturation represents their amplitude.*

Classification from V. Briane enables us to label trajectories and even their sub-parts automatically by motion type: confined motion (the particle is bound to a specific point), Brownian motion (the particle moves randomly), and directed motion (the particle moves in a determined direction). We then use this information to calculate diffusion coefficient and drift maps separately on each motion class with the most suitable formula.

[1] Hoze et al., Heterogeneity of AMPA receptor trafficking and molecular interactions revealed by superresolution analysis of live cell imaging, Proceedings of the National Academy of Sciences Oct 2012, 109 (42) 17052-17057; DOI: 10.1073/pnas.1204589109
[2] Briane et al., A statistical analysis of particle trajectories in living cells, Physical Review E, 2018
[3] Briane et al., A Sequential Algorithm to Detect Diffusion Switching along Intracellular Particle Trajectories, Bioinformatics, 2019.