



HAL
open science

Probabilistic overall reconstruction of membrane-associated molecular dynamics from partial observations in rod-shaped bacteria

Yunjiao Lu, Pierre Hodara, Charles Kervrann, Alain Trubuil

► **To cite this version:**

Yunjiao Lu, Pierre Hodara, Charles Kervrann, Alain Trubuil. Probabilistic overall reconstruction of membrane-associated molecular dynamics from partial observations in rod-shaped bacteria. QBI 2020 - Quantitative BioImaging Conference, Jan 2020, Oxford, United Kingdom. pp.1. hal-03087322

HAL Id: hal-03087322

<https://inria.hal.science/hal-03087322>

Submitted on 23 Dec 2020

HAL is a multi-disciplinary open access archive for the deposit and dissemination of scientific research documents, whether they are published or not. The documents may come from teaching and research institutions in France or abroad, or from public or private research centers.

L'archive ouverte pluridisciplinaire **HAL**, est destinée au dépôt et à la diffusion de documents scientifiques de niveau recherche, publiés ou non, émanant des établissements d'enseignement et de recherche français ou étrangers, des laboratoires publics ou privés.

Probabilistic overall reconstruction of membrane-associated molecular dynamics from partial observations in rod-shaped bacteria

Yunjiao Lu^{1,2}, Pierre Hodara¹, Charles Kervrann², Alain Trubuil¹

¹Inra, UR 1404, MaIAGE, Université Paris-Saclay, Jouy-en-Josas,

²Inria, Centre Rennes-Bretagne Atlantique, SERPICO Project Team, 35042, Rennes, France

Keyword: Total Internal Reflection (TIRF) Microscopy, Time-lapse microscopy, Multi object tracking, Image reconstruction, probabilistic modelling, stochastic processes, parametric estimation

Understanding the mechanisms that maintain the structure of rod-shaped bacteria is a challenging problem in cell biological research. We try to gain insight into this problem by observing the dynamics of the cell wall construction workers, the membrane-associated molecular machines (MMs) thanks to the recent development in bioimaging, especially with total internal reflection fluorescence microscopy (TIRFM). Due to the cylindrical form of the bacteria and the selective visualization of the TIRFM, only around one third of the perimeter can be observed. From the partial observed bacteria surface images, using single-particle tracking (SPT), earlier studies showed that a fraction of the MMs performs directed motion, across the image field quasi-orthogonally to the cylinder axis. No re-entry event considered, these motion segments were studied in an independent way. Here we address the problem of the connection of motion segments on a cylindrical surface, assuming that one MM may re-enters into the observed region (OR), a certain time after having left it. The directed MM motions are assumed as Brownian motion with drift, the birth and death events of the MMs are supposed to happen independently and uniformly on the surface. Given a set of observed segments entering and exiting the OR, we propose a probabilistic framework to calculate the probabilities of the events of birth, death and re-entry, based on speed and diffusion of the motion and the time of exit and entry. Even though two third of the surface is hidden as shown in Figure 1, this framework allows us to derive a computational procedure aiming at connecting segments belonging to the same trajectory, and then recovering directed MMs dynamics on the whole surface. The performance of the method is demonstrated on simulation data mimicking MMs dynamics observed in TIRFM. Further work will be focused on the application of the framework to real MMs motion segments, obtained by pre-processing TIRFM acquisitions using SPT.

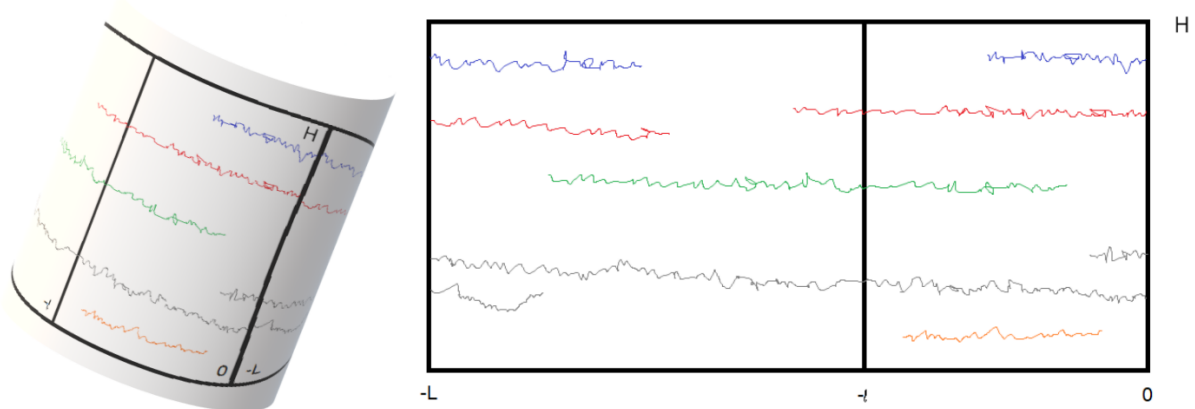


Figure 1: Trajectories on the cylinder and its 2D representation. The unobserved region is $(-L, -l] \times [0, H]$ and the observed region is $(l, 0] \times [0, H]$.