

Mathematical models for flagellar activation

Jessie LEVILLAIN, CMAP, Ecole polytechnique - Palaiseau

In order to compensate the lack of inertia in a fluid at a low Reynolds number, strategies involving non-reciprocal movement patterns need to be employed by swimmers at the microscopic scale [5]. Among them, the most common one is using beating filaments such as cilia, or flagella which has a characteristic pattern to maximize swimming efficiency. However, this motion cannot be easily reproduced when studying a simple elastic filament without any form of activation along its length. In this case, the wave propagating along the swimmer is attenuated very quickly [2, 4], which does not match the behaviors observed in the tails of swimming micro-organisms in biology, or in data-based simulations [7].

In practice, an entire structure propagating curvature variations is present along the flagellum. This structure, called axoneme, is mainly composed of pairs of filaments arranged in a circle, between which molecular motors walk [3, 6]. These motors are the active component which create bending along the flagellum, and are powered by a chemical component called Adenosine triphosphate (ATP).

In this talk, I will present a detailed mathematical model of the axoneme. I will particularly focus on the molecular motors' behavior, first through a two-state model, governed by Fokker-Planck equations. I will then introduce other more complex models to take into account the whole structure of this axoneme. I will study mathematically and numerically the influence of the ATP quantity on the system's behavior, and discuss its biophysical interpretation [1].

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