



Contribution ID: 1837 Type: **CLOSED - Oral (Student, In Competition) / Orale (Étudiant(e), inscrit à la compétition)**

Examining the role of bias versus swimming in superdiffusion

Tuesday, 30 May 2017 16:15 (15 minutes)

A key biophysical consideration in cellular biology is the role of motility. That is, can (and how does) a cell move in a preferred direction on its own accord (i.e., swim) for some physiological purpose (e.g., a bias due chemotactic gradient). One means to empirically characterize the result is by quantifying the so-called 'anomalous diffusion,' which directly arises from biases, of an ensemble of cells. Commonly, the observed response is that of superdiffusion, where the ensemble mean-squared displacement (MSD) is supra-linear (i.e., MSD exhibits a nonlinear time dependence with an exponent greater than unity). However, if the bias led to cell attraction (i.e. movement towards a localized high-oxygen concentration) the response is reversed. This suggests that quantification of the deviation from linearity can lead not only to distinguish cells which are capable of motility but also the degree, or strength, of their motion bias. Here we develop a heuristic computational model for *E. coli* motility to distinguish between swimming biases using the macroscopic effect on the MSD. Initial results indicate that objects which are motile, yet lack bias, exhibit characteristics consistent with normal diffusion. This observation motivates a deeper biophysical question as to how/if swimming and bias can be meaningfully disentangled and suggests that direct comparison to the diffusive motion, of similarly-sized not motile objects, under the same conditions is necessary.

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Session Classification: T4-7 Biomechanics and Fluid Dynamics (DPMB) | Biomécanique et dynamique des fluides (DPMB)

Track Classification: Physics in Medicine and Biology / Physique en médecine et en biologie (DPMB-DPMB)