

Abstract Submitted  
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**Large behavioral variability of motile *E. coli* revealed in 3D spatial exploration** N. FIGUEROA-MORALES, PMMH-ESPCI Paris, France. Penn State, PA, USA, T. DARNIGE, PMMH, U. Paris 6, France, V. MARTINEZ, U. of Edinburgh, UK, C. DOUARCHE, PMMH, U. Paris Sud, France, R. SOTO, DFI, U. de Chile, Chile, A. LINDNER, PMMH, U. Paris 7, France, E. CLEMENT, PMMH, U. Paris 6, France — Bacterial motility determines the spatio-temporal structure of microbial communities, controls infection spreading and the microbiota organization in guts or in soils. Quantitative modeling of chemotaxis and statistical descriptions of active bacterial suspensions currently rely on the classical vision of a run-and-tumble strategy exploited by bacteria to explore their environment. Here we report a large behavioral variability of wild-type *E. coli*, revealed in their three-dimensional trajectories. We found a broad distribution of run times for individual cells, in stark contrast with the accepted vision of a single characteristic time. We relate our results to the slow fluctuations of a signaling protein which triggers the switching of the flagellar motor reversal responsible for tumbles. We demonstrate that such a large distribution of run times introduces measurement biases in most practical situations. These results reconcile a notorious conundrum between observations of run times and motor switching statistics. Our study implies that the statistical modeling of transport properties and of the chemotactic response of bacterial populations need to be profoundly revised to correctly account for the large variability of motility features.

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