

Abstract Submitted  
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**Simulation of the flow field and tumbling dynamics of multiply flagellated bacterium** RONALD LARSON, NOBUHIKO WATARI, University of Michigan — To study the hydrodynamics of swimming of multi-flagellated bacteria, such as *Escherichia coli*, we develop a simulation method using a bead-spring model to account for the hydrodynamic and the mechanical interactions between multiple flagella and the cell body, the reversal of the rotation of a flagellum in a tumble and associated polymorphic transformations of the flagellum. This simulation reproduces the experimentally observed behaviors of *E. coli*, namely, a three-dimensional random-walk trajectory in run-and-tumble motion and steady clockwise swimming near a wall. Here we show using a modeled cell that the polymorphic transformation of flagellum in a tumble facilitates the reorientation of the cell, and that the time-averaged flow field near a cell in a run has double-layered helical streamlines. Moreover, the instantaneous flow field, which is strongly time-dependent, is more than 10-fold larger in magnitude than the time-averaged flow, large enough to affect the migration behavior of surrounding chemoattractants, with the Peclet number for these molecules being larger than one near a swimming cell.

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