

Modeling hydrodynamic interaction of bacterial flagella

May 17, 2017. 5 p.m.

수요일 오후 5시

#262, Science Hall, Yonsei U.

연세대학교 과학관 262호

Sookkyung Lim

Department of Mathematical Sciences,
University of Cincinnati

Bacteria such as *E. coli* swim through the fluid by utilizing their helical flagella, each of which is driven by a rotary motor. This flagellar motor is embedded in the cell body and it can turn either clockwise (CW) or counterclockwise (CCW), which will lead to either run or tumble. During a run, all of flagellar motors spin CCW while each filament forms a left-handed helix, and the hydrodynamic interaction of flagella causes the filaments to form a bundle that propels the cell forward. During a tumble, one or more flagellar motors reverse the direction of rotation and the motor reversal initiates the polymorphic transformation, which is a local change in helical pitch, radius, and the handedness.

In this work we present computational models (1) to demonstrate two mechanisms that drive polymorphic transformation by comparing to experimental data, and (2) to study flagellar bundling and unbundling. Kirchhoff rod theory is employed to describe each helical flagellum as a space curve associated with an orthonormal triad that measures the degree of bending and twisting of the rod. The elastic rod immersed in a viscous fluid applies the force and torque to the surrounding fluid and moves at the local fluid velocity whereas the triad rotates at the local angular fluid velocity.