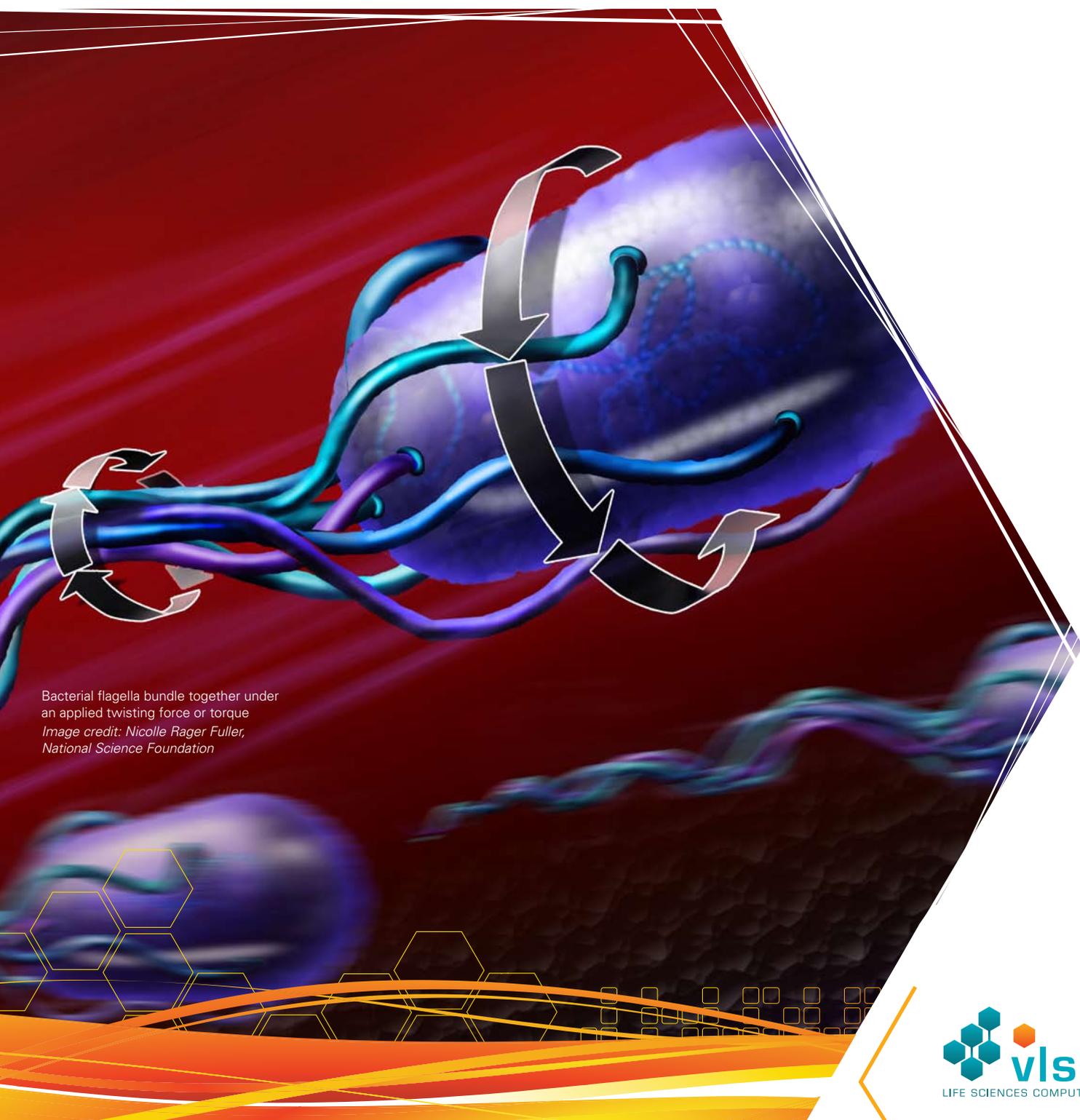


# HOW BACTERIA SWIM

Supercomputers are revealing how the corkscrew-like tails of bacteria work. The research is leading to a better understanding of bacterial life, and to a possible form of locomotion for micro-devices.

Tim Thwaites, Science Writer



Bacterial flagella bundle together under an applied twisting force or torque

*Image credit: Nicolle Rager Fuller, National Science Foundation*

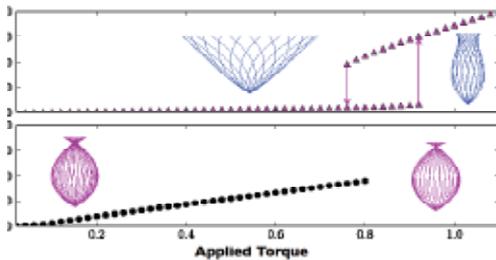
# “...peculiar things begin to happen...”



Sarah Clark. Image credit: David Paul

By modelling the characteristic motion of flagella, the corkscrew-like tails of bacteria, doctoral student Sarah Clark has proposed an explanation of why they tend to be helical rather than straight, and how multiple flagella bundle together for smooth rapid propulsion and break apart to allow changes of direction. It's all to do with their interaction with the viscous fluid surrounding them.

Such details are important to understand if flagella are ever to be used to drive micro-devices around the body, as Monash University mechanical engineer Assoc. Prof. James Friend and others have proposed. James is already working on such motors to drive miniature robots to transport catheters, carry cameras and deliver drugs.



(Above) A distinct transition from a cone shape (left) to a helical shape (right) is observed in naturally straight filaments as the applied twisting force or torque increases. (Below) Filaments which are naturally helical make no such transition.

Top View



Side View

Under certain simulated conditions two straight filaments will bundle together under applied torque (left), but near the transition stage the two filaments can hit each other and change shape constantly (middle and right).

Image credit: Sarah Clark

Flagella motion has been studied for more than 50 years. It's a classic problem, according to Sarah's supervisor at Monash University, Dr Prabhakar Ranganathan of Mechanical and Aerospace Engineering.

That's because it rapidly becomes very complicated—particularly once you recognise that flagella are flexible and not stiff, have a complex helical shape, operate in a fluid environment, and spin on their axis. “We are trying to understand how the fluid flow affects the shape, how the shape affects the fluid flow, and how that influences thrust,” Prabhakar says.

There's a further significant complication. Mathematical modelling shows that bacteria with a single flagellum would have no means of steering. They would only be able to swim in a straight line. But real bacteria change direction all the time.

One answer to this lies in the fact that most bacteria actually have multiple flagella. When all of the flagella drive in the same direction, they rapidly synchronise and bundle together as a single unit, and the organism moves in a straight line. But if one of the flagella in the bundle spins in the opposite direction, the fluid flows become almost chaotic, the bundle unravels, and the bacterium changes direction.

The mechanics of this is so complex that Sarah uses a supercomputer to capture all the intricate physical detail, and simulate the motion of bacterial flagella. She has modelled them as a single filament and a pair of filaments in a viscous fluid, varying the length, shape, flexibility and the torque or spinning force exerted on them. Sarah and Prabhakar are at the point of publishing what she has discovered so far.

At low torque a straight, flexible filament, tilted at an angle to its rotation axis, traces out a cone in fluid. As torque is increased, the filament goes through a distinct phase transition, finally snapping into a helical shape, which spins much faster and produces thrust. If the filament starts out as a helix, however, the phase transition is eliminated.

Under most conditions, a pair of straight filaments will simply go through the phase transition to become helical and then bundle together. If, however, they start close to the critical transition torque, and out of phase, peculiar things can begin to happen. “They bump into one another. One can knock the other into a twisted shape, and out again,” Prabhakar says. “By contrast, helical filaments rapidly synchronise and bundle together. It's all so smooth, it's almost boring.”

These simulations suggest why and how helical flagella evolved. It may seem simple, but the study demanded hundreds and hundreds of simulations over a huge range of conditions.

Each simulation takes one processor about a day to carry out. Without a supercomputer, it would have taken years just to collect the raw data. Realistically, the work would never have been done. But a supercomputer – initially in Canberra using National Computational Infrastructure facilities and then at Victorian Life Sciences Computation Initiative (VLSCI) in Melbourne – can calculate a whole set of conditions in parallel simultaneously.

In fact, Sarah uses Bruce, the VLSCI's SGI Altix x86 cluster. Now Prabhakar is planning studies on the formation of biofilms and the swarming motion of *Pseudomonas*, bacteria which can cause nasty infections in humans. These will require IBM Blue Gene, the most powerful computer VLSCI has to offer.

**For further information about this research contact Sarah Clark at [Sarah.Clark@monash.edu](mailto:Sarah.Clark@monash.edu).**

**To contact VLSCI, go to [www.vlsci.org.au](http://www.vlsci.org.au)**