

EFFECT OF SPATIAL CONFINEMENT ON HELICAL SWIMMING IN STOKES FLOW

Bin Liu^{*a)}, Kenneth S. Breuer^{*} & Thomas R. Powers^{*}

^{*}*School of Engineering, Brown University, 182 Hope Street, Providence, RI 02906, USA*

Small motile organisms often live in a complex fluid environment, where the hydrodynamic interactions due to the surrounding microstructures play crucial roles. The boundary element method (BEM) is, in principle, the most accurate and reliable computational tool in studying such fluid-structure interactions, but is limited by its relatively high computational cost. Implementations to this method with proper regularization or approximation have been applied to make this tool more feasible [1, 2]. However, it is still challenging to resolve high spatial resolution in 3D, especially when detailed swimming pattern matter and when the swimmer is subjected to a spatial confinement on the similar order of its length scales.

In situ, certain symmetry persists even in complex fluid-structure interactions, such as the helical symmetry of a long helical flagella that rotates and propels the surrounding fluid. To take full advantage of such symmetry in the flow structure, it is useful to map the force densities near the surface of structure to new spatial coordinates so that the these vectors compose a smaller set of individual values. One natural choice of the coordinate system is the one following the body-centerline of the helical filament. The boundary integral formulation can thus be mapped to a much reduced dimension. In the limit that the helix is infinitely long, these newly mapped force density are invariant along the body centerline, and a 2D boundary integral formulation can be reduced to 1D, without loss of any accuracies.

One application of this BEM with the implementation of flow symmetry is to study the effect of spatial confinements on micro-scale motile organisms, such as a bacterium swimming through a porous medium with the pore size of the same length as the bacterial flagella. For simplicity, the bacterium is regarded as a rigid helix and the porous media are modeled as cylindrical cavities with solid walls (shown in Fig. 1). A helical symmetry thus persists along the filament. The helix is constraint by external torque along its axial direction, but the net hydrodynamic force on the helix is zero so that this model helical flagellum swims force-free.

At given geometry and fixed rotation rate, we find that the helix always swim faster as the pore get narrower. However, at fixed power consumption, there exists an optimal pore size associated with the given helical geometry so that the helix swims fastest. More surprisingly, there exists a counter-intuitive dependence of this optimal pore size on the detailed helical geometry – a wider helix prefers a smaller pore size while a elongated one prefers a wider opening.

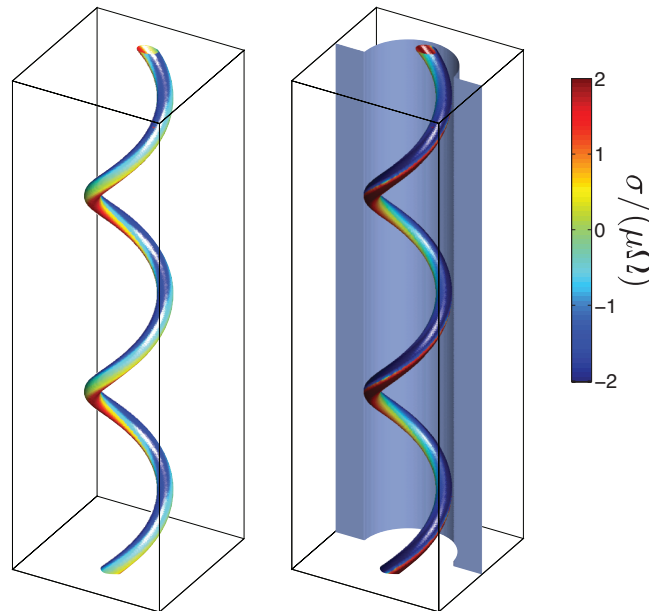


Figure 1. Comparison of the stress distribution on a helical filament that is subjected to external torque along its axial direction with (left panel) and without spatial confinement (right panel). The colormap shows the distribution of the normal stress σ , which is resolved with high spatial resolution and allows for accurate computation. When subjected to a spatial confinement, here, a circular pore (with a vertical cross-section illustrated), the stress are more sharply distributed as compared to swimming in free space at fixed power consumption.

^{a)} Corresponding author. E-mail: bin_liu@brown.edu.

References

- [1] Cortez R., Fauci L., and Medovikov A.: The method of regularized Stokeslets in three dimensions: Analysis, validation, and application to helical swimming. *Phys. Fluids* **17**: 031504, 2005.
- [2] Smith D. J.: A boundary element regularized Stokeslet method applied to cilia- and flagella-driven flow. *Proc. R. Soc. A* **465**: 3605 (2009)