Supplementary Materials

Trajectory of a Model Bacterium

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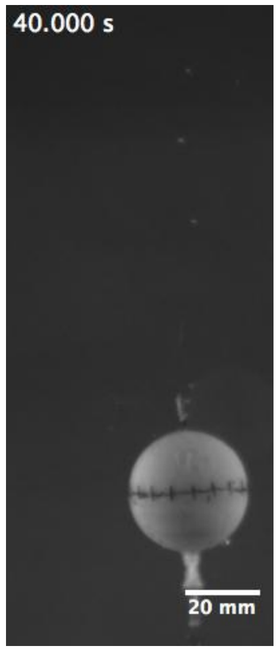
I. MACROSCOPIC MODEL BACTERIUM - MOVIE



Movie S1: Model bacterium was constructed and its motion was observed in low Reynolds number regime as described in the main text. The motion was imaged away from the tank walls at 125 frames per second. Scale bar: 20 mm.

The movie of the motion of the model bacterium is available as part of this supplement. A higher resolution version of the same movie can be accessed at (in AVI and MOV formats):

- https://drive.google.com/file/d/0B5JXM8vu1cQ-ZWpSNmg0NXg0OVU/view?usp=sharing
- https://drive.google.com/file/d/0B5JXM8vu1cQ-YnM3M3RHaEVONms/view?usp=sharing

II. LOW REYNOLDS NUMBER REGIME

This experiment was designed to verify that the translational motion of the head belongs to the assumed low Reynolds number flow regime. For this, a plastic sphere of the same dimensions as the head of the model bacterium is allowed to sediment under gravity. The spherical plastic shell is cut into halves, and its weight increased sufficiently (with metal rings) so that its net velocity due to buoyancy is close to the velocity at which the model bacterium propels itself. The sphere was imaged as it sediments towards the bottom of the tank, or rises to the top. The experiment was performed at 26.5° C at which fluid viscosity was measured to be approximately 0.945 Pa.s. It was observed that the sphere was neutrally buoyant with a mass of 24.944 gm, and was negatively buoyant with a mass of 24.964 gm at the measured terminal velocity of 0.56 mm/s downwards (average of 3 runs of more than 1000 frames each, SD of 0.02 mm/s). The theoretical sedimentation velocity was calculated to be 0.60 mm/s towards gravity using $6\pi\mu bv = \Delta mg$. The close agreement of theoretical and experimental velocities confirm the low Reynolds number regime. The small difference in the two weights resulting in significant velocity of the head also emphasizes the importance of carefully matching the weight of the bot with the fluid it displaces so that the observed motion is solely due to the motor thrust.

III. PROPULSION OF MODEL FLAGELLUM

This experiment was designed to measure the thrust force exerted by a rotating helix (model flagellum) in a highly viscous fluid and served as a benchmark study for the observed Reynolds number based on helix rotation of the model bacterium [1]. A 12-V, 60 rpm Vega ROBO kit motor (weighing 125 g) is powered by a DC source and connected to a rigid copper helix of varying dimensions (See Fig. S1 and table S1). The motor is fixed to a stand while the helix is lowered into a beaker containing silicone oil. The beaker rests on a weighing scale having a least count of 0.001 g. The external DC voltage and load determines the rotational frequency of the motor. The rotating helix exerts a thrust force on the surrounding fluid which is recorded on the weigh scale. High speed imaging of the rotating helix yields the angular frequency of the motor. There was a small extra force due to the rotation of part of the hook immersed in oil. This force was experimentally measured in the same setup by simply removing the flagellum from the coupling for each rotation rate. This extra force of hook rotation was subtracted from the measured force to obtain the force exerted only by the hook at the corresponding rotation rate. The experiments were performed with silicone oil of viscosity 29.4 (Oil 1) and 0.975 Pa-s (Oil 2) at 25° C. Two different helices were used for these experiments. The parameters for these are given in Table S1.

The observed force measurements were compared with theoretical estimates obtained from Lighthill SBT (Fig. S2). The MATLAB code from Rodenborn *et al* [1] was used.

		Helix A	Helix B
Pitch of helix	λ	11.25 mm	8.44 mm
Number of turns	N_λ	4	5
Radius of helix	R	6.75 mm	4.33 mm
Diameter of helix wire	2a	0.99 mm	0.54 mm

TABLE S1. Parameters for the propulsion experiment of Figure S1.

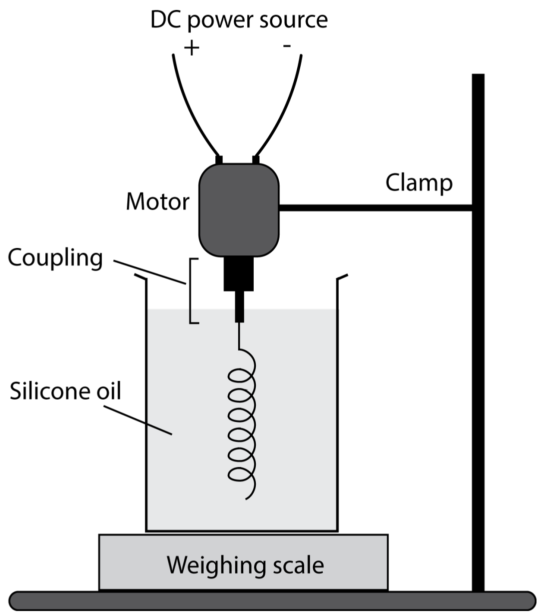


FIG. S1. Apparatus to study the propulsion by a rigid flagellum.

IV. COMPARISON WITH SLENDER BODY THEORY OF HIGDON

We compared our simulations with the predictions from the slender body theory of Higdon [3] and found that the dimensionless translational velocity of the bacterium is within 25% of Higdon's prediction for $L_c/b = 5$ (Fig. S3(B-C)). Here, $u = \mathbf{v} \cdot \mathbf{\Omega}/|\mathbf{\Omega}|$ and $c = \omega_{wave}/k$. As described in Results and Discussion, Higdon includes a collection of image singularities in addition to stokeslets on each flagellar element to ensure the no-slip boundary condition on the head's surface. Our simulations do not include the image singularities. We compared the translational velocity predicted by Higdon, which includes the force elements along the hook of the bot as well as image singularities throughout the flagellum in addition to the terms that our simulation includes. We find that around the relevant parameters for our experiment ($L_c/b = 5.8$ and $a/b = 0.034$), our simu-

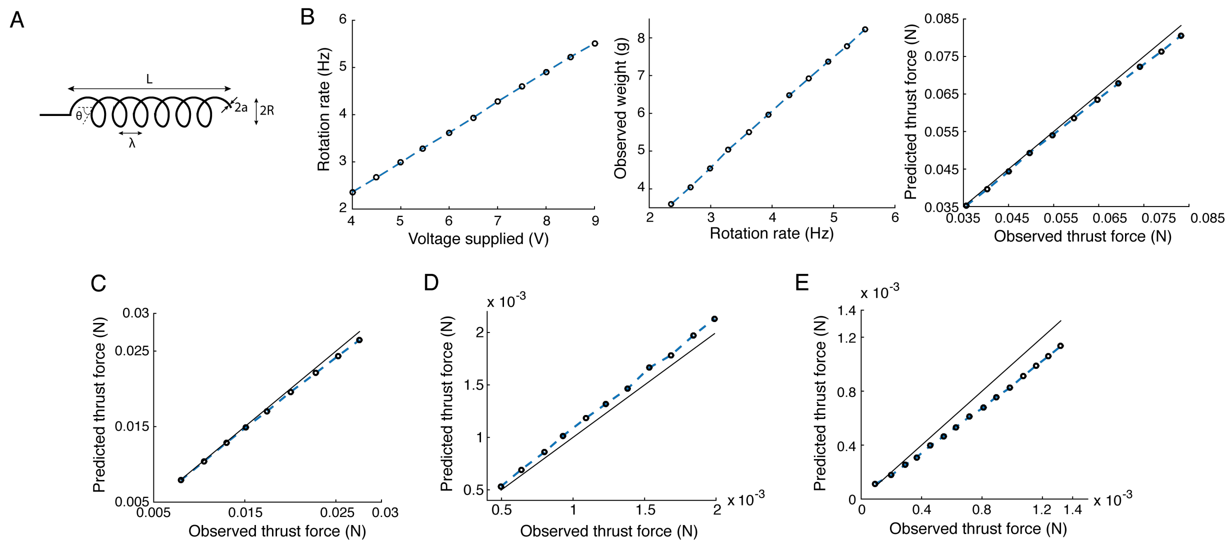


FIG. S2. **Propulsion by rigid flagellum**. (A) Schematic and parameters of the flagellum. (B) Rotation rate varies linearly with external DC voltage supplied for helix A in oil 1. The weight measured on the weighing scale increases proportionately with the observed flagellar rotation rate. Predicted thrust force was computed with SBT by Lighthill [2] and matches exactly with the observed thrust force. The corresponding measurements for helix B in oil 1 (C), helix A in oil 2 (D) and helix B in oil 2 (E) have been plotted. Data points for measured and predicted force are shown as black circles connected with dashed blue curve, and a 45° line is plotted in solid black. Error ranging from 0-4% was found between predicted and observed thrust force for (B) and (C), while there was 5-20% error for (D) and (E).

lation predicts lower velocity compared to that by Higdon's SBT by about 15% (Fig. S3(D-E)). This error may be ignored, especially considering the error in our experimental measurements are also roughly 15%. The reference translational velocity for Higdon's SBT in Fig. S3(D-E) were calculated using the MATLAB code generously provided by Professor Ashok Sanghani.

V. NUMERICAL SIMULATIONS

A MATLAB program is provided that simulates the entire trajectory of the bacterium in the laboratory frame using the geometry of the bacterium, flagellar rotation rate, buoyancy-balanced weight difference between the head and flagella and the angular tilt in the stationary bot. It is deposited as part of supplementary material. This program is based on the code from Rodenborn *et al* [5].

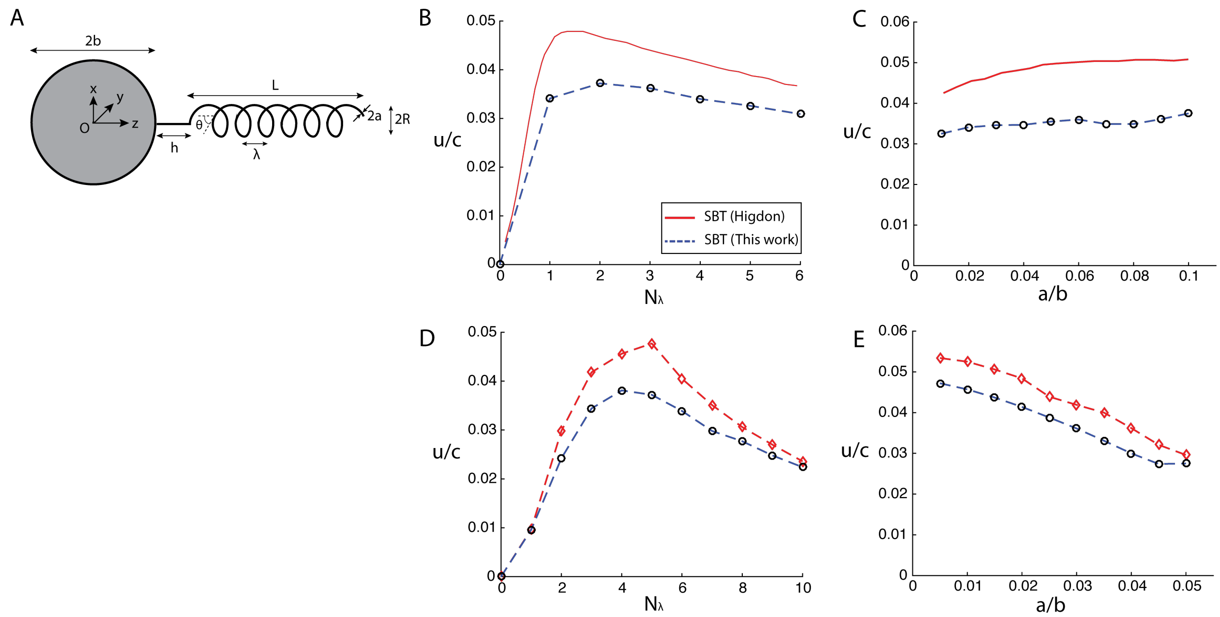
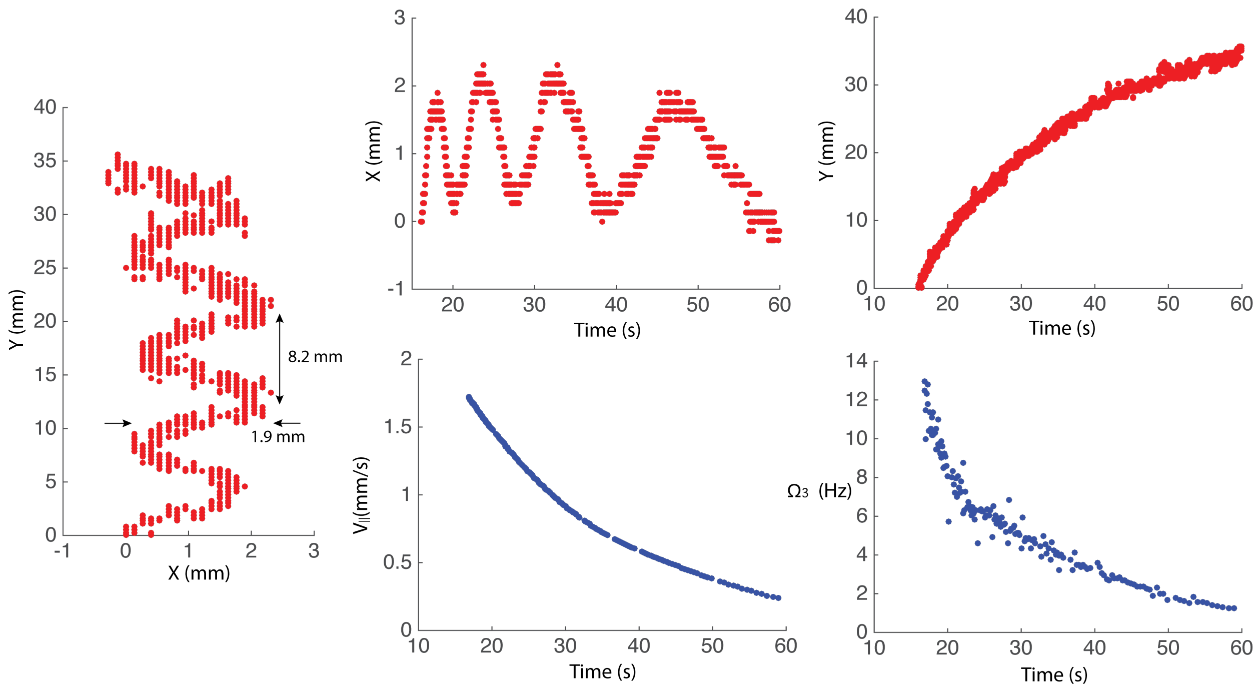
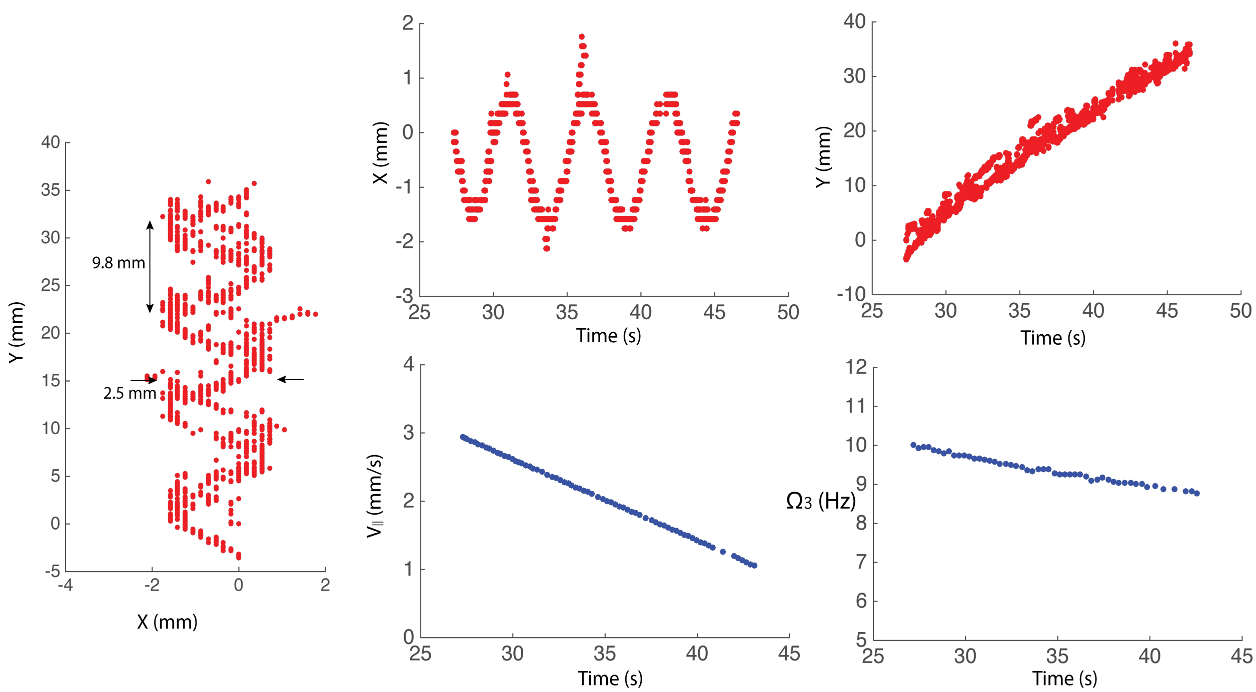


FIG. S3. (A) Schematic of the model bacterium. (B) Translational velocity component along the axis of the helical trajectory, rendered dimensionless by the wave speed and plotted with the number of wavelengths. Here, $L_c/b = 5, \theta = 45°, a/b = 0.02$. The parameter values correspond to Fig 3 of Higdon [3]. (C) Translational velocity is plotted with the ratio of wire radius to the head radius for $L_c/b = 5, \theta = 45°, N_\lambda = 1$. 'SBT (Higdon)' refers to the calculations including the modified Green's function that consist of stokeslets and their image singularities that ensure the no-slip boundary condition on the head surface, and 'SBT (This work)', which refers to the present work, ignores the image singularities in the calculations. (D-E) Dimensionless translational velocity is plotted with the number of wavelengths and against ratio of wire radius to the head radius for geometric parameters pertaining to our experimental bot. 'SBT (Higdon)' curves here also additionally include stokeslets and image singularities along the hook of the bot. For (D), $a/b = 0.034$ and for (E) $N_\lambda = 6$, and the other geometric parameters are described in Table I of the main text.

VI. MACROSCOPIC MODEL BACTERIUM - ADDITIONAL TRAJECTORIES

Additional trajectories obtained from model bacterium with similar geometric parameters have been depicted in Fig. S4. The pitch and the radius of wobble were reproducible and similar in magnitude across various experiments.


Y (mm)
X (mm)
8.2 mm
1.9 mm
X (mm)
Time (s)
Y (mm)
Time (s)
$V_{\parallel}$(mm/s)
Time (s)
Ω_3 (Hz)
Time (s)


Y (mm)
X (mm)
9.8 mm
2.5 mm
X (mm)
Time (s)
Y (mm)
Time (s)
$V_{\parallel}$ (mm/s)
Time (s)
Ω_3 (Hz)
Time (s)

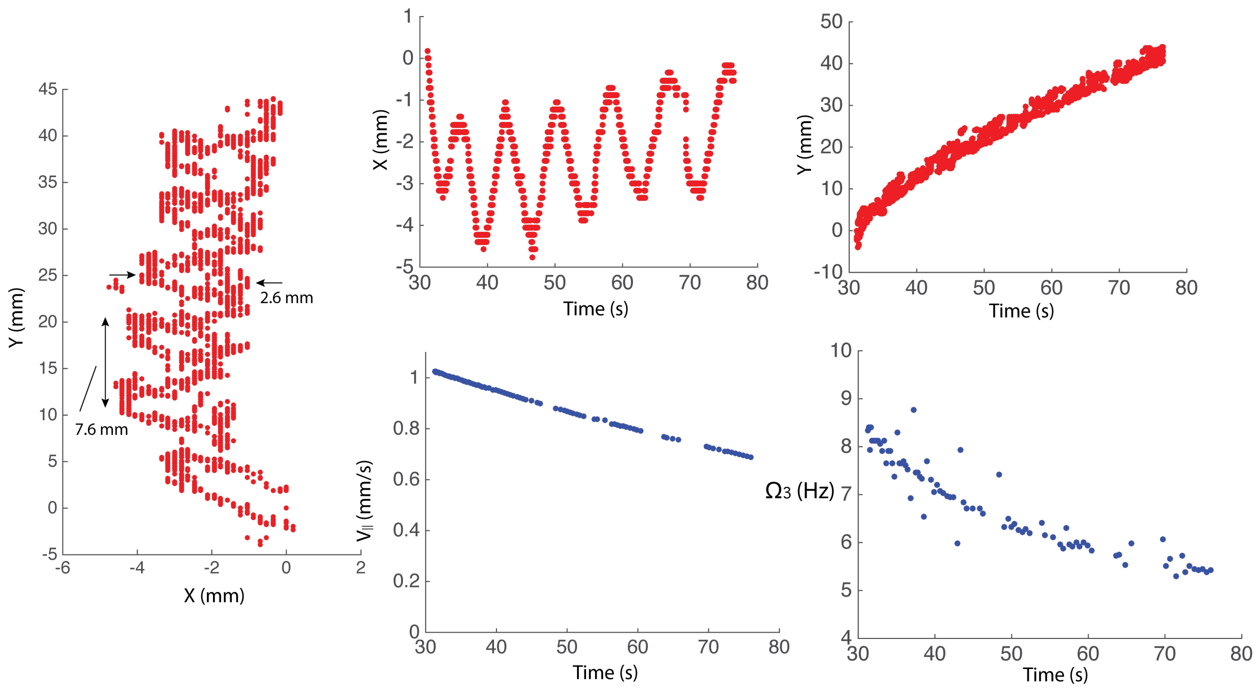


FIG. S4. Additional trajectories from model bacterium.

[1] Bruce Rodenborn, Chih-Hung Chen, Harry L. Swinney, Bin Liu, and H. P. Zhang, "Propulsion of microorganisms by a helical flagellum," Proc. Natl. Acad. Sci., **110**, 338–347 (2013).

[2] James Lighthill, "Flagellar hydrodynamics: The john von neumann lecture," SIAM Review, **18**, 161–230 (1976).

[3] J. J. L. Higdon, "The hydrodynamics of flagellar propulsion: helical waves," J . Fluid Mech., **94**, 331–351 (1979).