Electronic Supplementary Information (ESI) for

Implications of swimmers at interfaces on interfacial transport

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S1. Experimental construction of tracer paths

Swimmer displacements $\Delta\boldsymbol{x}_s$ over lag time $\tau = 0.2$s are expressed as active vectors; a polar coordinate system is constructed around each active vector with y axis in the direction of the displacement. Displacement vectors generated by the bacterium are reported for all active and passive pairs in this coordinate. Grid of points in this domain at position $\boldsymbol{x}'$ are generated with an interval of $2\ \mu m$ in cartesian coordinate (see Fig. S1a) or with an angle interval of $\pi/15$ (see Fig. S1b). Velocity vectors are measured at these grid points by properly ensemble averaging the passive vectors with relatively same position. Specifically, the passive vectors, $\Delta\boldsymbol{x}_p$, with their relative position to the swimmer $\boldsymbol{x_{sp}} = (r_{sp}, \varphi_{sp})$ expressed in polar coordinate, are binned with a tolerance of $|\boldsymbol{x}' - \boldsymbol{x}_{sp}| < \Delta R$, and $|\varphi - \varphi_{sp}| < \Delta\varphi$, see inset of Fig. S1a. The average correlation value in each bin is normalized with the magnitude of bacterial displacement to calculate induced displacement field at $\boldsymbol{x}'$. The number of passive vectors within the bin is greater than 10^6 and the bin size is chosen to increase with r to ensure statistical significance (details see [1]).

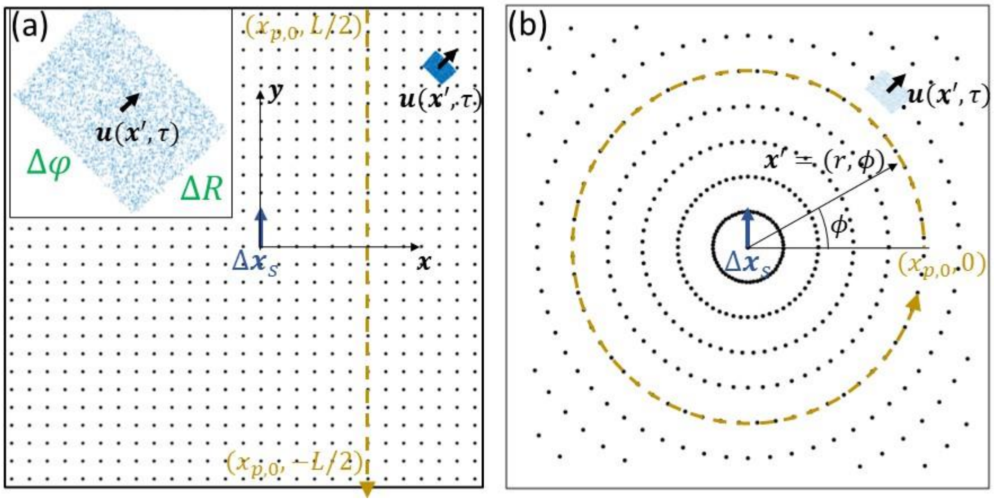

Fig. S1. Construct flow field in cartesian/polar coordinates. (a) To measure the flow field, a cartesian coordinate system at a domain with a size of $L = 120\ \mu m$ is constructed in which a swimming bacterium is placed at the origin, with its swimming direction rotated along the y axis. The passive displacements x_p are superposed, binned, and averaged to represent the velocity vector at x'. To construct the experimental tracer path with bacteria swim along straight path, the velocity vectors along the straight paths (yellow) are added. (b) A polar coordinate system is constructed, and velocity vectors are measured at the grid points. The experimental tracer path with bacteria swimming along circular path is constructed by integrating velocity vectors at the grid points along the circular paths (yellow).

S2. Numerical error to calculate tracer paths at finite separation distance

While no net hydrodynamic displacement of tracers is induced when the circular swimmer finishes a circle and tracers are well separated from the swimmer, displacement can occur for tracers and swimmers in closer proximity. In this limit, changes in the separation distance between swimmer and tracer $\boldsymbol{x}'$ cannot be neglected when calculating the fluid velocity. Thus, we numerically solve eqn (1) using Euler integration method to calculate the changes in their separation distance, $\boldsymbol{x}'(t) = \boldsymbol{x}_p(t) - \boldsymbol{x}_s(t)$, due to the finite displacements of tracers. The induced velocity $\boldsymbol{u}(\boldsymbol{x}'(t), \boldsymbol{q}(t))$ is integrated to find the position of the tracer $\boldsymbol{x}_p = \langle x_p, y_p \rangle$ and to calculate $\boldsymbol{x}'$. The Euler method is a first-order method, which generates the global error ϵ proportional to the step size Δt. To test the accuracy of our simulation, we estimate the error in net displacement of tracer, $\Delta \boldsymbol{x}_p$, when the swimmer completes one circle and detect its dependence in step size Δt (Fig.S2). We consider a situation when swimmer swims with $R_s = 2\ \mu m$, and is initially separated from the tracer by $r = 4\ \mu m$. The exact solution of $\Delta \boldsymbol{x}_p$ is approximated to the numerical solution with $\Delta t = 10^{-8}\ s$; $\Delta x_p \sim 0.5\ \mu m$ for a swimmer finishes one circle. The errors at different time steps are estimated as the difference between the solutions from the numerical integration and the exact solution. The error is found to be $\epsilon \ll \Delta x_p$, when $\Delta t < 10^{-3}$ shown in Fig. S2. To minimize the error and calculation time, we approximate the solution $\boldsymbol{x}_p$ with a step size of $\Delta t = 10^{-4}$.

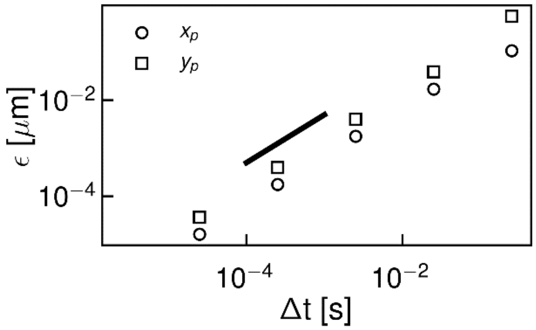

Fig. S2. Global integration error in calculating tracer path at finite separation distance. The global errors ϵ in calculating x_p (circle) and y_p (square) using different Δt are measured at the interval of swimmer completing one circle. The black line indicates that the global error increases linearly as Δt.

To further confirm that the explicit Euler scheme was performed at sufficiently small timesteps to resolve converged trajectories, paths predicted using $\Delta t = 10^{-4} s$ are compared to those predicted using $\Delta t = 5 \times 10^{-5} s$. The resulting trajectories superpose, as reported in Fig.S3. Predicted tracer displacement for particle initially at $x_{p,0} = \langle 4\ \mu m, 0 \rangle$ for $R_s = 2\ \mu m$, outside of the swimmer's circle are calculated using timestep $\Delta t = 10^{-4} s$ (Fig. S3a, black dots) and $\Delta t = 5 \times 10^{-5} s$ (Fig. S3a, red line). After 20 swimming circles, the position of tracer calculated from $\Delta t = 10^{-4} s$ compared to $\Delta t = 5 \times 10^{-5} s$ shows a difference of 0.016 µm. Compared to the total path length ~37 µm, the calculated difference is ~0.04% of the total displacements. Predicted tracer displacement for particle initially at $x_{p,0} = \langle 2\ \mu m, 0 \rangle$ for $R_s = 4\ \mu m$, inside the swimmer's circle are calculated using timestep $\Delta t = 10^{-4} s$ (Fig. S3b, black dots) and $\Delta t = 5 \times 10^{-5} s$ (Fig. S3b, red line). After 20 swimming circles, the position of tracer calculated from $\Delta t = 10^{-4} s$ compared to $\Delta t = 5 \times 10^{-5} s$ shows a difference of 0.032 µm. Compared to the total path length ~65.35 µm, the calculated difference is ~0.05% of the total displacements. The error in integration can be neglected in calculating Δx_p and the numerical integration results reveal the main features in tracer paths interacting with swimmers completing ~ 20 circles shown in Fig. 3c and 3d in the main text.

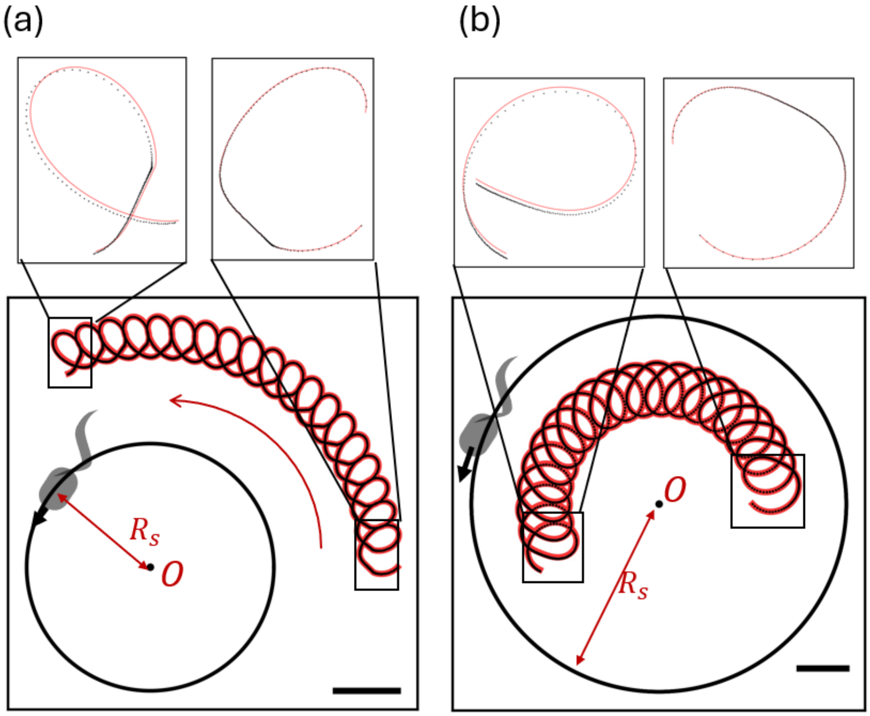

Fig. S3 (a) Predicted tracer displacement for particle initially at $x_{p,0} = \langle 4\ \mu m\ ,0\rangle$ for $R_s = 2\ \mu m$, outside of the swimmer's circle calculated from $\Delta t = 10^{-4}s$ (black dots) and $\Delta t = 5 \times 10^{-5}s$ (red line). (b) Predicted tracer displacement for particle initially at $x_{p,0} = \langle 2\ \mu m\ ,0\rangle$ for $R_s = 4\ \mu m$, inside the swimmer's circle calculated from $\Delta t = 10^{-4}s$ (black dots) and $\Delta t = 5 \times 10^{-5}s$ (red line).

S3. Example of pairwise interactions between parallel swimmers

Considering two misaligned swimmers initially located in parallel direction: the red bacterium is located in the quadrant of $\varphi = 26.56°$, $x = 4\ \mu m$ and $y = 2\ \mu m$ in the polar coordinate of grey swimmer. Based on the rotational field of "**S**" and "**B**" modes, both hydrodynamic modes will rotate the red bacterium CW. The grey bacterium initially located in the quadrant of $\varphi = 206.56°$of the red swimmer. The grey swimmer is displaced towards the red swimmer and is rotated CW contributed mostly by rotational field of **S** mode.

Fig. S4. Example trajectories of two neighboring swimmers reorienting and displacing each other.

S4. Numerical error to calculate tracer MSD interacting with multiple swimmers

The MSD of tracer displacements interacting with multiple swimmers are calculated using larger $\Delta t = 0.02s$ to save computational time. However, the MSD and diffusion coefficient extracted from tracer paths are less sensitive to computational error. We compared MSD calculated from tracer interacting with a single swimmer at minimal bacteria-tracer separation distance using $\Delta t = 0.02s$ and $\Delta t = 0.00001s$ to estimate the maximum error (smaller computational error generates as separation distance decays). The property of MSD (caging, non-caging, diffusive, or superdiffusive) is uncorrelated with step size (see Fig S4). However, we notice that using dt=0.02 s as step time can generate a maximum MSD error of approximately 7 μm^2 at lag time ~10s, which leads to a maximum error diffusion coefficient of 0.17 $\mu m^2/s$, an error of roughly 10%.

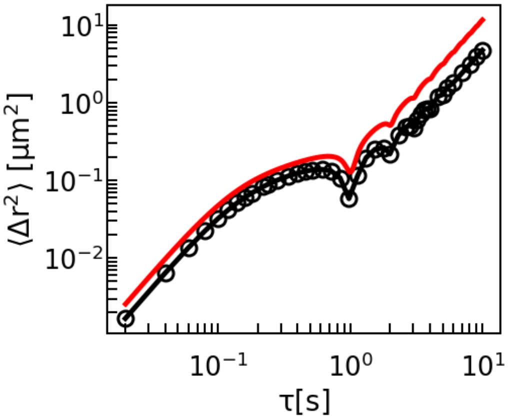

Fig.S5 Tracer MSD interacting with swimmer with a separation distance of $2\ \mu m$ calculated using step size of $\Delta t = 0.02s$ (black dots) compared with MSD (red line) calculated using $\Delta t = 0.00001s$.