Supporting Information

Idling Time of Swimming Bacteria near Particulate Surfaces Contributes to Apparent Adsorption Coefficients at the Macroscopic Scale under Static Conditions

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Figure S1 Schematic illustration of porous media interface configurations in capillary

Figure S2 Simulated bacterial distribution across difference porous media interface

Document S1. Possible porous media interface in capillary

Although both the hydroxypropyl methylcellulose augmented bacterial random motility and the Gelrite particulate suspension have increased viscosity, which helps to reduce the mixing between these two solutions to some extent, it is not possible to create an ideal sharp step-change between these two solutions, which makes determining the actual interface position in the capillary assay very difficult. We considered three configurations (concave, convex and slope) of the interface generated by the buffer solution and the Gelrite particulate suspension, as illustrated in Figure S1. Notice that, because the sizes of Gelrite particulates span from 50 to 500, the actual porous media interface configurations were more complicated than the following displayed three cases.

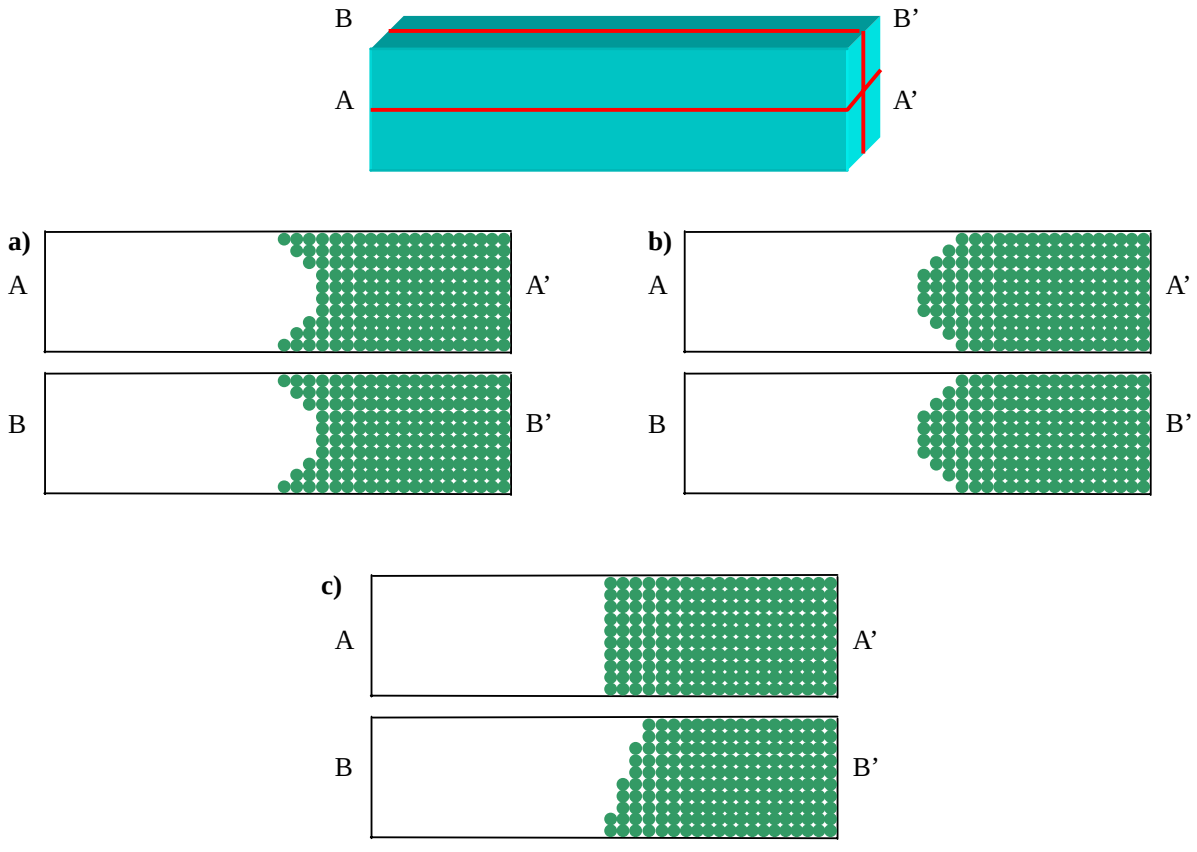
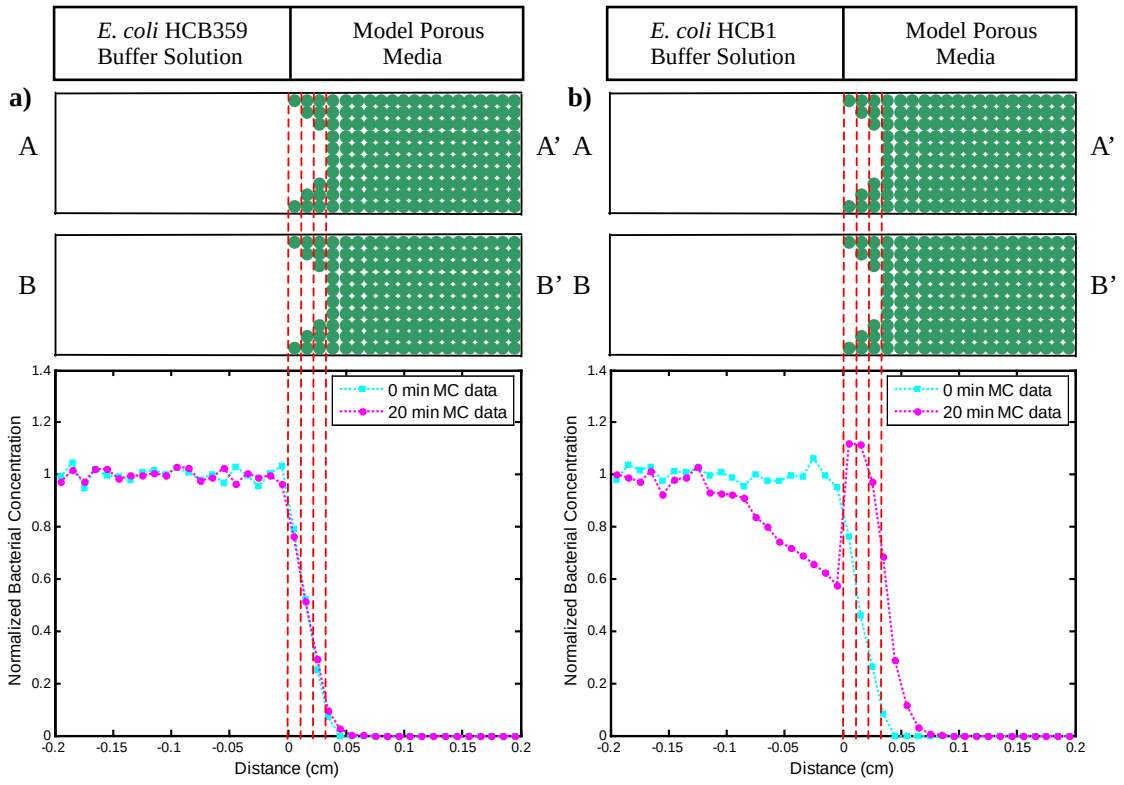


Figure S1. Schematic illustrations of porous media interface configurations in capillary represented by the cross section view A-A' and B-B' (a) concave, (b) convex, and (c) slope.

To conceptually identify the position of porous media interface created in the capillary, 40,000 non-motile tumbly mutant *E. coli* HCB359 and motile wild-type bacterial *E. coli* HCB1 swimming trajectories were generated by the Monte Carlo simulation algorithm in the simulation box with three different porous media interface configurations under the bacterial surface association mechanism, with $t_3 = 20\,\mathrm{s}$. The simulation results are further superimposed with the schematic porous media interface configurations in Figure S2.



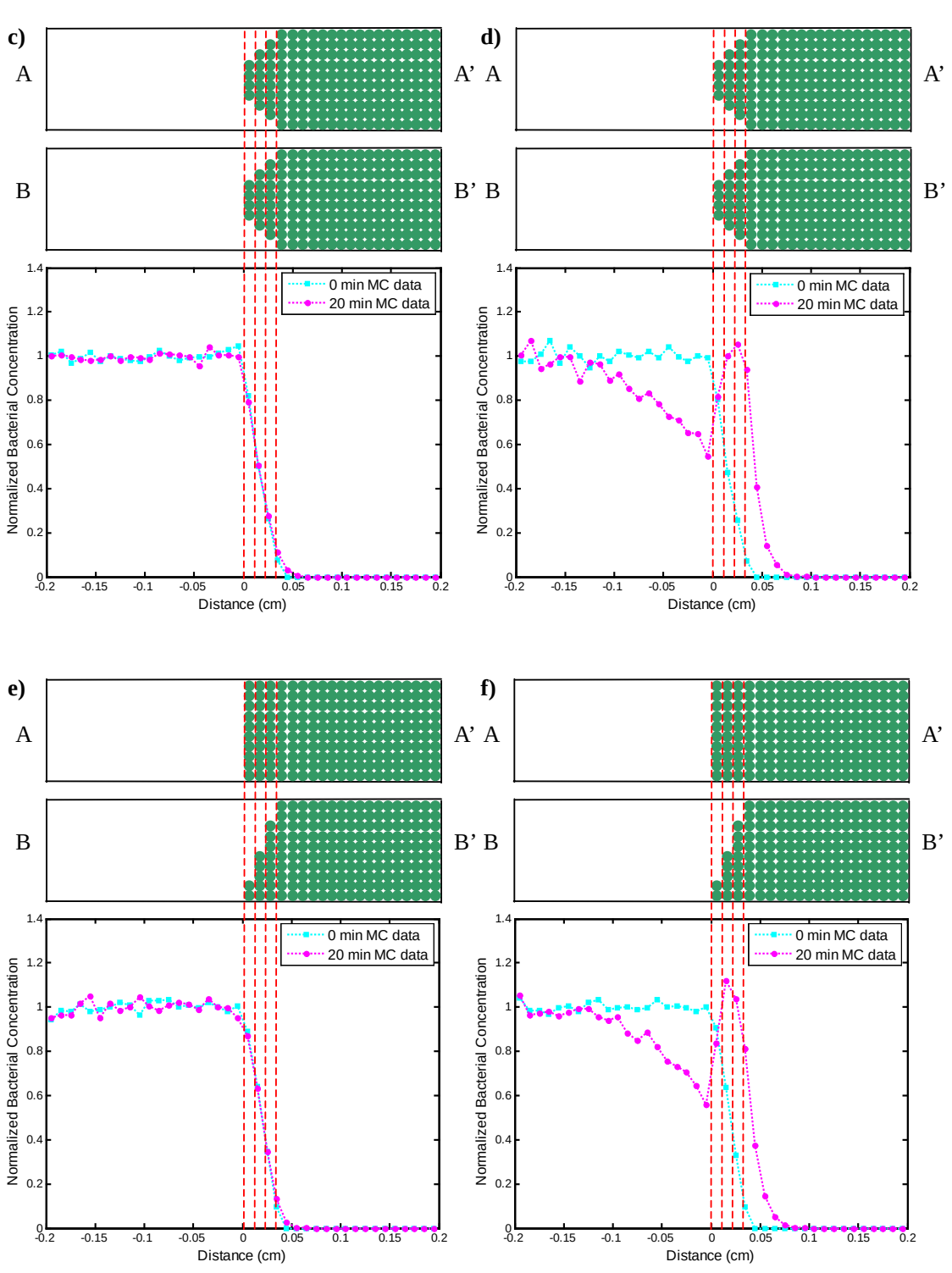


Figure S2. Normalized bacterial initial 0-min and final 20-min population distribution across three possible porous media interface: concave configuration (a) for non-motile tumbly mutant *E. coli* HCB359 and (b) for motile wild-type bacterial *E. coli* HCB1; convex configuration (c) for *E. coli*

HCB359 and (d) for *E. coli* HCB1; and slope configuration (e) for *E. coli* HCB359 and (f) for *E. coli* HCB1 predicted by the Monte Carlo simulations (MC data) under bacterial surface association mechanism: t_3 = 20s.

As seen in Figure S2, the initial bacterial distributions across the porous media interface are not the idealized sharp step-change styles. For non-motile tumbly mutant *E. coli* HCB359, for each interface configuration, there is a slight shift of the concentration distribution from the initial 0-min profile to the final 20-min profile. For motile wild-type bacterial *E. coli* HCB1, its accumulation peak will be located either in the mixing zone or the bulk porous media phase, depending on different mixing amounts and the interface configurations, but its trough point is consistently located in the bulk free solution phase, so this trough point is selected as the porous media interface observed from the capillary assay.