



Simulation of Bacterial Motion in Sterically Complex Environments

Matthew Kafker, Maria Dresser, Kentaro Hoeger, Tristan Ursell

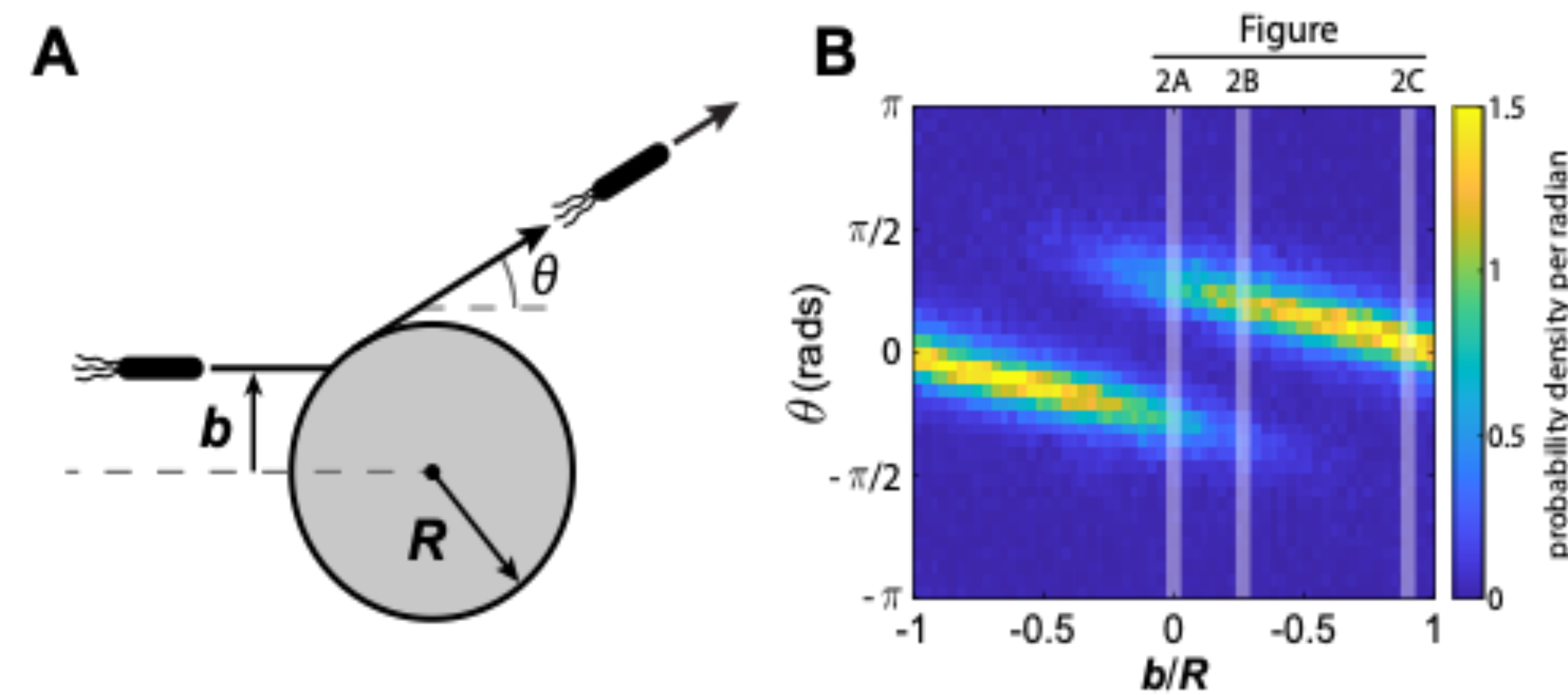
University of Oregon, Department of Physics, Eugene OR



How do bacteria move through complex spaces?

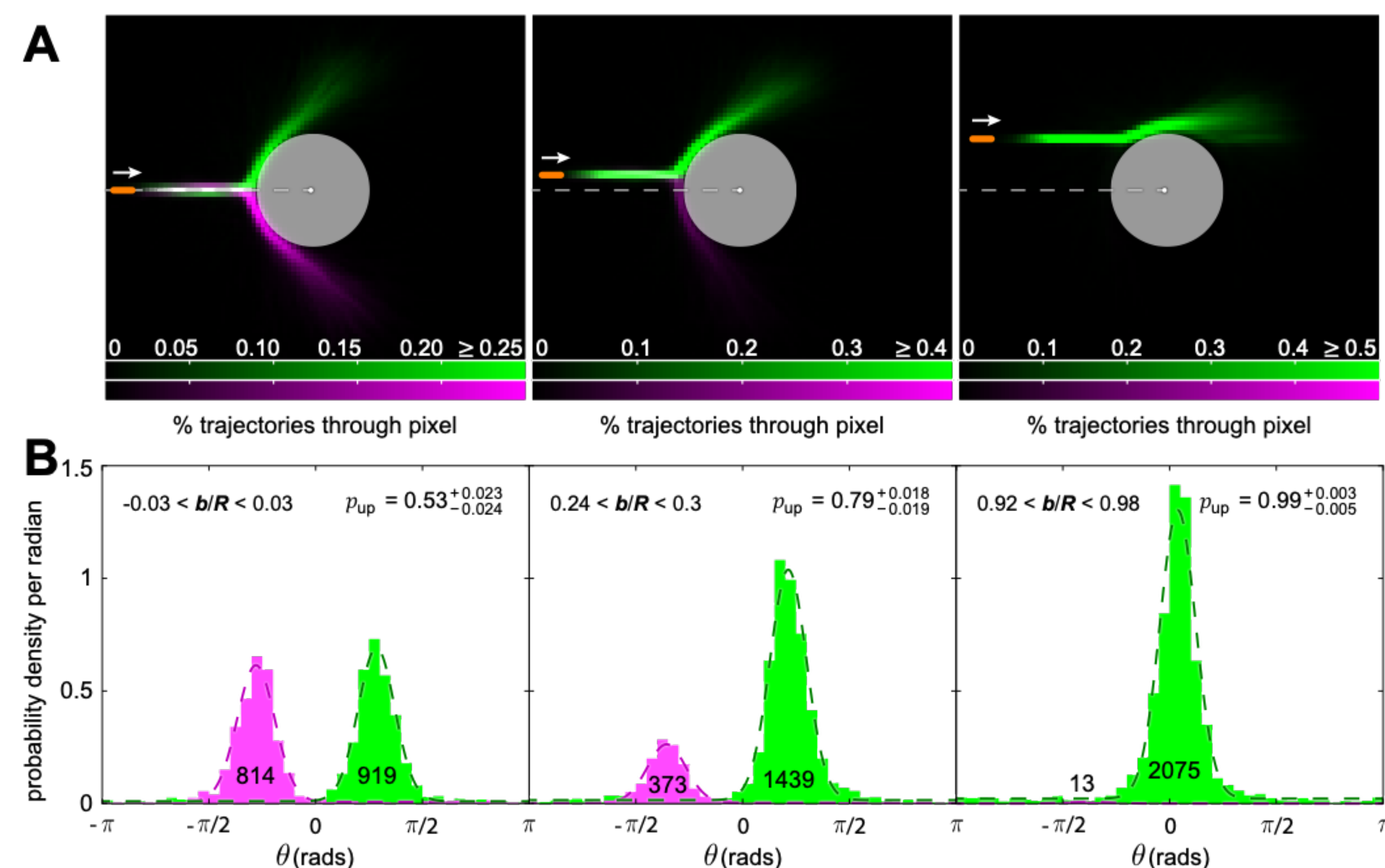
Many species of bacteria navigate complex and heterogeneous environments to search for metabolic resources and avoid toxins. Common among such complexities is steric structure – solid objects whose surface curvature alters bacterial trajectories upon impact. We investigate the effect of multiple interactions with steric structure on bacterial trajectories.

We characterized scattering of bacteria as they swam into vertical pillars of different radii. We use this as a simple model to understand how bacteria interact with solid, curved objects in their environment.



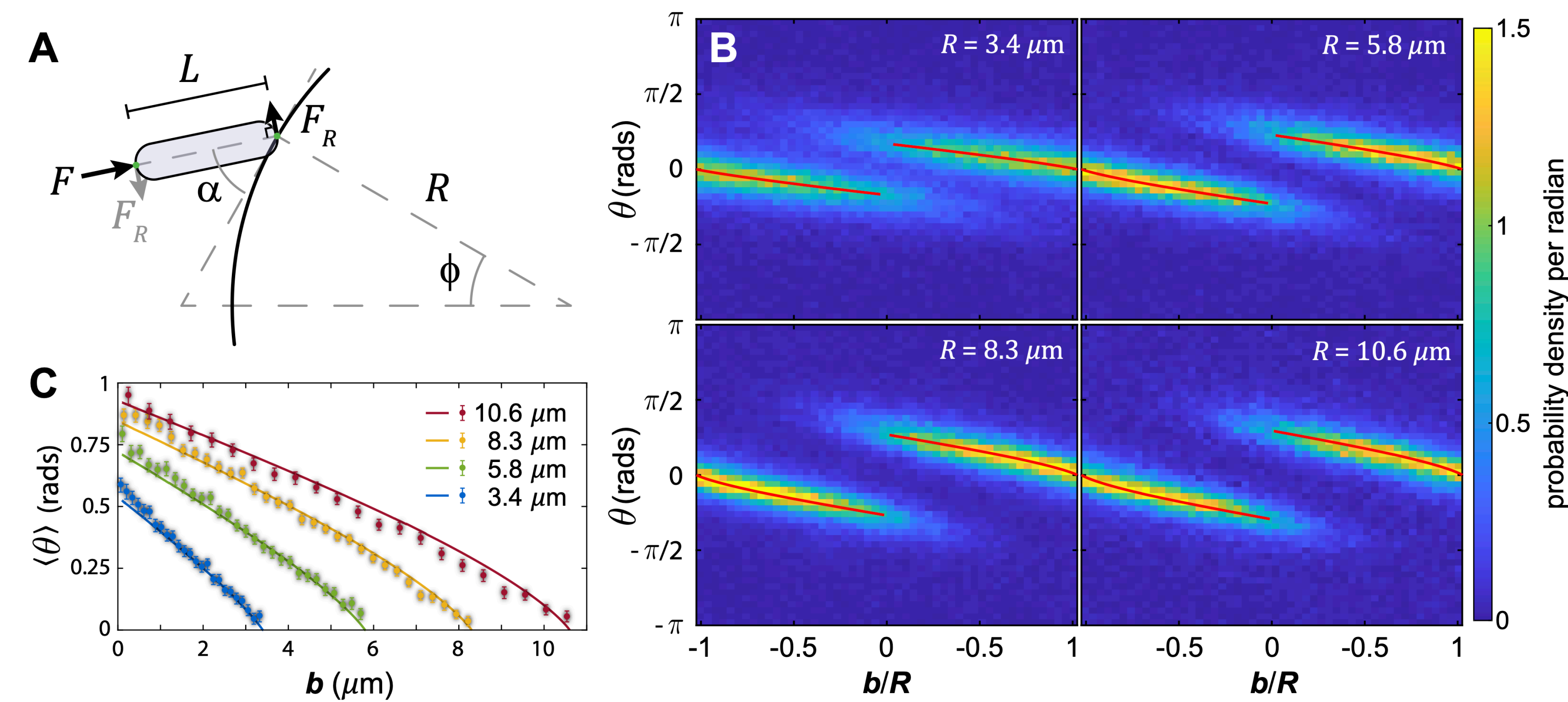
A.) Graphical definition of b , θ . B.) Probability distribution of θ v. b .

Using the impact parameter b and outgoing direction θ defined above, we describe the scattering process using a probability distribution. We see below that this probability distribution describes predominantly forward-scattering behavior.



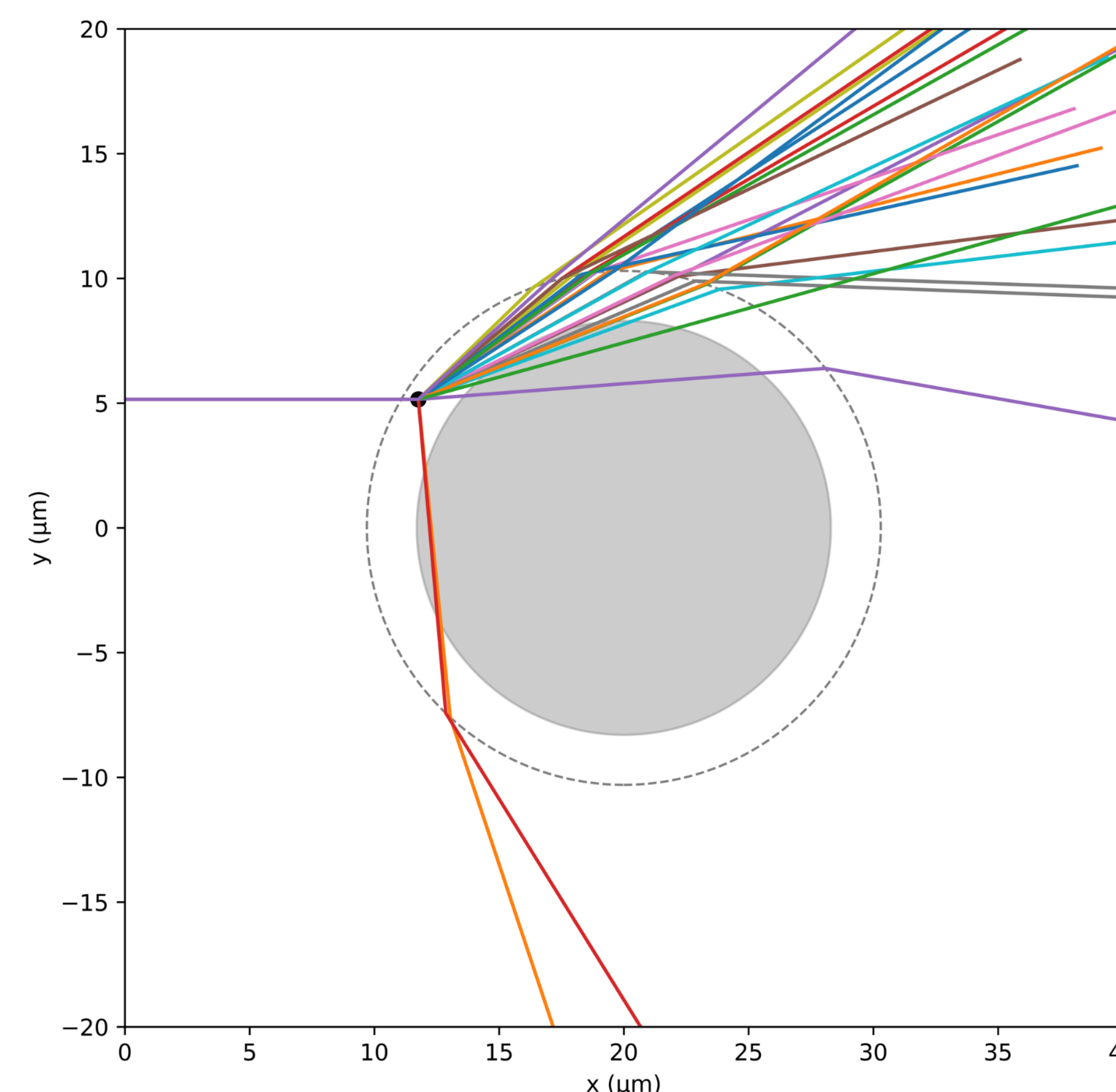
A.) Scattering characteristics for three values of b . B.) Theta histograms for trajectories from A.

We repeated these experiments with pillars of various radii.



A.) Mechanical analysis of scattering process. B.) Probability distribution of θ v. b for four pillar radii. C.) Mean outgoing direction θ vs. b for four pillar radii.

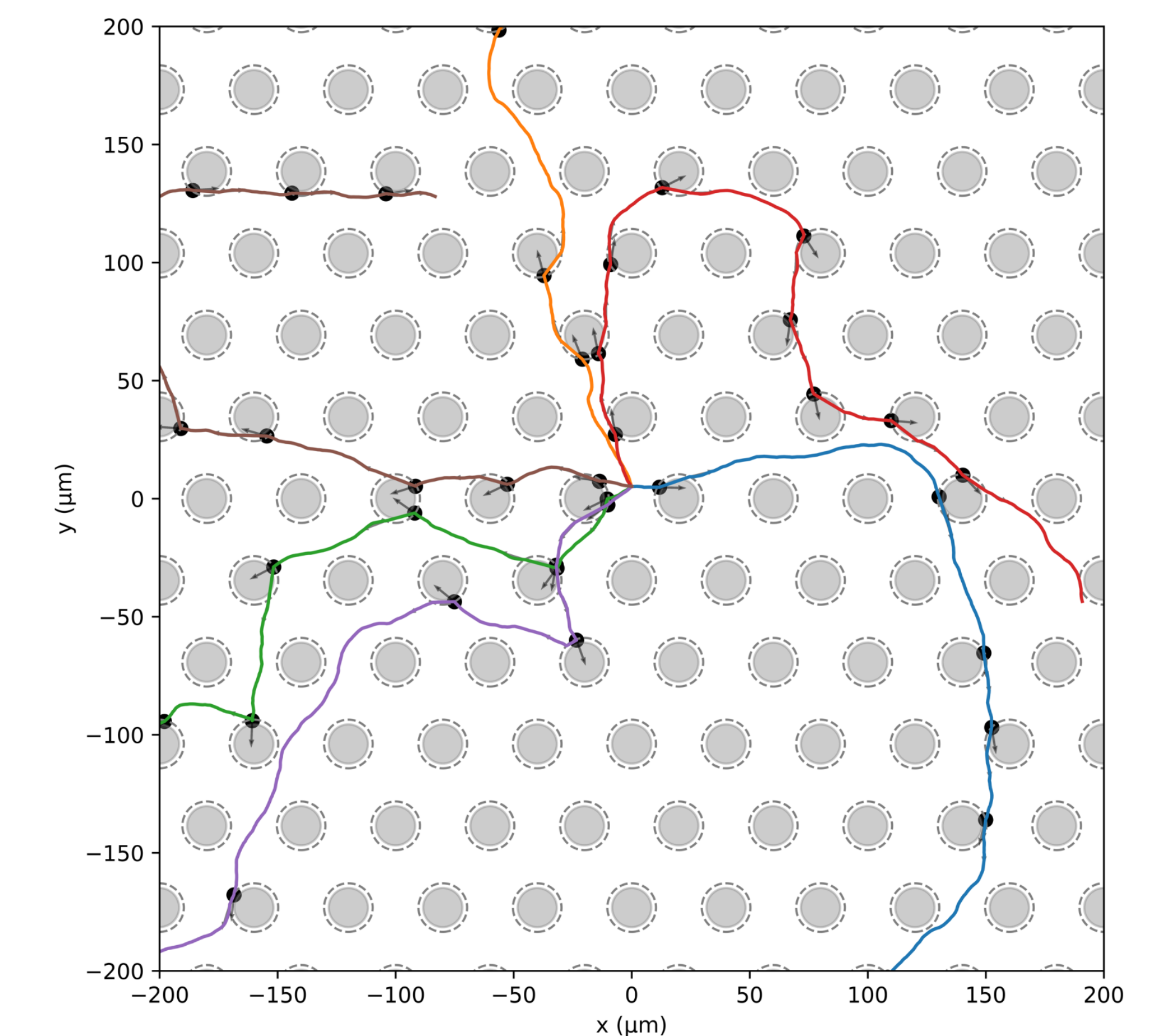
To investigate the effects of multiple interactions, we use an agent-based computer simulation of cells moving in 2D environments. Each environment presents simulated cells with steric objects in the form of circular pillars. Cells scatter with pillars according to the experimentally-derived probability distributions.



Simulated scattering of 25 cells at fixed b from $8.3\mu\text{m}$ pillar.

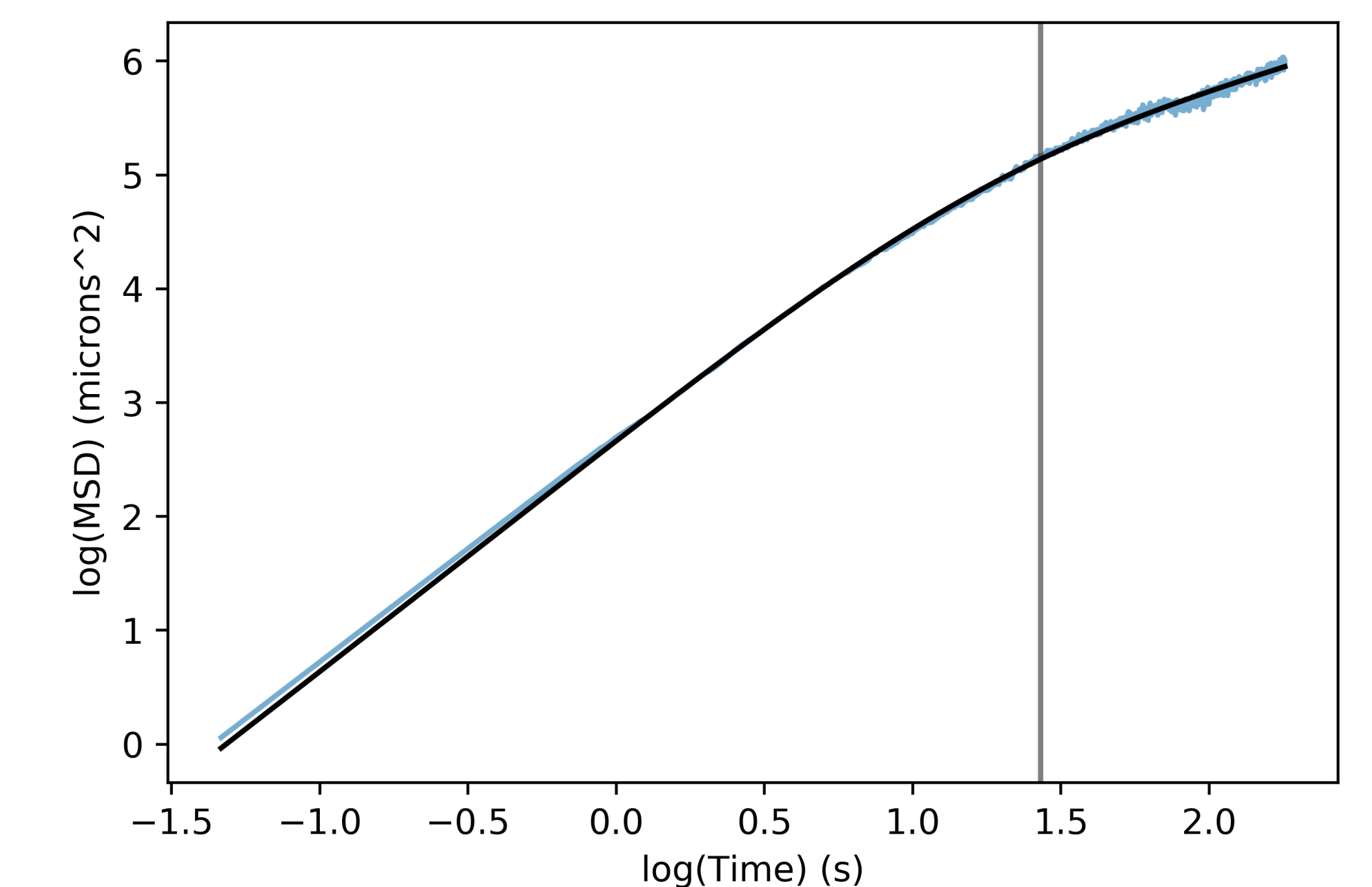
Once a cell enters the interaction radius (dashed circle), a scattering event is triggered. We model dynamics inside the interaction radius as a black box, connecting the point of entry to the point of exit with a straight line.

We visualize one such simulation below. When not scattering, cells undergo a persistent random walk.



Simulation of 7 cells in a hexagonal grid of pillars. Each cell is represented by a single color. Black dots indicate scattering.

To characterize motion of the ensemble of cells, we measure their mean squared displacement (MSD). Ensemble motion transitions from ballistic to diffusive at the vertical line in the figure below.



Log-log plot of MSD vs. time for a simulation of 50 cells swimming for 3 minutes. Blue curve is simulation data; black curve is fitted model.

References

- O. Sipos, K. Nagy, R. Di Leonardo, and P. Galajda, "Hydrodynamic Trapping of Swimming Bacteria by Convex Walls," *Phys. Rev. Lett.*, vol. 114, no. 25, p. 258104, Jun. 2015, doi: 10.1103/PhysRevLett.114.258104.
- P. D. Frymier, R. M. Ford, H. C. Berg, and P. T. Cummings, "Three-dimensional tracking of motile bacteria near a solid planar surface," *Proc. Natl. Acad. Sci.*, vol. 92, no. 13, pp. 6195–6199, Jun. 1995, doi: 10.1073/pnas.92.13.6195.

