Characterizing the relationship between bacterial motility and range expansion

Noah Pettinari[1] and Raghuveer Parthasarathy[1]

[1]Department of Physics, University of Oregon, Eugene, OR

Introduction

- Cellular motility is a well understood trait in bacteria, but its relation to larger scale range expansion has not been rigorously tested
- Run and tumble motility is characterized by long “runs” followed by short bouts of “tumbling”, or random reorientations of cells
- Current diffusion models do not incorporate features such as spatial structure into their predictions

Methods

- We examined five bacterial species
- In range expansion assays, bacteria were inoculated into low-density agar swim plates and left to grow for 24hr periods at 30°C
- In cellular tracking assays, bacteria were imaged in bulk gel using light sheet fluorescence microscopy

Figure 1: *Aeromonas* tracks in motility assay at 30°C.

Analysis

- Particle tracking was used to measure speed and tumble time distributions
- Image segmentation on swim plates to measure range expansion rates
- Calculated diffusion coefficient, compared to range expansion rates:

$$v_{range} = \sqrt{Dr}$$

Diffusion-driven range expansion

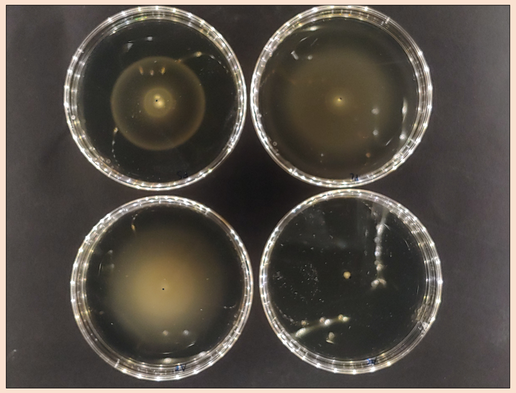

Figure 2: 0.2% agar swim plates growing at 30°C at 9 hours post-inoculation. From top left, clockwise: *Pseudomonas (PS), Plesiomonas (PL), Acinetobacter (AC), Aeromonas (AE)*.

Results

- Initial measurements of range expansion do not agree with predicted rates from pure diffusion

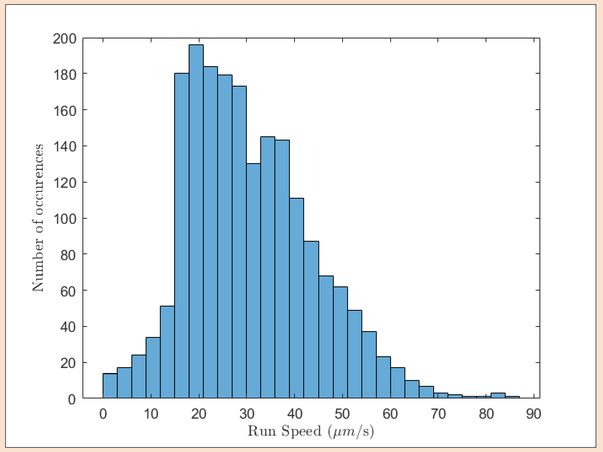

Figure 3: Speed distribution for a set of *Aeromonas* tracks, with a mean speed of 30 +/- 13 um/s.

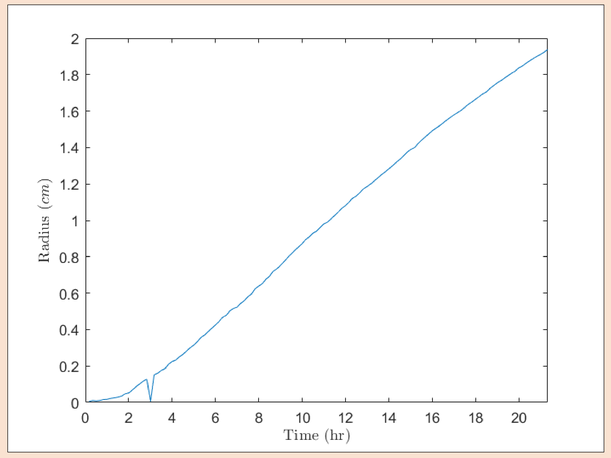

Figure 4: Radius of bacterial range over time. The plot indicates linear radial growth over time, with an approximate measured expansion rate of 0.27 um/s.

Future Directions

- Increase robustness of tracking analysis and improve image segmentation for improved measurements
- Examine multi-species interactions and their influence on motile behavior
- Measure “spatial diffusion” in structured regions at the cellular level

Acknowledgements

I would like to thank Vikram Sandhu, Elena Wall, the Parthasarathy Lab, and the Guillemin Lab for their support and assistance with this project. Thank you!

This work was supported by the National Institutes of Health (http://www.nih.gov/), under Awards P50GM09891 and P01GM125576-01

References

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