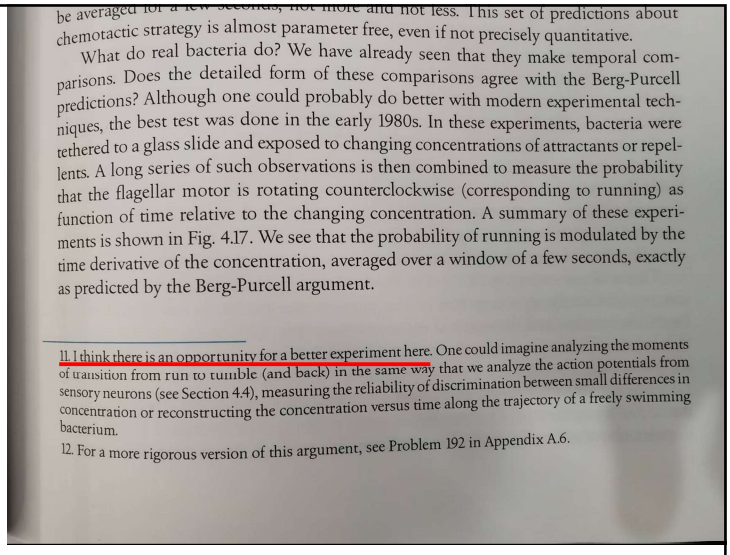
Quantitative principles in biological systems

3b. “Does biology care about bits?”

Fall 2026

Do *E. coli* count single molecules?



be averaged for a few seconds, not more and not less. This set of predictions about chemotactic strategy is almost parameter free, even if not precisely quantitative.

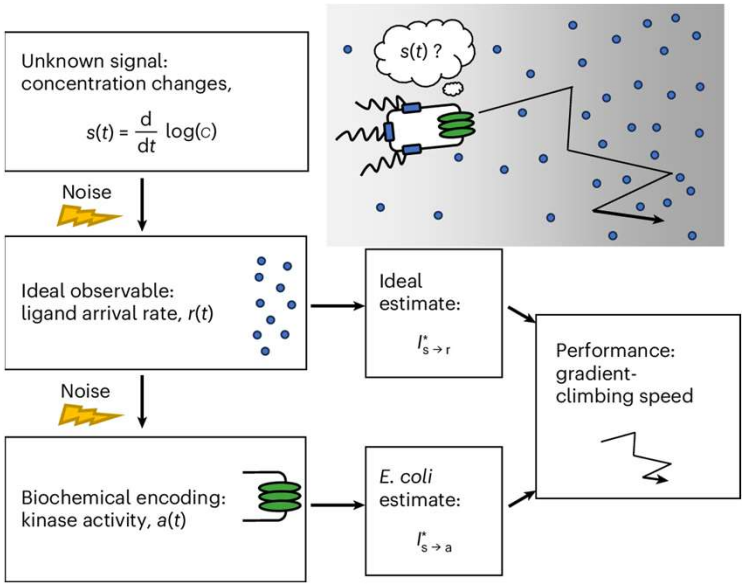
What do real bacteria do? We have already seen that they make temporal comparisons. Does the detailed form of these comparisons agree with the Berg-Purcell predictions? Although one could probably do better with modern experimental techniques, the best test was done in the early 1980s. In these experiments, bacteria were tethered to a glass slide and exposed to changing concentrations of attractants or repellents. A long series of such observations is then combined to measure the probability that the flagellar motor is rotating counterclockwise (corresponding to running) as function of time relative to the changing concentration. A summary of these experiments is shown in Fig. 4.17. We see that the probability of running is modulated by the time derivative of the concentration, averaged over a window of a few seconds, exactly as predicted by the Berg-Purcell argument.

11. I think there is an opportunity for a better experiment here. One could imagine analyzing the moments of transition from run to tumble (and back) in the same way that we analyze the action potentials from sensory neurons (see Section 4.4), measuring the reliability of discrimination between small differences in concentration or reconstructing the concentration versus time along the trajectory of a freely swimming bacterium.

12. For a more rigorous version of this argument, see Problem 192 in Appendix A.6.

“E. coli do not count single molecules”
https://www.biorxiv.org/content/10.1101/2024.07.09.602750v1.full
The title of this paper contradicts our expectations from unit 1. What is their argument?

Chemotaxis is a chain of information transmission ending at behavior.



Mattingly et al. *Nat Phys* (2026)

What did they measure?

- What is the relationship between velocity and signal?
- How did they measure CheA activity?
  - Why not use FRET between CheY and CheA?
- What was the difference between the measurements in their two papers?

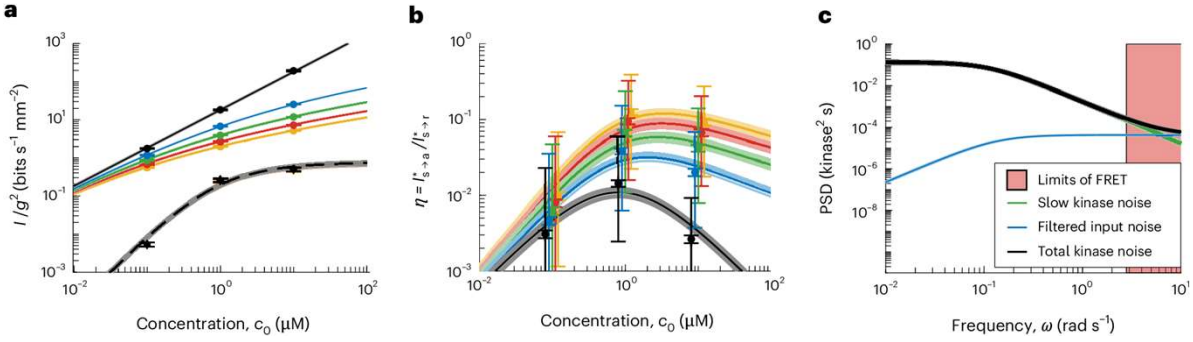
Mattingly et al. *Nat Phys* (2026)

What did they calculate?

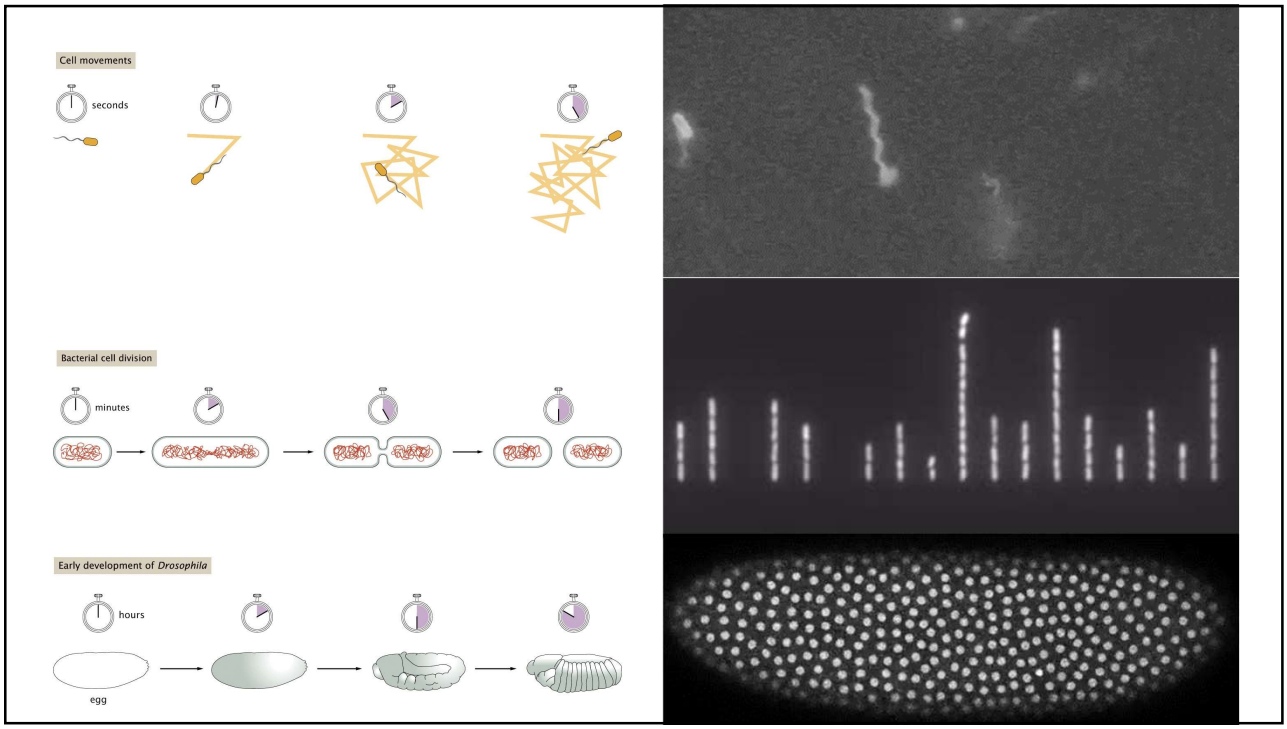
- What processes did they model?
  - $s \to r$ (stochastic processes), $r \to a$ (linear response plus noise), $a \to m$ (previous work), $m \to v$ (previous work), $v \to s$ (assumed negligible)
- How did they calculate information rate from signal to kinase activity $\dot{I}_{s\to a}$?
- How did they calculate $\dot{I}_{s\to r}$?
  - How can this task be possible without measuring r?
- What is the difference between $\dot{I}$ and $\dot{I}^*$?

Mattingly et al. *Nat Phys* (2026)

What was their question? ie Where did the conventional argument go wrong?



Mattingly et al. *Nat Phys* (2026)


Cell movements
seconds
Bacterial cell division
minutes
Early development of *Drosophila*
hours
egg