Calculating the Information Transmission Rate for (almost) *any* System

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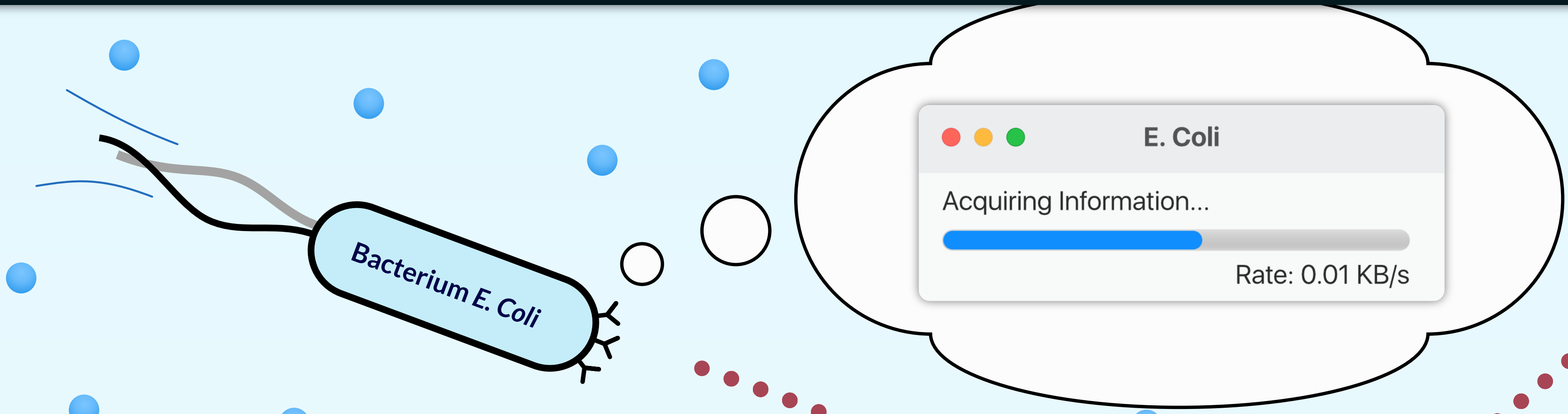
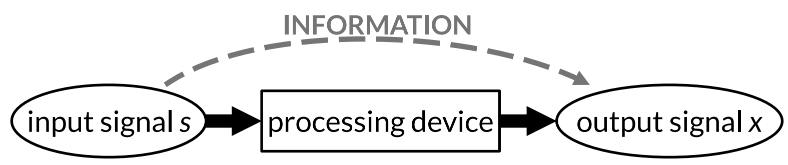


An Example System from Biology:
Bacteria like *E. coli* actively swim towards regions of high nutrient concentration. Inside of the bacterium a sophisticated chemical signaling network processes the information obtained from the cell's receptors. This information is used to guide the bacterium's movement.

PROBLEM

Information Measures



The **mutual information** I(*S*, *X*) quantifies how much information the output *x* contains about the input *s* (on average).

$$\mathrm{I}(S,X) = \iint \mathrm{d}s\,\mathrm{d}x\; \mathrm{P}(s,x)\log_2\frac{\mathrm{P}(s,x)}{\mathrm{P}(s)\mathrm{P}(x)}$$

However, to quantify the *speed/rate* of information transmission, we need to consider the case where *s* and *x* are not single values, but entire input/output **trajectories (i.e. time-series)**!

Speed of Information Transmission

The **information tranmission rate** is defined as the mutual information for long trajectories, divided by their duration/length *T*.

$$R = \lim_{T\to\infty}\frac{\mathrm{I}(\mathbf{S}_T,\mathbf{X}_T)}{T}$$

This is the quantity we want to compute!

The information transmission rate *cannot* be computed using standard techniques. Except for the simplest systems **approximations need to be used**.

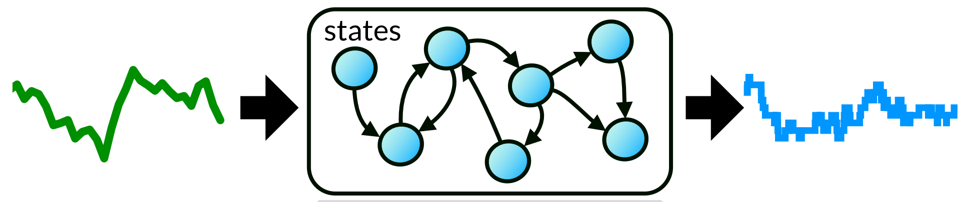
? **To compute the information transmission rate *exactly*, we need to**

- **obtain the probabilities of individual trajectories**
- **efficiently perform integrals in "trajectory space"**

SOLUTION

Model Building

We model our processing device as a stochastic system with different internal states and random transitions between these. Such models are widely used across many fields.



Master Equation

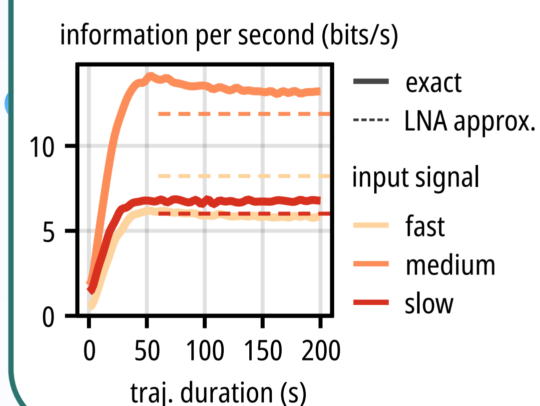
$$\frac{\mathrm{dP}_n(t)}{\mathrm{d}t} = \sum_k Q_{nk}\mathrm{P}_k(t)$$

$\mathrm{P}_n(t)$: probability of being in state *n* at time *t*.

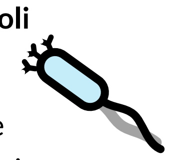
Novel Computational Scheme

- from the master equation we can compute the trajectory probability *exactly*.
- by leveraging Monte-Carlo simulation schemes developed in polymer physics, we can efficiently compute the necessary (path) integrals.

Results



Information Rate of E. Coli



- Our technique exactly computes the information transmission rate for a complex model of E. coli
- Typically used approximations can lead to very significant bias

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