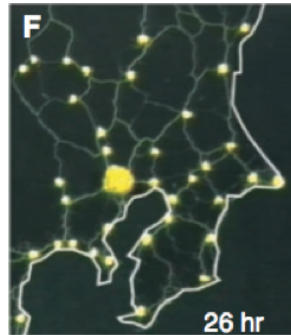
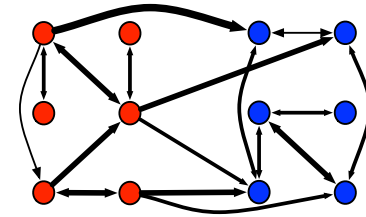
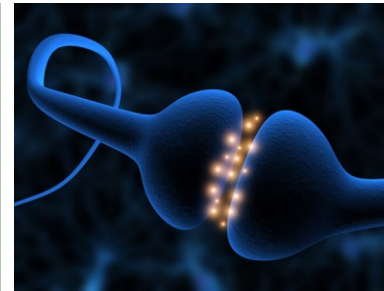


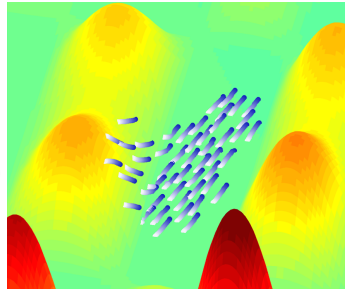
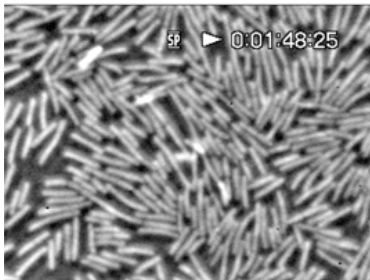
4 examples



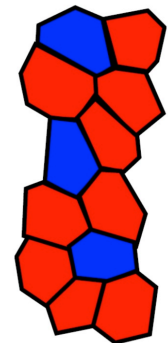
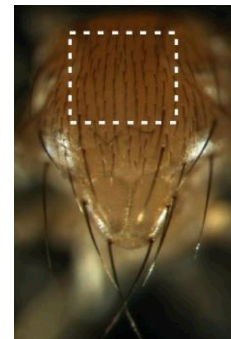
Slime mold foraging & MST construction
[Tero et al. *Science* 2010]



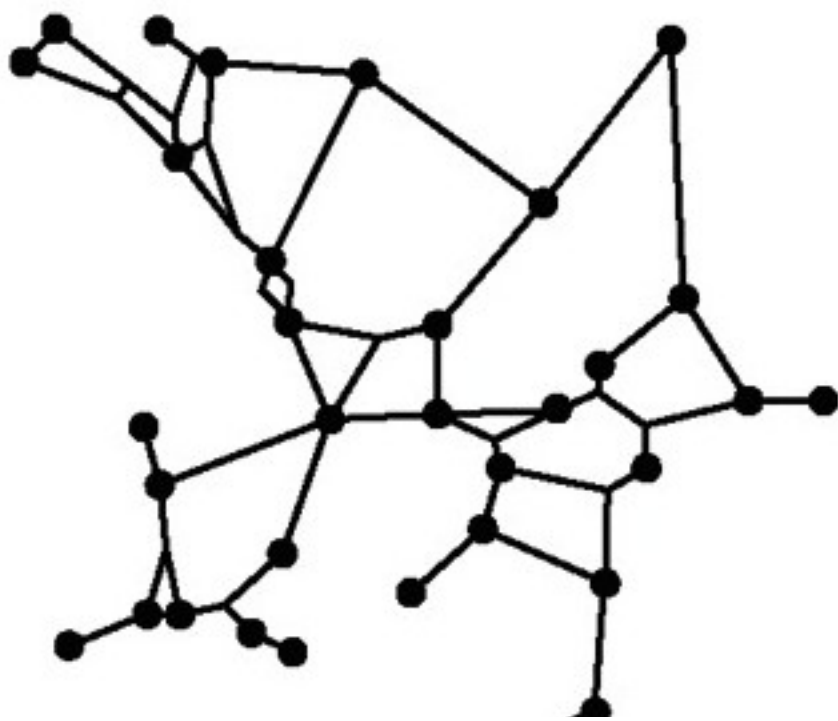
Synaptic pruning & network design



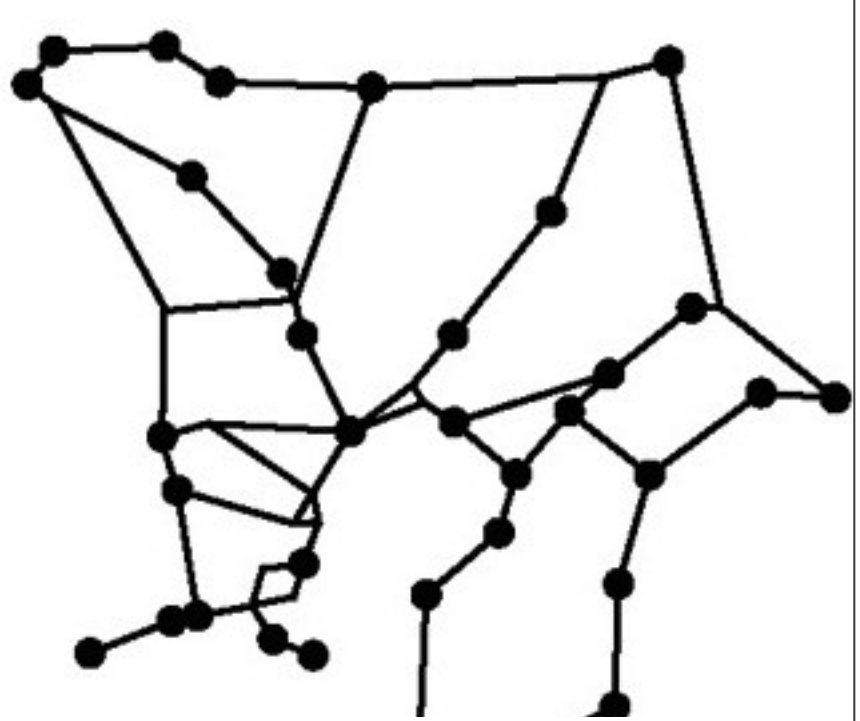
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Fly brain development & MIS
[Afek et al. *Science* 2010]



Slime mold network



Tokyo rail network

Very similar transport efficiency and resilience

Slime mold model

- Problem:
 - Design a network to connect food
- Platform:
 - Distributed (no centralized controller)
 - Food locations unknown
 - Message passing between nodes
- Algorithm:
 - Feedback: the greater the internal protoplasmic flow, the thicker the tube
 - Idea: reinforce preferred routes; remove unused or overly redundant edges
- Evaluation:
 - network efficiency, robustness, wiring

Slime mold algorithm

Start with meshed lattice

The flux through a tube (edge) is calculated as:

$$Q_{ij} = \frac{D_{ij} (p_i - p_j)}{L_{ij}}$$

Annotations for the equation:

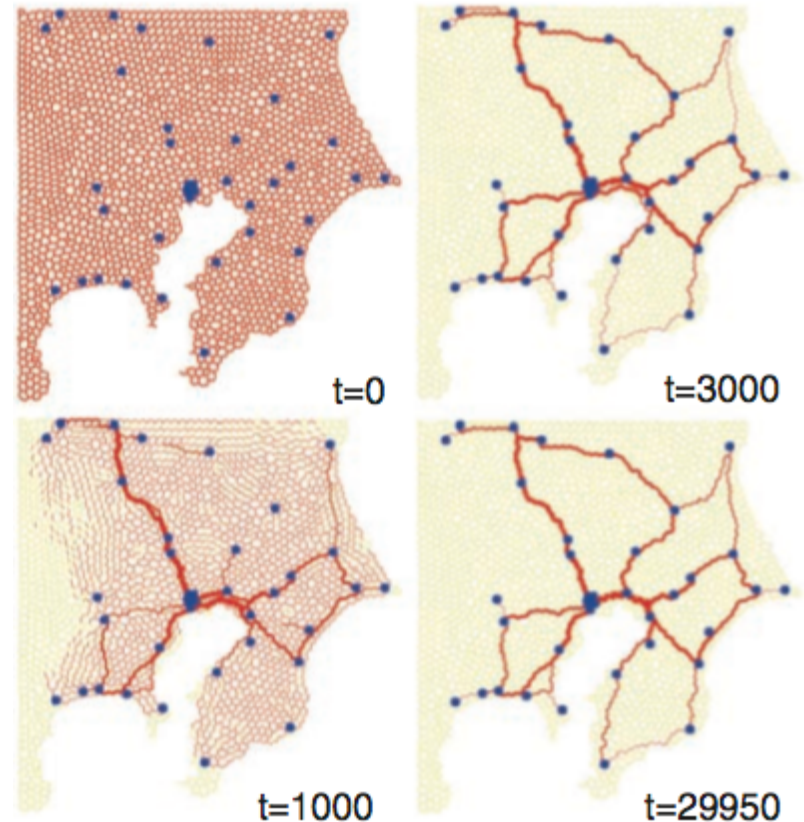
- $p_i - p_j$: Pressure difference between ends of tube
- D_{ij} : Conductance of tube
- L_{ij} : Length of tube

Think “network flow”: in each time step, choose two random food sources:

$$\sum_j Q_{1j} = I_0 \quad \text{Source pumps flow}$$

$$\sum_j Q_{2j} = -I_0 \quad \text{Sink consumes flow}$$

$$\sum_j Q_{ij} = 0 \quad \text{Else pass flow along (conservation)}$$



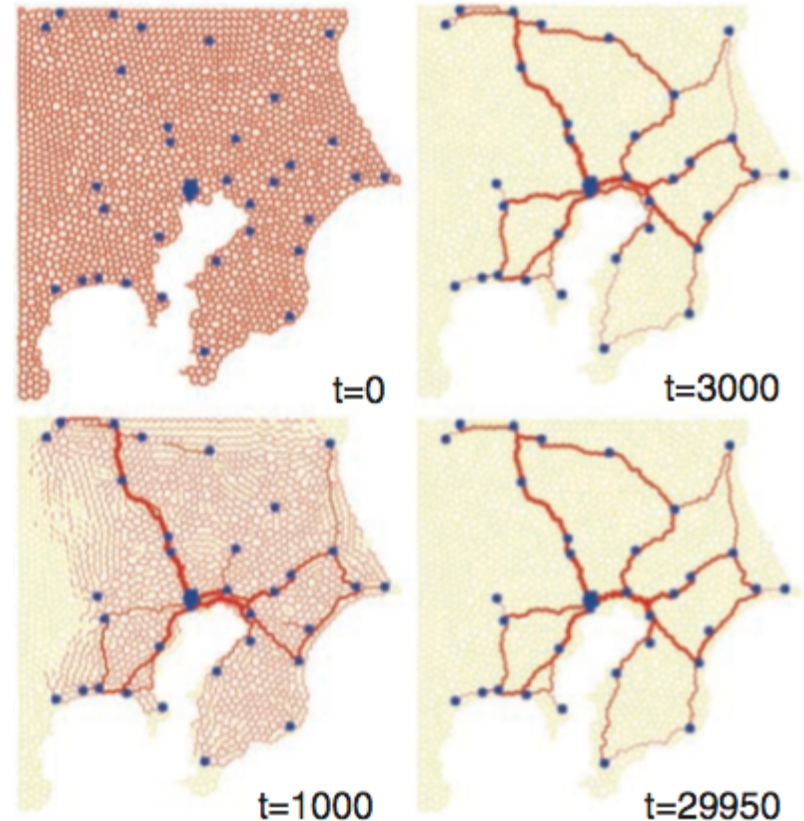
Update rule for tube weights

$$\frac{d}{dt}D_{ij} = f(|Q_{ij}|) - D_{ij},$$

First term: expansion of tubes in response to the flux

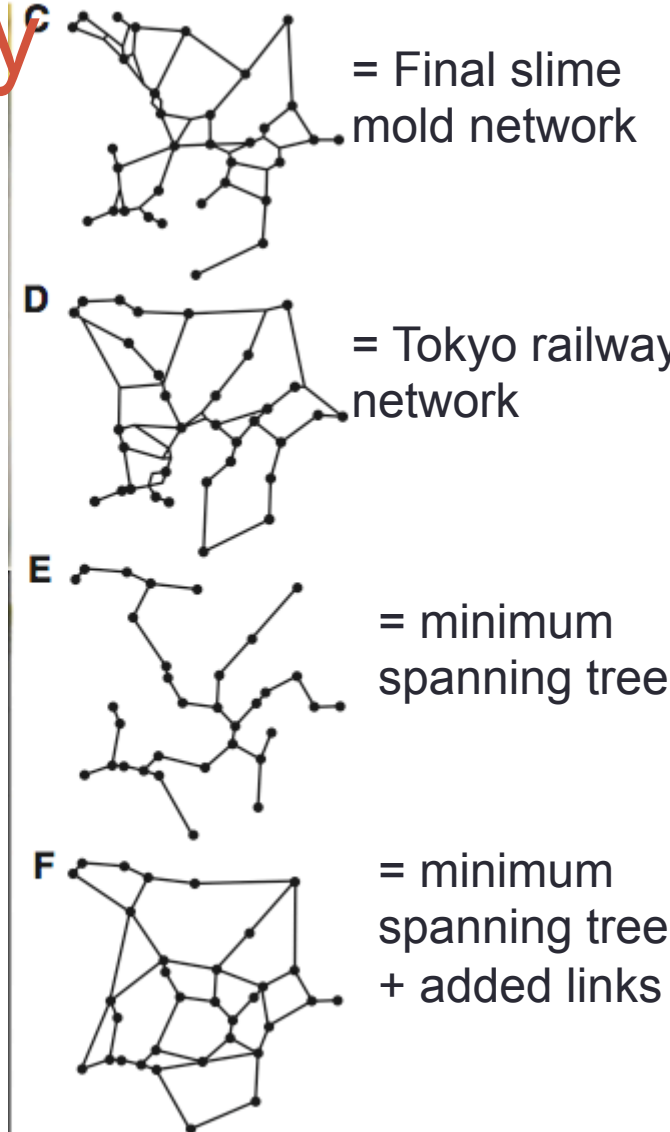
Second term: the rate of tube constriction; the tube gradually disappears if no flow

$f(|Q|)$ = sigmoidal curve

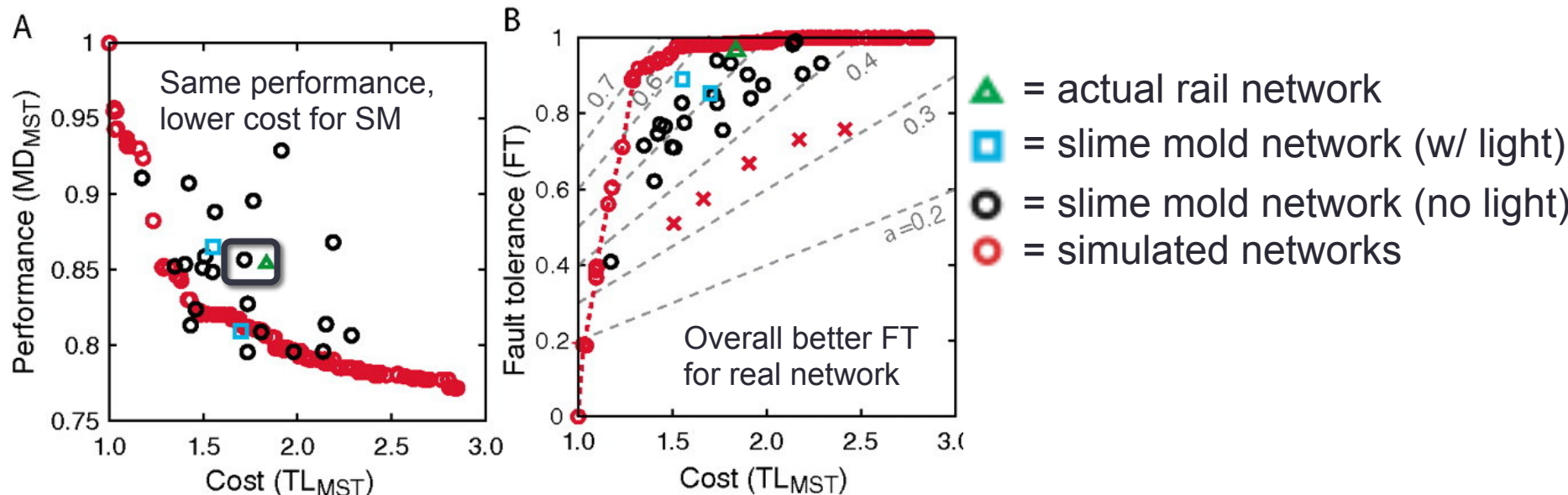


Evaluating network quality

- **TL** = wiring length used
- **MD** = avg minimum distance between any pair of food sources
- **FT** = tolerance to disconnection after single link failure



Slime mold and human-engineered networks have similar structural properties



Cost: $TL_{MST}(\triangle) = 1.80$ and $TL_{MST}(\circ) = 1.75 \pm 0.30$

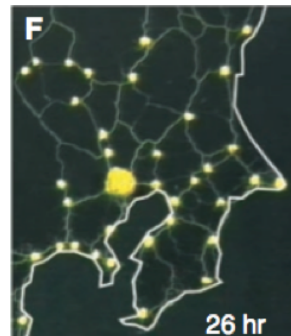
SIMILAR

Efficiency: $MD_{MST}(\triangle) = 0.85$ and $MD_{MST}(\circ) = 0.85 \pm 0.04$

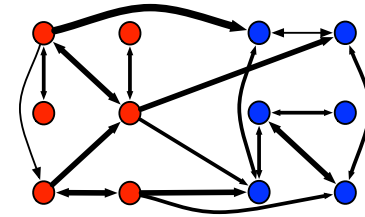
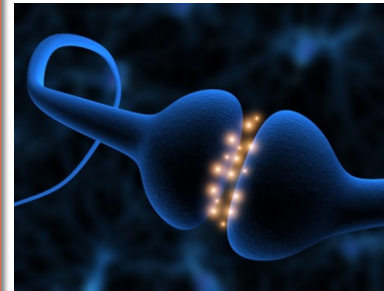
SIMILAR

Fault tolerance: 4% of links cause rail network disconnection; 14-20% for mold

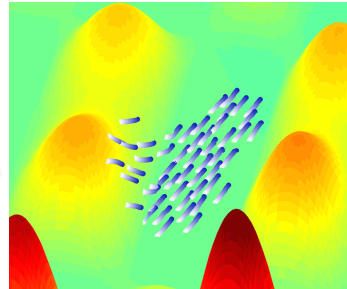
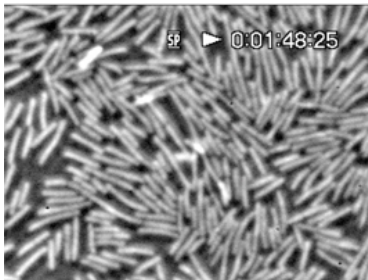
4 examples



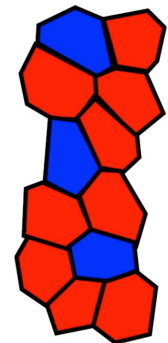
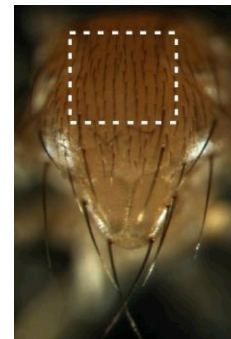
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Synaptic pruning & network design

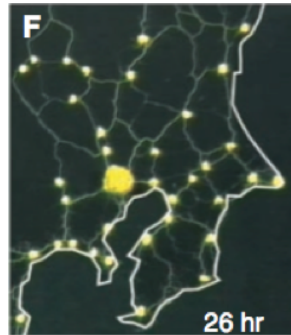


E coli foraging & consensus navigation
[Shklarsh et al. *PLoS Comput. Biol* 2013]

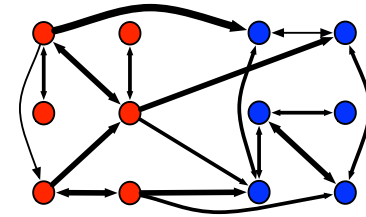
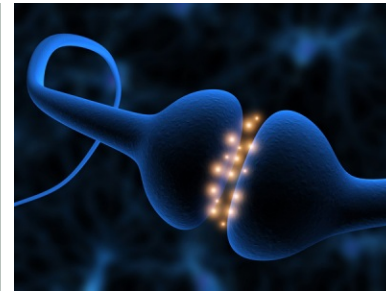


Fly brain development & MIS
[Afek et al. *Science* 2010]

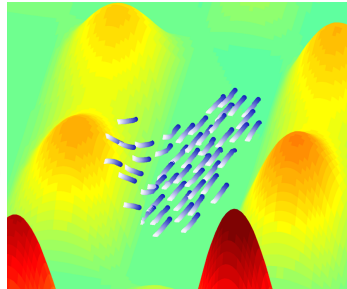
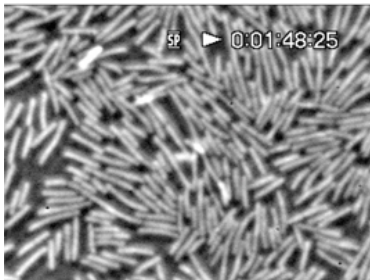
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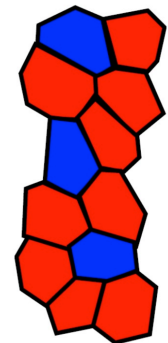
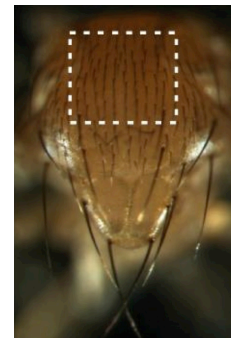
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Synaptic pruning & network design



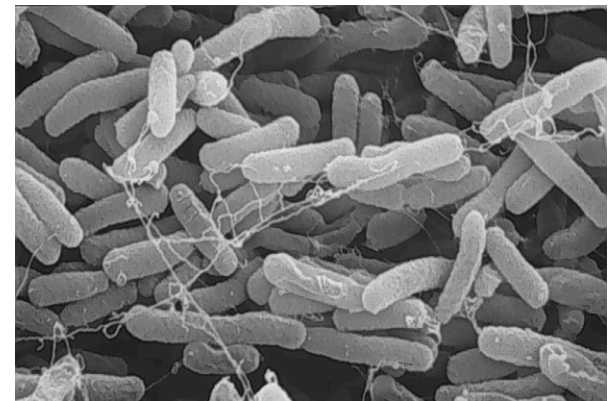
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Fly brain development & MIS
[Afek et al. *Science* 2010]

Bacterial foraging

- Problem: how does a collection of bacteria collectively navigate to find food in a complicated terrain?
- Platform:
 - Distributed (no centralized controller)
 - Food location unknown
 - Broadcast-like messages: individual and neighbor knowledge
 - Bounded message complexity [[see talk by Shashank Singh tomorrow](#)]
- Algorithm: (next slides)
- Evaluation:
 - Detection accuracy and time

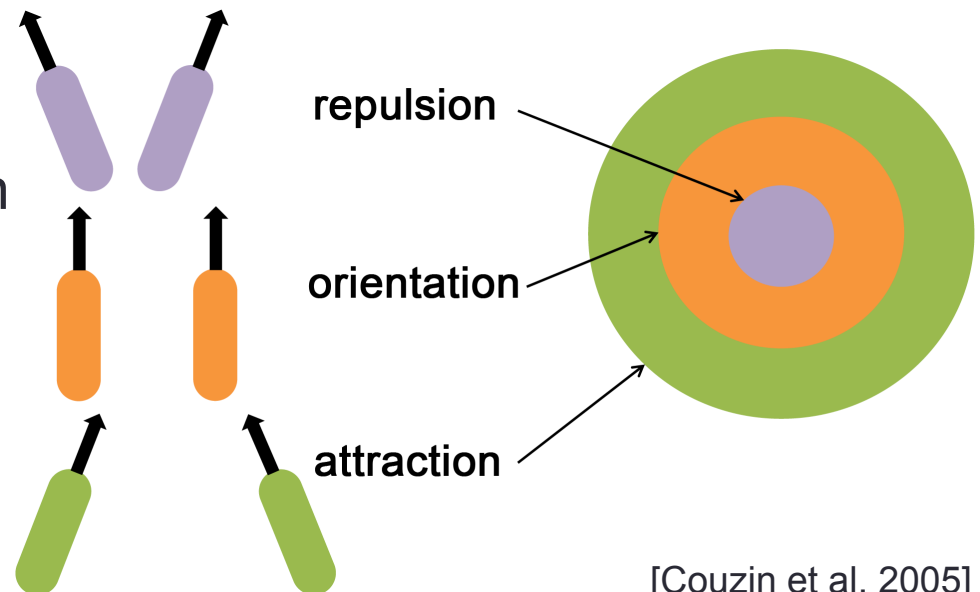


Bacterial chemotaxis

- Bacteria navigate via chemotaxis: move according to gradients in the chemical concentration (food)
- If low food concentration, tumble more (move randomly)

Bacteria also acquire cues from neighbors:

- Repulsion to avoid collision
- Orientation
- Attraction to avoid fragmentation

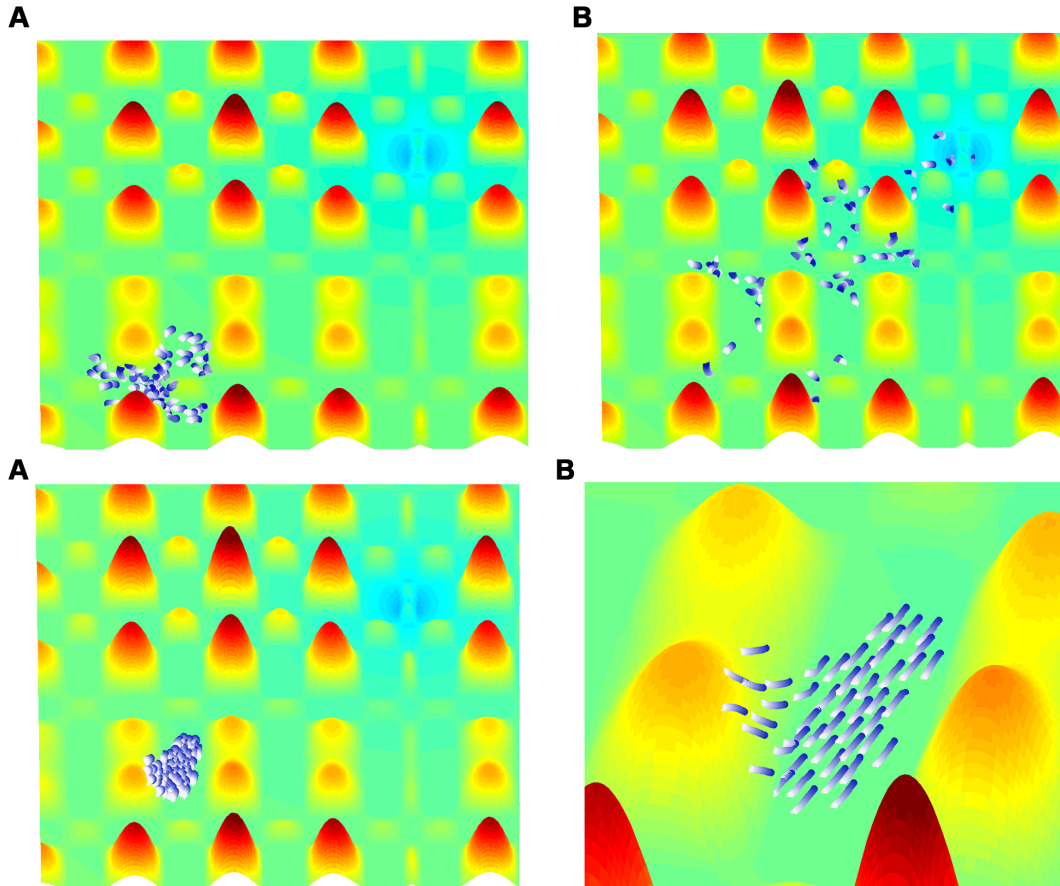


[Couzin et al. 2005]

Bacterial automata

- Treat bacteria as automata with two information sources:
 - Individual belief based on food source gradient
 - Interaction with neighbors' beliefs
- Parameter $w(i)_t$ controls how much bacterium i “listens” to its neighbors at time t

Analysis of different interaction weights



No interactions:
inefficient collective
navigation

Static interactions:
erroneous positive
feedback leads bacteria
astray: a subgroup gets
“bad” information and
leads others along an
incorrect trajectory

Solution: adaptive interaction weights

- Parameter $w(i)_t$ controls how much bacterium i “listens” to its neighbors at time t
- Adjust interaction weight $w(i)_t$ based on “self-confidence”:
 - When a bacteria finds a beneficial path (strong gradient), downweight $w(i)_t$ and listen less to neighbors
 - When unsure, upweight $w(i)_t$ to increase neighbor influence
- A simple interaction rule:

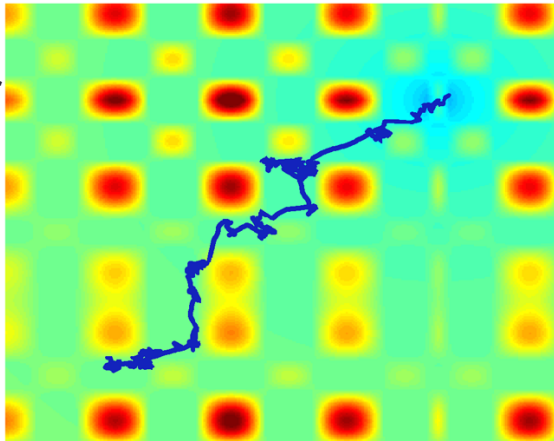
$$w_i(t) = \begin{cases} 1 & \text{if } \Delta c_i(t) \gg 0 \\ 0 & \text{else} \end{cases}$$

Change in gradient detected

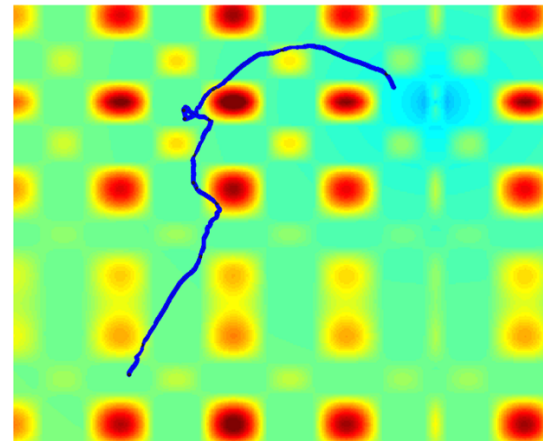


Plasticity of the interaction network leads to more efficient collective navigation

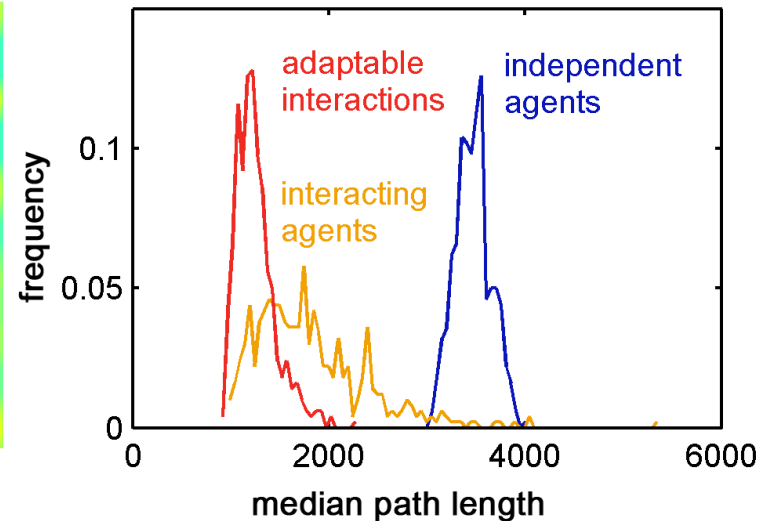
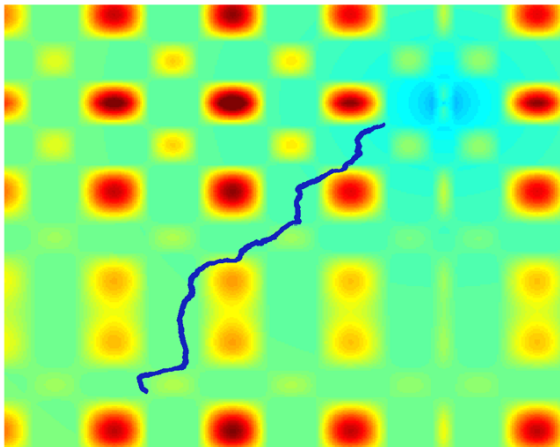
Random walk for independent agents



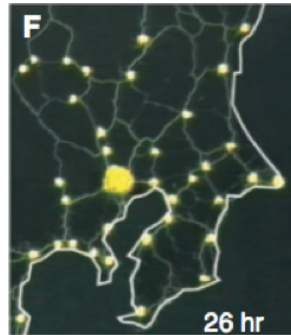
Some errors with fixed weights (static interactions)



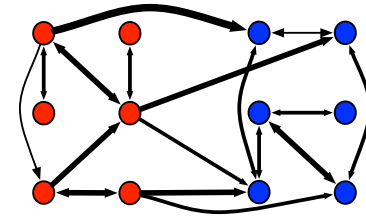
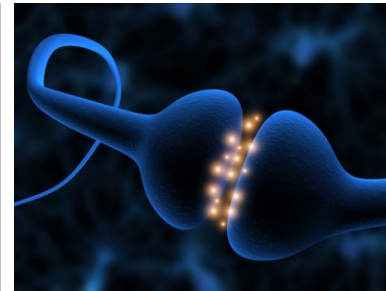
Fewer errors with adaptable interactions



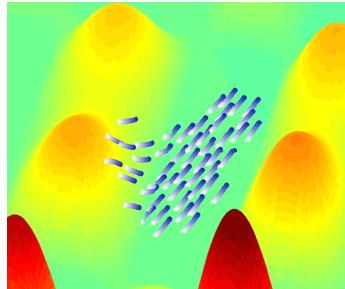
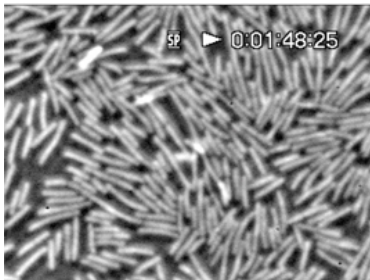
4 examples



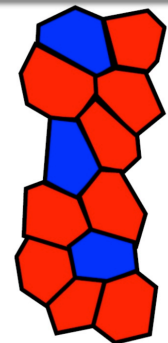
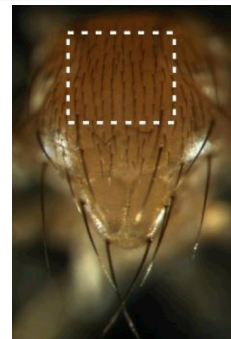
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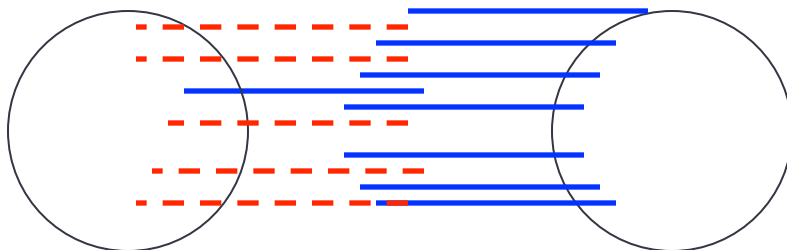
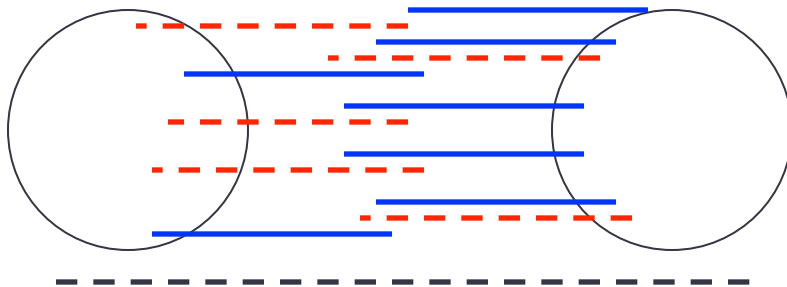
Trans vs. cis inhibition

———— Notch

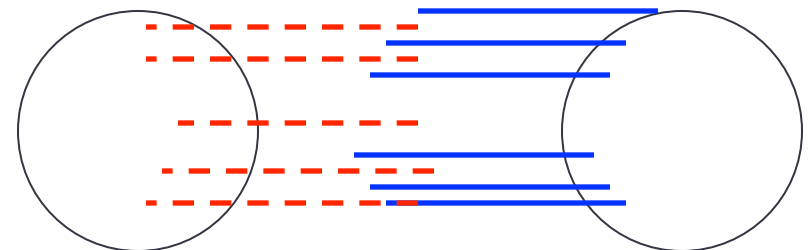
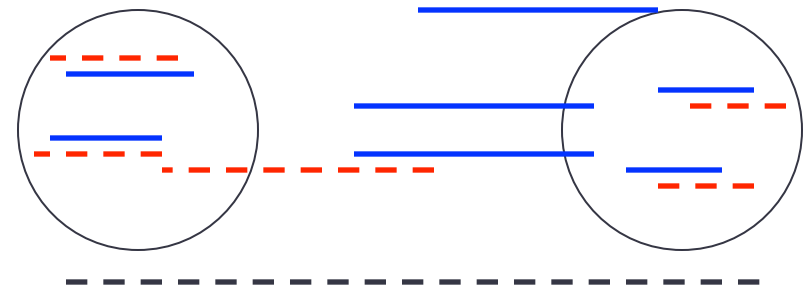
- - - - Delta

- Recent findings suggest that Notch is also suppressed in cis by delta's from the same cell
- Only when a cell is 'elected' it communicates its decision to the other cell

Trans model



Cis+Trans model



SOP selection in fruit flies

- During nervous system development, some cells are selected as sensory organ precursors (SOPs)
 - SOPs are later attached to the fly's sensory bristles
 - Like MIS, each cell is either:
 - Selected as a SOP; or
 - Laterally inhibited (via Delta-Notch signaling) by a neighboring SOP so it cannot become a SOP
- No two SOPs connected



MIS vs SOP

- Stochastic

- Proven for MIS
- Experimentally validated for SOP

- Constrained by time

- An uninhibited cell eventually becomes a SOP

- Reduced communication

- A node (cell) only sends messages if it joins the MIS

- Compared to previous algs:

- Unlike Luby, SOP cells do not know its number of neighbors (nor network topology)
- For SOP, messages are binary

Can we improve MIS algorithms by understating how the biological process is performed?

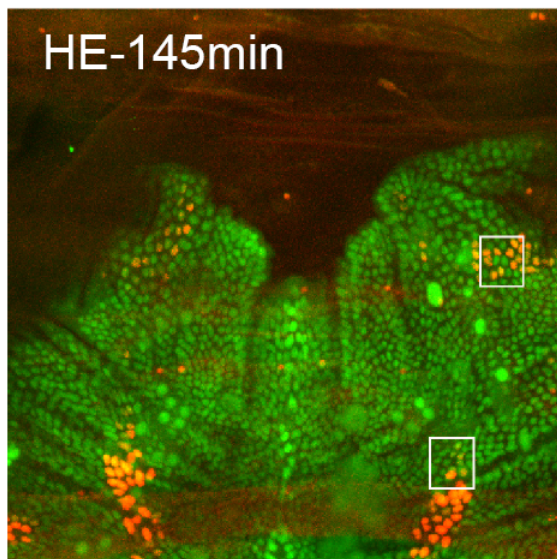
Maximal independent set 'on the fly'

- Problem: Elect a MIS
- Platform:
 - Distributed (no node receives all inputs or observes all outputs)
 - Binary message passing between nodes, and no knowledge of topology or number of neighbors (unlike Luby)
- Algorithm ingredients:
 - Stochastic (proven for MIS; experimentally validated for SOP)
 - Constrained by time (an uninhibited cell eventually becomes a SOP)
 - Low communication: a node only sends messages if it joins the MIS
- Evaluation:
 - Message complexity
 - Running time

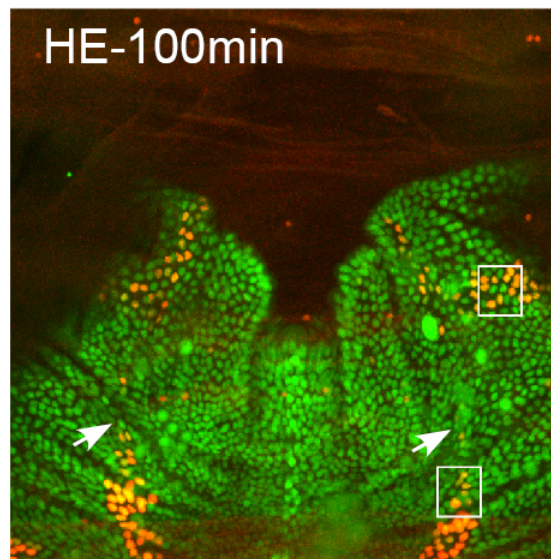
Can we improve MIS algorithms
by understating how the fly
solves this problem?

Movie

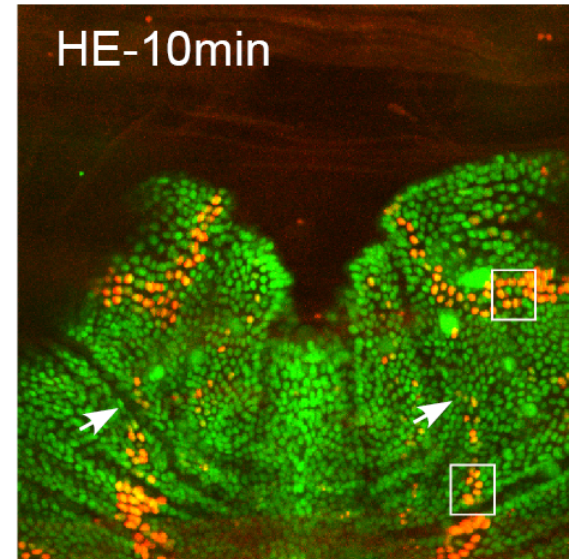
a1



a2

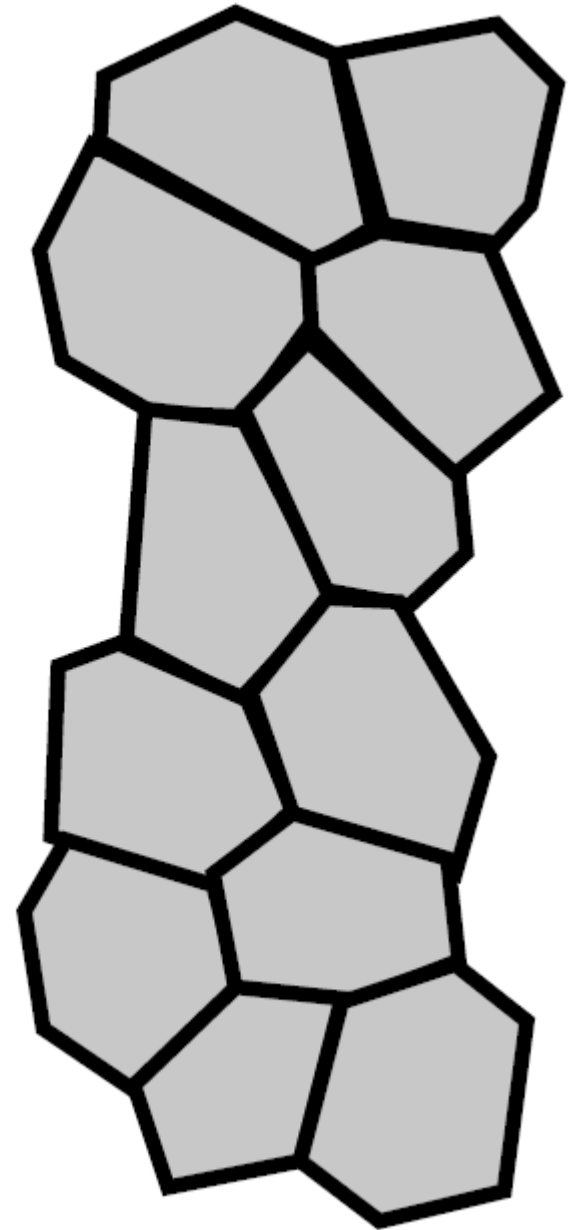


a3



Simulations

- 2 by 6 grid
- Each cell touches all adjacent and diagonal neighbors



Simulations

- A cell becomes a SOP by accumulating the protein Delta until it passes some threshold (nodes increase prob. of being elected as # of active nodes decreases)

Four models:

1. Accumulation

- Accumulating Delta based on a Gaussian distribution

2. Fixed Accumulation

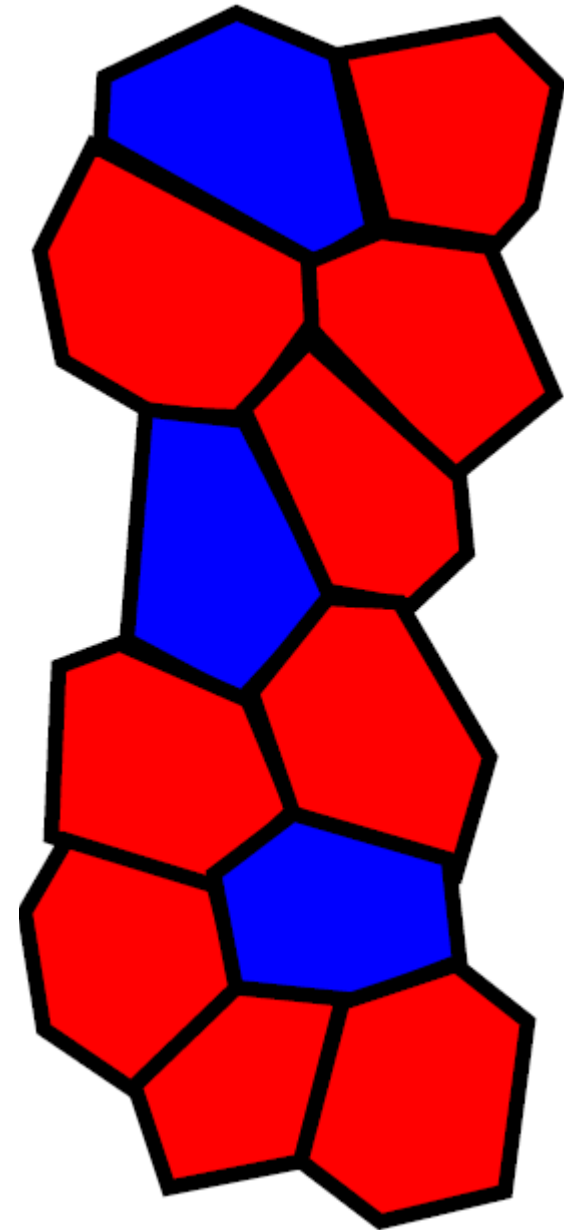
- Randomly select an accumulation rate only once

3. Rate Change

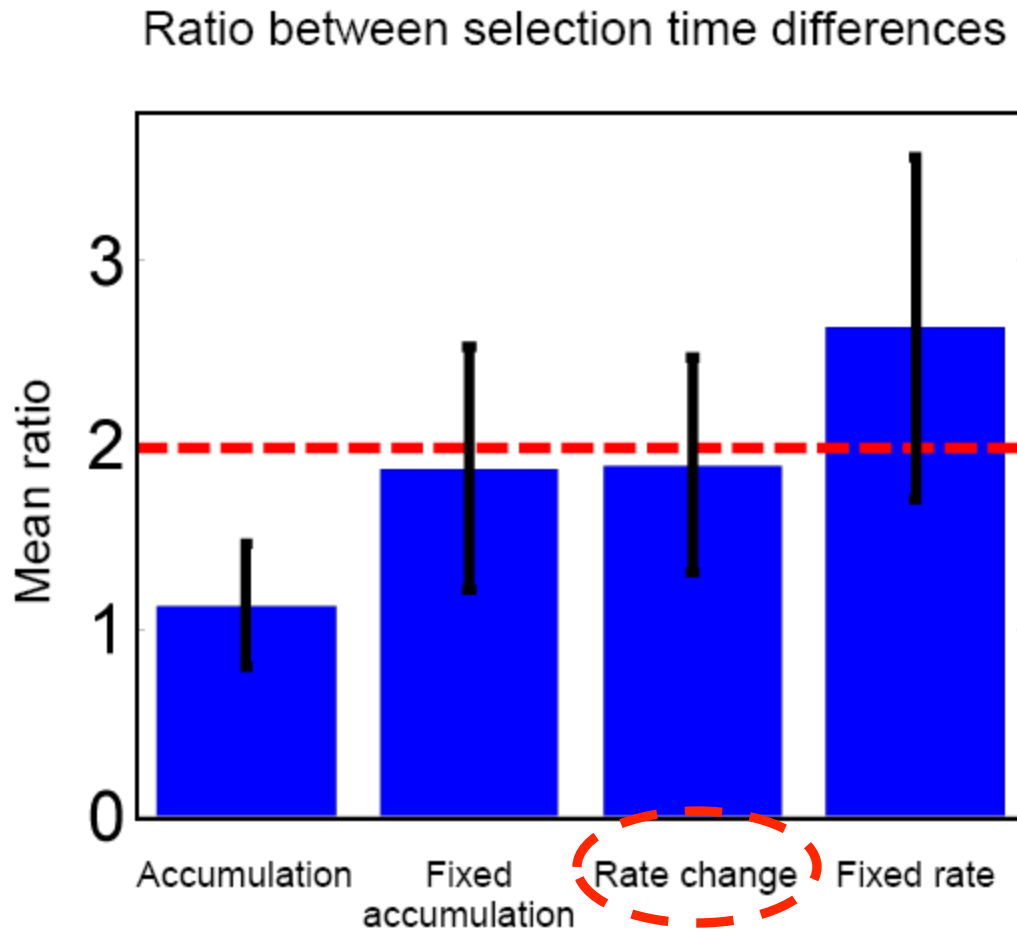
- Increase accumulation probability as time goes by using feedback loop

4. Fixed rate

- Fix accumulation probability, use the same probability in all rounds



Comparing time of selection experimentally and via simulations



New MIS Algorithm

MIS Algorithm (n, D) // n – upper bound on number of nodes

D - upper bound on number of neighbors

Table 1. MIS algorithm.

1. Algorithm: MIS (n, D) at node u
 2. For $i = 0: \log D$
 3. For $j = 0: M \log n$ // M is constant derived below
 4. * exchange 1 *
 5. $v = 0$
 6. With probability $\frac{1}{2^{\log D - i}}$ broadcast B to neighbors and set $v = 1$ // B is one bit
 7. If received message from neighbor, then $v = 0$
 8. * exchange 2 *
 9. If $v = 1$ then
 10. Broadcast B ; join MIS; exit the algorithm
 11. Else
 12. If received message B in this exchange, then mark node u inactive; exit the algorithm
 13. End
 14. End
 15. End
- W.h.p., the algorithm computes a MIS in $O(\log^2 n)$ rounds
- All msgs are 1 bit

Biological distributed algorithms

- Problem: what computational problem is the system trying to solve?
 - MIS, network construction, distributed search & consensus, task allocation
- Platform: what are the constraints and assumptions that need to be abided by?
 - Distributed, simple messages, dynamic networks, unknown environments, no UUIDs
- Algorithm: what strategy solves the problem within the platform?
 - Exploring broadly to deal with uncertainty, and then exploiting [see also Chris Reid tomorrow]
 - Feedback processes, to reinforce good solutions/edges/paths [slime mold, pruning]
 - Rates of communication/contact [MIS, pruning, ants]
 - The importance of stochasticity, to overcome noise & break symmetry
- Evaluation: what needs to be optimized?
 - Run-time efficiency, communication cost, flexibility, robustness, adaptation, resources
 - And their trade-offs! [MIS: higher run-time, lower complexity; pruning: wasteful but adaptive]

Conclusions

- What can biology contribute to distributed algorithms research?
 - New robust/flexible/adaptive algorithms
 - Revisiting problems with more or different constraints
- What can distributed algorithms contribute to biology research?
 - Formal models to evaluate performance and predict behavior
 - Identification of parameters critical for algorithmic optimization but ignored; raise new, testable hypotheses

Thanks!