Distributed Computing on the (Fruit) Fly

Yuval Emek

Distributed Computing Group ETH Zurich

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Distributed computing = power & limitations of computation in networks

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Synopsis

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Our mission: distributed computing in biological cellular networks

Yuval Emek (ETH Zurich)

Motivation

Selection of sensory organ precurser (SOP) cells = solving MIS [Afek, Alon, Barad, Hornstein, Barkai, Bar-Joseph 11]





2) Abstract models

3 Networked finite state machines

- Results
- MIS protocol

4 Conclusions

The structure of cells (eukaryotes)



Analogous to central processing unit

• Code = DNA





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 - Organized in chromosomes





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 - Controlled by concentration levels



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- Juxtacrine direct contact
 - respects network's topology
- Paracrine, endocrine
 - out of our scope

Delivery of message *m* from cell *s* to cell *t*

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 - Gap junction/receptor = port
 - No sense of direction
 - all neighbors look the same





Cell biology — a short intro

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Conclusions
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Perhaps we should aim for a network of FSMs?

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Highly regular topology

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Highly regular topology Synchronous environment

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 - one-two-many counting = discrete analogue for detecting different concentration levels

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nFSM — computability

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Observation (Anonymous networks)

Leader election and consensus are *impossible* under nFSM.

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Run-time:
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- Run-time bounds hold in expectation and w.h.p.
- Efficient algorithm = $\log^{O(1)} n$ run-time [Linial 92]

Every nFSM protocol designed to operate in a synchronous environment can be simulated in an asynchronous environment with a constant multiplicative run-time overhead.

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Makes life much easier for the protocol designer

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There exists an nFSM protocol that computes an MIS in any n-node graph in time $O(\log^2 n)$.

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Message passing model:

- O(log n) [Luby 86], [Alon, Babai, Itai 86]
- $\Omega\left(\sqrt{\log n}\right)$ [Kuhn, Moscibroda, Wattenhofer 04]
- Anonymous networks, constant size messages:
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The beeping model:

O(log² n)-O(log³ n)
 [Afek, Alon, Barad, Hornstein, Barkai, Bar-Joseph 11],
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Theorem

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Message passing model:

- $O(\Delta + \log^* n)$ [Barenboim, Elkin 09], [Kuhn 09]
- Ω(log* n) [Linial 92]
- $O(\log \Delta + \sqrt{\log n})$ [Schneider, Wattenhofer 10]
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- Anonymous (undirected) trees, constant size messages: Ω(log n) [Kothapalli, Onus, Scheideler, Schindelhauer 06]
- Directed trees:
 - $O(\log^* n)$ [Cole, Vishkin 86]
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Efficient algorithm: maximal matching

Under a small inevitable modification to the model, there exists an nFSM protocol that computes an MM in any n-node graph in time $O(\log^2 n)$.

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Lemma

For every nFSM protocol Π with bounding parameter b = 1, there exists an nFSM protocol Π^2 such that for every graph G, the execution of Π^2 on G simulates the execution of Π on G^2 with a constant multiplicative run-time overhead.

Corollary (Maximal 2-hop independent set)

There exists an nFSM protocol that computes a maximal 2-hop independent set for any n-node graph in time $O(\log^2 n)$.

Corollary (2-hop coloring)

Given some constant d, there exists an nFSM protocol that computes a 2-hop coloring with $(d^2 + 1)$ colors for any n-node graph satisfying $\Delta \leq d$ in time $O(\log n)$.

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Maximal k-hop independent set and k-hop coloring are impossible in anonymous networks for any $k \ge 3$.

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 - *u* must count the rounds in a phase (deciding when it ends)

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 - messages of logarithmic size
- Idea: transmit O(1) bits per round
 - logarithmically long phases
- Problem:
 - *u* must count the rounds in a phase (deciding when it ends)
 - phases must be aligned to guarantee fair competition

- Existing MIS algorithms rely on grouping rounds into phases: u competes with N(u) over joining the MIS
- Require either
 - calculations with super-constant variables
 - independent communication with each neighbor
 - messages of logarithmic size
- Idea: transmit O(1) bits per round
 - logarithmically long phases
- Problem:
 - *u* must count the rounds in a phase (deciding when it ends)
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- How can we decide if *u* joins MIS without long aligned phases?

MIS under nFSM — solution



• Relax requirement that phase is aligned and of predetermined length

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 - "softly" aligned
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• Tournament:

- length determined probabilistically
- "softly" aligned
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- Prove:
 - Amortized length of a tournament is $O(\log n)$ w.h.p.
 - Quarantee fair competition ⇒ const fraction of the edges is removed with const probability ⇒ O(log n) tournaments w.h.p.
1 Cell biology — a short intro

2) Abstract models

3 Networked finite state machines

- Results
- MIS protocol

4 Conclusions

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