# Distributed Computing on the (Fruit) Fly 

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## Synopsis

## Distributed network algorithms

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Mission: theory of distributed computing in biological cellular networks

## Motivation

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

(1) Cells as computing devices

## (2) Abstract distributed computing models

(3) Networked finite state machines
(4) Results

- MIS algorithm
(5) Conclusions


## Local computation

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- Analogous to CPU's current state


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(3) Affects $y$ 's gene expression
- Gap junction/receptor = port
- No sense of direction
- all neighbors look the same

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- \# message types grows with $n$


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Perhaps we should aim for a network of FSMs?

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Digital physics
Biological processes


Highly regular topology
(1) Cells as computing devices
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- one-two-many counting = discrete analogue for detecting different concentration levels
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- Run-time bounds hold in expectation and w.h.p.


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- run-time $=O(\log n)$
- Maximal Matching in arbitrary graphs (small model modification)
- run-time $=O\left(\log ^{2} n\right)$


## Additional general results

## Theorem (Synchronizer)

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

## Theorem (Computability)

In terms of their computational power, nFSM algorithms are (almost) equivalent to randomized linear-space Turing machines.
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The MIS problem: input: (arbitrary) network output: MIS


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- Problem:
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- Require either
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- messages of logarithmic size
- Idea: transmit $O(1)$ bits per step
- logarithmically long phases
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- How can we decide if $u$ joins MIS without long aligned phases?


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(2) Guarantee fair competition $\Longrightarrow$ const fraction of the edges is removed with const probability $\Longrightarrow$ $O(\log n)$ tournaments w.h.p.
(1) Cells as computing devices
(2) Abstract distributed computing models

3 Networked finite state machines
(4) Results

- MIS algorithm
(5) Conclusions


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