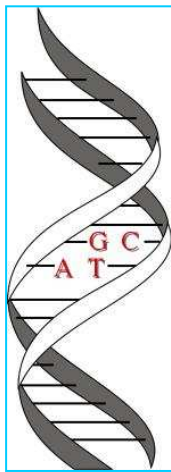


Looking Forward... Looking Inward

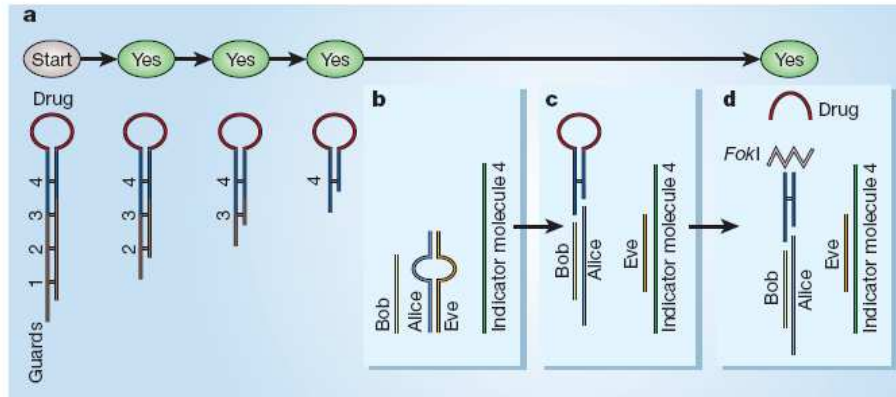
Anne Condon
University of British Columbia

DNA is programmable



DNA is programmable

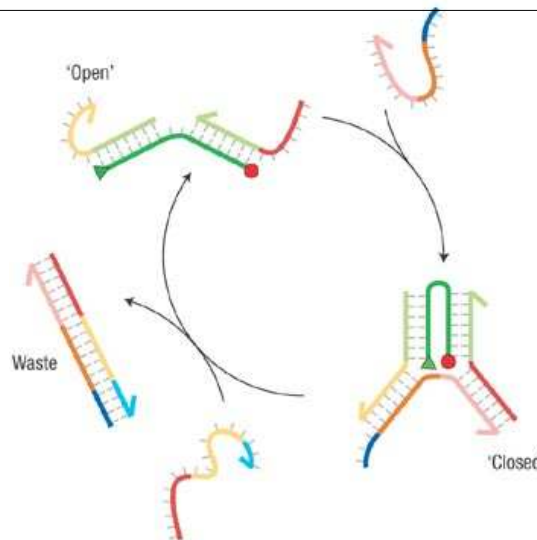
molecular automata | logic in motion | self-assembly



Benenson et al. Nature (2004)

DNA is programmable

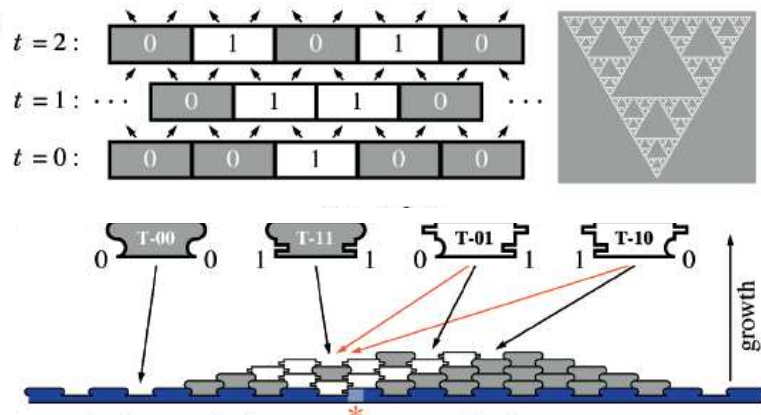
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Yurke, et al. Nature (2000)
Bath and Turberfield, Nature Nanotech (2007)

DNA is programmable

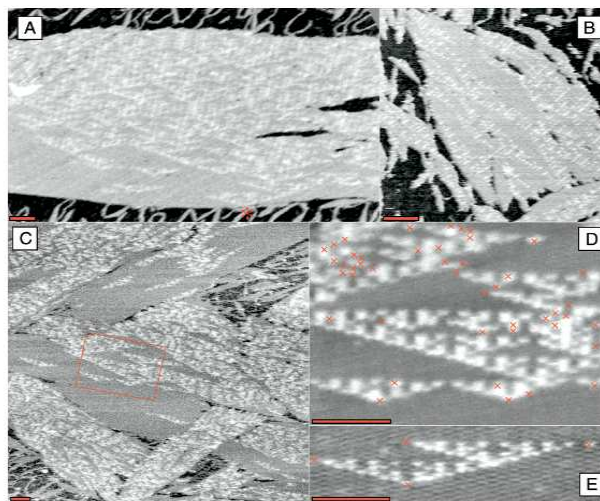
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Rothmund et al. PLoS Biology (2004)

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Rothmund et al. PLoS Biology (2004)

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- all of these are examples of stochastic processes
- challenges: predict their behavior, and learn to control errors that may arise

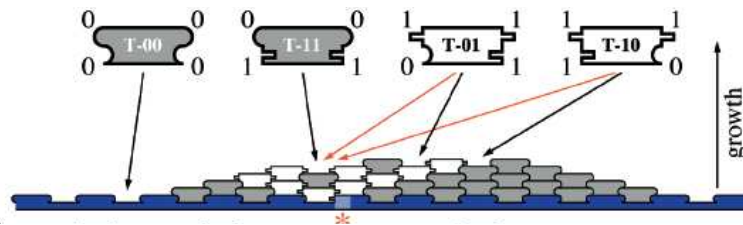
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stochastic model: tiles from a pool associate and dissociate from a single aggregate

$f(c)$: association rate of a tile type of concentration c to aggregate

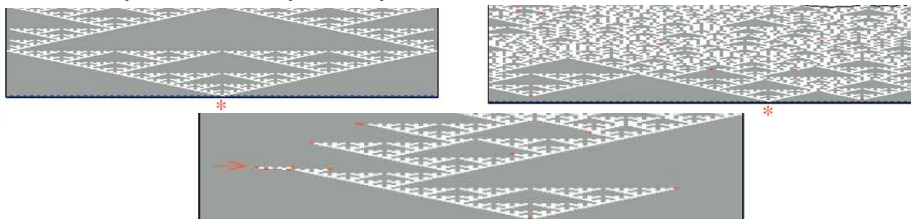
$r(b)$: disassociation rate of tile with b matching edges from aggregate



DNA is programmable

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- Can we provide mathematical insights or proofs of the following observations:
 - “slight quantitative variations in the model parameters can lead to striking qualitative differences in the observed error morphologies”
 - doubling the concentrations of T-00 and T-11 tiles leads to “a statistical preference for all-zero patches [which] actually increases the frequency and size of perfect Sierpinski patterns”



Reference

- **Algorithmic Self-Assembly of DNA Sierpinski Triangles.** *Paul W.K. Rothmund, Nick Papadakis, Erik Winfree.* [PLoS Biology](#) 2 (12) e424, 2004