Using cell colonies for computations

by reverse-engineering reaction-diffusion systems

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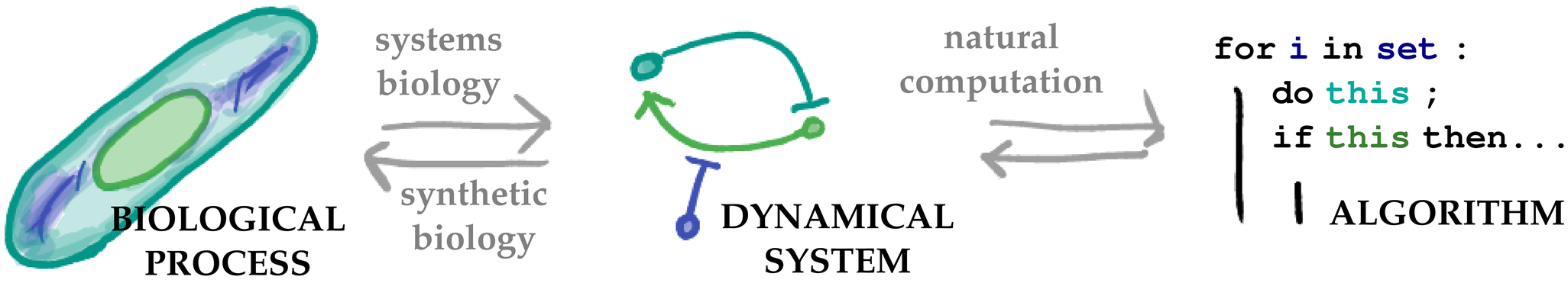

mappings between levels of abstraction from biological process to algorithm

Can bacterial colonies perform a fourier transform? What does a bacteria do? How would we manipulate it?
Bacteria already perform computations eg chemotaxis, lac system experimental figure + odes + network
genetic manipulation can supress/activate network segments We can cut-and-paste different network sections
- synthetic biology approaches
Can we cut-and-paste the right networks together to perform any arbitrary caclulation?

Algorithm → Dynamical System | Given a *response function* what is the *minimal* reaction network?

- 👍 Methods for the probabilistic inference of reaction networks exist [1]
- 👍 Mappings to and from algorithms pave the path towards programming in cells [2]
- 👎 No general mapping exists that takes model complexity into consideration

$$\partial_t \bar{\mathrm{p}}(t) = \overbrace{R(\rho)}^{\text{reaction}} + \underbrace{S(t)}_{\text{source}}$$

What is the general routine for *reducing complexity* in reaction networks?

- 👍 For *known time-scale separations* one can reduce models, introducing memory effects [3]
- 👎 There exist *no relevance determination* methods beyond empirical sensitivity analysis [4]

How does evolution lead to *complexity increase* in network motifs such as switches and clocks?

- 👍 Relationship between robustness and evolvability has been investigated [5]
- 👎 Evolutionary relationships between different chemical networks have not been quantified

Dynamical System | Given a *steady state pattern* what is the *minimal* reaction-diffusion network?

- 👍 Dynamics of local equilibria show promising analysis beyond linear stability [6]
- 👎 Need to design attractors in phase space; no description in phase space exists

$$\partial_t \rho(t) = \overbrace{R(\rho)}^{\text{reaction}} + \underbrace{D\,\partial_x^2 \rho(t)}_{\text{diffusion}}$$

$R(\rho)$ is a vector, multinomial in the components of ρ

References

[1] Nikhil Galagali. Bayesian inference of chemical reaction networks. 2016.
[2] Neil Dalchau, Gregory Szép, et al. Computing with biological switches and clocks. *Natural Computing*, 6 2018.
[3] George D.J. Phillies. Projection Operators and the Mori-Zwanzig Formalism. *Springer, New York, NY*, 2000.
[4] Luca Cardelli, Attila Csikász-Nagy, et al. Noise Reduction in Complex Biological Switches. *Scientific Reports*, 2016.
[5] Bryan C Daniels, Yan-Jiun Chen, et al. Sloppiness, robustness and evolvability in systems biology. *Current Opinion in Biotechnology*, 2008.
[6] J. Halatek and E. Frey. Rethinking pattern formation in reactiondiffusion systems. *Nature Physics*, 2 2018.