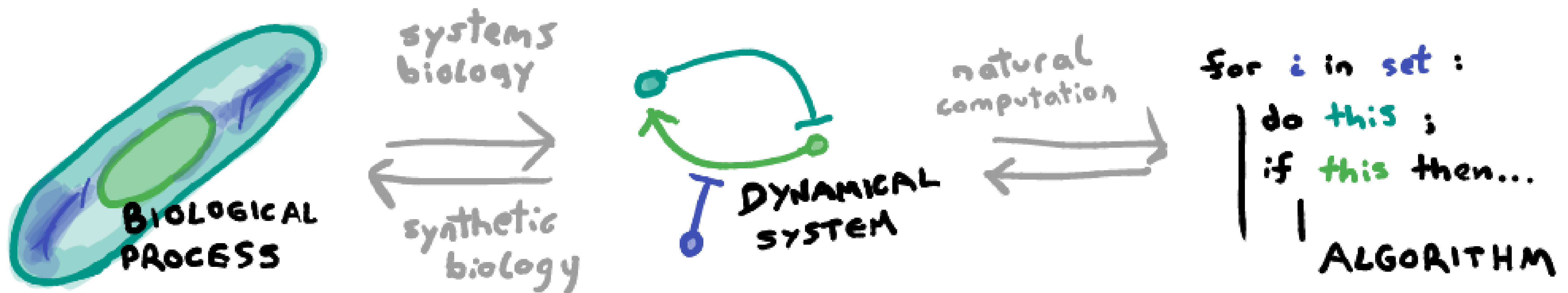


Gregory Szép, Luca Cardelli, Attila Csikász-Nagy



mappings between levels of abstraction from biological process to algorithm

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

- 👉 Mappings between algorithms and reaction networks pave the path towards programming in cells [1]
- 👎 No general mapping exists that takes model complexity into consideration

Biological Process → System | What is the *general routine* for *reducing complexity* in reaction networks?

- 👉 Time-scale separation allows reduction of component number; introducing delays and nonlinearity
- 👎 There exist no dimensionality reduction and parameter relevance methods for reaction networks

Biological Process → Dynamical System | How do *network motifs* such as *switches* and *clocks* evolve?

- 👉 Relationship between robustness and evolvability has been investigated [2]
- 👎 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 [3]
- 👎 Need to design attractors in phase space; no description in phase space exists

Biological Process → Dynamical System | How do *patterns* form across *growing cell populations*?

- 👉 Differential diffusion between cytosolic, membrane and inter-cellular components give rise to patterns
- 👎 Finite element reaction-diffusion simulations are computationally expensive

References

- [1] Neil Dalchau, Gregory Szép, et al. Computing with biological switches and clocks. *Natural Computing*, 6 2018.
- [2] Bryan C Daniels, Yan-Jiun Chen, et al. Sloppiness, robustness and evolvability in systems biology. *Current Opinion in Biotechnology*, 2008.
- [3] J. Halatek and E. Frey. Rethinking pattern formation in reactiondiffusion systems. *Nature Physics*, 2 2018.