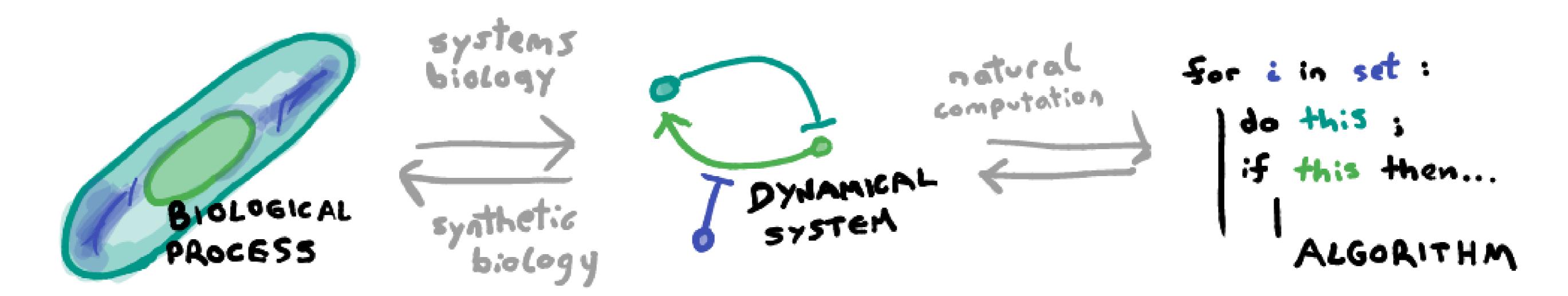


## Reverse-engineering natural computation





## Gregory Szép, Luca Cardelli, Attila Csikász-Nagy



mappings between levels of abstraction from biological process to algorithm

**Algorithm**  $\rightarrow$  **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]
- Dynamical structure function and Granger causality methods reconstruct networks from data
- No general mapping exists that takes model complexity into consideration

$$\partial_t \rho = R(\rho) + S(t)$$
source

Biological Process  $\rightarrow$  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]
- F 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

