On reverse-engineering natural computation

using reaction-diffusion approaches beyond linear stability

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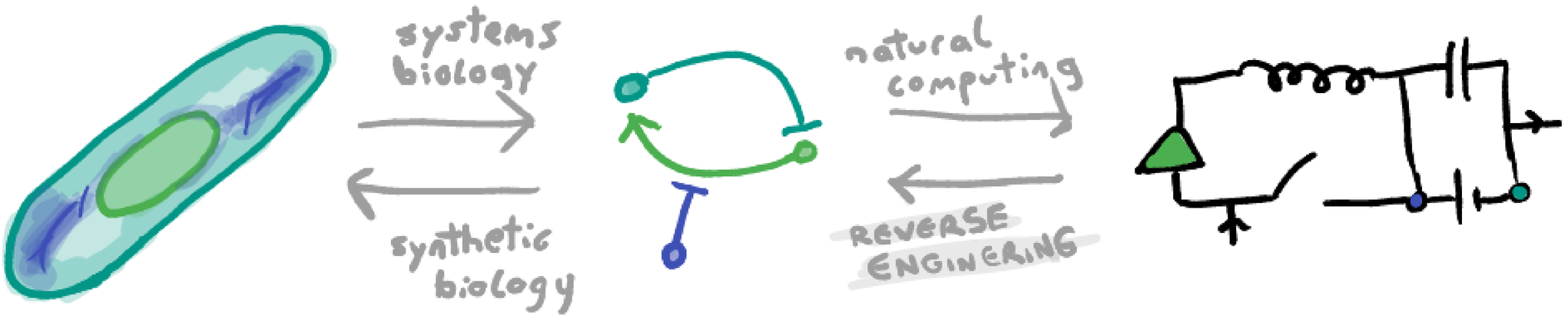
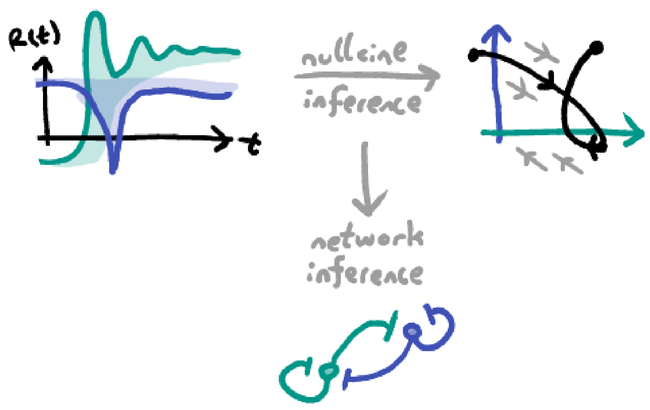


1 Evolution of response behaviour

Specific mappings have been explored between between algorithms, electrical engineering circuits and chemical reaction networks []. Understanding function of large biochemical networks from a computer science perspective guides experiments in synthetic biology and in-vitro reconstructive approaches [].

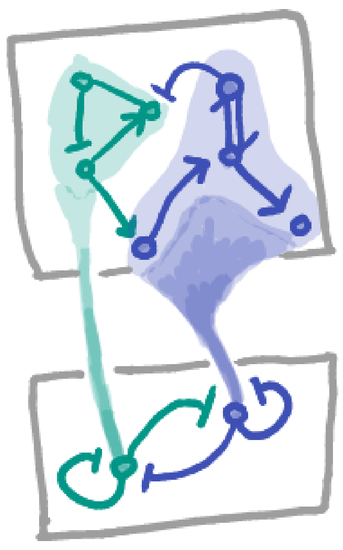
How does one design the *least complex* chemical reaction network that obeys a given *response function*?



The function of known biochemical networks such as the MAPK pathway, circadian rhythms and cell-cycles can be understood in terms of simple response functions; decompositions of large networks into switches and clocks are proposed in literature.

The networks found in nature are far from the least complicated realisations of particular response functions. The additional complexity can be explained by molecular evolutionary paths towards robust biological function [].

Can model reduction methods [] indentify relevant components, parameters [] and reduce complexity in reaction networks?



Using measures of relative complexity between two given networks, can we construct evolutionary trees and understand how primitive switches and clocks evolved?

2 Patterns in dynamic populations

Ever since turing formulated the differential diffusion condition [] for pattern formation, whether a biological pattern is truely driven by a diffusion instability or not has been a matter of debate and speculation.

It is conceivable that the differential diffusion condition is satisfied by the time-scale separation between cytosolic, membrane and intercellular reactions.

3 Geometrisation approach