

Automatic design in Synthetic Biology

Synthetic Biology has relied until now on rational design techniques to create novel functional genetic networks allowing the reprogramming of cells. However, their increasing size and complexity requires starting demanding computational methods to complement the design principles of biological circuits. The most challenging of them are those that mimic evolution to engineer a biological network. Circuits are computationally evolved by either modifying their topology or their kinetic parameters, and by using a fitness function to select for a targeted dynamics and maximal growth. We have applied these automatic approaches to design transcription, nucleic acids and metabolic networks. They allowed us to design of digital circuits, oscillators and memory devices. We will show how to use in silico evolution methods to take advantage from the recent advances on the understanding and engineering of modularity in biological networks.

This requires the design and construction of biological modules with context-independent targeted behaviour, which could be assembled in a combinatorial way to generate a desired dynamics. We have extended our procedure to the automatic assembly of biological part models, which will not only allow incorporating arbitrary kinetic models, but it will also allow the incorporation of experimental data back into the design process. We have also developed an automated method that allows the de novo design of metabolic pathways using a retrosynthetic algorithm. This tool will allow grafting new bioproduction pathways into a given cellular chassis.