

## Computational design of yeast synthetic gene circuits

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One of the main goals of Synthetic Biology is the development of software that drives the assembly of DNA circuits into cells. Our software, called “Parts & Pools”, permits the visual, drag and drop design of synthetic gene circuits in yeast and other eukaryotes. The name derives from the fact that, in our framework, gene circuits are made of two kinds of components: Parts (i.e., DNA sequences such as promoters, coding regions, and terminators) and pools which can contain proteins, RNA and chemicals. “Parts & Pools” as an add-on of ProMoT (Process Modeling Tool) is a collection of Python and Perl scripts. Each script generates a biochemical model for a DNA part or a pool. Models for circuit components are encoded in MDL (Model Definition Language) such that they can be loaded on ProMoT and used for complex circuit design. The model of a genetic circuit, which arises from the composition of the models of its components, can be exported to SBML (System Biology Markup Language) or Matlab language for simulations and analysis. Genetic networks are modeled according to full mass action kinetics. In order to generate models for components characterized by a large number of species and reactions (e.g., regulated promoters) “Parts & Pools” makes use of BioNetGen (rule-based modeling approach). Currently, we are working on several software improvements: A grammar for a textual circuit description, an export function to the Synthetic Biology Open Language (SBOL) and a connection to a database containing yeast sequences characterized in our lab.

### Biography

Mario Andrea Marchisio has obtained his PhD in Physics at the University of Trento, Italy in 2002. After working for four years at the CILEA computing center in Milan, Italy, he spent six years as a Post Doc at the ETH Zurich, Switzerland. Since September 2013, he is working as an Associate Professor in Synthetic Biology at the Harbin Institute of Technology, China.

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