CompuBioTic, a methodology for *de novo* design of vesicles performing programmed tasks

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Abstract

Synthetic biology aims at using biological parts in order to construct new programmed biological systems. The ambition of our project is to establish a methodology to design and construct synthetic biological systems made of protein elementary bricks and encapsulated within a non-living vesicle.

Within this perspective, we are constructing a catalogue of standardised and reusable protein parts for synthetic biology. The catalogue is a database containing well-characterized proteins and group of proteins playing defined roles, compatible with synthetic biological system engineering. An example is the role of "conditional sensor", which refers to molecules able to detect a biological signal and to give a conditional response to this signal. Each element is described with a biological processes formalisation language, Bio Ψ [1, 2]. It allows a formal and standardized description of the biological functions and processes at different levels of abstraction, and will allow automatic identification of biological components of interest in a biological database. It is also appropriate to dynamical (temporal and spatial) modelling and simulations. For this work, we used the Hsim software, a stochastic cellular automaton, and then studied the behaviour of the modelled system. We also characterized experimentally the parts of the catalogue and give them a score of "reusability" for synthetic biology.

We also aim at integrate these different software and databases in order to create a computer-assisted design tool for synthetic biology.

The catalogue counts fifteen main entries classified with respect to the scale of the system. A theoretical formal description of all the parts is available and some of them have been assay and characterized experimentally. For instance, we have encapsulated molecules implementing the "revealing" role entry in liposomes, and characterized it experimentally. We designed and model a theoretical system dedicated to early medical diagnosis task.

Keywords

Synthetic biology, catalogue, reusable components, proteins, vesicles, software tool

- [1] Mazière P., Parisey N., Aimar M. and Molina F. Formal description of TCA cycle based on elementary bricks of action, *J. Biosciences 2007, Vol32, N1, jan 2007 145-15*
- [2] P. Maziere, C. Granier, and F. Molina. A biological processes description scheme based on elementary bricks of action. J. Mol. Biol., 339:77–88, 2004