BIOGRAPHY

Francesc Posas is Professor of Biochemistry and Molecular Biology at the Department of Experimental and Health Sciences of the Universitat Pompeu Fabra (http://www.upf.edu/cellsignaling). After obtaining his doctorate in Biochemistry and Molecular Biology at the Universitat Autònoma de Barcelona (1995), he made his postdoctoral stay at Harvard University (Boston, USA). From 1999 leads the Cell Signaling Research Group (UPF). The group addresses how cells sense and respond to environmental changes, focusing on the characterization of signaling pathways in response to stress, particularly those controlled by the stress-activated MAP kinases of the Hog1/p38 family (SAPK). Using yeast S. cerevisiae as a model organism and higher eukaryotic cells, we analyze the molecular mechanisms of cells to respond and adapt to extracellular stimuli. A proper adaptation to stress involves the modulation of several basic aspects of cell biology. Among them, cell cycle and gene expression regulation. Recently, the group is also analyzing the basic signaling properties of the HOG pathway and how to alter them, and in the field of synthetic biology, they have implemented complex engineered networks to perform in vivo cellular computation.

Awards: Young Investigators from the Catalan Government (2001), EMBO Young Investigator Program (2000), EURYI to young investigators from the EU (ESF) (2004), EMBO member (2006), awarded with an ICREA Academia Researcher for University Professors (2009) and the “Carmen and Severo Ochoa” Award for Research in Molecular Biology (2011). He received a European Research Council Advanced Grant (ERC 2012).

PROJECT

European Research Council Advanced Grant

Project acronym: SYNCOM
Project full title: *Distributed Computation in Synthetic Consortia*

Synthetic biology is still far from producing flexible, programmable, scalable and predictable engineered constructs able to perform complex computations. The main problem has arisen from the fact that, in contrast to electronic designs where wires have identical nature, in a cell-based system each wire would correspond to a different molecular entity. In a joint effort between theoretical and experimental studies, we have established biological circuits with Distributed Computation capacity (Regot et al., 2011), opening the possibility to develop a novel method of properly design general purpose, LEGO-like multicellular systems able to partially avoid wiring limitation. Here, we propose to explore the limits of Distributed Computation in synthetic cellular systems. To this goal, we will extend our previous circuits to circuits with a higher complexity, never achieved to date as well explore the use of different cellular systems as a biological case study. Our preliminary data indicate that there are two aspects, which were not considered previously, that when combined with Distributed Computation, could permit a strong reduction or even eliminate the wires in biological computation; the first aspect is the use of inverse logic circuits and the second is the development of spatially restricted devices. We will set up the

theoretical framework of these novel aspects and establish in vivo circuits spatially restricted cellular systems.

To this end we propose

1) To use microfluidic devices for physically restricted cellular networks;
2) To implement circuits with mixed but physiologically isolated cells (without wires) with different computation capabilities.
In addition, we will extend these studies to obtain highly reprogrammable circuits. The combination of such approaches should demonstrate that biological computation is scalable, allows constructing arbitrary cell-based computing machines and breaks all current limitations concerning circuit complexity.