

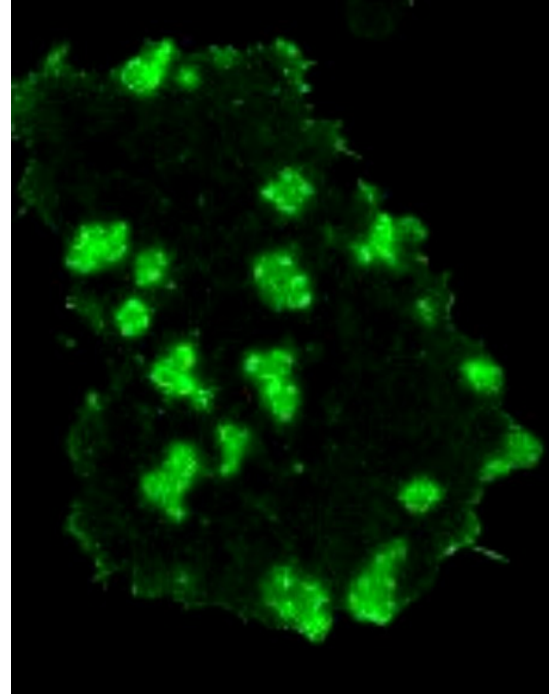
Training program in *Computational Biophysics*

TFG proposal

Computational modeling of pattern formation at the membranes of living cells

In living cells, certain proteins dynamically accumulate at specific regions of the cell membrane. This localized concentration of proteins can trigger mathematical instabilities in the underlying biochemical network, leading to cell polarization—that is, the spontaneous emergence of a distinct “front” and “back” of the cell. This symmetry breaking is a fundamental process in many forms of cellular organization and movement.

Beyond simple polarization, other dynamical behaviors can occur at the membrane. These include the formation of traveling waves, oscillations, and other non-stationary spatial patterns that continuously evolve over time. Such dynamic structures are particularly important for understanding how cells explore their environment, coordinate internal signaling, and ultimately achieve directed motion.



Proteins patterns at the membrane

Project details*Objectives*

The main goal is the interpretation of some experimental results in terms of mathematical modeling. We will describe these processes using stochastic reaction-diffusion equations, which provide a mathematical framework capable of capturing both the deterministic dynamics of pattern formation and the inherent fluctuations that arise from molecular noise;

$$\frac{dc}{dt} = F(c, k_i) + D \nabla^2 c + G(c) \xi(x, t)$$

The first term corresponds to the biochemical reactions, where one of the parameters of k_i is controlled by the constrain of the available amount of proteins, the second term to the diffusion process and the last term proportional to ξ corresponds to stochastic fluctuations

Methods

We are going to employ finite differences to numerically integrate the stochastic reaction diffusion equations. We discretize in space to calculate the diffusion term and the integration in time is done with an equivalent to the simple Euler method but for stochastic equations. This project demands a strong knowledge on programming.

Activities

- Reading literature about protein pattern formation at membranes.
- Writing and testing code in c++/python or similar
- Validating the output of the code and comparing it with experimental results
- Develop and use visualisation tools for the interpretation of the results
- Publishing a repository of the codes
- Writing and defending the bachelor's thesis

Supervisors and host research groups

- Dr. Sergio Alonso (BIOCOM-SC, <https://biocomsc.upc.edu/en>).

Valued characteristics of the candidates

- Programming knowledge, especially c++, or Python
- Basic knowledge in linux or intention to learn it.

Practical information

Application: Send your CV and motivation letter to s.alonso@upc.edu

Further information: You can contact to s.alonso@upc.edu