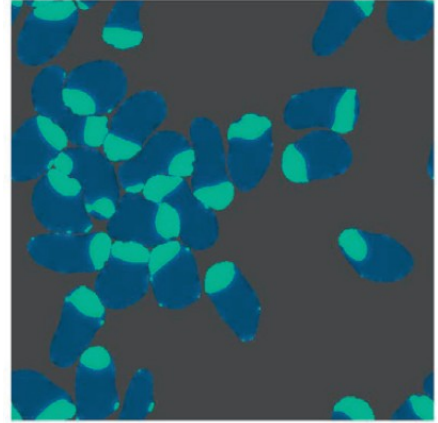


Training program in Computational Biophysics

TFG/TFM proposal

**Computational modeling of accumulate
dynamics 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. Such model of cell polarization can be employed, together with a phase field model for the shape of the cell, to model cell motion and in particular to model the dynamics among interactive cells, and in the aggregation processes. In the figure we show a particular snapshot of the dynamical repulsive interactions among a set of cell (represented by the green front and the blue back) using periodic boundary conditions.



Proposal: We propose a project to be conducted during the academic year 2026/2027. The project is to simulate numerically, using the phase field approach, the interaction among a set of cells trying to understand elastic and other properties of the group of accumulated cells

References: Moreno E, Großmann R, Beta C and Alonso S (2022) From Single to Collective Motion of Social Amoebae: A Computational Study of Interacting Cells. Front. Phys. 9:750187.

Supervisor: Sergio Alonso (s.alonso@upc.edu)

Candidate profile: Last course of Engineering Physics and/or Mathematics at UPC.

Centre: Escola Politècnica Superior d'Edificació de Barcelona, EPSEB (Barcelona).

Application: Sent CV (including grades) and a motivational letter to the head of the program (Clara Prats, clara.prats@upc.edu).

Funding: Research group BIOCOS-SC will offer an INIREC contract to the three best candidates that want to carry out any of the project associated with this training program in Computational Biophysics in the academic year 2026/2027.