

MEP/BEP project: New protein functions in a stochastic yeast-polarization model

Goal: Implement newly discovered protein functions in a model for yeast cell polarity

Methods: *In silico* stochastic modelling, C++, reaction-diffusion and phase separation physics

Introduction

In the *in vitro* wet lab work we do, we find exciting new protein properties and functions. However, the cell environment is quite different from the *in vitro* environment and thus these functions are not observed in the living cell. By building a model, we have a platform to explore the interface of observed protein functions on macro dynamics of yeast cell polarity establishment. We have built a stochastic model that implements both reaction-diffusion based dynamics and phase separation onto a simulated yeast cell.

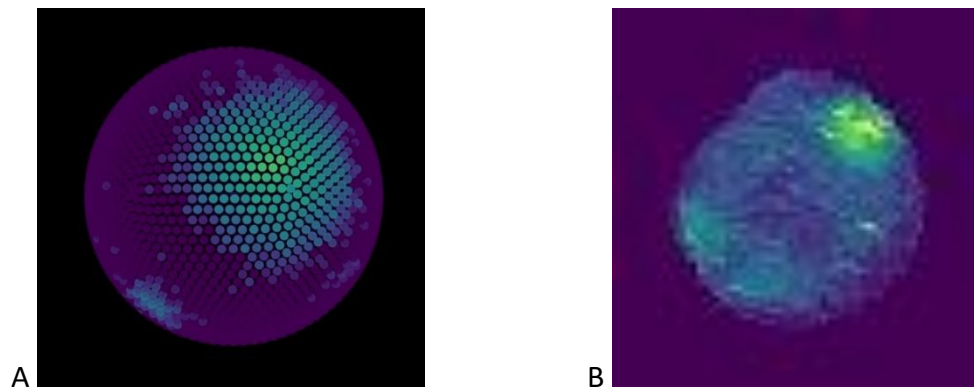


Figure 1. A) Simulated polarized yeast cell. B) Scanning confocal image of a polarized yeast cell with fluorescently labelled Cdc42.

Project description

For this *in silico* project, you will work on the implementation of newly found protein properties to the already existing stochastic yeast-polarization model. You will work on converting biological and chemical concepts about proteins into a physics formalism. The project provides a nice challenge for students interested in pattern formation dynamics, thermodynamics, stochastic modelling, reaction-diffusion systems, and phase separation.

This project is done together with the Jos Zwannikken lab.

Requirements

This project is suitable for students with a background in physics, nanobiology or biophysics. Some coding experience would be beneficial for this project, but is not required. This project is quite physics minded, so interest and curiosity towards statistical physics and phase separation physics are nice.

Contact

If you're interested in this project or if you have questions/suggestions, feel free to contact me, Nynke Hetteema, at n.m.hetteema@tudelft.nl.