

Cell biophysics : phase diagrams, phase portraits and trajectories

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Stripped-down experimental systems that contain a limited number of purified proteins allow for deciphering the mechanisms of cell division and motility as well as cellular functions based on membrane deformation. Such controlled conditions allow us to propose and challenge physical modelling where physical parameters can be varied. For example, cytoskeletal dynamics, reproduced on liposome membranes, generate inward and outward membrane deformations (Figure 1) that depend on membrane tension and the structural details of cytoskeletal architectureⁱ. Besides, a static study of buckling/wrinkling of actin-covered liposomes under osmotic deflation demonstrates the elastic nature of the actin cytoskeletonⁱⁱ.

My new project at LPENS addresses how the cytoskeleton interacts with the nucleus during cell motility through narrow constrictionsⁱⁱⁱ. We apply an inference method derived from a Langevin equation approach to learn the dynamical equations describing nuclear trajectories and shape changes.

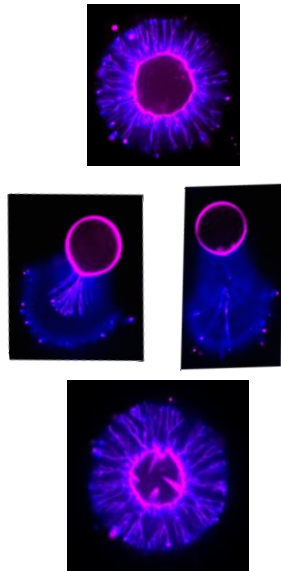


Figure 1: The dynamic actin cytoskeleton (marked by the presence of capping proteins, *Alexa Fluor 488 C5-maleimide*, green) is able to deform the membrane (*TexasRed-DHPE*, red) inward (spikes towards the liposome center) and outward (tubes emanating from the liposome membrane) and propel them through the formation of a comet-like structure. Liposomes have a diameter of 10 to 20 microns.

References

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ⁱⁱ R. Kusters, C. Simon, R. Lopes Dos Santos, V. Caorsi, Sangsong Wu, J.-F. Joanny, P. Sens, **C. Sykes**, "Actin shells control buckling and wrinkling of biomembranes" *Soft Matter*, **15**, 9647 – 9653 doi: 10.1039/c9sm01902b (2019)

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