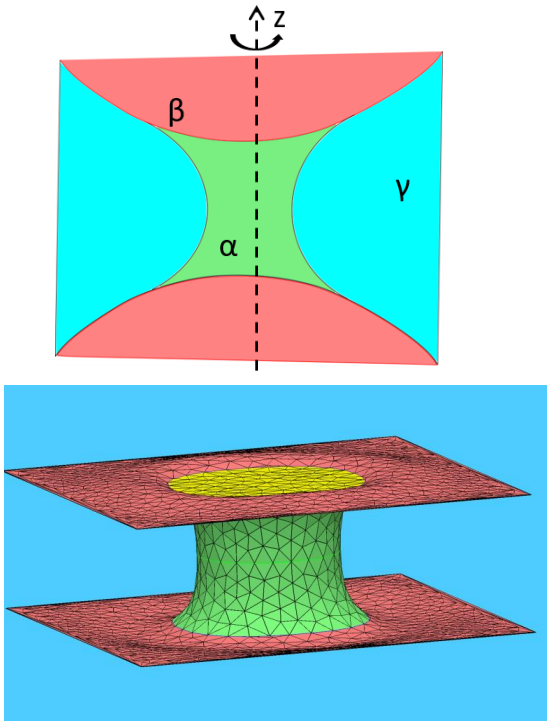
Research Area:

I believe that my understanding of fluid dynamics, thermodynamics, biomedical instrumentations, systems biology, and statistical mechanics has self-propelled me towards living active matter, and research in general. My research interests include soft matter physics, wetting phenomena, non-Newtonian rheology, membrane biophysics, colloidal clusters, artificial micro-swimmers, multiphase flow, and lattice Boltzmann simulations.

Research Experience:

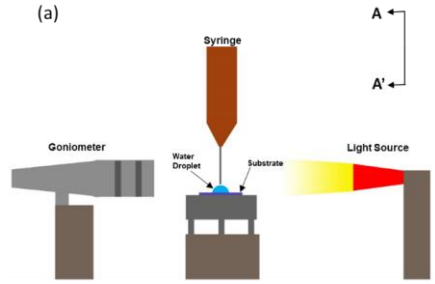
Capillary Bridges: Nucleation, Growth and Forces between the vesicles

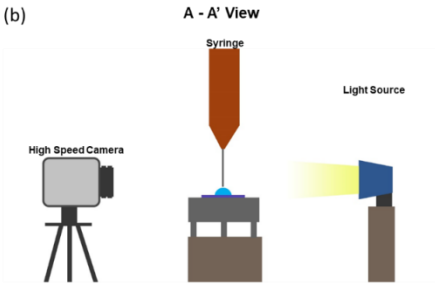
Although negligible at large scales, capillary forces may become dominant over gravity and other surface forces at small length scale. A small amount of liquid bridging two solid membranes may result in a strong adhesion due to surface tension as well as Laplace pressure. Using the software Surface Evolver, a computational model of a capillary bridge formed by a liquid droplet between two vesicles was developed in order to a) study the forces between the vesicles and the impact of varying various physical parameters and b) investigate nucleation and formation and the role of membrane confinement. The platform is interactive and allows user to input and vary the physical parameters such as the bending rigidities, surface tension values and volume of the system. The software then minimizes the energy taking into account all the aforementioned energies, and helps to determine the final configuration of the system.

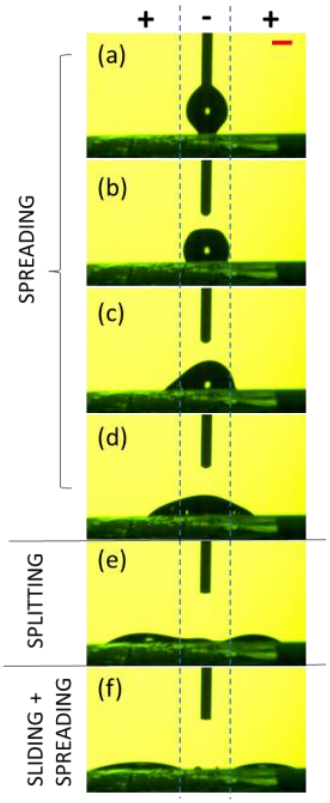


Droplet Dynamics on Patterned surfaces

In recent years, there has been a significant investigation in droplet microfluidics, and droplet splitting, in particular, owing to its immense applications in areas of drug discovery, high-throughput screening, nanotechnology, lab-on-chip devices, and material synthesis. We have used an efficient and novel technique for substrate fabrication which can thereafter be exploited to split droplets using the alternating wettability contrast (up to 100°). In essence, a micro-sized water droplet is dispensed on the hydrophobic region, neighboring hydrophilic regions on both sides, and splitting is observed. The motion of such a droplet has been understood as the superposition of sliding of the center of mass and the spreading of the droplet perimeter initially, leading to its splitting into two daughter droplets and their subsequent motion. The dependence of the droplet splitting process on the wettability difference, Δθ, has been investigated. The velocity was analyzed as a function of Δθ, while also considering minimization of energy.

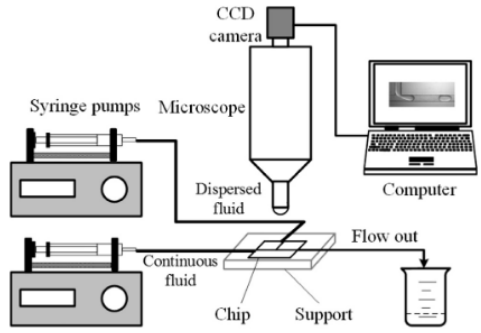


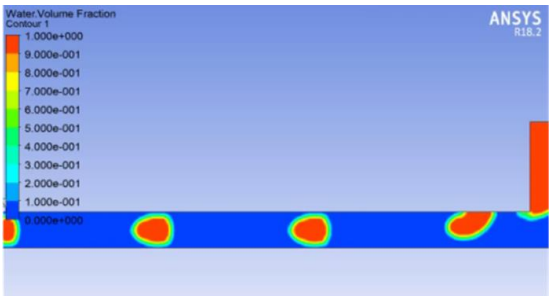




PDMS Micro-particle Generation in a T-junction for Hemodynamic Studies

The study of hemodynamics is of vital importance as they help to assess this relationship between the cardiovascular system and the oxygen needs of the body's tissues. Such assessments are designed to allow medical professionals to make proper decisions for their patients and help diagnose and prevent CVDs. To perform such studies and in vitro experiments of blood flow, blood analogue fluids are generally used to avoid the ethical and practical considerations involved with using blood. To account for the flexibility of the RBCs, we used PDMS particles in the suspension. Here we present a study to produce PDMS micro-particles, to be used in biomimetic fluids, by droplet microfluidics using a T-junction. As the advantages of this technology, it miniaturises the volume of reagents consumed as well as gives highly mono-dispersed particles.





The Useful Suspects: Investigating new neighbors and relatives of the NF-kB family

Nuclear Factor-kB (NF-kB) family transcription factors are central regulators of cellular decision after inflammatory signals and stresses. These members of the NF-kB family (RelA, RelB, c-Rel, NF-kB1, and NF-kB2) act pleiotropically to specify transcriptional programs important for cell proliferation and apoptosis. Previous studies have shown the canonical and non-canonical signaling pathways of the NF-kB family. However, there is limited understanding on their crosstalk and the regulated biological functions. Here, we aim to identify genes that are phenotypically, genetically and epigenetically similar to the NF-kB family. We found that two classes of genes showing a cell-type specific correlation with the NF-KB family transcription factors. Our established analysis platform can help establish unknown gene-gene interactions useful for predicting genetic networks of associated phenotypes.