Abstract: This talk will cover two of my recent papers in cell biology, where local stability analysis provided insights into protein network dynamics. In the first paper, we investigate the pattern formation of a reaction-diffusion model for protein clustering in the plasma membrane. We obtain theoretical estimates for diffusion-driven instabilities of the protein aggregates based on the Turing mechanism. Our main result is a threshold phenomenon: a sufficiently high feedback reaction between the membrane and cytosolic proteins promotes the formation of a single-patch spatially heterogeneous steady state. In the second paper, we discuss GTPase molecular switches and a network between monomeric (m) and trimeric (t) GTPases that have been recently found in experiments. We develop a nonlinear ordinary differential equation model and provide explicit formulae for the steady states of the system. By performing a local stability analysis, we systematically investigate the role of the different connections between the GTPase switches. Interestingly, a coupling of the active mGTPase to the GEF of the tGTPase is sufficient to provide two locally stable states that can be interpretable biologically. When we add a feedback loop to the coupled system, two other locally stable states emerge. Our findings reveal that coupling these two different GTPase motifs can dramatically change their steady-state behaviors and shed light on how such coupling may impact signaling mechanisms in eukaryotic cells.

Professor Stolerman is joining the Department of Mathematics this spring 2022 as an expert in applications of mathematics to cell biology and related topics.