Life finds a way: Mathematical modeling of the spatiotemporal dynamics and organization of complex biological systems

Mathematical models, data analytics, statistical analysis, and visualization techniques are valuable tools in the effort to determine the mechanisms that drive the spatiotemporal dynamics and organization of complex biological systems. In the first part of this talk, I will discuss how mathematical modeling enhances understanding of the immune response to human infection with the bacteria Mycobacterium tuberculosis (Mtb), which results in the formation of unique, emergent lung structures called granulomas. Due to the duration and dynamic nature of this immune response (years to decades), as well as the involvement of processes that occur over tissue, cellular, and molecular scales, we take a multiscale and mechanistic computational modeling approach. We build a hybrid agent-based model through which we generate simulated granulomas whose range of spatial configurations reflects the heterogeneity observed experimentally, and we investigate how the behavior of neutrophils contributes to Mtb protection versus pathology. In the second part of this talk, I will present a coarse-grained, entropic polymer chain model for the genome in living yeast cells, a highly dynamic system where entropic interactions and nuclear confinement drive the formation of domains of high chromosomal interaction, known as topologically associating domains. Specifically, I will discuss modeling and visualization techniques for nucleolus dynamics, and show that enrichment of dynamic chromosomal crosslinks drives phase separation of the nucleolus. Through our work, we hope to advance understanding of these systems — broadly, the eukaryotic genome and the immune response to infectious disease — beyond current experimental capabilities.