CIRC Symposium Series 2025-2026

Leveraging Machine Learning to Estimate Survival Curves with Current Status Data

Charlie Wolock, PhD
Department of Biostatistics and Computational Biology

In many epidemiological study designs, time-to-event outcomes may be subject to current status sampling: rather than observing the outcome itself, the investigator observes each study participant at a single monitoring time, recording a binary indicator of whether the event has occurred by that time. Such study design results in an extreme form of interval censoring. Existing nonparametric methods for current status data typically require independence between the monitoring time and the event time, which may be unrealistic in practice. We propose an approach to estimating the survival curve of a time-to-event outcome under current status sampling using tools from semiparametric efficiency theory and shape-constrained estimation. Our method allows for monitoring processes that are informed by measured covariates and employs machine learning tools to flexibly estimate nuisance parameters. We devise a sensitivity analysis approach investigating the degree to which the resulting estimates change under deviations from conditionally uninformative monitoring. We use the proposed methods to estimate the duration of COVID-19 symptoms using data from a university community.

Quantifying Free Energy of Phase Separation in Model Lipid Membranes

Akshara Sharma
Department of Biochemistry and Biophysics

Cell membranes contain a large number of lipid species and are capable of complex behavior like the formation of laterally ordered structures. Liquid-liquid phase separation of lipids has been captured in model membranes that undergo cholesterol-dependent phase separation into liquid-ordered and liquid-disordered domains by preferential lateral organization. While experimental studies of phase separation have provided insight into the formation of these domains and their structural properties, thermodynamic understanding of the phenomenon lags far behind. Recent work from our lab has demonstrated that the free energy landscape of phase separation can be estimated by simulating coarse-grained models of lipid bilayers with the weighted ensemble protocol. One major result of this initial work was that the effectiveness of the approach was very sensitive to the choice of the variable used to track phase separation. While the clustering-based collective variable was effective, it has several limitations, most notably that it is difficult to interpret structurally. Here, I present recent work that develops and analyzes a new collective variable based on mixing entropy and compares it to prior results. I discuss our new results in the form of free energy curves, calculated ΔΔG values, and other convenient features of our new CV calculation algorithm. This is a step towards optimizing our pipeline for calculation of the free energy landscape and provide more accurate thermodynamics of model lipid bilayer systems.

Friday, April 17, 2026
11:30 am - 1 pm
Wegmans Hall 1400

University of Rochester