Inference of Dynamic Networks in Biological Systems

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Biological systems are complex dynamic networks. In this talk, I will introduce GOBI (General Model-based Inference), a simple and scalable method for inferring regulatory networks from time-series data. GOBI can infer gene regulatory networks and ecological networks that cannot be obtained with previous causation detection methods(e.g., Granger, CCM, PCM). I will then introduce Density-PINN (Physics-Informed Neural Network), a method for inferring the shape of the time-delay distribution of interactions in a network. The inferred shape of time-delay distribution can be used to identify the number of pathways that induce a signaling response against antibiotics. This solves the long-standing mystery, the major source of cell-to-cell heterogeneity in response to stress. Finally, I will talk about how to accurately infer epidemic parameters by using realistic time delay distribution for latent and infectious periods.

References

[1] Jo H, Hong H, Hwang H,J, Chang W, Kim JK, Density Physics-Informed Neural Network reveals sources of cell heterogeneity in signal transduction, Cell Patterns (2023)

[2] Park SH, Ha S, Kim JK, A general model-based causal inference overcomes the curse of synchrony and indirect effect, Nature Communications (2023)

[3] Hong H, Eom E, Lee H, Choi S, Choi B, Kim JK, Overcoming Bias in Estimating Epidemiological Parameters: A Bayesian Approach with Realistic History-Dependent Disease Spread Dynamics (Under review))