THE UNIVERSITY OF CHICAGO | **DEPARTMENT OF STATISTICS**

Statistics Colloquium

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"Integrative Deep Multi-Learning for Biclustering and Predicting Cancer Drug Responses: Leveraging Omics and Drug Molecular Data"

Monday April 8, 2024, at 11:30 AM
Jones 303, 5747 S. Ellis Avenue
Pre-Seminar refreshments will be served at 11:00 AM in Jones 303

Abstract

Precision medicine in cancer treatment leverages the complex relationship between cancer biology and drug molecules, hindered by the genetic complexity of cancer and diverse drug structures. We introduce Integrative Multi-Task Deep Biclustering (IMTDB), merging cancer omics, drug data, and drug response to pinpoint cancer cell lines sensitive to specific drugs based on their molecular profiles. IMTDB uses biclustering to identify these sensitive subsets and predict drug sensitivity with enhanced accuracy by iterating between learning cell line and drug embeddings and their response mappings. This approach helps identify tailored treatment strategies by revealing the molecular signatures driving drug response. IMTDB's capability to group unseen cell lines and compounds facilitates quick screening, marking a potential significant step towards personalized cancer therapy. Our validation through simulations and diverse datasets underscores IMTDB's potential in identifying precise treatment options.