

SEMINARIO ALEATORIO 458

FROM STATISTICAL METHODS TO BIOLOGICAL DISCOVERY: NETWORK INFERENCE AND BIOMARKER DISCOVERY

RESUMEN:

Modern biological datasets, including gene expression, microbiome, genomic, and environmental data, present significant statistical and computational challenges because of their high dimensionality, complex dependency structures, and biological heterogeneity. In this seminar, I will present several statistical and machine-learning methods that I have developed to address these challenges and demonstrate their applications to a range of biological and biomedical problems.

I will first introduce wpLogicNet, a Bayesian mixture-model framework for reconstructing gene regulatory networks and inferring combinatorial logic gates directly from continuous gene-expression data. I will then present CMiNet, a consensus framework that integrates multiple microbiome network-inference algorithms with bootstrap-based stability analysis to construct reliable microbial association networks, together with MiNAA, a network-alignment algorithm for comparing biological networks across different conditions.

Next, I will discuss HighDimMixedModels.jl, a penalized mixed-effects framework for biomarker discovery in clustered, high-dimensional omics datasets, and demonstrate its applications to transcriptomics, GWAS, and microbiome studies. I will also present machine-learning approaches for soil microbiome analysis, in which integrating microbial sequencing data with environmental variables improved the prediction of potato yield and common scab disease. In addition, consensus-based strategies identified robust microbial biomarkers associated with disease.

Overall, this seminar demonstrates how statistical methodology, machine learning, and network-based approaches can be combined to develop interpretable, scalable, and reproducible computational tools for biological discovery.

Presentado por



ROSA AGHDAM

PhD in Statistics (Shahid Beheshti University. Teheran Iran, 2015). Actualmente ocupa la posición de Scientist en el Wisconsin Institute for Discovery (WID) en USA. Previamente fue Postdoctoral Researcher en el WID (2022-2024) y Senior Research Fellow en el Institute for Research in Fundamental Sciences en Iran (2020-2022).

Sus áreas de interés incluyen: Gene regulatory network inference, Microbiome network analysis, Machine learning and statistical methods, Sequencing-based data analysis, Cancer genomics and systems biology, Reproducible computational biology.

Detalles del evento:

Fecha: Viernes 7 de agosto, 2026

Hora: 13:00

Ubicación: Salón 310, ITAM
Campus Río Hondo