INTERNATIONAL GENETIC EPIDEMIOLOGY SOCIETY

Save The Date: Friday, March 6, 2026

11 am (EST), 8 am (PST) and 5 pm (CET)

Dear IGES members,

IGES hosts regular virtual journal clubs throughout the year to increase IGES members' familiarity with emerging and classic literature in genetic epidemiology and to foster discussion and networking among members. This month's journal club introduces joint sparse canonical correlation analysis (jsCCA), a multistage method that integrates multi-omics data (copy number aberrations, methylation, expression) with clinical outcomes to identify interpretable, outcome-associated molecular modules in cancer. Make plans to attend our next meeting!

Title: "Identifying genes associated with disease outcomes using joint sparse canonical correlation analysis-An application in renal clear cell carcinoma" (*Genet Epidemiol*. 2024 Dec;48(8):414-43).

Article: https://onlinelibrary.wiley.com/doi/10.1002/gepi.22566

Abstract (adapted from the original abstract):

Cancer genomics studies often have multiple interconnected data modalities that are related but have captured different molecular features of the tumor. Connecting multiple such modalities jointly with a tumor-related outcome while maintaining interpretability has proven to be a difficult problem. We present joint sparse canonical correlation analysis (jsCCA), a multistage pipeline for integrating high-dimensional multi-omics data with clinical outcomes. jsCCA extends sparse canonical correlation analysis to simultaneously link patterns of multiple data modalities, namely copy number aberrations (CNA), DNA methylation, and gene expression, while retaining only small, interpretable sets of features in each layer.

jsCCA detects potentially orthogonal gene components that are highly correlated with sets of methylation sites which in turn are correlated with sets of CNA sites. We then connect these multivariate “gene components” to the outcome. Applying jsCCA to TCGA clear cell renal cell carcinoma data (n = 515), we identify eight components representing coordinated CNA–methylation–expression modules. These components highlight regulatory relationships including a putative pathway where CNAs on 10q25 and methylation near SIX5 influence ASAH1 expression, which is strongly associated with tumor stage. Two components also modify the association between smoking and tumor stage and are enriched for immune, inflammatory, and hypoxia pathways. Our framework offers a general, interpretable strategy for outcome-driven analysis of multimodal omics in cancer genetic epidemiology.

Registration Link:

https://msm-edu.zoom.us/meeting/register/wTw95QXXRZKEfwgKcdMC8A

After registering, you will receive a confirmation email containing information about joining the meeting.

Bio:

Diptavo Dutta joined the Division of Cancer Epidemiology and Genetics as an Earl Stadtman tenure-track investigator in the Integrative Tumor Epidemiology Branch (ITEB) in August 2022. Before that, he earned his Ph.D. in biostatistics from the University of Michigan at Ann Arbor and subsequently was a postdoctoral fellow at Johns Hopkins University. Dr. Dutta’s research program utilizes genetic, transcriptomic, proteomic, and other ‘omics’ data to study cancer etiology, especially focusing on kidney cancer and breast cancer.

Do you have any suggestions for interesting topics, papers, or presenters for further talks? Or would you like to support us in organizing the Journal Club? Please contact Dr. Silke Szymczak (silke.szymczak@uni-luebeck.de)

On behalf of the organizing team of the IGES Journal Club,
Silke Szymczak
Heejong Sung
Cheryl Cropp