

BIOSTATISTICS SEMINAR



Sandra Safo, PhD
Assistant Professor in
Division of Biostatistics,
University of Minnesota

Joint Nonlinear Association and Prediction of Multi-view Data

Improvements in technologies produce an unprecedented amount of diverse but related data (e.g., genetics, proteomics, metabolomics) that, in addition with clinical data, can be leveraged to effectively predict an outcome and to identify important variables. Recent work show that prediction methods that leverage the strengths of these multi-faceted or multi-view data simultaneously (i.e., one-step methods) have enormous potential to yield more powerful findings than two-step methods: association followed by prediction. Existing one-step methods have focused on linear associations. The relationships between data from multiple sources, and data from multiple sources and an outcome, however, are too complicated to be understood solely by linear methods. We propose kernel-based methods for joint nonlinear association and regression or classification studies for data from multiple sources. The methods model the nonlinear association between multi-view data together with learning the prediction model and also identify variables contributing to the overall association of the different data types and the variation in the outcome. We demonstrate the effectiveness of our methods on a set of synthetic and real datasets.

Thursday November 12, 2020

3:00 pm - 4:00 pm

Zoom meeting: Please also find a link in the email invite, with the password.

<https://uncsph.zoom.us/j/92138801086?pwd=Y0lINUNQcS9lZERjalVhbVZSZ3AwQT09>



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