Department of Biostatistics and Bioinformatics Seminar

Thursday, March 28, 2024

12:00 pm – 1:00 pm – **IN PERSON – CNR-AUDITORIUM-LOBBY LEVEL**

Jie Chen, PhD
Professor, Department of Biostatistics
Interim Chair, Department of Biostatistics, Data Science and Epidemiology
Augusta University

ABSTRACT

Retrospective detection of multiple change points: Methods and Applications

Developing methods for searching multiple change points in data streams lately became trendy in many practical problems. Change point analysis has a wide range of applications in fields such as statistical quality control, finance, economics, climate study, medicine, health sciences and genomics. Two of the central questions need to be answered in change point analysis are to test if there are change points presented in the data and to estimate the unknown change point loci when the change points exist. Depending on the specific underlying problem, change point analysis can be done retrospectively (off-line) or prospectively (on-line). In this talk, I will first provide a brief review of how (retrospective) multiple change points detection problem has been handled in the literature. Then, I will discuss the problem of modelling sequencing data of multiple subjects for genomic feature discovery. Taking into consideration of the correlated structure of high throughput genomic data, we used the framework of a fused Lasso latent feature model to detect multiple change points in multiple profiles, and further propose a modified information criterion for the tuning parameter selection when searching for common features shared by multiple samples. Simulation studies and application on DNA-sequencing data showed that the proposed approach can effectively identify individual genomic features of a single subject profile and common genomic features for multiple subjects. This is based on a joint work with S. Deng.

If you wish to meet with Dr. Jie Chen,
please contact (Porchia.Arnold@emory.edu) if interested by Tuesday, March 26, 2024.