Yale Center for Biomedical Data Science
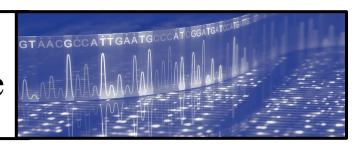
CBDS Seminar Series

"Innovative Approaches to Analyze Sequence Data to Elucidate Disease Etiology"

Suzanne Leal, PhD

Director of the Center for Statistical Genetics, Columbia University

The Innovative Approaches to Analyze Sequence Data to Elucidate Disease Etiology lecture will bring current studies into a historical prospective where it has been debated whether it is advantageous to analyze families or population based data and demonstrate for sequence-based studies both data types play an important role in elucidating the genetic etiology of Mendelian and Complex Traits. Methodology to analyze sequence data for Mendelian traits will be presented and the identification of FAM92A, for postaxial polydactyly using both pedigree and mouse data will be provided as an example. The talk will then discuss analyzing sequence data for complex traits using aggregate association methods. The computational tool, SEQSpark will be described, which allows for that analysis of large epidemiological datasets due to its processing capabilities. Lastly, nonparametric linkage analysis which has been very recently revised for the analysis of rare variants will be presented which in addition to aggregate association analysis can be used to analyze family-based sequence data.

Wednesday, February 5, 2020
4 p.m. to 5 p.m. Seminar
Brady Auditorium
310 Cedar Street