LAUFER CENTER
FOR PHYSICAL AND QUANTITATIVE BIOLOGY

Seminar 2017

New methods for measuring natural selection and predicting deleterious variants in noncoding regions of the human genome

Many genetic variants that influence phenotypes of interest are located outside of protein-coding genes, yet existing methods for identifying such variants have poor predictive power. I will describe a new computational method, called LINSIGHT, that substantially improves the prediction of noncoding nucleotide sites at which mutations are likely to have deleterious fitness consequences, and which, therefore, are likely to be phenotypically important. LINSIGHT combines a generalized linear model for functional genomic data with a probabilistic model of molecular evolution. The method is fast and highly scalable, enabling it to exploit the 'big data' available in modern genomics. I will show that LINSIGHT outperforms the best available methods in identifying human noncoding variants associated with inherited diseases.
In addition, ……..

Full abstract, please visit http://laufercenter.stonybrook.edu/seminar

Adam Siepel
Professor, Watson School of Biological Sciences & Chair,
Simons Center for Quantitative Biology
Cold Spring Harbor Laboratory

Friday October 13, 2017

2:30 PM Laufer Center 101

Host: Steve Skiena

Refreshments: Hub 110 after seminar

Stony Brook University

For a disability related accommodation, please call 631-632-5400