MTH-994
Machine learning for biological and biomedical data I: Basic algorithms (Fall 2017)
Instructor: Professor Guowei Wei
Michigan State University

Biology is believed to be the last forefront of natural sciences. The exponential growth of biological data has paved the way for biological sciences to transform from qualitative, phenomenological and descriptive to quantitative, analytical and predictive. Machine learning, the major workhorse of artificial intelligence and data science, has become a driving force behind this historic transformation. This course will discuss the theoretical foundation of basic machine learning algorithms, including support vector machines, decision tree learning, association rule learning, artificial neural networks, deep learning, manifold learning, Bayesian networks, representation learning, similarity and metric learning, genetic algorithms, etc. Emphasis will be given to their application potentials to large biological and biomedical data sets.

MTH-994
Machine learning for biological and biomedical data II: Applications (Spring 2018)
Instructor: Professor Guowei Wei
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In the post-omics era, the availability of high-throughput sequencing strategies have resulted in genomics, proteomics and metabolomics. Omics aims at the integrative studies of whole set biomolecular information that translates into the structure, function, and evolution of living organisms. Currently, the Protein Data Bank has accumulated more than 130 thousand structure and the GenBank has collected near 200 million sequences. Understanding the rules of life from these massive data sets as well as making use of these rules for health science is a major mission of biosciences in the 21st Century. This course will focus on how to use machine learning and deep learning algorithms for scientific discovery from a wide variety of real data in bioinformatics, biophysics, bioimaging, biomedical science and bioengineering. Particular emphasis will be given to the machine learning predictions of phenomics from genomics aided by ChIA-PET and/or trait information and structure-function relationship from massive biomolecular data sets.