Department of Computer Science--Colloquium Series

Impact of different loss functions in training DNN for understanding regulatory roles of DNA sequence in DNA methylation

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Date: Friday, Nov 10th,2023
Time: 10am-11am
Location: Petty 213

Abstract:

Functional genomic events, such as DNA methylation, regulate gene expression by moderating chromatin state, playing critical roles in various important biological processes, such as X-chromosome inactivation and aging. Their aberrant activities have been linked to several diseases such as cancers, immunological disorders, and neurological disorders. In a given cell, variations in functional genomic events across the genome is known to be regulated by the sequence content in the spatial neighborhood of respective genomic locus. However, specific DNA sequence patterns that regulate functional genomic events remain largely unknown. The deep neural networks, excelling in feature learning from unstructured data, holds the premises in identifying and characterizing such sequence patterns. In this talk, I will present the results from one of our very recent efforts in this direction, training deep neural networks to predict DNA methylation from DNA sequence. We studied the impact of the use of different loss functions, specifically cross-entropy loss and hinge loss in network training on various aspects of the trained network, including the prediction performance, learned sequence patterns, and uncertainly in predictions.

Biography:

Jiangwen Sun is an assistant professor at Old Dominion University, Computer Science Department. He received his doctorate degree from University of Connecticut. He has broad multidisciplinary research interests, including machine learning, data mining, medical informatics, and bioinformatics. He is particularly interested in pursuing precision medicine by developing and applying advanced machine learning techniques and other data analytics to analyze data from various dimensions of life at the systems-level.