SCIENCE AT THE EDGE

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"*Modeling to interpret genomes (via protein structure and function) and networks (via network inference and modeling)*"

This talk will describe two computational biology problems that sit on the border between large scale learning and detailed modeling and will describe projects that combine machine learning and modeling to interpret genomes (via protein structure and function) and genomes (via network inference and modeling). In the first part I will describe new work to predict protein structure genome wide (in collaboration with IBM's world community grid). Methods to annotate the many thousands of protein families with no known function in metagenomics data include structure prediction with Rosetta, followed by deep learning methods to predict protein function from an integration of sequence, structure and network data. The second part of the talk will detail a recent effort to learn networks for multiple cell types in the immune system. Multi-task learning approaches to network inference that scale biophysically motivated network inference to very large data-sets will be demonstrated in model organisms and then applied to the mammalian immune system. Lastly, I will discuss the merits of combining modeling and learning approaches in computational biology.

FRIDAY, FEBRUARY 16, 2018
11:30 AM, ROOM 1400 BPS

Refreshments at 11:15

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