Data-Driven Models for Protein Binding and Mutagenesis Effects

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Frontiers in Computational and Information Sciences
Seminar Series

Presented by…

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Abstract: Despite many decades of research into physical and statistical potentials, many challenges remain in characterizing protein energetics. By recasting problems in structural biology as classification questions, new ways of utilizing experimental data emerge. The use of physics-based features in classification models allows us to learn many underlying physical principles of protein structure from the evolutionary record and experimental data. Several successful examples of such models will be presented, including predictive models for alanine scanning and mutagenesis, protein design, and the identification of nucleotide binding sites on protein surfaces.

Bio: Julie Mitchell is an Associate Professor of Mathematics and Biochemistry at the University of Wisconsin. As an Assistant Professor, she founded the BACTER Institute for computational biology, serving as its Director from 2004-2012. Her professional honors include a Alfred P Sloan award in Molecular Biology. Prior to moving to Wisconsin in 2003, she was a postdoc and later promoted to Project Scientist at the San Diego Supercomputer Center at UC San Diego. Her PhD in Mathematics was awarded in 1998 from UC Berkeley, where she studied with Morris Hirsch, one of the founders of the field of dynamical systems. Mitchell's current research focuses on the development of physics-based data-driven models for protein structure and interaction. She is particularly interested to "learn" the physical principles of protein interaction from the evolutionary record and has made notable contributions to the prediction of mutagenesis effects on protein-protein interactions.

More info: http://www.math.wisc.edu/~mitchell/

Monday, March 18

BSF 1007
Darwin Room

11:00 am