学术报告会

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The Predictive Power of Machine Learning Techniques in Data-driven Biomedical Knowledge Discovery: My Structural Bioinformatics Journey

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Abstract:

Structural bioinformatics is the branch of bioinformatics which is concerned with the analysis and prediction of the three-dimensional structure of biological macromolecules on a genomic scale by developing computational methods. Recently, machine learning techniques based on statistical learning have provided efficient solutions to challenging problems that were previously considered difficult to address. In this talk, by combining my research experiences, I highlight some important recent developments in the prediction and analysis of functional residues or sites that are based on such methods. In particular, I focus on two tasks in structural bioinformatics, i.e. predicting protease-specific substrate cleavage sites and predicting enzyme catalytic sites from sequence and/or structural information. I dig deeper into the predictions, showing how machine learning methods can extract the predictive power and to what extent heterogeneous features derived at different levels (i.e. sequence, structure, and network) of the data samples can contribute to the model's performance. Some of the existing difficult issues/problems will also be discussed in the talk.

Biography:

Jiangning Song is a Senior Research Fellow and group leader at the Department of Biochemistry and Molecular Biology, School of Biomedical Sciences, Faculty of Medicine, Nursing and Health Sciences, Monash University, Melbourne, Australia. His research focuses on bioinformatics, systems biology, machine learning, systems pharmacology and enzyme engineering. He has co-authored 101 publications, with >1200 citations. His research has won a number of academic awards, including the JSPS Postdoctoral Fellowship, CAS Hundred Talents Fellowship and Australian NHMRC Peter Doherty Biomedical Fellowship and Future Research Leadership at Monash University.