学术报告会

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Harnessing the power of machine-learning techniques to address the 'sequence labeling' problem in the era of biomedical big data

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Abstract:

Recent advances in high-throughput sequencing have significantly contributed to an ever-increasing gap between the number of gene products ('proteins') whose function is well characterised and those for which there is no functional annotation at all. Experimental techniques to determine the protein function are often expensive and time-consuming. Recently, machine-learning (ML) techniques based on statistical learning have provided efficient solutions to challenging problems of sequence classification or annotations that were previously considered difficult to address. In this talk, by combining our recent research progress, I will highlight some important developments in the prediction of two representative sequence labeling problems in computational biology, i.e. i.e. 'target substrate labeling' and 'active site labeling', based on the high-dimensional, noisy and redundant information derived from sequences and the 3D structure. I will illustrate how ML methods can extract the predictive power from a variety of features that are derived from different aspects of the data can contribute to the model performance.

Biography:

Dr. Stephen J. Song is a Senior Research Fellow and Group Leader in the Cancer and Infection and Immunity Programs in the Biomedicine Discovery Institute (BDI), and Department of Biochemistry and Molecular Biology, School of Biomedical Sciences, Faculty of Medicine, Nursing and Health Sciences, Monash University, Melbourne, Australia. Trained as a bioinformatician and data-savvy scientist, he has a very strong specialty in Artificial Intelligence, Bioinformatics, Comparative Genomics, Cancer Genomics, Computational Biomedicine, Data Mining, Infection and Immunity, Machine Learning, Proteomics, and 'Biomedical Big Data', which are highly sought-after expertise and skill sets in the data-driven biomedical sciences. Ranked as one of the top-performing young Australian bioinformaticians, he was awarded a four-year NHMRC Peter Doherty Biomedical Fellowship (2008-2012) with his supervisor ARC Federation and Laureate Fellow Prof James Whisstock, Director of the ARC Centre of Excellence in Advanced Molecular Imaging, Monash University, and Scientific Head of EMBL Australia. Dr. Song is an Associate Investigator (AI) of the ARC Centre of Excellence in Advanced Molecular Imaging at Monash University. He is a formal member of the Monash Centre for Data Science and the Monash Bioinformatics Platform.