

中央研究院統計科學研究所

學術演講

講題：Statistical and Computational Approaches for the Identification of Novel Viruses and Virus-host Interactions

演講人：Prof. Fengzhu Sun (孫豐珠教授)

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時間：2018年12月20日 (星期四) 下午14:00-15:30

地點：中央研究院統計科學研究所6005會議室(環境變遷研究大樓A棟)

※茶會：下午15:30開始

Abstract

Viruses play important roles in controlling bacterial population size, altering host metabolism, and have broader impacts on the functions of microbial communities, such as human gut, soil, and ocean microbiomes. However, the investigations of viruses and their functions were vastly underdeveloped. Metagenomic studies provide enormous resources for the identifications of novel viruses and their hosts. We recently developed a k-mer based method, VirFinder, for the identification of novel virus contigs in metagenomic samples [1]. Applications to a liver cirrhosis metagenomic data suggest that viruses play important roles in the development of the disease. We also developed an alignment-free statistic, VirHost-Matcher, for the identification of bacterial hosts of viruses [2] and machine learning based approaches to identify new viruses infecting particular hosts with a relative large number of infecting viruses [3]. Recently we also developed an integrative approach for predicting virus-host interactions [4].

1. J Ren, NA Ahlgren, et al. (2017) *Microbiome* 5(1):69
2. NA Ahlgren, J Ren, et al. (2017) *Nucleic Acids Research* 45(1):39-53
3. MG Zhang, et al. (2017) *BMC Bioinformatics (APBC2017)* 18 (3), 60
4. WL Wang, J Ren et al. (2018) Under Review.