

JOINT EVENT

10th International Virology Summit
&
4th International Conference on Influenza & Zoonotic Diseases
July 02-04, 2018 | Vienna, Austria



Taijiao Jiang

Institute of Basic Medical Sciences-CAMS, China

Bioinformatic approaches to infectious diseases

Due to the development of high throughput sequencing technologies, large-scale sequencing of pathogens, such as influenza viruses and HIV, has not only become a routine work in surveillance of infectious diseases, but also become indispensable in identification of newly emerging infectious disease in their outbreaks. Besides, analyses of these large-scale sequence data of pathogens will significantly enhance our understanding towards the evolution of diseases, promoting new strategies for prevention and control of these viruses. This research mainly focuses on modeling the evolution of infectious disease from gene data and epidemiological data. Many computational methods have been developed in this lab to understand the origin and evolution of influenza viruses. They were demonstrated to be helpful in influenza vaccine recommendation, estimating the mortality burden and disease lethality, sourcing newly emerging influenza viruses, and so on. They have made a significant influence in the field of bioinformatics and informatics of infectious diseases. Among them, in collaboration with China CDC, the new methods developed for vaccine recommendation of human influenza viruses have now been in use in China CDC for assisting flu vaccine strains selection.

Recent Publications

1. Zhaozhong Zhu, Zheng Zhang, Wenjun Chen, Zena Cai, Xingyi Ge, Haizhen Zhu, Taijiao Jiang, Wenjie Tan, Yousong Peng (2018) The neuropathology of alcohol-related brain damage Predicting the receptor-binding domain usage of the coronavirus based on kmer frequency on spike protein. *Infect Genet Evol* 2018 Jul 4;61:183-184.
2. Taijiao Jiang et al (2018). Genome-wide RNA-Seq identifies Fas/FasL-mediated tumoricidal activity of embryonic stem cells *Int J Cancer* 2018 May 20;142(9):1829-1841
3. Yousong Peng, Xiaodan Li, Hongbo Zhou, Aiping Wu, Libo Dong, Ye Zhang, Rongbao Gao, Hong Bo, Lei Yang, Dayan Wang, Xian Lin, Meilin Jin, Yuelong Shu, Taijiao Jiang (2018) Continual Antigenic Diversification in China Leads to Global Antigenic Complexity of Avian Influenza H5N1 Viruses. *Sci Rep* 2018 May 31;8:46994.
4. Xiao Ding, Jiejian Luo, Lijun Quan, Aiping Wu, Taijiao Jiang (2017) Evolutionary genotypes of influenza A (H7N9) viruses over five epidemic waves in China. *Infect Genet Evol* 2017 Nov 22;55:269-276.

Biography

Taijiao Jiang has completed his PhD in Biochemistry and Molecular Biology at the Institute of Biochemistry and Cell Biology-Chinese Academy of Sciences in 1999 and his Master Degree in Computer Science from Yale University in 2003. After his Postdoc researches in Yale Biology Department (1999-2002) and MIT Biology Department (2003-2005), he got a Professorship at Institute of Biophysics Chinese Academy of Sciences. In 2015, he joined at the Chinese Academy of Medical Sciences & Peking Union Medical College and cofounded the Suzhou Institute of Systems Medicine. He is the Director of Center of Biomedical Big Data of Chinese Academy of Medical Sciences. He has published more than 40 papers in reputed journals and has been serving as the President of Bioinformatics Branch of the Chinese Biophysics Society since 2017.

taijiao@ibms.pumc.edu.cn