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Channing Microbiome Seminar September 9th (Friday), 2022, 9AM (ET)

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Novel methods in microbiome data integration and their applications

Abstract: The close association between gut microbiota dysbiosis and human diseases is being increasingly recognized. However, contradictory results are frequently reported as confounding effects exist. The lack of unbiased data integration methods also impedes the discovery of disease-associated microbial biomarkers from different cohorts. Here, we propose an algorithm, NetMoss, for assessing shifts of microbial network modules to identify robust biomarkers associated with various diseases. Compared to previous approaches, the NetMoss method shows better performance in removing batch effects. Through comprehensive evaluations on both simulated and real datasets, we demonstrate that NetMoss has great advantages in the identification of disease-related biomarkers. Based on analysis of pandisease microbiota studies, there is a high prevalence of multidisease-related bacteria in global populations. We believe that large-scale data integration will help in understanding the role of the microbiome from a more comprehensive perspective and that accurate biomarker identification will greatly promote microbiome-based medical diagnosis.

Bio: Dr. Fangqing Zhao is a Professor of Beijing Institutes of Life Science, Chinese Academy of Sciences (BIOLS). His research interests include developing novel computational approaches for exploring noncoding RNAs and human microbiomes. He obtained his PhD in marine genomics from Institute of Oceanology, Chinese Academy of Sciences in 2006. Dr. Zhao conducted his Postdoc research in the Department of Biochemistry and Molecular Biology at Pennsylvania State University from 2006 to 2010. Since 2011, he has been appointed as a Principal Investigator (100-Talent Plan) by Beijing Institutes of Life Science, Chinese Academy of Sciences. He has been awarded with National Science Fund for Distinguished Young Scholars (2020), and has published more than 50 research papers in high-profile journals including Cell, Gut, Nature Biotechnology, Nature Computational Science, Nature Communications, etc.

Selected publications:

1. Li Z, Zhang B, Wang N, Zuo Z, Wei H & **Zhao F***. A novel peptide protects against diet-induced obesity by suppressing appetite and modulating the gut microbiota. *Gut*, 2022 doi: 10.1136/gutjnl-2022-328035
2. Xiao L, Zhang F & **Zhao F***. Large-scale microbiome data integration enables robust biomarker identification. *Nature Computational Science*, 2022, 2: 307-316.
3. Wu W, Zhang J, Cao X, Cai Z & **Zhao F***. Exploring the cellular landscape of circular RNAs using full-length single-cell RNA sequencing. *Nature Communications*, 2022, 13(1):3242.
4. Yang J, Hou L, Wang J, Xiao L, et al., Zhao Y* & **Zhao F***. Unfavourable intrauterine environment contributes to abnormal gut microbiome and metabolome in twins. *Gut*, 2022 doi: 10.1136/gutjnl-2021-326482
5. Yu Y, Zhang B, Ji P, Zuo Z, Huang Y, Wang N, Liu C, Liu SJ & **Zhao F***. Changes to gut amino acid transporters and microbiome associated with increased E/I ratio in *Chd8^{-/-}* mouse model of ASD-like behavior. *Nature Communications*, 2022, 13(1):1151.
6. Zhang J, Hou L, Zuo Z, Zhang X, Xue Y & **Zhao F***. Comprehensive profiling of circular RNAs with nanopore sequencing and CIRI-long. *Nature Biotechnology*, 2021, 39:836-845.
7. Xiao L, Wang J, Zheng J, Li X & **Zhao F***. Deterministic transition of enterotypes shapes the infant gut microbiome at an early age. *Genome Biology*, 2021, 22:243.
8. Wang J, Li Z, Ma X, Du L, Jia Z, Cui X, Yu L, Xiao L, Zhang B, Fan H & **Zhao F***. Translocation of vaginal microbiota is involved in impairment and protection of uterine health. *Nature Communications*, 2021, 12:4191.
9. Jia N, Wang J, Shi W, Du L, Sun Y, et al., Tick Genome and Microbiome Consortium, **Zhao F*** & Cao WC*. Large-scale comparative analyses of tick genomes elucidate their genetic diversity and vector capacities. *Cell*, 2020, 182(5):1328-1340
10. Zhang J, Chen S, Yang J & **Zhao F***. Accurate quantification of circular RNAs identifies extensive circular isoform switching events. *Nature Communications*, 2020, 11:90.