BRIGHAM AND WOMEN'S HOSPITAL

HARVARD MEDICAL SCHOOL

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Department of Medicine
Channing Division of Network Medicine

Channing Microbiome Seminar
April 14 (Friday), 2023, 9AM (ET)

Zoom: https://us02web.zoom.us/j/81070959105?pwd=RFJNd3dSZmR6dXJZNjJiYVVzQ3NEQT09
Meeting ID: 810 7095 9105
Passcode: 984617

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Nanopore sequencing and Natural Language Processing in Microbiome analysis and translation

Microbiome as a research field is largely driven by technical advances, including sequencing technology and analytical methods. Firstly, our group works on applying Oxford Nanopore Technology in the sequencing and assembly of microbiome data, in which we demonstrated that with ONT reads we can increase the quality of metagenomic assembly and recover large number of structural variations (SVs, insertion/deletion/translocations), and the SVs define strains within bacterial species with significant differences in metabolic potential (Chen 2022 Nat Comms); we also expanded the ONT sequencing in mycobiome research by sequencing longer barcodes (full rRNA operon) and constructed a reference database (FRODO, Lu 2022 Mole Ecol). Secondly, our collaborative work in autoimmune diseases revealed gut microbial protein components that contribute to the pathogenesis of lupus (Chen 2021 Arthritis & Rheuma; Chen2023 Sci Bull), and protective peptide from tonsillar microbiome for rheumatoid arthritis (Li 2022 Adv Sci). Based on these inspirations, we decided to apply Natural Language Processing to systematically discover functional proteins in the gut microbiome, and successfully recovered 178 antimicrobial peptides (AMPs), in which many are potent against antibiotic-resistant bacteria in vitro and in vivo (Ma 2022 Nat Biotech; Guardian "Scientific stories of the year"). We are further expanding NLP in microbial protein discovery (Adv Sci, in revision) and potentially modification/design.

Short Bio:
2008-2010, European Union EM master, studied in Ghent University, Belgium/Oviedo University Spain/Bremen University, Germany
2010-2014, PhD in Bioinformatics with John Baines, Max-Planck Institute for Evolutionary Biology, Ploen, Germany
2014-2017, Postdoc in Jeroen Raes lab, KU Leuven/Flemish Institute for Biotechnology, Leuven, Belgium
2017-now, group leader of Bioinformatics and Computational Biology, Institute of Microbiology, CAS Beijing

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