

Xin (David) Zhao

Microbiome Researcher | Data Scientist

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[LinkedIn](#)

[GitHub](#)

EDUCATION

University of Alberta - Doctorate, Food Science and Technology

September 2013 - November 2018

Edmonton, AB

Jiangnan University - Master's, Food Science and Technology

September 2009 - July 2012

Jiangsu, China

Wuhan University of Science and Engineering - Bachelor's, Bioengineering

September 2005 - July 2009

Hubei, China

WORK EXPERIENCE

Freelance - Data Analyst in Microbiome and Health

May, 2022 - current

Edmonton, AB

- Provided advisory services with the SyMBIOTA Lab researchers on 2 scientific publications
- Implemented 5 projects using real-world data with R, documenting statistical procedures with Markdown
- Developed GitHub pages to share R analytic pipelines with beginners in microbiome analytics

SyMBIOTA Lab, Dept of Pediatrics, University of Alberta -

Microbiome Epidemiology Researcher

August 2020 - December 2021

Edmonton AB

- Developed predictive models for childhood obesity that outperformed literature models by 27%
- Presented 2 conference posters to the audience with different background
- Published 2 peer-reviewed papers on microbiome and health areas
- Helped colleagues solve analytic problems, co-authoring a paper with 1000 views in months
- Supported 3 graduate students in biostatistics and R programming

Freelance - Data Research Analyst

November, 2019 - July, 2020

Edmonton, AB

- Took time to transit from a career in experimental microbiology to computational biology
- Completed certified courses on R programming
- Completed the Public Health and Epidemiology Certification
- Reached out to professors at the University of Alberta to plan research projects

Microbiology Lab, Dept of Agri., Food & Nutrition, University of Alberta -

Food Microbiology Researcher

August 2013 - May 2018

Edmonton AB

- Developed a bioinformatics pipeline to annotate bacterial transporters' genes using genome data

- Cooperated with bioinformaticians to sequence genomes and analyze phylogenetic trees of probiotics strains
- Identified taxonomy of gut bacteria in humans, swine, and poultry with molecular methods
- Conducted a piglet trial by collecting intestinal samples and analyzing qPCR data
- Mentored 2 students to operate instruments in the Biosafety Level II Laboratory

PROJECTS

Machine learning prediction of childhood obesity

- Developed predictive models based on microbiome data of a population of 2500 infants
- Recognized and solve technical problems in machine learning modeling with R
- Interpreted statistical outcomes in the biological context for the general audience

Risk factors evaluation for infant microbiome development

- Studied the association between prenatal factors and infant microbiome in a cohort study
- Conducted ordination analysis on 16S sequence microbiota data and environmental variables
- Identified confounding variables by literature review and Directed Acyclic Graphs

Comparative genomics of gut and sourdough lactobacilli

- Closed probiotic genomes with PCR and Sanger sequencing methods
- Analyzed phylogenetic trees based on core genomes to confirm host-specific lineages
- Identified positive selection genes to explain the diversification of the lactobacilli population
- Constructed sugar metabolism pathways for probiotics with the KEGG server

Toxin genotyping of foodborne pathogen

- Prepared culture media to sample foodborne pathogens in chicken
- Drafted the SOP on computational analysis of *C. perfringens* toxins

Use of probiotics as antibiotics alternative for piglets

- Designed and implemented the daily feeding regime for the piglet experiment
- Developed PCR primers to detect probiotics in pig gut microbiota with the strain resolution

Biochemical assay of antibiotics-utilizing human commensal microbiota

- Evaluated antimicrobial resistance of gut bacteria using the disk diffusion method
- Investigated biochemical factors that affect metabolism by gut microbiota
- Validated hypothesized metabolism pathways with HPLC-MS spectra and literature review

CERTIFICATIONS

- Ethical Conduct for Research Involving Humans (TCPS 2: CORE 2022) (Panel on Research Ethics)
- Workplace Hazardous Materials Information System (WHMIS) (University of Alberta)
- R Programming ([Coursera](#), Credential ID 9V7ATEJB7HUR)
- Epidemiology for Public Health Specialization ([Coursera](#), Credential ID 7ZH2XA38AFQJ)

SKILLS

Language

R (R Studio); SQL; HTML; CSS

Computational Skills

Multivariate Statistics; Correlation and Regression; Hypothesis Testing; Supervised Learning; Unsupervised Learning; Data Exploratory Analysis; Data Visualization; Bioinformatics (standalone BLAST toolkit, MEGA 5, MAUVE, Geneious and KEGG server); GitHub

Domain Knowledge

Food Microbiology; Molecular Microbiology; Biostatistics; Microbiome Epidemiology; Applied Machine Learning

Laboratory Techniques

Biosafety Level II Laboratory Practice; qPCR; Primer Design; Bacterial Identification; Comparative Genomics; Phylogenetics; Gel Electrophoresis; RNA Expression; Experiment Design

CONFERENCE PRESENTATIONS (PRESENTING AUTHOR IS UNDERLINED)

- Xin Zhao, Kelsea M Drall, Sarah Bridgman, Mandal Rupasri, Allan B Becker, Piush J Mandhane, Theo J Moraes, Malcolm R Sears, Stuart E Turvey, Padmaja Subbarao, James A Scott, and Anita L Kozyrskyj. Effect of infant vitamin D drops on fecal glycerol, propylene glycol, and microbiota at 3 months of age, **Slide show**, at Having IMPACTT: Advancing Microbiome Research, Virtual Symposium, June 2021.
- Xin Zhao, and Michael G. Gänzle. Genetic and phenotypic analysis of carbohydrate metabolism and transport in *Lactobacillus reuteri*. **Poster presentation**, at 12th International Symposium on Lactic Acid Bacteria, in Egmond aan Zee, the Netherlands, August 2017.
- Xin Zhao, Jingshui Zheng, Xiaoxi B. Lin, and Michael G. Gänzle. Comparative genomics *Lactobacillus reuteri* from sourdough reveals adaptation of an intestinal symbiont to food fermentations, **Oral presentation**, at VIth Sourdough Symposium, in Nantes, France, October 2015.

PUBLICATIONS

- Xin Zhao, Sarah L. Bridgman, Kelsea M. Drall, Hein M. Tun, Piush J. Mandhane, Theo J. Moraes, Elinor Simons, Stuart E. Turvey, Padmaja Subbarao, James A. Scott, and Anita L. Kozyrskyj. "Infant vitamin D supplements, fecal microbiota and their metabolites at 3 months of age in the CHILD study cohort" [Biomolecules 13\(2\),\(2023\): 200](#)
- Yuanyao Chen, Xin Zhao, Wolfgang Moeder, Hein M. Tun, Elinor Simons, Piushkumar J. Mandhane, Theo J. Moraes et al. "Impact of Maternal Intrapartum Antibiotics, and Caesarean Section with and without Labour on Bifidobacterium and Other Infant Gut Microbiota." [Microorganisms 9, no. 9 \(2021\): 1847](#)
- Xin Zhao, Weilan Wang, A. Blaine, S. T. Kane, R. T. Zijlstra, and M. G. Gänzle. "Impact of probiotic *Lactobacillus* sp. on autochthonous lactobacilli in weaned piglets." [Journal of Applied Microbiology 126, no. 1 \(2019\): 242-254](#)
- Xin Zhao. "Genomic and phenotypic comparison of *Lactobacillus reuteri* isolates from food and intestinal ecosystems provides insights to probiotics applications" [Ph.D. Thesis](#) (2018)
- Xin Zhao, and Michael G. Gänzle. "Genetic and phenotypic analysis of carbohydrate metabolism and transport in *Lactobacillus reuteri*." [International Journal of Food Microbiology 272 \(2018\): 12-21](#)
- Yan Yang, Xin Zhao, Minh HA Le, Ruurd T. Zijlstra, and Michael G. Gänzle. "Reutericyclin producing *Lactobacillus reuteri* modulates development of fecal microbiota in weanling pigs" [Frontiers in Microbiology 6 \(2015\): 762](#)

- Jinshui Zheng, **Xin Zhao** (co-first author), Xiaoxi B. Lin, and Michael Gänzle. "Comparative genomics *Lactobacillus reuteri* from sourdough reveals adaptation of an intestinal symbiont to food fermentations" [*Scientific Reports* 5, no. 1 \(2015\): 1-11](#)
- **Xin Zhao**, Tian Fengwei, Wang Gang, Liu Xiaoming, Zhang Qiuxiang, Zhang Hao, and Chen Wei. "Isolation, identification and characterization of human intestinal bacteria with the ability to utilize chloramphenicol as the sole source of carbon and energy" [*FEMS Microbiology Ecology* 82, no. 3 \(2012\): 703-712](#)