Qiyun Zhu, Ph.D.

Assistant Professor
Arizona State University

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EDUCATION

- **Ph. D.** in Biological Sciences (evolutionary biology focus) — 2014
  University at Buffalo, The State University of New York
    - Advisor: Katharina Dittmar
    - Dissertation: Molecular evolution and ecology of fleas and flea-associated microbial organisms in light of horizontal gene transfer.
- **M. S.** in Biological Sciences (molecular biology focus) — 2009
  University at Buffalo, The State University of New York
- **B. S.**, in Biological Sciences — 2007
  Fudan University

ACADEMIC APPOINTMENTS

- **Assistant Professor** — 2020 – present
  School of Life Sciences; Biodesign Center for Fundamental and Applied Microbiomics,
  Arizona State University
- **Postdoctoral Scholar** — 2016 – 2020
  Department of Pediatrics, University of California San Diego
  Supervisor: Rob Knight
- **Postdoctoral Fellow** — 2014 – 2016
  Department of Genomic Medicine, J. Craig Venter Institute
  Supervisor: Sarah Highlander
- **Research Assistant** — 2008 – 2011
  New York State Center of Excellence in Bioinformatics and Life Sciences
- **Undergraduate Researcher** — 2005 – 2007
  Fudan University, Lab of Molecular Immunology

PEER-REVIEWED PUBLICATIONS

Google Scholar profile: https://scholar.google.com/citations?user=mjkV0pUAAAAJ

Total papers: **86**, citations: **36,052**, *h*-index: **48**, *i*10-index: **81**.

- Sun F, Wang K, Dong X, et al. The Microbial Bile Acid Metabolite 3-oxo-LCA Inhibits Colorectal Cancer Progression. *Cancer Research*. doi: 10.1158/0008-5472.CAN-24-3898.
- Flores-Ramos S, Siguenza N, Zhong W, et al. Diurnal Characterization of Metatranscriptomics Yields Bacterial Transgenes with Pronounced Metabolic Effects. *Cell Host & Microbe*. 2025. 33(7):1057-72.e5.
- Jiang Y, Aton M, Zhu Q, Lu YY. Modeling microbiome-trait associations with taxonomy-adaptive neural networks. *Microbiome*. 2025. 13(1):87.
- Bandoo RA, Kraberger S, Ozturk C, et al. Identification of diverse bacteriophages associated with bees and hoverflies. *Viruses*. 2025. 17(2):201.

- Martino C, Kellman BP, Sandoval DR, et al. SARS-CoV-2 infectivity can be modulated through bacterial grooming of the glycocalyx. *mBio*. 2025. Feb 25:e04015-24.

- Jiang Y, Liao D, Zhu Q, Lu YY. PhyloMix: Enhancing microbiome-trait association prediction through phylogeny-mixing augmentation. *Bioinformatics*. 2025. Jan 12:btaf014.

- Rocha ST, Shah DD, Zhu Q, Shrivastava A. The prevalence of motility related genes within the human oral microbiota. *Microbiology Spectrum*. 2024. e0126424.

- Lund MC, Hopkins A, Dayaram A, et al. Diverse microviruses circulating in invertebrates within a lake ecosystem. *Journal of General Virology*. 2024. 105(11). doi: 10.1099/jgv.0.002049.

- Dong X, Sun F, Secaira-Morocho H, et al. The dichotomous roles of microbial modified bile acids, 7-oxo-DCA and isoDCA in intestinal tumorigenesis. *Proceedings of the National Academy of Sciences*. 2024. 121(47):e2317596121.

- Secaira-Morocho H, Chede A, Gonzalez-de-Salceda L, et al. An evolutionary optimum amid moderate heritability in prokaryotic cell size. *Cell Reports*. 2024. 43(6):114268.

- Lee M, Kaul A, Ward JM, et al. House dust metagenome and pulmonary function in a U.S. farming population. *Microbiome*. 2024. 12(1):129.

- Griffiths JA, Yoo BB, Thuy-Boun PS, et al. Peripheral Neuronal Activation Shapes the Microbiome and Alters Gut Physiology. *Cell Reports*. 2024. 43(4):113953.

- Liu Y, Ritchie S, Teo SM, et al. Integration of polygenic and gut metagenomic risk prediction for common diseases. *Nature Aging*. 2024. 4(4):584-94.

- Sepich-Poore GD, McDonald D, Kopylova E, et al. Robustness of cancer microbiome signals over a broad range of methodological variation. *Oncogene*. 2024. 43(15):1127-48.

- Burcham Z, Belk AD, McGivern BB, et al. A conserved interdomain microbial network underpins cadaver decomposition despite environmental variables. *Nature Microbiology*. 2024. 9(3):595-613.

- Balaban M, Jiang Y, Zhu Q, McDonald D, Knight R, Mirarab S. Generation of accurate, expandable phylogenomic trees with uDANCE. *Nature Biotechnology*. 2024. 42(5):768-77.

- McDonald D, Jiang Y, Balaban M, et al. Greengenes2 unifies microbial data in a single reference tree. *Nature Biotechnology*. 2024. 42(5):715-718.

- Pavia MJ, Chede A, Wu Z, Cadillo-Quiroz H, Zhu Q. BinaRena: a dedicated interactive platform for human-guided exploration and binning of metagenomes. *Microbiome*. 2023. 11(1):186.

- Fu T, Huan T, Rahman G, et al. Paired microbiome and metabolome analyses associate bile acid changes with colorectal cancer progression. *Cell Reports*. 2023. 42(8):112997.

- Wang Z, Dalton KR, Lee M, et al. Metagenomics reveals novel microbial signatures of farm exposures in house dust. *Frontiers in Microbiology*. 2023. 14:1202194.

- Morton JT, Jin DM, Mills RH, et al. Multi-level analysis of the gut–brain axis shows autism spectrum disorder-associated molecular and microbial profiles. *Nature Neuroscience*. 2023. 26(7):1208-1217.

- Singh K, Pituch P, Zhu Q, et al. Distinct Nausea Profiles Are Associated With Gastrointestinal Symptoms In Oncology Patients Receiving Chemotherapy. *Cancer Nursing*. 2023. 46(2):92-102.

- Jiang Y, Balaban M, Zhu Q, Mirarab S. DEPP: Deep Learning Enables Extending Species Trees using Single Genes. *Systematic Biology*. 2023. 72(1):17-34.

- Liu Y, Teo SM, Meric G, et al. The gut microbiome is a significant risk factor for future chronic lung disease. *Journal of Allergy and Clinical Immunology*. 2022. 151(4):943-52.

- Shaffer JP, Nothias LF, Thompson LR, et al. Standardized multi-omics of Earth's microbiomes reveals microbial and metabolite diversity. *Nature Microbiology*. 2022. 7(12):2128-50.

- Haziza LN, Sepich-Poore GD, Livyatan I, et al. Pan-cancer analyses reveal cancer type-specific fungal ecologies and bacteriome interactions. *Cell*. 2022. 185(20):3789-806.e17.

- Hakim D, Wandro S, Zengler K, et al. Zebra: Static and Dynamic Genome Cover Thresholds with Overlapping References. *mSystems*. 2022. e00758-22.

- Gonzalez CG, Mills RH, Zhu Q, et al. Location-Specific Signatures of Crohn's Disease at a Multi-omics Scale. *Microbiome*. 2022. 10(1):133.

- Gauglitz JM, West KA, Bittremieux W, et al. Enhancing untargeted metabolomics using metadata-based source annotation. *Nature Biotechnology*. 2022. 40(12):1774-9.

- Zhu Q, Huang S, Gonzalez A, et al. Phylogeny-aware analysis of metagenome community ecology based on matched reference genomes while bypassing taxonomy. *mSystems*. 2022. e00167-22.

- Armstrong G, Martino C, Morris J, et al. Swapping Metagenomics Preprocessing Pipeline Components Offers Speed and Sensitivity Increases. *mSystems*. 2022. e01378-21.

- Liu Y, Méric G, Havulinna AS, et al. Early prediction of incident liver disease using conventional risk factors and gut-microbiome-augmented gradient boosting. *Cell Metabolism*. 2022. 34(5):719-30.e4.

- Gonzalez CG, Mills RH, Kordahi MC, et al. The Host-Microbiome Response to Hyperbaric Oxygen Therapy in Ulcerative Colitis Patients. *Cellular and Molecular Gastroenterology and Hepatology*. 2022. 14(1):35-53.

- Jasbi P, Mohr AE, Shi X, et al. Microbiome and metabolome profiles of high screen time in a cohort of healthy college students. *Scientific Reports*. 2022. 12(1):1-17.

- Needham BD, Funabashi M, Adame MD, et al. A gut-derived metabolite alters brain activity and anxiety behavior in mice. *Nature*. 2022. 602(7898):647-53.

- Qin Y, Havulinna AS, Liu Y, et al. Combined effects of host genetics and diet on human gut microbiota and incident disease in a single population cohort. *Nature Genetics*. 2022. 54(2):134-42.

- Mills RH, Dulai PS, Vázquez-Baeza Y, et al. Multi-omics analyses of the ulcerative colitis gut microbiome link *Bacteroides vulgatus* proteases with disease severity. *Nature Microbiology*. 2022. 7(2):262-76.

- Balaban M, Jiang Y, Roush D, Zhu Q, Mirarab S. Fast and Accurate Distance-based Phylogenetic Placement using Divide and Conquer. *Molecular Ecology Resources*. 2022. 22(3):1213-27.

- Singh KP, Kober KM, Ernst B, et al. Multiple Gastrointestinal Symptoms Are Associated With Chemotherapy-Induced Nausea In Patients With Breast Cancer. *Cancer Nursing*. 2022. 45(3):181-89.

- Armstrong G, Cantrell K, Huang S, et al. Efficient computation of Faith's phylogenetic diversity with applications in characterizing microbiomes. *Genome Research*. 2021. 31(11):2131-37.

- Zhu Q, Hou Q, Huang S, et al. Compositional and genetic alterations in Graves' disease gut microbiome reveal specific diagnostic biomarkers. *The ISME Journal*. 2021. 15(11):3399-411.

- Huang S, Jiang S, Huo D, et al. Candidate probiotic *Lactiplantibacillus plantarum* HNU082 rapidly and convergently evolves within human, mice, and zebrafish gut but differentially influences the resident microbiome. *Microbiome*. 2021. 9(1):151.

- Sun Z, Huang S, Zhang M, et al. Challenges in Benchmarking Metagenomic Profilers. *Nature Methods*. 2021. 18(6):618-26.

- Jiao JY, Fu L, Hua ZS, et al. Insight into the function and evolution of Wood-Ljungdahl pathway in *Actinobacteria*. *The ISME Journal*. 2021. 15(10):3005-18.

- Karst SM, Ziels RM, Kirkegaard RH, et al. High-accuracy long-read amplicon sequences using unique molecular identifiers with Nanopore or PacBio sequencing. *Nature Methods*. 2021. 18(2):165-9.

- Tripathi A, Vázquez-Baeza Y, Gauglitz JM, et al. Chemically informed analyses of metabolomics mass spectrometry data with Qemistree. *Nature Chemical Biology*. 2021. 17(2):146-51.

- Cantrell K, Fedarko MW, Rahman G, et al. EMPress Enables Tree-Guided, Interactive, and Exploratory Analyses of Multi-omic Data Sets. *mSystems*. 2021. 6(2):e01216-20.

- Bhagwat G, Zhu Q, O'Connor W, et al. Exploring the Composition and Functions of Plastic Microbiome Using Whole-Genome Sequencing. *Environmental Science & Technology.* 2021. 55(8):4899-913.

- Leão T, Wang M, Moss N, et al. Multi-Omics Characterization of the Natural Product Potential of Tropical Filamentous Marine Cyanobacteria. *Marine Drugs*. 2021. 19(1):20.

- Lin W, Zhang W, Paterson GA, et al. Expanding magnetic organelle biogenesis in the domain Bacteria. *Microbiome*. 2020. 8(1):152.

- Asnicar F, Thomas AM, Beghini F, et al. Precise phylogenetic analysis of microbial isolates and genomes from metagenomes using PhyloPhlAn 3.0. *Nature Communications*. 2020. 11(1):2500.

- Hillmann B, Al-Ghalith GA, Shields-Cutler RR, et al. SHOGUN: a modular, accurate, and scalable framework for microbiome quantification. *Bioinformatics*. 2020. 36(13):4088-90.

- Estaki M, Jiang L, Bokulich NA, et al. QIIME 2 enables comprehensive end-to-end analysis of diverse microbiome data and comparative studies with publicly available data. *Current Protocols in Bioinformatics*. 2020. 70(1):e100.

- McCall L, Callewaert C, Zhu Q, et al. Home chemical and microbial transitions across urbanization. *Nature Microbiology*. 2020. 5(1):108-15.

- Zhu Q, Mai U, Pfeiffer W, et al. Phylogenomics of 10,575 genomes reveals evolutionary proximity between domains Bacteria and Archaea. *Nature Communications*. 2019. 10(1):5477.

- Sanders JG, Nurk S, Salido RA, et al. Optimizing sequencing protocols for leaderboard metagenomics by combining long and short reads. *Genome Biology*. 2019. 20(1):226.

- Bolyen E, Rideout JR, Dillon MR, et al. Reproducible, interactive, scalable and extensible microbiome data science using QIIME 2. *Nature Biotechnology*. 2019. 37(8):852-57.

- Fu T, Coulter S, Yoshihara E, et al. FXR Regulates Intestinal Cancer Stem Cell Proliferation. *Cell*. 2019. 176(5):1098-1112.e18.

- Mills RH, Vázquez-Baeza Y, Zhu Q, et al. Evaluating Metagenomic Prediction of the Metaproteome in a 4.5-Year Study of a Patient with Crohn's Disease. *mSystems*. 2019. 4(1):e00337-18.

- Xu ZZ, Amir A, Sanders J, et al. Calour: an Interactive, Microbe-Centric Analysis Tool. *mSystems*. 2019. 4(1):e00269-18.

- Zhu Q, Dupont CL, Jones MB, et al. Visualization-assisted binning of metagenome assemblies reveals potential new pathogenic profiles in idiopathic travelers' diarrhea. *Microbiome*. 2018. 6(1):201.

- Fang X, Monk JM, Nurk S, et al. Metagenomics-based, strain-level analysis of *Escherichia coli* from a time-series of microbiome samples from a Crohn's disease patient. *Frontiers in Microbiology*. 2018. 9:2559.

- Hillmann B, Al-Ghalith G, Shields-Cutler R, et al. Evaluating the information content of shallow shotgun metagenomics. *mSystems*. 2018. 3(6):e00069-18.

- Minich JJ, Zhu Q, Xu ZZ, et al. Microbial effects of livestock manure fertilization on freshwater aquaculture ponds rearing tilapia (*Oreochromis shiranus*) and North African catfish (*Clarias gariepinus*). *MicrobiologyOpen*. 2018. e00716.

- Tripathi A, Marotz C, Gonzalez A, et al. Are microbiome studies ready for hypothesis-driven research? *Current Opinion in Microbiology*. 2018. 44:61-69.

- Hua ZS, Qu YN, Zhu Q, et al. Genomic inference of the metabolism and evolution of the archaeal phylum Aigarchaeota. *Nature Communications*. 2018. 9(1):2832.

- McDonald D, Hyde E, Debelius JW, et al. American Gut: an Open Platform for Citizen Science Microbiome Research. *mSystems*. 3(3):e00031-18.

- He Y, Kosciolek T, Tang J, et al. Gut microbiome and magnetic resonance spectroscopy study of subjects at ultra-high risk for psychosis may support the membrane hypothesis. *European Psychiatry*. 2018. 53:37-45.

- Washburne AD, Morton JT, Sanders J, McDonald D, Zhu Q, Oliverio AM, Knight R. Methods for phylogenetic analysis of microbiome data. *Nature Microbiology*. 2018. 3(6):652.

- Knight R, Vrbanac A, Taylor BC, et al. Best practices for analysing microbiomes. *Nature Reviews Microbiology*. 2018. 16(7):410-422.

- Minich JJ, Zhu Q, Janssen S, et al. KatharoSeq Enables High-Throughput Microbiome Analysis from Low-Biomass Samples. *mSystems*. 2018. 3(3):e00218-17.

- Kapono CA, Morton JT, Bouslimani A, et al. Creating a 3D microbial and chemical snapshot of a human habitat. *Scientific Reports*. 2018. 8(1):3669.

- Thompson LR, Sanders JG, McDonald D, et al. A communal catalogue reveals Earth's multiscale microbial diversity. *Nature*. 2017. 551(7681):457-63.

- Lin W, Paterson GA, Zhu Q, et al. Origin of microbial biomineralization and magnetotaxis during the Archean. *Proceedings of the National Academy of Sciences*. 2017. 114(9):2171-76.

- Yang Y, Zhu Q, Liu S, Zhao C, Wu C. The origin of Chinese domestic horses revealed with novel mtDNA variants. *Animal Science Journal*. 2017. 88(1):19-26.

- Li W, Richter RA, Jung Y, Zhu Q, Li RW. Web-based bioinformatics workflows for end-to-end RNA-seq data computation and analysis in agricultural animal species. *BMC Genomics*. 2016. 17(1):761.

- Dittmar K, Zhu Q, Hastriter MW, Whiting MF: On the probability of dinosaur fleas. *BMC Evolutionary Biology*. 2016. 16(1):9.

- Liu Y, Yu Y, Duan W, et al. Home storage significantly impairs Bifidobacteria survival in powered formula for infants and young children in the Chinese market. *International Journal of Dairy Technology*. 2015. 68(4):495-502.

- Han X, Chen Y, Wang L, et al. RNA: an expanding view of function and evolution. *Evolutionary Bioinformatics*. 2015. Suppl. 1:77-9.

- Zhu Q, Hastriter MW, Whiting MF, Dittmar K. Fleas (Siphonaptera) are Cretaceous, and evolved with Theria. *Molecular Phylogenetics and Evolution*. 2015. 90:129-39.

- Brook CE, Bai Y, Dobson AP, et al. *Bartonella* spp. in fruit bats and blood-feeding ectoparasites in Madagascar. *PLOS Neglected Tropical Diseases*. 2015. 9(2):e0003532.

- Zhu Q, Kosoy M, Dittmar K. HGTector: an automated method facilitating genome-wide discovery of putative horizontal gene transfers. *BMC Genomics*. 2014. 15:717.

- Zhu Q, Kosoy M, Olival KJ, Dittmar K. Horizontal transfers and gene losses in the phospholipid pathway of *Bartonella* reveal clues about early ecological niches. *Genome Biology and Evolution*. 2014. 6(8):2156-69.

- Kazemian M, Zhu Q, Halfon MS, Sinha S. Improved accuracy of supervised CRM discovery with interpolated Markov models and cross-species comparison. *Nucleic Acids Research*. 2011. 39(22):9463-72.

- Kantorovitz MR, Kazemian M, Kinston S, et al. Motif-blind, genome-wide discovery of cis-regulatory modules in *Drosophila* and mouse. *Developmental Cell*. 2009. 17(4):568-79.

- Liu Y, Zhu Q, Zhu N. Recent duplication and positive selection of the *GAGE* gene family. *Genetica*. 2008. 133(1):31-5.

- Liu Y, Zhu Q, Zhu N. Rapid HLA-DR fluorotyping based on melting curve analysis. *Immunological Investigations*. 2007. 36(4):507-21.

BOOK CHAPTERS

- Sanders J, Lin H, Zhu Q, Morton JT. Pipelines and Databases— Microbiome Analysis. In *Manual of Molecular Microbiology: Fundamentals and Applications*. Ed. Hayden RT., Carroll KC, Dekker JP, McAdam AJ, Wolk DM. pp. 296-313. John Wiley & Sons, Hoboken, NJ. 2025.

- Zhu Q, Mirarab S. Assembling a Reference Phylogenomic Tree of Bacteria and Archaea by Summarizing Many Gene Phylogenies. In *Environmental Microbial Evolution - Methods in Molecular Biology*. Ed. Luo H. pp. 137-165. Humana, New York, NY. 2022.

- Dittmar K, Zhu Q, Hastriter MW, Whiting MF. Evolutionary history of Siphonaptera: fossils, origins, vectors. In *Parasite Diversity and Diversification - Evolutionary Ecology Meets Phylogenetics*. Ed. Morand S, Krasnov BR, Littlewood DTJ. p. 230. Cambridge University Press. 2015.

BIOINFORMATICS TOOLS (SELECTED)

GitHub profile: https://github.com/qiyunzhu

- **Scikit-bio**: Versatile Python library for bioinformatics.
- **Woltka**: Phylogeny-guided shotgun metagenomic data analysis tool.
- **Web of Life** (WoL): Reference phylogenetics tree of bacterial and archaeal genomes.
- **BinaRena**: Interactive graphical interface for manual observation and binning of metagenomic contigs.
- **HGTector**: Genome-wide detection of horizontal gene transfer based on BLAST hit distribution statistics.

PRESENTATIONS (SELECTED)

- Zhu Q. Open-source microbiome and multi-omic data science with scikit-bio. *MCBIOS*. Salt Lake City, USA. 2025. (invited)

- Zhu Q, Morton JT, McDonald D, et al. Expanding Python library scikit-bio for efficient multi-omic data integration and complex community modeling. *ISMB and BOSC*. Montreal, Canada. 2024.

- Zhu Q. Decoding the fungal dimension of microbiomes. Pre-conference webinar of *Microbiome Data Congress*. Virtual. 2023.

- Secaira-Morocho H, Gonzales-de-Salceda L, Chede A, et al. A comprehensive analysis of diversity and evolution of cell size among bacterial and archaeal species. *Evolution*. Albuquerque, USA. 2023.

- Roush D, Hakim D, Gonzalez A, et al. Synchronized decoding of functional capacities and compositions of metagenomes in a sweep. *RECOMB-CG*. San Diego, USA. 2022.

- Zhu Q. BinaRena: Interactive Visualization and Binning of Metagenomic Contigs. *RECOMB-CG*. San Diego, USA. 2022.

- Zhu Q, Mai U, Pfeiffer W, et al. A Reference Phylogeny of More Than 10,000 Microbial Genomes. *ASM Microbe*. Atlanta, USA. 2018. (oral + poster)

- McCall L, Callewaert C, Zhu Q, et al. Impact of Urbanization and Westernization on the Human-Environment Microbiome and Metabolome. *ASM Microbe*. Atlanta, USA. 2018.

- Zhu Q, Jones MB, Highlander SK. Pathogen Discovery in Travelers' Diarrhea of Unknown Etiology by Metagenomic Sequencing. *ASM-NGS*, Washington, D.C., USA. 2015.

- Zhu Q, Dittmar K. Systematic detection of horizontal gene transfer patterns in Rickettsia using a new method based on Blast hit distribution statistics. *SMBE*. Chicago, USA. 2013.

- Zhu Q, Dittmar K. HGTector: a new approach to prediction of horizontal gene transfer based on Blast hit distribution statistics. *GLBIO*. Pittsburgh, USA. 2013.

RESEARCH GRANTS

- NAIRR Pilot: **NAIRR250131**. Accelerating protein function annotation via distilled language models. Role: PI (100%). Amount: 20,000 GPU hours. 2025 – 2026

- NSF DBI: **2412446**. Center: PIPP Phase II: Theme 4: Pandemic ESCAPE: Environmental Surveillance Center for Assessing Pathogen Emergence. Role: Senior personnel (23%). ASU PI: Matthew Scotch. Lead PI: Scott Berry (UKY). Amount: $6,094,449. 2024 – 2031

- ABRC: **RFGA2023-008-15**. Enhancing infectious disease detection in Arizona: novel computational approaches to pathogen identification in microbiome data. Role: PI (100%). Amount: $225,000. 2024 – 2027

- DOE BER: **DE-SC0024320**. Expanding Python library scikit-bio for efficient multi-omic data integration and complex community modeling. Role: Lead PI (50%). Co-Is (subawards): James Morton (Gutz Analytics), Rob Knight (UC San Diego). Amount: $1,049,998. 2023 – 2026

- NSF XSEDE: **BIO210103**. Inference and application of a largest and hierarchically organized microbial reference phylogeny. Role: Lead PI. Co-PIs: Rob Knight, Siavash Mirarab, and Wayne Pfeiffer. Amount: Computing resources (equivalent to $10,513.40). 2021 – 2022

TEACHING EXPERIENCE

Instructor, Arizona State University

- **BIO/MBB/MAT 355**: Introduction to Computational Molecular Biology (3 credits) 2021 – present
- **BIO/MIC 494/598**: Microbiome Data Science (3 credits) 2021 – present
- Guest lectures: MIC 598: Microbial Diversity and Environmental Processes, BIO 549: Phylogenetic Biology and Analysis, SEA 598: Marine Microbial Ecology Seminar, EVO 610: Research Areas of Evolution, MIC 501: Foundations in Microbiology, BIO/MIC 498/591: Programming for Biologists

- Quantitative Research for the Life and Social Sciences Program   2021

Teaching assistant, University at Buffalo

- BIO 200: Evolutionary Biology, BIO 201: Cell Biology, BIO 400/500: Bioinformatics and Genome Analysis, BIO 205/215: Biological Chemistry, BIO 302: Molecular Biology

MENTORING EXPERIENCE

Research group (Zhu Lab), Arizona State University

- Software engineer: 1, postdoctoral scholars: 4, graduate students: 9, undergraduate students: 16, high school student: 1, summer intern students: 2.

Thesis advisory committee member, Arizona State University

- Doctorate: 14, Master's: 5, Bachelor's: 2.

ACADEMIC SERVICES

Peer-reviewer for journals

- *Advanced Science, Bioinformatics, Bioinformatics and Biology Insights, BMC Genomics, BMC Microbiology, Cell Reports Methods, eLife, European Journal of Clinical Microbiology & Infectious Diseases, Evolutionary Bioinformatics, Frontiers in Microbiology, Gene* (Elsevier), *Genome Biology, IEEE/ACM Transactions on Computational Biology and Bioinformatics, Journal for ImmunoTherapy of Cancer, Journal of Hazardous Materials, Microbial Ecology, Microbiological Research, Microbiome, Molecular Metabolism, mSystems, Nature Biotechnology, Nature Communications, Nature Reviews Genetics, npj Biofilms and Microbiomes, Nucleic Acids Research, PeerJ, PLOS Computational Biology, PLOS One, PLOS Pathogens, PNAS Nexus, Scientific Reports, SOJ Genetic Science.*

Peer-reviewer for whole books

- Springer Nature

Peer-reviewer for funding agencies

- Department of Energy (DOE), USA, German Research Foundation (DFG), Germany, National Institutes of Health (NIH), USA, National Science Foundation (NSF), USA, Oak Ridge Associated Universities (ORAU), USA

Guest editor for journal

- *Evolutionary Bioinformatics*   2014 – 2015

Conference organization

- **Workshop organizer and instructor**: Multi-omic data integration for microbiome research using scikit-bio. *ISMB*. Montreal, Canada   2024
- **Committee member and session chair**: *Microbiome Data Congress*. Boston, USA   2023
- **Session chair**: Bioinformatics, Genomics (co-chair: Kaixiong Ye). *ICIBM*. Philadelphia, USA   2022
- **Session chair**: Metagenomics & Genome Rearrangments. *RECOMB-CG*. San Diego, USA   2022