

CURRICULUM VITAE

Di Wu, PhD

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PERSONAL INFORMATION

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EDUCATION

<u>Institution</u>	<u>Degree</u>	<u>Date Conferred</u>	<u>Major</u>
University of Harvard Department of Statistics Department of Biostatistics Dana Farber Cancer Institute Brigham and Women's Hospital US	Postdoc	Apr 2015	Biostatistics Bioinformatics
University of Melbourne Institute of Medical Research Bioinformatics Division Australia	Ph.D.	Dec 2012	Statistical Bioinformatics
Case Western Reserve University School of Medicine Department of Epidemiology & Biostatistics US	M.S.	May 2006	Biostatistics
Shanghai Jiao Tong University Department of Biotechnology China	B.S.	June 1998	Biotechnology

PROFESSIONAL EXPERIENCE

2021 – present	Associate Professor, Division of Oral and Craniofacial Health Sciences, Adams School of Dentistry, University of North Carolina at Chapel Hill, NC
2021 – present	Research Associate Professor, Department of Biostatistics, Gillings School of Global Public Health, University of North Carolina at Chapel Hill, NC
2019 – present	Full member, Computational Medicine (compMed) University of North Carolina at Chapel Hill, NC
2018 – present	Full member, Cancer Genetics UNC Lineberger Comprehensive Cancer Center, University of North Carolina at Chapel Hill, NC
2016 – present	Core Member of Bioinformatics and computational Biology (BCB) in The Biological & Biomedical Sciences Program (BBSP) University of North Carolina at Chapel Hill, NC
2015 – present	Core Member, Carolina Health Informatics Program (CHIP), University of North Carolina at Chapel Hill, NC
2015 – 2021	Assistant Professor, Division of Oral and Craniofacial Health Sciences, Adams School of Dentistry, University of North Carolina at Chapel Hill, NC
2015 – 2021	Research Assistant Professor, Department of Biostatistics, Gillings School of Global Public Health, University of North Carolina at Chapel Hill, NC
2011 – 2015	Postdoctoral Fellow, Department of Statistics, Harvard University, Cambridge, MA
2011 – 2015	Postdoctoral Fellow, Biostatistics, Dana-Farber Cancer Institute, Boston, MA
2011 – 2015	Postdoctoral Fellow, Division of Genetics, Harvard Medical School and the Brigham and Women’s Hospital, Boston, MA
2007 – 2011	Biostatistician (part-time), Center for Cancer Research, Monash Institute of Medical Research, Clayton, Victoria, Australia
2006 – 2007	Biostatistician, Center for Cancer Research, Monash Institute of Medical Research, Clayton, Victoria, Australia

2004 – 2006	Research Assistant III, Department of Pathology, Case Western Reserve University, Cleveland, OH
2003 – 2004	Research Assistant II, Case Comprehensive Cancer Center, Case Western Reserve University, Cleveland, OH
2001 – 2003	Research Assistant I & II, Department of Pathology, Case Western Reserve University, Cleveland, OH
1998 – 2001	Research Assistant, Shanghai Institute of Biochemistry, Chinese Academy of Science, China

HONORS & AWARDS

2018	Junior Faculty Development Award, UNC-Chapel Hill
2018	Finalist, Joseph Lister Award for Young Investigators, American Association for Dental Research (AADR)
2010	Chinese Government Award for Outstanding Self-Financed Students Abroad
2010	Edith Moffat Overseas Travel Scholarship, Walter and Eliza Hall Institute, Australia
2007-2010	Australian Postgraduate Award, University of Melbourne, Australia
2009	Student Travel Bursary, AMATA Conference, Sydney, Australia
2007	Student Travel Bursary, MGED and AMATA Conference, Brisbane, Australia
2007	Travel Scholarships, ICE-EM Australian Graduate School in Mathematics
1995	Scholarship for Excellence, Shanghai Jiao Tong University, China

BIBLIOGRAPHY

Books & Book Chapters:

1. **Wu D**, Gantier MP. Normalization of Affymetrix miRNA Microarrays for the Analysis of Cancer Samples. *Microarray Data Analysis Methods and Applications* part of the *Methods in Molecular Biology Series* Ed. 2015; DOI:10.1007/7651_2015_239: 1-10.
2. Divaris K, Shungin D, Rodriguez-Cortes A, Basta PV, Roach J, Cho H, **Wu D**, Ferreira Zandona AG, Ginnis J, Ramamoorthy S, Kinchen JM, Kwintkiewicz J, Butz N, Ribeiro AA, Azcarate-Peril MA. The supragingival biofilm in early childhood caries: clinical and laboratory protocols and bioinformatics pipelines supporting metagenomics,

metatranscriptomics, and metabolomics studies of the oral microbiome. *Methods Mol Biol.* 2019;1992(40): 525-548

3. **Wu D.** Karhade D, Pillai M, Jiang M, Huang L, Li G, Cho H, Roach J, Li Y, Divaris K. Machine learning and deep learning in genetics and genomics . *Machine Learning in Dentistry*. Springer Nature Switzerland AG. 2021. doi.org/10.1007/978-3-030-71881-7_13. p p163-181

Submitted articles

1. Pillai M, **Wu D.** Validation approaches for computational drug repurposing: a review. Revision
2. Simancas-Pallares M, Gormley A, Shrestha P, Gu Yu, Cho H, Spangler H, Burk Z, Smith M, Dashper S, Burgner D, Zandona A, Ginnis J, Vann W, Esberg A, Roach J, Ribeiro Apoen, **Wu D.** Silva M, Lif Holgersson P, Haworth S, Johansson I, North K, Divaris K. Evidence for clinical subtypes of early childhood caries. 2024
3. Binghao Yan, **Wu D.** Differential Expression Analysis for Metatranscriptomics with Sample-Paired Metagenomics Data. 2024

<https://www.biorxiv.org/content/10.1101/2022.12.08.519567v1.abstract>

Refereed papers/journal articles

1. Cheng X, An J, Lou J, Gu Q, Ding W, Droby GN, Wang Y, Wang C, Gao Y, Anand JR, Shelton A, Satterlee AB, Mann B, Hsiao YC, Liu CW, Lu K, Hingtgen S, Wang J, Liu Z, Miller CR, **Wu D.** Vaziri C*, Yang Y*. Trans-lesion synthesis and mismatch repair pathway crosstalk defines chemoresistance and hypermutation mechanisms in glioblastoma. *Nature Communications*. 15, Article number: 1957 (2024). *co-corresponding author.
2. Wang H, Divaris K, Pan B, Li X, Lim JH, Saha G, Barovic M, Giannakou D, Korostoff JM, Yu B, Sen S, Moss K, **Wu D.** Beck JD, Ballantyne CM, Natarajan P, North KE, Netea MG, Chavakis T, and Hajishengallis G. DNMT3A-driven clonal hematopoiesis promotes inflammatory bone loss. *Cell*. Accepted, Apr 2024.
3. Kandala K, Archer HR, Moss KL, White B, Thomas BR, Milner BE, **Wu D.** Weintraub JA. Comparison of Initial Treatment Decisions between In-person Exams and Asynchronous Teledentistry Exams for People with Special Healthcare Needs . *Journal of the American Dental Association*. Accepted. May (2024).
4. Zhang X, Joseph S, **Wu D.** Bowser JL, Vaziri C. The DNA Damage Response (DDR) landscape of endometrial cancer defines discrete disease subtypes and reveals therapeutic opportunities. *NAR Cancer*. Volume 6, Issue 2, June 2024, zcae015, <https://doi.org/10.1093/narcan/zcae015>

5. Yang J, Zhuang H, Li J, Nunez-Nescolarde AB, Luo N, Chen H, Li A, Qu X, Wang Q, Fan J, Bai X, Ye Z, Gu B, Meng Y, Zhang X, **Wu D**, Sia Y, Jiang X, Chen W, Combes AN, Nikolic-Paterson DJ, Yu X. The secreted micropeptide C4orf48 enhances renal fibrosis via an RNA-binding mechanism. *The Journal of clinical investigation*. 134(10):e178392. 2024. <https://doi.org/10.1172/JCI178392>.
6. Lyu R, Qu Y, Divaris K, **Wu D**. Methodological Considerations in Longitudinal Analyses of Microbiome Data: A Comprehensive Review. *Genes*. 15(1), 51. 2024. doi.org/10.3390/genes15010051
7. Park JE, Smith MA, Alsten SCV, Walens A, **Wu D**, Hoadley KA, Troester MA, Love MI. DiffSig: Associating Risk Factors With Mutational Signatures. *Cancer Epidemiol Biomarkers Prev*. 33 (5): 721–730. 2024. <https://doi.org/10.1158/1055-9965.EPI-23-0728>
8. Yang Y, Alves T, Miao MZ, Wu YC, Li G, Lou J, Hasturk H, Dyke TV, Kantarci A*, **Wu D***. Single-Cell Transcriptomic Analysis of Dental Pulp and Periodontal Ligament Stem Cells. *Journal of Dental Research*. Volume 103, Issue 1, 2024 Jan. <https://doi.org/10.1177/002203452312052>. *co-corresponding author.
9. Cho H, Liu C, Tang B, Lin B, et al Love M, Divaris K, **Wu D**. Comprehensive evaluation of methods for differential expression analysis in metatranscriptomics. *Briefings in Bioinformatics*. Aug 2023. <https://doi.org/10.1093/bib/bbad279>
10. Miao MZ, Su QP, Cui Y, Bahnson EM, Li G, Wang M, Yang Y, Collins JA, **Wu D**, Gu Q, Chubinskaya S, Diekman BO, Yamada KM, Loeser RF. Redox-active endosomes mediate $\alpha 5 \beta 1$ integrin signaling and promote chondrocyte matrix metalloproteinase production in osteoarthritis. *Science Signaling*. Vol 16, Issue 809, Oct 2023, DOI: 10.1126/scisignal.adf829
11. Schrank T, Kothari A, Weir WH, Stepp AH, Rehmani H, Liu X, Wang X, Sewell A, Li X, Tasoulas J, Kim S, Yarbrough G, Xie Y, Flamand Y, Marur S, **Wu D**, Burtness B, Anderson KS, Baldwin A, Yarbrough WG, Issaeva N. Non-canonical HPV carcinogenesis drives radio-sensitization of head and neck tumors. *PNAS*. 2023 Aug 8;120(32):e2216532120. doi: 10.1073/pnas.2216532120
12. Babikow E, Ghaltakhchyan N, Livingston T, Qu Y, Liu C, Hoxie A, Sulkowski T, Bocklage C, Marsh A, Phillips ST, Mitchell KB, Ribeiro AD, Jackson TH, Roach J, **Wu D**, Divaris K, and Jacox LA. Longitudinal Microbiome Changes in Supragingival Biofilm Transcriptomes Induced by Orthodontics. *JDR Clinical & Translational Research*, 2023, <https://doi.org/10.1177/23800844231199393>. Oct
13. Pan Y, Landis J, Moorad R, **Wu D**, Marron JS, and Dittmer DP. A new Poisson probability paradigm for single cell RNA-seq clustering. *BMC Bioinformatics*. (2023) 24:256. <https://doi.org/10.1186/s12859-023-05349-2>. June 17

14. Cho H, Ren Z, Divaris K*, Roach J, Lin B, Liu C, Azcarate-Peril A, Simancas-Pallares M, Shrestha P, Orlenko A, Ginnis J, North K, Zandona AF, Ribeiro A, **Wu D***, Koo H*. Selenomonas sputigena acts as a pathobiont mediating spatial structure and biofilm virulence in early childhood caries. *Nat Commun* 14, 2919 (2023). <https://doi.org/10.1038/s41467-023-38346-3>; *co-corresponding author. May
15. Cho H, Liu C, Preisser J, **Wu D**. A bivariate zero-inflated negative binomial model for identifying underlying dependence with application to single cell RNA sequencing data. *Statistical Methods in Medical Research*. 32(7), 2023 May
16. Lin BM, Cho H, Liu C, Roach J, Ribeiro AA, Divaris K, **Wu D**. BZINB Model-Based Pathway Analysis and Module Identification Facilitates Integration of Microbiome and Metabolome Data. *Microorganisms*. March 2023; 11(3):766. <https://doi.org/10.3390/microorganisms11030766>
17. Fang Y, Potter G, **Wu D**, Zhu H, Liu M. Addressing Multi-Site Functional MRI Heterogeneity through Collaborative Learning for Multi-Target Brain Disease Identification. *Human Brain Mapping*. 44 (11), 4256-4271, May 2023
18. Anand J, Chiou L, Sciandra C, Zhang X, Hong J, **Wu D**, Zhou P, Vaziri C, Roles of trans-lesion synthesis (TLS) DNA polymerases in tumorigenesis and cancer therapy, *NAR Cancer*, Volume 5, Issue 1, March 2023, zcad005, <https://doi.org/10.1093/narcan/zcad005>
19. Bose C, valentine G, Philips K, Boggess K, Moss K, Barros S, Marchesan J, **Wu D**, O'Shea TM, Peralta-Carcelen M, Goldstein R, Ramamurthy R, Beck J. Antepartum periodontitis treatment and risk of offspring screening positive for autism spectrum disorder. *Journal of Perinatology*. Jan 2023. Volume 43, pages 470–476 (2023) Apr
20. Wu T, Wu Y, Jiang D, Sun W, Zou M, Vasamsetti SB, Dutta P, Leers SA, **Wu D**, Li G. SATB2, coordinated with CUX1, regulates IL-1 β -induced senescence-like phenotype in endothelial cells by fine-tuning the atherosclerosis-associated p16INK4a expression. *Aging Cell*. 22 (2), e13765 (2023) Feb
21. Zhang J, Lu S, Miyuraj W, et al, Liu Y, **Wu D**, Kevin M, Ashutsh M, Zeng E, Lei Y, Zhang S. TRAF3IP2-IL-17 axis strengthens the gingival defense against pathogens. *Journal of Dental Research*. Jan 2023, Vol. 102(1) 103–115 (2023)
22. Buren EV, Hu M, Cheng L, Wrobel J, Wilhelmsen K, Su L, Li Y, **Wu D**. TWO-SIGMA-G: A New Competitive Gene Set Testing Framework for scRNA-seq Data Accounting for Inter-Gene and Cell-Cell Correlation. *Briefings in Bioinformatics*. Volume 23, Issue 3, May 2022, DOI: 10.1093/bib/bbac084.
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26. Li T, Samuel TM, Zhu Z, Howell B, Cho S, Baluyot K, Hazlett H, Elison JT, Wu D, Hauser J, Sprenger N, Zhu H, Lin W. Jointly analyzing the association of human milk nutrients with cognition and temperament traits during the first 6 months of life. *Frontiers in Nutrition*. 2022. <https://doi.org/10.17615/depg-p094>

27. Schrank TP, Landess L, Stepp WH, Rehmani H, Weir WH, Lenze N, Lal A, **Wu D**, Kothari A, Hackman TG, Sheth S, Patel S, Jefferys SR, Issaeva N, Yarbrough WG. Comprehensive Viral Genotyping Reveals Prognostic Viral Phylogenetic Groups in HPV16-Associated Squamous Cell Carcinoma of the Oropharynx. *Molecular Cancer Research*. July 2022. DOI: 10.1158/1541-7786.MCR-21-0443

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29. Yu W, Gu Q, **Wu D**, Zhang W, Li G, Lin L, Lowe JM, Hu S, Li TW, Zhou Z and Miao, MZ 2022. Identification of potentially functional circRNAs and prediction of circRNA, miRNA, mRNA regulatory network in periodontitis: Bridging the gap between bioinformatics and clinical needs. *Journal of Periodontal Research*, 2022, 57(3), pp.594-614.

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31. Nosrat A, Yu P, Verma P, Dianat O, **Wu D**, Fouad AF. Was the COVID-19 Pandemic Associated with an Increased Rate of Cracked Teeth. *Journal of Endodontics*. 2022. DOI: 10.1016/j.joen.2022.07.002

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33. Yu L, Cao C, Zhang M, Gu Q, Gao H, Balic J, Xu D, Zhang L, Ying L, Xu D, Yang Y, **Wu D**, He B, Jenkins B, Liu Y, Li X, Li J (2022). Complete loss of miR-200 family induces EMT associated cellular senescence in gastric cancer. Accepted. *Oncogene*. 2022.
34. Wu T; Jiang D, Zou M, Sun W, **Wu D**, Cui,J, Huntress I, Peng Xinxia, Li G (2022). Coupling high throughput mapping with proteomics analysis delineates cis-regulatory elements at high resolution . *Nucleic Acid Research*. DOI: 10.1093/nar/gkab890
35. Xie J, Cho H, Lin B, Pillai M, Heimisdottir L, Bandyopadhyay D, Zou F, Roach J, et al Divaris K, **Wu D** (2021). Improved Metabolite Prediction Using Microbiome Data-Based Elastic Net Models. *Front. Cell. Infect. Microbiol.*, 25 October 2021. DOI: 10.3389/fcimb.2021.734416
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37. Nosrat A, Dianat O, Verma P, Yu P, **Wu D**, Fouad A (2021). Endodontics specialists' practice during the initial outbreak of COVID-19. Oct 2021, *Journal of Endodontics*. DOI: 10.1016/j.joen.2021.09.015 As the #2 item on this Coronavirus Briefing from the AAE
38. Karhade DS, Roach J, Shrestha P, Simancas-Pallares MA, Ginnis J, Burk ZJS, Ribeiro AA, Cho H, **Wu D**, Divaris K. (2021) An Automated Machine Learning Classifier for Early Childhood Caries. *Pediatr Dent*. May 15;43(3):191-197.
39. Yang Y, Sun H, Zhang Y, Zahng T, Gong J, Wei Y, Duan YG, Shu M, Yang Y, **Wu D***, Yu D*. (2021) Dimensionality reduction by UMAP reinforces sample heterogeneity analysis in bulk transcriptomic data. *Cell Report*. July, 2021, doi: 10.1016/j.celrep.2021.109442. *Co-corresponding author
40. Cho S, Zhu Z, Li T, Baluyot K, Howell BR, Hazlett HC, Elison JT, Hauser J, S Norbert, **Wu D**, Lin W. (2021) Human milk 3'-Sialyllactose is positively associated with language development during infancy. *The American Journal of Clinical Nutrition*. May, 2021, 4.doi: 10.1093/ajcn/nqab103
41. Rosa T, Neves A, Azcarate-Peril MA, Divaris K, **Wu D**, Cho H, Moss K, Paster J, Chen T, Freitas-Fernandes LB, Fidalgo TKS, Lopes R, Valente AP, Arnold RR, Ribeiro AA. (2021) The Bacterial Microbiome and Metabolome in Caries Progression and Arrest. *The Journal of Oral Microbiology*. doi.org/10.1080/20002297.2021.1886748. June 16, 2021.
42. Zhang S, Philips KH, Moss K, **Wu D**, Adam H, Selvin E, Demmer RT, Pankow J, Norby F, Mustapha IZ, Beck JD. (2021) Periodontal and Risk of Incident Diabetes in the Atherosclerosis Risk in Communities (ARIC) Study: A BMI-modified Association. *J Clinical Endocrinology & Metabolism*; <https://doi.org/10.1210/clinem/dgab337>. JCEM's Featured Article of the week.

43. Shallal-Ayzin M, Trinh T, Yeung W, Tawil PZ, Cl H, **Wu D**, Khan AA. (2021) A Prospective Analysis of the Correlation between Postoperative Pain and Vital Pulp Therapy. *The Frontiers in Dental Medicine*. Feb 22, 2021.
44. Yip J, Liu C, **Wu D**, Fouad A. (2021) The association of apical periodontitis and type 2 diabetes mellitus: A large hospital network cross-sectional case-controlled study.. *The Journal of the American Dental Association*. Jan 11, 2021. doi.org/10.1016/j.adaj.2021.01.005
45. Zou M, Jiang D, Wu T, ZHANG X, ZHao Y, **Wu D**, Sun W, Cui J, Moreland L, Li G. (2021) Post-GWAS functional studies reveal an RA-associated CD40 induced NF-kB signal transduction and transcriptional regulation network targeted by class II HDAC inhibitors. *Human Molecular Genetics*. 2021 Jan doi.org/10.1093/hmg/ddab032
46. Lou JT, Yang Y, Gu QS, Price BA, Qiu YH, Fedoriw Y, Desai S, Mose LE, Chen B, Tateishi S, Parker JS, Vaziri C, **Wu D**. (2021) Rad18 mediates specific mutational signatures and shapes the genomic landscape of carcinogen-induced tumors in vivo. *Nucleic Acid Research Cancer*, 2021 Jan 06; 3(1) zcaa037, doi.org/10.1093/narcan/zcaa037
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48. Wang N, Du N, PengY, Yang K, Shu Z, CHANG K, **Wu D**, Yu J, Zhou Y, Li X, Liu B, Gao Z, Zhnag R, Zhou X. (2021) Network Patterns of Herbal Combinations in Traditional Chinese Clinical Prescriptions. *Frontiers in pharmacology*. 2021, Jan. doi: 10.3389/fphar.2020.590824
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52. Guo ZL, Wang G, Wu B, Chou WC, Cheng L, Zhou CL, Lou JT, **Wu D**, Su LS, Zheng JN, Ting J, Wan YY. (2020) DCAF1 regulates Treg senescence via the ROS axis during immunological ageing. *J Clin Invest*, 2020 Jul 30;136466. doi: 10.1172/JCI136466.

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54. Zhong W, Dong L, Poston TB, Spracklen CN, **Wu D**, Darville T, Mohlke K, Li Y, Li Q and Zheng X. (2020) Inferring Causal Networks from Mixed Observational Data Using Directed Acyclic Graphs. *Frontiers in Genetics*. 2020 Feb 7;11:8. doi: 10.3389/fgene.2020.00008. eCollection 2020.
55. Divaris K, Slade GD, Ferreira Zandona AG, Preisser JS, Ginnis J, Simancas-Pallares MA, Agler CS, Shrestha P, Karhade DS, Ribeiro AA, Cho HY, Gu Y, Meyer BD, Joshi AR, Azcarate-Peril MA, Basta PV, **Wu D**, North KE. (2020) Cohort profile: ZOE 2.0—a community-based genetic epidemiologic study of early childhood oral health. *Int. J. Environ. Res. Public Health* 2019, Nov 1; 17(21):8056; <https://doi.org/10.3390/ijerph17218056>
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- Clear Cell Carcinoma. *Eur J Cancer*. 2015 Sep;51(13):1831-42. doi: 10.1016/j.ejca.2015.05.011. Epub 2015 Jun 6.
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- Human Genetics in Rheumatoid Arthritis Guides a High-Throughput Drug Screen of the Cd40 Signaling Pathway. *PLoS Genet.* 2013 May;9(5):e1003487. doi: 10.1371/journal.pgen.1003487. Epub 2013 May 16.
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87. Lim E, Vaillant F, **Wu D**, Forrest NC, Pal B, Hart AH, Asselin-Labat ML, Gyorki DE, Ward T, Partanen A, Feleppa F, Huschtscha LI, Thorne HJ, kConFab, Fox SB, Yan M, French JD, Brown MA, Smyth GK, Visvader JE, Lindeman GJ. (2009) Aberrant Luminal Progenitors as the Candidate Target Population for Basal Tumor Development in Brca1 Mutation Carriers. *Nat Med.* 2009 Aug;15(8):907-13. doi: 10.1038/nm.2000. Epub 2009 Aug 2.
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91. Kong Q, Huang S, Zou W, Vanegas D, Wang M, **Wu D**, Yuan J, Zheng M, Bai H, Deng H, Chen K, Jenny AL, O'Rourke K, Belay ED, Schonberger LB, Petersen RB, Sy MS, Chen SG, Gambetti P. (2005) Chronic Wasting Disease of Elk: Transmissibility to Humans Examined by Transgenic Mouse Models. *J Neurosci*. 2005 Aug 31;25(35):7944-9. doi: 10.1523/JNEUROSCI.2467-05.2005.
92. Kong Q, Huang S, **Wu D**, Wang M, Vanegas D, Bai H, Deng H, Chen K, Zou W, Jenny AL, O'Rourke K, Sy M., Chen SG and Gambetti P. (2004) Transmissibility of chronic wasting disease of elk and deer to humans. *J Neuropathology and Experimental Neurology*. 63:515.

Published Refereed Abstracts

1. **Wu D**. A Novel Deep Learning Interpolation Method for Irregularly-Sampled Longitudinal Microbiome Data. Poster. J Dent Res 2024 (IADR/AADR/CADR).
2. **Wu D**. Microbial Omics Data Integration to Compare Oral and Gut Bacterial Association With Diseases (ECC and IBD). Invited Talk. J Dent Res 2022 (IADR/AADR/CADR).
3. **Wu D**. Integrative Analysis of Metagenome, Metatranscriptome and Metabolome Applied in a Cohort of Early Childhood Caries (ECC). Invited Talk. J Dent Res 2021 (IADR/AADR/CADR).
4. **Wu D**, Cho H, Simancas-Pallares MA, Ginnis J, Ferreira Zandona AG, Divaris K. Understanding the Early Childhood Caries Microbiome: Integrative Metatranscriptomics-Metagenomics Analyses. Invited Talk. J Dent Res 2019;98 (Spec Iss A): 3072291 (IADR/AADR/CADR).
5. Shungin D, Simancas-Pallares MA, Ginnis J, Ferreira Zandona AG, **Wu D**, Divaris K. Characterizing Supragingival Biofilm Metatranscriptome And Metagenome In Early Childhood Caries. J Dent Res 2019;98 (Spec Iss A): 3181468 (IADR/AADR/CADR).
6. Ribeiro AA, Rosa T, Neves AA, Azcarate-Peril MA, Divaris K, **Wu D**, Cho H, Paster BJ, Chen T, Fidalgo T, Freitas-Fernandes LB, Valente A, Arnold R. The Oral Microbiome and Metabolome in Caries Initiation and Arrestment. J Dent Res 2019;98 (Spec Iss A): 3072291 (IADR/AADR/CADR).

7. Heimisdottir LH, Cho H, Ginnis J, Simancas-Pallares MA, Ferreira Zandoná MA, Shungin D, **Wu D**, Divaris K. Metabolomics Insights in Early Childhood Caries. *J Dent Res* 2019;98 (Spec Iss A): 3072291 (IADR/AADR/CADR).
8. Li G, Chen M, Li G, **Wu D**, Lian C, Sun Q, Shen D. A longitudinal MRI study of amygdala and hippocampal subfields for infants with risk of Autism, Annual meeting of Organization for Human Brain Mapping. Rome Italy. GLMI 2019. Lecture Notes in Computer Science, Vol 11849. Springer, Cham.
9. **Wu D**, Gupta A, Moss K, Morelli T, Beck J, Offenbacher S. Novel patient level and teeth level classification on PAVE study to compare community and periodontal treatment outcomes. International Association for Dental Research (IADR). London, UK. *J Dent Res* 2018;97 (Spec Iss B): 2959972.
10. Divaris K, Cho H, **Wu D**, Roach J, Rodríguez Cortés A, Basta PV, Ferreira Zandoná AG, Ginnis J, Meyer BD, Hu S, Simancas-Pallares MA, Butz N, Azcarate-Peril MA. Supragingival Biofilm Transcriptomics in Early Childhood Oral Health. *J Dent Res* 2018;97 (Spec Iss B): (IADR/CED).
11. **Wu D**, Wang R, Teles F, Integrative Statistical Analysis of the Microbiome, Metabolome and Inflammation Data in Fanconi Anemia to Understand Oral Cancer Causality. American Association for Dental Research (AADR), Florida. *J Dent Res* 2018;97 (Spec Iss A): 2865782.
12. **Wu D**, Moss K, Morelli T, Beck J, Offenbacher S. Extracting dental school periodontal records to measure treatment outcomes and risk modification. American Association for Dental Research (AADR)/IADR, San Francisco, CA. *J Dent Res* 2017;96 (Spec Iss A):2640139.
13. Morelli T, Moss KL, Beck J, Preisser JS, **Wu D**, Divaris K, Offenbacher S. Periodontal Profile Classes Predict Periodontitis Progression and Tooth Loss. *J Dent Res* 2017;96 (Spec Iss A): 0129 (IADR/AADR/CADR).

Invited Oral Presentations and Unpublished Abstracts

Local

2024 Interpretable prediction using machine learning methods in longitudinal microbiome data. CompMed Program. UNC-Chapel Hill, NC. Yifan, PhD in my group.

2023 BGOB: A new deep learning method for microbiome time series analysis
CompMed Program. UNC-Chapel Hill, NC. Yixiang, PhD in my group.

2023 Panelist, Machine Learning in EHR. Carolina Health Informatics Program (CHIP) annual Analytics and Machine-Learning in Maternal-Health Intervention (AMMI) 2023 Conference UNC-Chapel Hill, NC. (Apr)

- 2022 High dimensional multi-modality omics data integration to understand cancer genome, microbiome and single cells. Bioinformatics and Computational Biology Program. UNC-Chapel Hill, NC.
- 2022 Novel statistical methods to integrate microbiome sequencing data. CompMed Program. UNC-Chapel Hill, NC.
- 2021 A comprehensive evaluation of metatranscriptomic differential expression analysis methods. CompMed Program. UNC-Chapel Hill, NC. Hunyong Cho, PhD in my group.
- 2020 A computational pipeline for single cell RNA-seq analysis to reveal how HIV infection and persistent IFN-I signaling affect immune cells. CompMed Program. UNC-Chapel Hill, NC.
- 2020 High dimensional omics data integration to understand cancer genome, microbiome and single cells. Genetics Department. BCB program. UNC-Chapel Hill, NC
- 2019 Transcriptional gene set tests and microbial omics data analysis. Biostatistics Department Seminar, UNC-Chapel Hill, NC.
- 2017 Extracting dental school periodontal records to measure treatment outcomes for precision medicine. UNC Perio Expo. UNC-Chapel Hill, Chapel Hill, NC.
- 2016 Biostatistics Seminar Series - NC TraCS, Colloquium Seminars - Bioinformatics and Computational Biology, and Center for Image Analysis and Informatics. UNC-Chapel Hill, Chapel Hill, NC.
- 2015 Oral cancer susceptibility and causality: integrative analysis of the microbiome, metabolome and inflammation in Fanconi Anemia. Dental Research Day. UNC School of Dentistry. UNC-Chapel Hill, Chapel Hill, NC.
- 2015 A mixture model for contamination detection in target DNaseq. UNC Lineberger Comprehensive Cancer Center. UNC-Chapel Hill, Chapel Hill, NC.
- 2015 Cancer personalized medicine. UNC Health Informatics Program. UNC-Chapel Hill, Chapel Hill, NC.
- 2015 RNAseq data analysis. UNC Genetics. UNC-Chapel Hill, Chapel Hill, NC.
- 2014 Genomic data integration to discover/repurpose drugs for complex diseases. School of Dentistry. UNC-Chapel Hill, Chapel Hill, NC.
- 2014 Genomic data integration to discover/repurpose drugs for complex diseases. Biostatistics Department. UNC-Chapel Hill, Chapel Hill, NC.

National

- 2024 LP-Micro: Explainable Prediction using machine learning methods on clinical outcomes from Longitudinal microbiome data. STATGEN, Pittsburg. (Invited)
- 2024 LBZINB pathway analysis to integrative microbiome and metabolome data. ENAR, Baltimore. (Invited)
- 2023 Methodological considerations in oral microbiome investigations and application to a study of early childhood caries. Meeting of Task Force on Design and Analysis in Oral Health Research. New York NY. (Invited) May
- 2023 ODE-Based Deep Learning Interpolation for Irregularly- Sampled Longitudinal Microbiome Data. Eastern North American Region. International Biometric Society. (ENAR), Nashville TN. (Invited)
- 2022 Integrative Analysis of Metagenome, Metatranscriptome and Metabolome Applied in a Cohort of Early Childhood Caries (ECC). Forsyth Institute, Harvard University, Boston.
- 2022 Panel list for standards and harmonization of metabolomics data from gut microbiome studies taking place at IMMSA workshop. NIST-Hosted Workshop on Standards for Microbiome and Multi'Omics Measurements. Aug 2022. Boulder, Colorado
- 2022 Cell-cell interaction analysis for single cell RNAseq (scRNAseq) data, Joint Statistical Meetings (JSM), Washington DC. (Invited)
- 2020 Gene set testing methods for single cell RNAseq (scRNAseq) data, Joint Statistical Meetings (JSM), Philadelphia, PA. (online) (Invited)
- 2019 A bivariate zero inflated negative binomial model for gene-gene dependence in single cell RNAseq, Joint Statistical Meetings (JSM), Denver, CO. (Invited)
- 2018 Integrative causal analysis of microbiome, metabolome and inflammation data to understand oral cancer mechanism. Symposium-International Chinese Statistical Association (ICSA), New Brunswick, NJ. (Invited)
- 2017 Classification method of dental electronic health record (EHR) data potentially improves precision treatment. American Medical Informatics Association (AMIA) Annual Meeting, Washington, DC.
- 2014 ROMER, ranked based rotation gene set test. Joint Statistical Meetings (JSM), Boston, MA.
- 2014 Introduction to novel gene set tests. Bioconductor Annual Meeting, Boston, MA.
- 2014 Data integration for drug repurposing. Symposium-International Chinese Statistical Association (ICSA), Portland, OR.

- 2014 Genomic data integration to discover/repurpose drugs for complex diseases. Cleveland Clinic Foundation, Cleveland, OH.
- 2014 Genomic data integration to discover/repurpose drugs for complex diseases. Massachusetts General Hospital, Harvard Medical School, Cambridge, MA.
- 2014 Genomic data-based drug discovery/repurposing. Biostatistics Department, MD Anderson Cancer Center, Houston, TX.
- 2013 The Genotype-Tissue Expression (GTEx) retreat, Cambridge, MA.
- 2013 Integrating GWAS data with drug information for drug repurposing. Program in Quantitative Genomics, Harvard School of Public Health, Boston, MA.
- 2013 Gene set tests in breast cancer, stem cell and drug repurposing. Institute for Stem Cell Biology and Regenerative Medicine, Stanford University, Palo Alto, CA.
- 2012 Novel gene set tests in breast cancer and stem cell research. Symposium-International Chinese Statistical Association (ICSA). Cambridge, MA.
- 2012 Bayesian Gene Set Test. Eastern North American Region/International Biometric Society Meeting (ENAR), Washington DC.
- 2012 shRNA data analysis using limma. Broad Institute, Project Achilles Group.
- 2012 shRNA data analysis using limma. Dana Farber Institute, Matthew Meyerson group, Boston, MA.
- 2011 Gene set testing, stem cells and breast cancer. The high dimension data seminar in Biostatistics Department, Harvard University, Boston, MA.
- 2010 Analysis of transcriptional signatures reveals the cell of origin for breast cancer subtypes. Harvard University, Broad Institute, Dana Farber Cancer Institute, Boston, MA. John Hopkins University, MD Anderson Cancer Center, Stanford University.
- 2010 ROAST: rotation gene set tests for complex microarray experiments. 18th Annual International Conference on Intelligent Systems for Molecular Biology (ISMB). Boston, MA.

International

- 2023 LBZINB pathway analysis for microbiome and metabolome data integration. ISMB. Lyon. (Poster) Aug 2023
- 2023 Single-Cell Plus – Data Science Challenges in Single-Cell Research, Banff International Research Station for Mathematical Innovation and Discovery (BIRS). BANFF TN. (Invited) July 2023

- 2022 A Gaussian Mixture Model of logRatio to Integrate Metagenome and Metatranscriptome Data. EcoStat conference. Ryukoku University, Kyoto, Japan. (online) (Invited)
- 2019 Evaluation of statistical methods for differential expression analysis in microbiome metatranscriptomics data. Symposium-International Chinese Statistical Association (ICSA), Hangzhou, China.
- 2019 Understanding early child cavities by analysis of metatranscriptomics and metagenomics, American Association for Dental Research (AADR)/IADR, Vancouver, Canada.
- 2019 Microbial association with the age-adjusted mullen score in a longitudinal study of children's early life – Baby Connectome Project (BCP), 6th International Conference on Nutrition & Growth (N&G 2019), Valencia, Spain.
- 2018 Comparison of statistical methods to analyze metatranscriptome data for differential abundance in an early childhood oral health study, International Association for Dental Research (IADR), London, UK.
- 2018 Statistical methods to access gene-gene associations in single cell RNA seq data, ISCA-China, Qingdao, China.
- 2016 A mixture model for contamination detection in target DNA seq, the 3rd Taihu International Statistics Forum, Shanghai, China.
- 2013 Genomic data-based drug discovery/repurposing. Ontario Institute for Cancer Research. University of Toronto, Canada.
- 2012 CD40 pathway analysis, Shandong Academy of Sciences, Jinan, China.
- 2011 Investigation of gene-gene interaction in GWAS data and eQTL data. WEHI. Melbourne, Australia.
- 2010 Analysis of transcriptional signatures reveals the cell of origin for breast cancer subtypes. National Information and Communications Technology Australia (NICTA), Melbourne, Australia.
- 2010 Analysis of transcriptional signatures reveals the cell of origin for breast cancer subtypes. The Eskitis Institute for Cell and Molecular Therapies, Brisbane, Australia.
- 2009 Patterns across data sets: finding the cell origin of basal-like breast tumours. Bioinformatics Australia. Melbourne, Australia.
- 2009 Patterns across data sets: finding the cell origin of basal-like breast tumours. The 9th Annual Australian Microarray and Associated Technologies Association (AMATA-9). Sydney, Australia.

- 2008 Roast, a gene set testing method for laboratory generated microarray data. The 8th Annual Australian Microarray and Associated Technologies Association (AMATA-8). Dunedin, New Zealand.
- 2008 Residual space permutation for gene set testing in designed microarray experiments. Australian Statistical Conference, Melbourne, Australia.
- 2007 An empirical Bayes approach used in microarray data analysis. Graduate Statistics Course of Australian Mathematical Sciences Institute (AMSI), Brisbane, Australia.
- 2007 Gene set enrichment tests in microarray experiments with small sample sizes. The 10th annual Microarray and Gene Expression Data Society meeting (MGED-10) and the 7th Annual Australian Microarray and Associated Technologies Association (AMATA-7). Brisbane, Australia.

Patents:

- 2023 Compositions comprising human milk oligosaccharides for use in a subject to support language development, Submitted application. Dec 2019. UNC. Weili Lin, **Di Wu**, Tengfei Li, Ziliang Zhu and Seoyoon Cho. Docket No. 3712036-03567. US Patent App. 17/756,987. Approved 2023
- 2009 ‘Gene expression profiles and uses therefor’ WEHI, Geoffrey LINDEMAN, Jane Visvader, Gordon Smyth, **Di Wu**. PCT number pending. Priority Date: 6th May 2009. Provisional patent Application No. AU2009901989. Human breast stem and luminal progenitor cells.

Digital and other novel forms of scholarship: Software Developed

- 2023 R package BZINB-immPath. <https://github.com/blin24/BZINB-iMMPath>. BZINB model-based pathway analysis for microbiome and metabolome data.
- 2023 DE analysis of metatranscription data
<https://github.com/Hunyong/microbiome2020>
- 2023 Joint Imputation for microbiome data.
<https://github.com/lcw68/jointImpute>
- 2022 R package InteGratio. <https://github.com/lcw68/integratio>. Iteration analysis using Gaussian Mixture for microbiome DNaseq and RNAseq data.
- 2021-2022 R package JointImputation. <https://github.com/lcw68/jointImpute>. Joint imputation method on microbiome DNaseq and RNAseq data.

- 2021 R package ENVIM available in gitHub <https://github.com/jialiux22/ENVIM>). It's to use elastic net variable importance model (ENVIM) for the metabolite prediction in a metabolomics profile via metagenomic and metatranscriptomic data at the gene-level. "Improved Metabolite Prediction Using Microbiome Data-Based Elastic Net Models". *Front. Cell. Infect. Microbiol.* DOI: 10.3389/fcimb.2021.734416
- 2019 R package BZINB available in CRAN <https://cran.r-project.org/web/packages/bzinb/index.html> and gitHub <https://github.com/Hunyong/BZINB>. 'bzinb: Bivariate Zero-Inflated Negative Binomial Model Estimator', by Hunyong Cho, Chuwen Liu, Jinyoung Park, **Di Wu**. It provides a maximum likelihood estimation of Bivariate Zero-Inflated Negative Binomial (BZINB) model or the nested model parameters. Also estimates the underlying correlation of a pair of count data. The paper draft is submitted to Biometrics and is currently under review. The draft can be found in BioRxiv <https://www.biorxiv.org/content/10.1101/2020.03.06.977728v2>
- 2019-2021 R package twosigma available in gitHub <https://github.com/edvanburen/twosigma>. It's a TWO-component SInGle cell Model-based Association method for differential expression (DE) analyses in single-cell RNA-seq (scRNA-seq) data. The first component models the probability of "drop-out" with a mixed-effects logistic regression model and the second component models the (conditional) mean expression with a mixed-effects negative binomial regression model. It also allows random effects due to the correlation among cells with-in a sample for better Type I error control. The paper draft is submitted and currently under review. It can be found in BioRxiv <https://www.biorxiv.org/content/10.1101/709238v2>. In 2021, we added new functions as the gene set test for single cell RNASeq data, named "Two-Sigma-G".
- 2007-15 R package LIMMA. Ritchie ME, Phipson B, Wu D, Hu Y, Law CW, Shi W, Smyth GK (2015). "limma powers differential expression analyses for RNA-sequencing and microarray studies." *Nucleic Acids Research*, 43(7), e47. doi: [10.1093/nar/gkv007](https://doi.org/10.1093/nar/gkv007).
- 2010 R function *roast* in LIMMA Package. Wu D, Lim E, Vaillant F, Asselin-Labat ML, Visvader JE, Smyth GK. 2010. ROAST: rotation gene set tests for complex microarray experiments. *Bioinformatics*. 26(17):2176-82
- 2007 R function *camera* function for the correlation adjusted mean rank gene set analysis in LIMMA Package to estimate variance-inflation factor for means of correlated genes. See <https://rdrr.io/bioc/limma/src/R/geneset-camera.R>. **Wu D, Smyth GK. Camera: A Competitive Gene Set Test Accounting for Inter-Gene Correlation. Nucleic Acids Res 2012;4017: e133, epub date: 2012/05/29 PMC3458527**

TEACHING ACTIVITIES

Major Teaching and Administrative Responsibilities

UNC Adams School of Dentistry

Course Participation

2022, 2023 Lecturer, ORTP 901: Research in Craniofacial Sciences
2017-2021 Lecturer, DENG 703: Applied Research Methods
1 hour – Spring/Fall ~28 MS students

UNC Biostatistics

Course Participation

2024 BIOS 781-001: Genetic Data Analysis
2023-2024 BIOS 694: Honor thesis
2020-2024 BIOS 994: PhD thesis
2021 Lecturer, BIOS 784: Introduction to Computational Biology
1 hour – Spring ~30 PhD students
2019-2023 Lecturer, BIOS 785: Statistical Methods for Gene Expression Analysis
1 hour – Fall ~30 PhD students
2017 Lecturer, BIOS 784: Introduction to Computational Biology
1 hour – Fall ~30 PhD students

UNC Information and Library Sciences

Course Participation

UNC Information and Library Sciences
2017 Lecturer, INLS 890: Health Informatics-Advanced Special Topics
1 hour – Fall ~30 PhD students

UNC Bioinformatics and Computational Biology Curriculum

Course Participation

UNC Bioinformatics and Computational Biology Curriculum
2020-2023 co-mentor, BBSP BCB First Year PhD Groups
1 hour – Fall ~30 PhD students
2016 Lecturer, BCB 720: Introduction to Statistical Modeling
1 hour – Fall ~30 PhD students

MENTORING ACTIVITIES

Undergraduate research projects mentored/supervised

2023-2023 DCM Analysis of Microbiome and Metabolome in Oral Biofilm Reveals Key ECC associated Interaction Modul. Maya Yin, Undergraduate, honor student, Biostatistics, University of North Carolina at Chapel Hill, Primary Mentor: Di Wu

2022-2023 An Assessment of Automated Quantitative Structure-Activity Relationship Modeling on Drug Discovery for Novel Treatment of Blood Disorder.

- Parnika Agrawal, Undergraduate, honor student, Biostatistics
University of North Carolina at Chapel Hill, Primary Mentor: Di Wu
- 2017-2021 Clustering analysis of single cell RNAseq data
Brian Chen (now PhD at Biostat), Research Intern, Biostatistics
University of North Carolina at Chapel Hill, Primary Mentor: Di Wu
- 2018-2019 Weighted inference of gene expression variability in single cell RNAseq
data for gene set tests: a replication study
Jie He, Undergraduate, honor student, Biostatistics
University of North Carolina at Chapel Hill, Primary Mentor: Di Wu
The defense was approved with highest honors
- 2012-2013 Lung cancer subtype classification using gene set tests.
Yushu Pang, Summer Intern, Statistics
Harvard University. Primary Mentor: Jun Liu, co-mentor: Di Wu
- MS degree thesis mentoring
- 2020- 2021 Childhood Obesity, Early Childhood Caries, and Oral Microbiome: A
secondary Biostatistical Analysis of ZOE 2.0.
Seung-Hyun Lee. MS in Public Health, University of North Carolina at
Chapel Hill, Primary Mentor: Di Wu
- 2020 ChIP-seq data analysis in causal pathways.
Ty Darnell. MS in Biostatistics, University of North Carolina at
Chapel Hill, Primary Mentor: Di Wu
- 2020 Multi-mediator analysis in causal pathways.
Arryn Panagos. MS in Biostatistics, University of North Carolina at
Chapel Hill, Primary Mentor: Di Wu
- 2020 Analysis of functional genomics and electronic dental/medical records of
oral diseases.
Amrita Tembhe. MS in Public health, University of North Carolina at
Chapel Hill, Primary Mentor: Di Wu
- 2019 Evaluation of library size effect on normalization and differential
abundance testing methods for microbiome sequencing data.
Karen Chen. MS in Biostatistics, University of North Carolina at
Chapel Hill, Primary Mentor: Di Wu
- 2019 Cell population analysis in single cell RNAseq data.
Liyong. MS in Biostatistics, University of North Carolina at
Chapel Hill, Primary Mentor: Di Wu

- 2018 Exploration of gene expression variability in single cell RNAseq data for gene set tests.
Yiling Liu. MS in Biostatistics, University of North Carolina at Chapel Hill, Primary Mentor: Di Wu
- 2017 Validation of periodontal and tooth profile classification system for determining periodontitis treatment outcomes: aimed at precision medicine.
Ayushi Gupta. MS in Health Informatics, University of North Carolina at Chapel Hill, Carolina Health Informatics Program (CHIP)
Primary Mentor: Di Wu
- 2015 The analgesic effect of a new ibuprofen formulation on odontogenic pain.
Tanjit Taggar. MS in School of Dentistry. University of North Carolina at Chapel Hill, Primary advisor: Asma Khan. Co-Advisor: Di Wu

MD/PhD degree mentoring

- 2022- Bioinformatics and Computational Biology, cardiac reprogramming
Rachelle Ambrose. MD/PhD in School of Medicine, University of North Carolina at Chapel Hill, Co- Mentor: Di Wu and Li Qian
- 2021-2022 Immune, HIV and Leukemia
Sophie Maharry. MD/PhD in School of Medicine, University of North Carolina at Chapel Hill, Co- Mentor: Di Wu and George Fedoriw

PhD degree mentoring

- 2023-present Statistical causal methods of genomics data.
Walter Chen. PhD in Biostatistics, University of North Carolina at Chapel Hill, Co-Mentor: Di Wu and Yun Li
- 2023-present Statistical methods for single cell and spatial transcriptome data
Yishu Zhang. PhD in Biostatistics, University of North Carolina at Chapel Hill, Primary-Mentor: Di Wu
- 2023-present Computational methods of genomics data.
Leyu Dai. PhD in Health Informatics, University of North Carolina at Chapel Hill, Primary-Mentor: Di Wu
- 2023-present Statistical methods of data integration in cancer genomics data.
Eunchong Kang. PhD in Biostatistics, University of North Carolina at Chapel Hill, Primary-Mentor: Di Wu
- 2022-present Deep learning methods for precision medicine.
Yifan Dai. PhD in Biostatistics, University of North

- Carolina at Chapel Hill, Co-Mentor: Di Wu and Yufeng Liu
- 2021-present Deep learning methods for time series data in microbiome and EHR.
Yixiang Qu. PhD in Biostatistics, University of North
Carolina at Chapel Hill, Co-Mentor: Di Wu and Joseph G. Ibrahim
- 2023-present Statistical methods for microbiome data integration methods.
Jialiu Xie. PhD in Biostatistics, University of North
Carolina at Chapel Hill, Primary Mentor: Di Wu
- 2022-2023 Statistical methods for cell-cell communications in single cell and spatial
transcription data analysis.
Chenghao Wang. PhD in Biostatistics, University of North
Carolina at Chapel Hill, Primary Mentor: Di Wu
- 2022-present EHR data analysis for drug repurposing of Head and Neck Cancer.
Pradham Tanikella. PhD in Genetics (**BCB in BBSP**), University of North
Carolina at Chapel Hill, Primary Mentor: Di Wu
- 2022-present Single cell (spatial) transcriptome data analysis methods in cancer studies.
Benjamin Bulen. DrPH at Biostatistics, University of North
Carolina at Chapel Hill, Primary Mentor: Di Wu
- 2021-present Joint analysis of metagenomics and metatranscriptomics data.
Chuwen Liu. PhD in Biostatistics, University of North
Carolina at Chapel Hill, co-Mentor: Di Wu and Xiaojing Zheng
- 2020-present Cell trajectory estimation using single cell (spatial) transcriptome data
with biological replicates.
Ji-Eun Park. PhD in Biostatistics, University of North
Carolina at Chapel Hill, Co- Mentor: Di Wu and Michael Love
- 2019-2024 Data integration for pathway analysis across Metagenome,
Metatranscriptome, and Metabolome.
Bridget Lin. PhD in Biostatistics, University of North
Carolina at Chapel Hill, Primary Mentor: Di Wu
(Now at UNC)
- 2019-2022 Estimation of matrix of Poisson parameters in single cell RNAseq data.
Yue Pan. PhD in Biostatistics, University of North
Carolina at Chapel Hill, Co-Mentor: Di Wu and Steve Marron
(Now at St Jude Children's Hospital)
- 2017-2022 Computational drug repurposing validation strategies.
Malvika Pillai. PhD in Public Health Informatics, University of North
Carolina at Chapel Hill, Primary Mentor: Di Wu

(Now a postdoc fellow at Stanford University)

- 2017-2021 Precision Medicine Methodology development with application to survival and Genomics data.
Hunvong Cho. PhD in Biostatistics, University of North Carolina at Chapel Hill, Co-Mentor: Di Wu and Michael Kosorok (Now a postdoc fellow at Amazon)
- 2017-2020 Improved statistical methods to analyze single cell RNAseq data: association method and gene set tests.
Eric Van Buren. PhD in Biostatistics, University of North Carolina at Chapel Hill, Co-Mentor: Di Wu and Yun Li (Now a postdoc fellow, Biostatistics at Harvard University)

PhD thesis committee membership

- 2022-present Meethila Gade. PhD in Division of Pharmacotherapy and Experimental Therapeutic, University of North Carolina at Chapel Hill, Primary Mentor: Erin Heinzen
- 2022-present Alice Woolard. PhD in Genetics (**BCB** in BSP), University of North Carolina at Chapel Hill,
Primary Mentor: Shawn Gomez
- 2022-present Gaith Droby. PhD in BBSP, University of North Carolina at Chapel Hill,
Primary Mentor: Cyrus Vaziri
- 2022-2024 Increasing diversity with statistical methods in genetics studies. Quan Sun. PhD in Biostatistics, University of North Carolina at Chapel Hill, Primary Mentor: Yun Li
- 2022-2024 Deciphering association signals from Genome-Wide Association Studies. Weifang Liu. PhD in Biostatistics, University of North Carolina at Chapel Hill, Primary Mentor: Yun Li
- 2022-2024 Metabolite prediction models in UK Biobank: A metabolome-wide association study (MWAS),
Le Huang. PhD in Genetics (**BCB** in BSP), University of North Carolina at Chapel Hill,
Primary Mentor: Yun Li
- 2020-2022 Anthony Shawn Abrantes. PhD in Biostatistics, University of North Carolina at Chapel Hill, Primary Mentor: Yun Li
- 2020-2022 Developing Statistical Methods in Genetics.
Jonathan Rosen. PhD in Biostatistics, University of North Carolina at Chapel Hill, Primary Mentor: Yun Li

- 2020-2021 Methods for characterizing Chromatin Interactions
Taylor Lagler. PhD in Biostatistics, University of North Carolina at Chapel Hill, Primary Mentor: Yun Li
- 2020-2021 Transcriptome-wide association studies: challenges, solutions, and future directions.
Amanda Tapia, PhD in Biostatistics, University of North Carolina at Chapel Hill, Primary Mentor: Yun Li
- 2020-2021 Deconvolution and Network construction by single cell RNA sequencing Data.
Meichen Dong. PhD in Biostatistics, University of North Carolina at Chapel Hill, Primary Mentor: Fei Zou and Yuchao Jiang
- 2019-present Defining novel genome maintenance mechanisms in Head and neck squamous cell carcinoma
Deepika Jayaprakash. PhD in Oral and Craniofacial Biomedicine, University of North Carolina at Chapel Hill
Primary Mentor: Cyrus Vaziri
- 2019-2020 Evaluation and Incorporation of uncertainty quantification in differential transcript usage in bulk RNAseq and single cell RNAseq.
Scott Van Buren. PhD in Biostatistics, University of North Carolina at Chapel Hill, Primary Mentor: Naim Rashid and Mike Love
(Now Bioinformatics Scientist - Harvard University)
- 2019-2020 Clustering of Bulk RNA-Seq and Missing Data Methods in Deep Learning.
David Lim. PhD in Biostatistics, University of North Carolina at Chapel Hill, Primary Mentor: Naim U. Rashid and Joseph G. Ibrahim
- 2019-2021 Statistical Methods to analyze Hi-C data.
Cheynna Crowley. PhD in Biostatistics, University of North Carolina at Chapel Hill, Primary Mentor: Yun Li
- 2018-2021 Microbiol 16s and RNA-Seq data integration in plants.
Isai Salas-Gonzalez. PhD in Genetics (**BCB**), University of North Carolina at Chapel Hill, Primary Mentor: Jeff Dangl
- 2017-2018 Cluster Ensemble Methods for Single Cell RNA-Seq Data and Deconvolution of Bulk Hi-C Data.
Ruth Huh. PhD in Biostatistics, University of North Carolina at Chapel Hill, Primary Mentor: Yun Li
- 2016 Statistical Methods in Cell Type Abundance Estimation and eQTL

Mapping.

Doug Wilson. PhD in Biostatistics. University of North Carolina at Chapel Hill, Primary Mentor: Wei Sun

MS thesis research committees

- 2021-2022 Microbiome study in the orthodontic patient cohort
Taneisha Livingston. MS in Adams School of Dentistry, University of North Carolina at Chapel Hill, Primary Mentor: Laura Jacox
- 2019-2020 Metabolomics Insights in Early Childhood Caries.
Lara Heimisdottir. MS in Adams School of Dentistry, University of North Carolina at Chapel Hill, Primary Mentor: Kimon Divaris
- 2019-2020 Influences on dental caries and overweight/obesity among preschool-age children in North Carolina.
Meredith Davis. MS in Adams School of Dentistry, University of North Carolina at Chapel Hill, Primary Mentor: Kimon Divaris
- 2018-2019 Changes and oral microbiome shifts in HIV and patients following periodontal therapy.
Karin Schey. MS in Adams School of Dentistry, University of North Carolina at Chapel Hill, Primary Mentor: Jennifer Webster-Cyriaque
- 2016-2018 Oral microbiome changes associated with fixed prosthodontic restoration
Sarah Lee. MS in Adams School of Dentistry, University of North Carolina at Chapel Hill, Primary Mentor: Kimon Divaris

Honor research committees

- 2022 Single-cell Multi-omics analysis reveals Gene Regulatory Network at Single-cell Level during Early Stage of Direct Cardiac Reprogramming
Bella Qian. BS honor in Biostatistics, University of North Carolina at Chapel Hill, Primary Mentor: Yuchao Jiang

GRANTS AND CONTRACTS

Active and recent (see updated other supports)

- 2024(JUNE)-26 NIH/NINDS R21: “Genotype-informed single-cell transcriptomic profiling of mosaic brain tissue”
Role: Co-investigator, 5%
Principal Investigator: Erin Heinzen
- 2023-24 UNC LCCC Pilot Grant: “Drug Repurposing for Head and Neck Cancer using

- Genomics Data Integration and Electronic Health Records”
 Total Award: \$50,000 (one year)
 Principal Investigator: Di Wu
- 2023-28 NIH/NIAID P01: “Determinants of HIV broadly neutralizing antibody precursor induction in infants”
 Role: Co-investigator, 10%. Co-lead the data-coordination center.
 Principal Investigator: De Paris, Kristin
- 2021-26 NIH/NIA R01: “Comprehensive functional genomic analysis of the multi-disease associated CDKN2A/B locus”
 Role: Co-investigator, 5%
 Principal Investigator: Gang Li
- 2021-26 NIH/NIA R01: “Computational Diffusion MRI for Studying Early Human Brain Development”
 Role: Co-investigator, 6%
 Principal Investigator: Pew-Thian Yap
- 2021-25 NIH/NIA R01: “Longitudinal Mapping of Human Brain Development in the First Years of Life”
 Role: Co-investigator, 6%
 Principal Investigator: Pew-Thian Yap
- 2022-25 NIH/NIA R01: “Multi-Site Neuroimage Harmonization for Personalized Brain Disorder Analysis”
 Role: Co-investigator, 5%
 Principal Investigator: Mingxia Liu
- 2021-25 NIH/ NIGMS R01: “Development of a cavitation enhancement technology to access archived tissues for epigenetic-based biomedical research”
 Role: Co-investigator, 4%
 Principal Investigator: Pattenden
- 2019-24 NIH-NCI R01: “Establishing MAGE-A4/RAD18 as a novel cancer-specific chemotherapeutic target”
 Total Award: \$413,559
 Role: Co-investigator, 6% effort
 Principal Investigator: Cyrus Vaziri
- 2018-23 NIH/NIEHS R01: “Pathological Reprogramming of DNA Damage Signaling in Neoplastic Cells” (with extension)
 Total Award: \$302,167
 Role: Co-investigator, 9% effort

Principal Investigator: Cyrus Vaziri

Completed

- 2020-2021 Pilot Award, UNC Computational Medicine: “A novel computational pipeline for single cell RNA-seq analysis to reveal the role of type-I IFN in HIV-induced immune dysfunction and viral persistence”
Total Award: \$50,000 (with extension)
Principal Investigator: Di Wu
- 2018-23 NIH-NCI R01: “Defining Mechanisms of Pathological Trans-Lesion Synthesis During Carcinogenesis.”
Total Award: \$334,841
Role: Co-investigator, 16.6% effort
Principal Investigator: Cyrus Vaziri
- 2019-22 NIH/NIDCR R03: “Investigating the Microbial Basis of Early Childhood Caries via Metagenomics and Metatranscriptomics Analyses”
Total Award: \$200,000
Principal Investigator: Di Wu -- 25% effort
(with no-cost extension)
- 2020 Pilot Award, UNC NC TraCS: “determination of genital mucosal T cell responses involved in protection from Chlamydia trachomatis in women using single cell RNA sequencing analysis”
Total Award: \$50,000
Co-Investigator: Di Wu (January 2020-December 2020) -- 0% effort
- 2019-20 UNC Lineberger Developmental Award: “Validating Trans-Lesion Synthesis as a Novel Therapeutic Target in Glioblastoma”
Total Award: \$200,000
Co-Investigator: Di Wu (January 2019-December 2020) -- 0% effort
- 2018-19 UNC Lineberger Developmental Award: “Quantitative Imaging Data in a Community-Based Mammography Registry: A Feasibility Study”
Total Award: \$140,000
Co-Investigator: Di Wu (January 2018-December 2019) 0% effort
- 2018-19 Pilot Award, UNC Center for Environmental Health and Susceptibility (CEHS): “Defining novel Chk2 functions in suppression of UV-induced skin carcinogenesis”
Total Award: \$25,000
Principal Investigator: Di Wu (January 2018-March 2019)
- 2016 NIH-NINDS R21: “Using High Throughput Approach to Identify/Characterize Functional Variants on Multiple Sclerosis”

Total Award: \$273,045
Sub Principal Investigator: Di Wu 5% effort

2011-2015 Australian National Health and Medical Research Council (NHMRC) Early Career Overseas Fellowship: “Epistatic and cross-tissue analysis for human gene expression traits”
Total Award: \$340,000
Principal Investigator: Di Wu 100% effort

PROFESSIONAL SERVICE & SOCIETY MEMBERSHIPS

Scientific Review

2021- 2024 NIH ad-hoc review: R03, R21, R01, K

2015 Scientific Peer Reviewer -- Australian National Health and Medical Research Council

National and International

2024 Oral Session organizer for IMS-APRM Invited Sessions. Emerging opportunities in omics data and longitudinal/functional data analysis. 2024 Melbourne, Australia (Jan)

2023 Panel organizer, Machine Learning in EHR. Carolina Health Informatics Program (CHIP) annual Analytics and Machine-Learning in Maternal-Health Intervention (AMMI) 2023 Conference UNC-Chapel Hill, NC. (Apr)

2022 Symposium Organizer: American/International Association of Dental Research (AADR/IADR) Chengdu, China (Virtual)

2021 Symposium Organizer: American/International Association of Dental Research (AADR/IADR) Washington, DC (Virtual)

2020 Symposium Organizer: American/International Association of Dental Research (AADR/IADR) Washington, DC (Conferences cancelled due to Pandemic)

2019 Session Organizer: International Chinese Statistical Association (ICSA), Hangzhou, China

2018 Symposium Organizer: International Association of Dental Research (IADR), London, UK

2018 Poster Reviewer: American Medical Informatics Association (AMIA), San

Francisco, CA

- 2018 Oral Session Chair: American Association of Dental Research (AADR), Fort Lauderdale, FL
- 2018 Poster Session Chair: American Association of Dental Research (AADR), Fort Lauderdale, FL
- 2012-2015 Mentor: Harvard Graduate Women in Science and Engineering, Cambridge, MA
- 2014 Oral Session Chair: International Chinese Statistical Association (ICSA), Portland, OR
- 2014 Judge: American Society of Human Genetics (ASHG), DNA Day Essay Contest, San Diego, CA
- 2013 Member: Harvard University Postdoc Advisory Board, Cambridge, MA
- 2012 Session Chair: International Chinese Statistical Association (ICSA), Boston, MA
- 2012 Coordinator: Sino-American Pharmaceutical Professionals Association New England (SAPA-NE) Annual Conference, Boston, MA
- 2011 Coordinator: Australia-China Biomedical Research Conference (ACABS), Melbourne, Australia

University of North Carolina-Chapel Hill

- 2023-present Faculty Appointment and Promotion Committee (PTAC) Member, UNC Adam School of Dentistry
- 2023-present Executive Committee Member: Curriculum in Bioinformatics and Computational Biology, UNC School of Medicine
- 2023-present Member: Faculty Search Committee, Pathology Department, Tenure-track Assistant Professor, UNC School of Medicine
- 2023-present Member: Faculty Search Committee, Oral Cancer, Open Track, Department of Oral Craniofacial Health Science, UNC Adam School of Dentistry
- 2023-present Retreat organizing committee, Biostatistics, UNC Gillings School of Public Health
- 2022-2023 Member: Faculty Search Committee, Biostatistics Department, Assistant Professor, UNC Adam School of Dentistry

- 2017-present Member: UNC Bioinformatics and Computational Biology (BCB) PhD Admissions Committee
- 2021-present Member: UNC Admissions Committee for the PhD in Biomedical and Health Informatics program, Carolina Health Informatics Program (CHIP)
- 2021-present Executive Committee Member of PhD program, Oral & Craniofacial Biomedicine (OCBM) at UNC
- 2020 Reviewer, COVID-19 Gillings Innovation Laboratory (GIL) proposals, UNC Gillings School of Public Health
- 2020 Member: Faculty Search Committee, Tenure-track Assistant Professor, Biomedical Research Imaging Center, Department of Radiology, UNC School of Medicine
- 2020 Poster Judge: UNC Adams School of Dentistry Dental Research Day
- 2018 Member: Tenure Track Faculty Search Committee, jointly in UNC Adams School of Dentistry, Division of Oral and Craniofacial Health Sciences (OCHS), and in the UNC School of Medicine, Department of Orthodontics and Biomedical Research Imaging Center
- 2018 Poster Judge: Annual Student Research Day, UNC School of Medicine
- 2018 Speaker: Faculty Research Showcase. UNC Gillings School of Global Public Health
- 2017 Member: UNC Admissions Committee Biological and Biomedical Sciences Program (BBSP) Foreign Admissions Committee
- 2017 Faculty: UNC Health Informatics Program (CHIP) Training Program T15
- 2016 Member: UNC Biostatistics Computing Committee
- 2016 Member: UNC Admissions Committee for the Master of Professional Science in Biomedical and Health Informatics program, Carolina Health Informatics Program (CHIP)

Editorial boards and peer review activity

- 2023 Ad hoc Reviewer – Bioinformatics, Briefings in Bioinformatics, Nucleic Acids Research

- 2022 Ad hoc Reviewer -- Briefings in Bioinformatics, Nucleic Acids Research
- 2020/2021 Topic Editor for Research Topic “Genetics and Molecular Mechanisms of Oral and Esophageal Squamous Cell Carcinoma“ in Journal of *Frontier in Oncology*
- 2020 Ad hoc Reviewer -- Briefings in Bioinformatics, Bioinformatics (twice), Bioscience Reports, Nucleic Acids Research Cancer
- 2019 Ad hoc Reviewer -- Proceedings of the National Academy of Sciences
- 2018 Ad hoc Reviewer – Nature Method, Genetics in Medicine, Genome Biology, Bioinformatics
- 2017 Ad hoc Reviewer – PLoS Computational Biology, PLoS One, Gene, Nature Scientific Report, Molecules (from MDPI), International Journal of Gynecological Cancer, OncoImmunology, IEEE/ACM Transactions on Computational Biology and Bioinformatics, Genetics in Medicine, Bioinformatics
- 2016 Ad hoc Reviewer – Statistics in Medicine, PLoS One, Statistics in Biosciences, Journal of the American Statistical Association (JASA), Bioinformatics
- 2015 Ad hoc Reviewer – Nucleic Acids Research, BMC Bioinformatics, PLoS One, International Journal of Dentistry, PLoS Computational Biology, Bioinformatics, Biometrics
- 2014 Ad hoc Reviewer – Biometrics, Nucleid Acids Research, PLoS One, Statistics in Medicine, IEEE/ACM Transactions on Computational Biology and Bioinformatics, Bioinformatics, Briefings in Bioinformatics
- 2014 Lead Guest Editor -- Cancer Informatics journal supplement (Libertas Academica)
- 2013 Ad hoc Reviewer – Biomarkers in Cancer, PLoS One, Bionformatics
- 2012 Ad hoc Reviewer – Nucleic Acids Research, Genomics, Proteomics and Bioinformatics-Elsevier, Bioinformatics

Society Memberships

- 2016-present Member: American/International Association of Dental Research (AADR/IADR)
- 2015-present Member: American Statistical Association (ASA)
- 2017-2018 Member: American Medical Informatics Association (AMIA)