CURRICULUM VITAE

PERSONAL INFORMATION

Name: **Yun Li**
Work address: 5043 Genetic Medicine Building, 120 Mason Farm Rd., Chapel Hill, NC 27599
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EDUCATION

PhD, University of Michigan, Ann Arbor, MI, 2004-2009, Biostatistics
MS, Bowling Green State University, Bowling Green, OH, 2002-2004, Applied Statistics
MA, Bowling Green State University, Bowling Green, OH, 2001-2002, Communication Studies
B.S., Shanghai Jiaotong University, China, 1997-2001, English (Finance and Business)
Second B.S., Shanghai Jiaotong University, China, 1998-2001, Computer and Application

PROFESSIONAL EXPERIENCE

Professor of Genetics, UNC, Chapel Hill, NC, 2021-
Professor of Biostatistics, UNC, Chapel Hill, NC, 2021-
Adjunct Associate Professor, Applied Physical Sciences, UNC, Chapel Hill, NC 2019-
Director, Data Science Core, Intellectual and Developmental Disabilities Research Center (IDDRC) , UNC, Chapel Hill, NC, 2015-
Associate Professor of Genetics, UNC, Chapel Hill, NC, 2015-2021
Associate Professor of Biostatistics, UNC, Chapel Hill, NC, 2015-2021
Adjunct Assistant Professor of Computer Science, UNC, Chapel Hill, NC, 2012-2018
Member, Carolina Center for Genome Sciences, UNC, Chapel Hill, NC, 2009-
Assistant Professor of Genetics, UNC, Chapel Hill, NC, 2009-2015
Assistant Professor of Biostatistics, UNC, Chapel Hill, NC, 2009-2015

HONORS AND AWARDS

2023 Research.com Best Female Scientists 2023 (Genetics world ranking 367)
2015- Faculty Member, Theta Chapter of the Delta Omega Society
2014 Thomson Reuters Highly Cited Researcher
2013 Junior Faculty Development Award, UNC
2012 Jefferson-Pilot Fellowship in Academic Medicine, School of Medicine, UNC
2008-2009: Rackham Predoctoral Fellowship, University of Michigan
2008: ASHG Trainee Award in Predoctoral Basic
2008: Rackham One-Term Dissertation Fellowship, University of Michigan

2007: March of Dimes Scholarship on Medical & Experimental Mammalian Genetics
2006, 2007: Rackham Travel Grant, University of Michigan
2005: Best Performance on Qualifying Examination, University of Michigan
2004: Robert A. Patton Book Scholarship, Bowling Green State University
2004: Ronald Benton Scholarship, Toledo Section, American Society for Quality
2003: Wray Jackson Smith Scholarship, American Statistical Association
2001: Level 1 (highest) in International Japanese Proficiency Test
1998-1999: Harler Scholarship for Excellence in German Language Studies
1997-2001: Annual Academic Scholarship, Shanghai Jiaotong University
1997-1998: Yan Kuanhu Fund Scholarship for Excellent Performance
1997-1998: Scholarship of the Metrobank Foundation

BIBLIOGRAPHY

Refereed original research:

* indicates first or co-first authorship
indicates corresponding authorship
underscore indicates lab member

As of 4/22/2024 on Google Scholar, publications below have a total of 111,261 citations, with an H-index score of 91 and an i10-index of 207.

1. Sun Q, Yang Y, Rosen JD, Chen J, Li X, Guan W, Jiang MZ, Wen J, Pace RG, Blackman SM, Bamshad MJ, Gibson RL, Cutting GR, O'Neal WK, Knowles MR, Kooperberg C, Reiner AP, Raffield LM, Carson AP, Rich SS, Rotter JI, Loos RJF, Kenny E, Jaeger BC, Min YI, Fuchsberger C#, **Li Y#** (2024) MagicalRsq-X: A cross-cohort transferable genotype imputation quality metric. *Am J Hum Genet*. S0002-9297(24)00116-2. doi: 10.1016/j.ajhg.2024.04.001. PMID: 38636510.

2. Shan Y, Huang C, **Li Y**, Zhu H (2024) Merging or ensembling: integrative analysis in multiple neuroimaging studies. *Biometrics* 80(1) https://doi.org/10.1093/biomtc/ujae003

3. Hou K, Gogarten S, Kim J, Hua X, Dias JA, Sun Q, Wang Y, Tan T; Polygenic Risk Methods in Diverse Populations (PRIMED) Consortium Methods Working Group; Atkinson EG, Martin A, Shortt J, Hirbo J, **Li Y**, Pasaniuc B, Zhang H (2024) Admix-kit: an integrated toolkit and pipeline for genetic analyses of admixed populations. *Bioinformatics* 40(4):btae148. doi: 10.1093/bioinformatics/btae148. PMID: 38490256 PMCID: PMC10980565.

4. Jeng XJ, Hu Y, Sun Q, **Li Y** (2024) Weak signal inclusion under dependence and applications in genome-wide association study. *Ann. Appl. Stat*. 18(1): 841-857 (March 2024). DOI: 10.1214/23-AOAS1815

5. Sun Q, Rowland BT, Chen J, Mikhaylova AV, Avery C, Peters U, Lundin J, Matise T, Buyske S, Tao R, Mathias RA, Reiner AP, Auer PL, Cox NJ, Kooperberg C, Thornton TA, Raffield LM, **Li Y#** (2024) Improving polygenic risk prediction in admixed populations by

explicitly modeling ancestral-differential effects via GAUDI. *Nat Commun*. 15(1):1016. PMID: 38310129. PMCID: PMC10838303.

6. Reynolds LM, Houston DK, Skiba MB, Whitsel EA, Stewart JD, **Li Y**, Zannas AS, Assimes TL, Horvath S, Bhatti P, Baccarelli AA, Tooze JA, Vitolins MZ (2024) Diet Quality and Epigenetic Aging in the Women's Health Initiative. *J Acad Nutr Diet*. S2212-2672(24)00002-9. PMID: 38215906. DOI: 10.1016/j.jand.2024.01.002.

7. Hughes O, Bentley AR, Breeze CE, Aguet F, Xu X, Nadkarni G, Sun Q, Lin BM, Gilliland T, Meyer MC, Du J, Raffield LM, Kramer H, Morton RW, Gouveia MH, Atkinson EG, Valladares-Salgado A, Wacher-Rodarte N, Dueker ND, Guo X, Hai Y, Adeyemo A, Best LG, Cai J, Chen G, Chong M, Doumatey A, Eales J, Goodarzi MO, Ipp E, Irvin MR, Jiang M, Jones AC, Kooperberg C, Krieger JE, Lange EM, Lanktree MB, Lash JP, Lotufo PA, Loos RJF, Ha My VT, Peralta-Romero J, Qi L, Raffel LJ, Rich SS, Rodriquez EJ, Tarazona-Santos E, Taylor KD, Umans JG, Wen J, Young BA, Yu Z, Zhang Y, Ida Chen YD, Rundek T, Rotter JI, Cruz M, Fornage M, Lima-Costa MF, Pereira AC, Paré G, Natarajan P, Cole SA, Carson AP, Lange LA, **Li Y**, Perez-Stable EJ, Do R, Charchar FJ, Tomaszewski M, Mychaleckyj JC, Rotimi C, Morris AP, Franceschini N (2024) Genome-wide study investigating effector genes and polygenic prediction for kidney function in persons with ancestry from Africa and the Americas. *Cell Genom*. 4(1):100468. PMID: 38190104. PMCID: PMC10794846.

8. Skinner HG, Palma-Gudiel H, Stewart JD, Love SA, Bhatti P, Shadyab AH, Wallace RB, Salmoirago-Blotcher E, Manson JE, Kroenke CH, Belsky DW, **Li Y**, Whitsel EA, Zannas AS (2024) Stressful life events, social support, and epigenetic aging in the Women's Health Initiative. *J Am Geriatr Soc*. 72(2):349-360. PMID: 38149693.

9. Chen J, Mu W, **Li Y**, Li D (2023) On the Identifiability and Interpretability of Gaussian Process Models. 37th Conference on Neural Information Processing Systems (NeurIPS 2023). https://doi.org/10.48550/arXiv.2310.17023

10. Rosen J, Lee L, Abnousi A, Chen J, Wen J, Hu M#, **Li Y#** (2023) HPTAD: A computational method to identify topologically associating domains from HiChIP and PLAC-seq datasets. *Comput Struct Biotechnol J*. https://doi.org/10.1016/j.csbj.2023.01.003. PMID: 38213897. PMCID: PMC10782010.

11. Ren X, Yang H, Nierenberg JL, Sun Y, Chen J, Beaman C, Pham T, Nobuhara M, Takagi MA, Narayan V, **Li Y**, Ziv E, Shen Y (2023) High-throughput PRIME-editing screens identify functional DNA variants in the human genome. *Mol Cell*. 83(24):4633-4645.e9. PMID: 38134886. PMCID: PMC10766087.

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13. Guintivano J, Byrne EM, Kiewa J, Yao S, Bauer AE, Aberg KA, Adams MJ, Campbell A, Campbell ML, Choi KW, Corfield EC, Havdahl A, Hucks D, Koen N, Lu Y, Mægbæk ML, Mullaert J, Peterson RE, Raffield LM, Sallis HM, Sealock JM, Walker A, Watson HJ, Xiong Y, Yang JMK, Anney RJL, Gordon-Smith K, Hubbard L, Jones LA, Mihaescu R, Nyegaard M, Pardiñas AF, Perry A, Saquib N, Shadyab AH, Viktorin A, Andreassen OA, Bigdeli TB, Davis LK, Dennis CL, Di Florio A, Dubertret C, Feng YA, Frey BN, Grigoriadis S, Gloaguen E, Jones I, Kennedy JL, Krohn H, Kunovac Kallak T, **Li Y**, Martin NG, McIntosh AM, Milgrom J, Munk-Olsen T, Oberlander T, Olsen CM, Ramoz N, Reichborn-Kjennerud T, Robertson Blackmore E, Rubinow D, Skalkidou A, Smoller JW, Stein DJ, Stowe ZN, Taylor V, Tebeka S, Tesli M, Van Lieshout RJ, van den Oord EJCG, Vigod SN, Werge T, Westlye LT, Whiteman DC, Zar HJ; Major Depressive Disorder Working Group of the Psychiatric Genomics Consortium; Wray N, Meltzer-Brody S, Sullivan P (2023) Meta-Analyses of Genome-Wide Association Studies for Postpartum Depression. *Am J Psychiatry*. 180(12):884-895. PMID: 37849304.

14. Yang X, Wen J, Yang H, Jones IR, Zhu X, Liu W, Li B, Clelland CD, Luo W, Wong MY, Ren X, Cui X, Song M, Liu H, Chen C, Eng N, Ravichandran M, Sun Y, Lee D, Van Buren E, Jiang MZ, Chan CSY, Ye CJ, Perera RM, Gan L, **Li Y#**, Shen Y# (2023) Functional characterization of Alzheimer's disease genetic variants in microglia. *Nat Genet*. 55(10):1735-1744. PMID: 37735198. PMCID: PMC10939305. (Associated Research Briefing: Linking non-coding variants to function in microglia in Alzheimer's disease *Nat Genet*. 55: 1615–1616. PMID: 37749247 DOI: 10.1038/s41588-023-01503-x)

15. Lee L, Yu M, Li X, Zhu C, Zhang Y, Yu H, Chen Z, Mishra S, Ren B, **Li Y#**, Hu M# (2023) SnapHiC-D: a computational pipeline to identify differential chromatin contacts from single-cell Hi-C data. *Brief Bioinform*. doi: 10.1093/bib/bbad315. Online ahead of print. PMID: 37649383.

16. Lee L, Yu H, Jia BB, Jussila A, Zhu C, Chen J, Xie L, Hafner A, Mishra S, Wang DD, Strambio-De-Castillia C, Boettiger A, Ren B, **Li Y#**, Hu M# (2023) SnapFISH: a computational pipeline to identify chromatin loops from multiplexed DNA FISH data. *Nat Commun*. 14(1):4873. doi: 10.1038/s41467-023-40658-3. PMID: 37573342. PMCID: PMC10423204.

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28. Chen J*, Luo T*, Jiang M, Liu J, Gupta GP#, **Li Y**# (2023) Cell composition inference and identification of layer-specific spatial transcriptional profiles with POLARIS. *Sci Adv*. 9(9):eadd9818. doi: 10.1126/sciadv.add9818. PMID: 36857450.

29. Liyanage JSS et al (2022) A Versatile and Efficient Novel Approach for Mendelian Randomization Analysis with Application to Assess the Causal Effect of Fetal Hemoglobin on Anemia in Sickle Cell Anemia. *Mathematics* 10(20), 3743; https://doi.org/10.3390/math10203743.

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35. Sun Q, Yang Y, Rosen JD, Jiang MZ, Chen J, Liu W, Wen J, Raffield LM, Pace RG, Zhou YH, Wright FA, Blackman SM, Bamshad MJ, Gibson RL, Cutting GR, Knowles MR, Schrider DR, Fuchsberger C#, **Li Y#** (2022) MagicalRsq: Machine-learning-based genotype imputation quality calibration. *Am J Hum Genet*. doi: 10.1016/j.ajhg.2022.09.009. PMID: 36198314.

36. Jain P, Binder AM, Chen B, Parada H Jr, Gallo LC, Alcaraz J, Horvath S, Bhatti P, Whitsel EA, Jordahl K, Baccarelli AA, Hou L, Stewart JD, **Li Y**, Justice JN, LaCroix AZ (2022) Analysis of Epigenetic Age Acceleration and Healthy Longevity Among Older US Women. *JAMA Netw Open*. 5(7):e2223285. PMID: 35895062.

37. Chen J*, Liu W*, Luo T*, Yu Z, Jiang MZ, Wen J, Gupta GP, Giusti P, Zhu H, Yang Y, **Li Y#** (2022) A comprehensive comparison on cell-type composition inference for spatial transcriptomics data. *Brief Bioinform.* bbac245. doi: 10.1093/bib/bbac245. PMID: 35753702.

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A, Schlessinger D, Uda M, Ruokonen A, Jarvelin MR, Waterworth DM, Vollenweider P, Peltonen L, Mooser V, Abecasis GR, Wareham NJ, Sladek R, Froguel P, Watanabe RM, Meigs JB, Groop L, Boehnke M, McCarthy MI, Florez JC, Barroso I (2009) Novel genetic loci implicated in fasting glucose homeostasis and their impact on type 2 diabetes risk. *Nature Genetics* 42: 105-116. PMID: 20081858. PMCID: PMC3018764. (*I performed imputation and association analysis in the FUSION cohorts*.)

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Galver LM, Fan JB, Gunderson K, Murray SS, Oliphant AR, Chee MS, Montpetit A, Chagnon F, Ferretti V, Leboeuf M, Olivier JF, Phillips MS, Roumy S, Sallée C, Verner A, Hudson TJ, Kwok PY, Cai D, Koboldt DC, Miller RD, Pawlikowska L, Taillon-Miller P, Xiao M, Tsui LC, Mak W, Song YQ, Tam PK, Nakamura Y, Kawaguchi T, Kitamoto T, Morizono T, Nagashima A, Ohnishi Y, Sekine A, Tanaka T, Tsunoda T, Deloukas P, Bird CP, Delgado M, Dermitzakis ET, Gwilliam R, Hunt S, Morrison J, Powell D, Stranger BE, Whittaker P, Bentley DR, Daly MJ, de Bakker PI, Barrett J, Chretien YR, Maller J, McCarroll S, Patterson N, Pe'er I, Price A, Purcell S, Richter DJ, Sabeti P, Saxena R, Schaffner SF, Sham PC, Varilly P, Altshuler D, Stein LD, Krishnan L, Smith AV, Tello-Ruiz MK, Thorisson GA, Chakravarti A, Chen PE, Cutler DJ, Kashuk CS, Lin S, Abecasis GR, Guan W, **Li Y**, Munro HM, Qin ZS, Thomas DJ, McVean G, Auton A, Bottolo L, Cardin N, Eyheramendy S, Freeman C, Marchini J, Myers S, Spencer C, Stephens M, Donnelly P, Cardon LR, Clarke G, Evans DM, Morris AP, Weir BS, Tsunoda T, Johnson TA, Mullikin JC, Sherry ST, Feolo M, Skol A, Zhang H, Zeng C, Zhao H, Matsuda I, Fukushima Y, Macer DR, Suda E, Rotimi CN, Adebamowo CA, Ajayi I, Aniagwu T, Marshall PA, Nkwodimmah C, Royal CD, Leppert MF, Dixon M, Peiffer A, Qiu R, Kent A, Kato K, Niikawa N, Adewole IF, Knoppers BM, Foster MW, Clayton EW, Watkin J, Gibbs RA, Belmont JW, Muzny D, Nazareth L, Sodergren E, Weinstock GM, Wheeler DA, Yakub I, Gabriel SB, Onofrio RC, Richter DJ, Ziaugra L, Birren BW, Daly MJ, Altshuler D, Wilson RK, Fulton LL, Rogers J, Burton J, Carter NP, Clee CM, Griffiths M, Jones MC, McLay K, Plumb RW, Ross MT, Sims SK, Willey DL, Chen Z, Han H, Kang L, Godbout M, Wallenburg JC, L'Archevêque P, Bellemare G, Saeki K, Wang H, An D, Fu H, Li Q, Wang Z, Wang R, Holden AL, Brooks LD, McEwen JE, Guyer MS, Wang VO, Peterson JL, Shi M, Spiegel J, Sung LM, Zacharia LF, Collins FS, Kennedy K, Jamieson R, Stewart J (2007) Genome-wide detection and characterization of positive selection in human populations. *Nature* 449(7164): 913-8. PMID: 17943131. PMCID: PMC2687721.

264. The International HapMap Consortium (2007) A second generation human haplotype map of over 3.1 million SNPs. *Nature* 449: 851-861. PMID: 17943122. PMCID: PMC2689609. (total 250 co-authors. *I performed basic quality control of genotypes from different labs*.)

265. Scott JL, Mohlke KL, Bonnycastle LL, Willer CJ, **Li Y**, Duren WL, Erdos MR, Stringham HM, Chines PS, Jackson AU, Prokunina-Olsson L, Ding CJ, Swift AJ, Narisu N, Hu T, Pruim R, Xiao R, Li XY, Conneely KN, Riebow NL, Sprau AG, Tong M, White PP, Hetrick KN, Barnhart MW, Bark CW, Goldstein JL, Watkins L, Xiang F, Saramies J, Buchanan TA, Watanabe RM, Valle TT, Kinnunen L, Abecasis GR, Pugh EW, Doheny KF, Bergman RN, Tuomilehto J, Collins FS, Boehnke M (2007) A genome-wide association study of type 2 diabetes in Finns detects multiple susceptibility variants. *Science* 316: 1341-1345. PMID: 17463248. PMCID: PMC3214617. (*I performed genotype imputation and contributed to meta-analysis with two other studies*.)

266. Li M, Atmaca-Sonmez P, Othman M, Branham KE, Khanna R, Wade MS, **Li Y**, Liang L, Zareparsi S, Swaroop A and Abecasis GR (2006) *CFH* haplotypes without the Y402H coding variant show strong association with susceptibility to age-related macular

degeneration. *Nature Genetics* 38**:** 1049-1054. PMID: 16936733. PMCID: PMC1941700. (*I performed haplotype association analysis*.)

Manuscripts Submitted/In Press

Omitted. Please visit https://yunliweb.its.unc.edu/publications.html for preprints.

Review articles:

267. Zhong W, Liu W, Chen J, Sun Q, Hu M, **Li Y#** (2022) Understanding the function of regulatory DNA interactions in the interpretation of non-coding GWAS variants. *Front Cell Dev Biol.* doi: 10.3389/fcell.2022.957292. PMID: 36060805.
268. Liu W*, Zhong W*, Chen J, Huang B, Hu M, **Li Y#** (2022) Understanding Regulatory Mechanisms of Brain Function and Disease through 3D Genome Organization. *Genes* 13(4):586. PMID: 35456393.
269. Yu M, **Li Y**, Hu M (2022) Mapping chromatin loops in single cells. *Trends Genet.* 38(7):637-640. PMID: 35400543.
270. **Li Y#**, Hu M, Shen Y (2018) Gene Regulation in the 3D Genome. *Hum Mol Genet*. 27(R2):R228-R233. PMID: 29767704. PMCID: PMC6061806.
271. **Li Y**, Willer CJ, Sanna S, Abecasis GR (2009) Genotype imputation. *Annual Review Genomics and Human Genetics* 10: 387-406. PMID: 19715440. PMCID: PMC2925172.

Book chapters:

- Li G, Zhang G, **Li Y#** (2022). "DNA Methylation Imputation Across Platforms." Methods Mol Biol 2432: 137-151.
- Wu D, Karhade DS, Pillai M, Jiang MZ, Huang L, Li G, Cho H, Roach J, **Li Y**, Divaris K (2021). Machine Learning and Deep Learning in Genetics and Genomics. Machine Learning in Dentistry, Springer: 163-181.

Invited oral presentations:

2024	Department of Biostatistics, Johns Hopkins University
2024	University of Pennsylvania Biomedical Data Science Seminar Series
2024	Department of Human Genetics, Emory School of Medicine
2023	3rd annual conference of Clinical Research En lighten And Transform Era(CREATE), Shanghai, China
2023	Keynote speaker at the International Genetic Epidemiology Society 32nd Annual Meeting, Nashiville, TN
2023	UNC Data Science Day
2023	Online genomics seminar, Department of Biostatistics, Columbia University
2023	Biomedical Engineering Department, Johns Hopkins University
2023	Centre for Computational Biology Seminar, Duke-NUS, Singapore
2023	School of Public Health, National University of Singapore (NUS), Singapore
2023	12th ICSA International Conference, Hong Kong, China
2023	2023 ICSA China Conference, Chengdu, Sichuan, China
2023	International Congress of Human Genetics, Cape Town, South Africa
2023	Genomics and Personalized Medicine, Vanderbilt University, Nashiville, TN
2023	Longitudinal Studies Section, the National Institute on Aging (NIA), Virtual

2022 CAMP workshop, IGVF Consortium, Virtual
2022 Department of Human Genetics, University of Chicago
2022 Integrating Imaging and Omics Working Group, 4D Nucleome Project, virtual
2022 TOPMed All Hands call, virtual
2022 Department of Statistics, Florida State University
2022 ENAR 2022, Virtual
2022 School of Medicine, Shanghai Jiao Tong University, Virtual
2021 Department of Genetics and Genomic Sciences at the Icahn School of Medicine at Mount Sinai, Virtual
2021 The Charles Bronfman Institute For Personalized Medicine, MSSM, Virtual
2021 Spatial Biology US Congress, Virtual
2021 Department of Biostatistics, Virginia Commonwealth University, Virtual
2021 WNAR 2021, Virtual
2021 UCSF Pharmaceutical Sciences and Pharmacogenomics, Virtual
2021 Center for Public Health Genomics, University of Virginia, Virtual
2021 Department of Biology, Penn State University, Virtual
2020 2020 ICSA Applied Statistics Symposium, Virtual
2020 Colorado Center for Personalized Medicine, University of Colorado-Denver, Aurora, CO
2020 MidAtlantic Bioinformatics Conference, Virtual
2020 Department of Computational Medicine and Bioinformatics, University of Michigan, Virtual
2019 The 11th ICSA International Conference, Hanzhou, Zhejiang Province, China
2019 Biomedical Informatics, Ohio State University, Columbus, OH
2019 The 17th SCBA International Symposium, Kunming, Yunan Province, China
2019 ENAR 2019 Spring Meeting, Philadelphia, PA
2019 Duke Center for Statistical Genetics and Genomics, Inaugural Talk, Durham, NC
2019 BIRS Workshop, "Frontiers in Single-cell Technology, Applications and Data Analysis", Banff, Alberta, Canada
2018 Joint Statistical Meeting, Vancouver, British Columbia, Canada
2018 Workshop on high dimensional statistics: theory and applications, Changchun, Jilin Province, China
2018 Department of Statistics, University of California, Riverside, CA
2018 Joint GSP-TOPMed Analysis Workshop, Nashville, TN
2017 IBW2017, the Thirteenth International Bioinformatics Workshop, Haerbin, Heilongjiang Province, China
2017 2017 IMS-China International Conference on Statistics and Probability, Nanning, Guangxi Province, China
2017 Department of Public Health Sciences, University of Chicago, Chicago, IL
2017 Department of Preventative Medicine, University of Southern California, Los Angeles, CA
2017 Department of Biostatistics, University of Michigan, Ann Arbor, MI
2017 Department of Pediatrics, Baylor College of Medicine, Houston, TX
2016 Cancer Institute and Hospital, Chinese Academy of Medical Sciences, Beijing, China
2016 Vanderbilt Genetics Institute, Vanderbilt University, Nashville, TN

2016 School of Public Health, Shanghai Jiaotong University, Shanghai, China
2016 2016 Joint Statistical Meeting in Chicago, IL
2016 The 4th IBS-China International Biostatistical Conference, Shanghai, China
2016 Center for Statistical Genetics, University of Michigan, Ann Arbor, MI
2016 Division of Biostatistics, Department of Population Health, New York University School of Medicine, New York, NY
2015 Department of Biostatistics, University of Minnesota, Minneapolis, MN
2015 Department of Mathematics, Bowling Green State University, Bowling Green, OH
2015 Institute for Behavioral Genetics, University of Colorado, Boulder, CO
2015 Institute for Personalized Medicine (IPM), Penn State University, Hershey, PA
2015 ENAR, the International Biometric Society, Miami, FL
2014 Department of Biomathematics, University of California, Los Angeles, CA
2014 Department of Biostatistics, Harvard University, Boston, MA
2014 Department of Biostatistics, University of Pittsburgh, Pittsburgh, PA
2014 Nanjing Medical University, Nanjing, Jiangsu Province, China
2014 Centre for Genomic Sciences, the University of Hong Kong, Hong Kong, China
2014 The Hong Kong University of Science and Technology, Hong Kong, China
2014 Department of Biostatistics, University of Pittsburgh, Pittsburgh, PA
2014 Department of Statistics, Purdue University, West Lafayette, IN
2014 Department of Biostatistics, Columbia University, New York
2013 2013 Triangle Statistical Genetics Conference, Durham, North Carolina
2013 2013 Joint Statistical Meeting in Montreal, Canada
2013 Department of Computer Science, Jiangnan University, Wuxi, China
2013 The Second Taihu International Statistics Forum
2013 ICSA/ISBS (International Chinese Statistical Association/International Society of Biopharmaceutical Statistics) Joint Statistical Conference in Washington, D.C.
2013 2013 ENAR (Eastern North American Region International Biometric Society, Orlando, Florida
2012 Department of Human Genetics, Emory University, Atlanta, Georgia
2012 Department of Epidemiology and Biostatistics, Case Western Reserve University, Cleveland, Ohio
2012 2012 ICSA Applied Statistics Symposium
2011 Quantitative Genomics Seminar Series, Division of Human Genetics at Cincinnati Children's Hospital, University of Cincinnati
2010 8th ICSA International Conference, Guangzhou, China
2010 Section of Molecular Epidemiology, Leiden University Medical Center, Leiden, The Netherlands
2010 Division of Biostatistics, Washington University School of Medicine
2010 2010 ICSA Applied Statistics Symposium
2010 National Institute of Environmental Health Sciences
2010 Center for Genomics and Personalized Medicine Research, Wake Forest University
2010 Cancer Institute and Hospital, Chinese Academy of Medical Sciences (CAMS)
2009 Genetics, University of North Carolina
2009 Lady Davis Institute of Medical Research, Department of Epidemiology, Biostatistics and Occupational Research, McGill University

2009 School of Public Health, Yale University
2009 Biostatistics, University of North Carolina
2009 Genetics and Genomic Sciences, Mount Sinai School of Medicine, New York
2007 McKusick-Nathans Institute of Genetic Medicine, Johns Hopkins University
2007 Pharmacogenetics, GlaxoSmithKline
2007 ICSA Symposium

TEACHING RECORD

CLASSROOM TEACHING

Course/Module Director:

BCB723: Topics in Statistical Genetics and Genomics, 7.5 lecture hours
Spring 2024, 16 students
Spring 2023, 12 students
Spring 2022, 12 students and 1 auditor
Spring 2021, 9 students and 1 auditor
Spring 2020, 10 students and 1 auditor
Spring 2019, 9 students and 1 auditor
Spring 2018, 8 students

Bios782/BCB725: Statistical Methods in Genetic Studies
Fall 2022, 13 students, 24 lecture hours
Fall 2020, 19 students and 1 autitor, 22.5 lecture hours

Bios782: Statistical Methods in Genetic Studies,
Fall 2018, 12 students and 2 auditors, 21 lecture hours
Fall 2016, 21 students, 22.5 lecture hours

BCB720: Introduction to Statistical Modeling, 12 lecture hours
Fall 2016, 24 students

EPI889: Advanced Genetic Epidemiology – High Throughput Data Analysis
12 lecture hours
Fall 2016, 12 students
Fall 2014, 5 students
Fall 2012, 18 students

Bios735: Statistical Computing, 9 hours for lecturing/leading discussions
Fall 2015, 22 students
Fall 2013, 23 students

Bios781: Statistical Methods in Genetic Mapping, 3 hours for guest lecturing
Spring 2022
Spring 2020

BCB725/Bios681: Introduction to Statistical Genetics,
3 credit hours (24 hours for lecturing/leading discussions),
Spring 2015, 9 students
Spring 2012, 17 students

Guest Lectures at UNC:

BIOS/BCB785: Statistical Methods for Gene Expression Analysis,

1.5 lecture hours, Fall 2020
1.5 lecture hours, Spring 2019

BCB710: Bioinformatics Colloquium,
1.5 lecture hours, 2009, 2010, 2013, 2015, 2019, 2020

EPID743: Genetic Epidemiology, 1.5 contact hours, 2010-2020

BIOS781: Statistical Methods in Genetic Mapping
3.0 lecture hours, Spring 2024
3.0 lecture hours, Spring 2022
1.5 lecture hours, Spring 2020
4.5 lecture hours, 2018

BCB720: Introduction to Statistical Modeling,
1.5 lecture hours, Fall 2015, 2017, 2018

BCB720: Introduction to Statistical Modeling,
12 lecture hours, Fall 2016, 24 students

BIOS784: Computational Biology, 4.5 contact hours, 2013, 2015

BIOS740: Statistical Methods for Genetic Association Studies,
4.5 lecture hours, 2012, 2014

Lectures outside UNC:

- ✧ 2019 Banff International Research Station (BIRS) Workshop on Single-cell Technology, Applications and Data Analysis
- ✧ Joint Statistical Meeting (JSM) Professional Development Continuing Education Course on Analysis of Genome-Wide Sequencing Association Studies, jointly taught with Xihong Lin and Michael Wu - 2014
- ✧ 2014 Workshop on Emerging Statistical Challenges and Methods For Analysis of Massive Genomic Data in Complex Human Disease Studies, Banff International Research Station for Mathematical Innovation and Discovery, Banff, Canada.
- ✧ 2014 Workshop on Big Data in Genetics and Toxicogenomics, Durham, NC
- ✧ Short Course on Genetic Epidemiology, Nanjing Medical University, Nanjing, China - 2013
- ✧ Short Course on Next Generation Sequencing: Technology and Statistical Methods, UAB in Birmingham, Alabama – 2012
- ✧ ICSA Short Course on the Analyses of Next Generation Sequencing Studies, Boston, 2012
- ✧ Statistical Genetics Short Course, Chapel Hill, North Carolina, 2010 summer
- ✧ Short Course “SNP’s and Human Diseases”, Erasmus MC, Rotterdam, the Netherlands, 2010
- ✧ Graduate Student Instructor for Biostat605 (Introduction to SAS), University of Michigan, 2008

MENTORING

High School Student Research Advisor:

2022-2023 Archita Khaire, North Carolina School of Science and Mathematics, early admitted into MIT

Undergraduate Student Research Advisor:

2023- Katherine Xing, B.S. student, Department of Biostatistics, UNC-CH

2023- Guning Shen, B.S. student, Biology and Computer Science
2022- Theo Wu, B.S. student, Departments of Biostatistics and Mathematics, UNC-CH
2022-2024 Hongyu Yu, B.S. student, Department of Biostatistics, UNC-CH
2022-2023 Ellen Hu, B.S. student, Department of Biostatistics, UNC-CH
2022-2023 Sara O'Brien, B.S. student, Department of Biostatistics, UNC-CH
2020-2021 Yingxi Kaylee Yang, B.S. student, Department of Statistics, Sun Yat-Sen University. Current Position: Ph.D. student, Statistics and Data Science, Yale University
2020-2022 Alice Y. Sun, B.S. student, Department of Biostatistics, Department of Biology, UNC-CH. Current Position: MS student in Biomedical Informatics, Stanford University
2019-2020 Daniel Malawsky, B.S. student, Department of Biostatistics, UNC-CH. Current Position: Ph.D. student, Sanger Institute
2018-2019 Qian Zhang, B.S. student, Statistics, Tsinghua University. Current Position: Ph.D. student, Statistics, Purdue University
2018-2019 Quan Sun, B.S. student, Mathematics and Applied Mathematics, Zhejiang University. Current Position: Ph.D. student, Biostatistics, UNC-CH
2018-2019 Wenwen Mei, B.S. student (first generation college student), Department of Biostatistics, UNC-CH. Current Position: Ph.D. student, Biostatistics, UNC-CH
2017-2018 Zoey Hou, B.S. student, Department of Financial Risk Management, Central University of Finance and Economics. Current Position: Ph.D. student, Applied Mathematics, Northwestern University
2017-2018 Jun Yin, B.S. student in biotechnology, Beijing Normal University. Current Position: Data Scientist, CVS Health
2016-2017 Eric Zhou, B.S. student, Department of Computer Science, UNC-CH. Current Position: Backend Software Engineer at IBM

Master's Student Advisor:

2023- Wenrong Wu, M.S. student, Caraolina Health Informatics Program
2023- Ruochen Li, M.S. student, Department of Biostatistics, UNC-CH.
2022- Yunfei Fan, M.S. student, Department of Biostatistics, UNC-CH.
2022-2024 Dinelka Nanayakkara, M.S. student, Department of Biostatistics, UNC-CH.
2022-2024 Caiwei Xiong, M.S. student, Department of Biostatistics, UNC-CH.
2022-2024 Xinyue Zeng, M.S. student, Department of Biostatistics, UNC-CH.
2022-2024 Jingying Wang, M.S. student, Department of Biostatistics, UNC-CH.
2022-2023 Jiawen Du, M.S. student, Department of Biostatistics, UNC-CH. Current Position: Ph.D. student, Department of Biostatistics, UNC-CH
2022-2023 Lingbo Zhou, M.S. student, Department of Biostatistics, UNC-CH. Current Position: Ph.D. student, Department of Biostatistics, UNC-CH
2020-2022 Wanjiang Wang, M.S. student, Department of Biostatistics, UNC-CH. Current Position: Ph.D. student in Population Health, Northeastern University
2020-2021 Zhentao Yu, M.S. student, Department of Biostatistics, UNC-CH. Current Position: Ph.D. student, Department of Biostatistics, UNC-CH
2019-2020 Yueting Wang, M.S. student, Department of Biostatistics, UNC-CH. Current Position: Ph.D. student, University of Pittsburgh
2017-2019 Madeline Kowalski, M.S. student, Department of Biostatistics. Current position:

MD/PhD student at New York University School of Medicine
2016-2018 Cheynna Crowley, M.S. student, Department of Biostatistics. Current position: Principal Statistician, GlaxoSmithKline in Waltham, MA

Doctoral Student Thesis Advisor:

2023- Jiawen Du, Ph.D. student, Department of Biostatistics
2023- Lingbo Zhou, Ph.D. student, Department of Biostatistics
2023- Walter Chen, Ph.D. student, Department of Biostatistics
2022- Elena Kharitonova, Ph.D. student, Department of Biostatistics
2022- Wyliena Guan, Ph.D. student, Department of Biostatistics
2022- Sean Conneely, MD/Ph.D. student, Curriculum in Bioinformatics and Computational Biology (co-mentoring with Dr. Juliano)
2022- Amar Marthi, Ph.D. student, Department of Epidemiology (co-mentoring with Dr. Franceschini)
2022- Shuai Huang, Ph.D. student, Department of Biostatistics
2022- Will/Chenwei Tang, Ph.D. student, Department of Biostatistics
2022- Frank Ockerman, Ph.D. student, Department of Biostatistics
2021- Emma Wilson, Ph.D. student, Curriculum in Bioinformatics and Computational Biology (co-mentoring with Dr. Mohlke)
2021- Brian Chen, Ph.D. student, Department of Biostatistics
2020- Jiawen Chen, Ph.D. student, Department of Biostatistics
2020-2024 Le Huang, Ph.D. student, Curriculum in Bioinformatics and Computational Biology
2019-2024 Quan Sun, Ph.D. student, Department of Biostatistics
2020-2023 Tianyou Luo, Ph.D. student, Department of Biostatistics. Current position: Machine Learning Scientist, Tempus Labs.
2022 Ruixuan Shang, Ph.D. student, Department of Biostatistics
2021 Ben Bodek, Ph.D. student, Department of Biostatistics
2021-2023 Xiaoqi Li, Ph.D. student, Caraolina Health Informatics Program.
2020-2021 Chanhwa Lee, Ph.D. student, Department of Biostatistics.
2019-2023 Weifang Liu, Ph.D. student, Department of Biostatistics. Current position: Biostatistician II, Foundation Medicine, Boston
2018-2022 Minzhi Jiang, Ph.D. student, Department of Applied Physical Sciences. Current position: Post-doctoral fellow, Department of Biostatistics, Johns Hopkins University
2018-2022 Bryce Rowland, Ph.D. student, Department of Biostatistics (NSF Graduate Research Fellowship recipient 2019-2022). Current position: Assistant Professor, Department of Biostatistics; Senior Research Scientist at the Collaborative Studies Coordinating Center, UNC-CH
2016-2021 Jon Rosen, Ph.D. student, Department of Biostatistics. Current position: Post-doctoral fellow, Department of Genetics, UNC-CH
2016-2021 Yue Shan, Ph.D. student, Department of Biostatistics. Current position: Clinical statistician, Hengrui Medicine Co.,Ltd., Shanghai
2017-2021 Amanda Tapia, Dr.PH student, Department of Biostatistics. Current position: Post-doctoral fellow, University of Pittsburgh
2016-2021 Taylor Lagler, Ph.D. student, Department of Biostatistics (NSF Graduate

Research Fellowship recipient 2017-2020). Current position: Statistician at The Lubrizol Corporation

2017-2021 Gang Li, Ph.D. student, Department of Statistics and Operation Research. Current position: Post-doctoral fellow, University of Washington

2018-2020 Cheynna Crowley, Dr.PH student, Department of Biostatistics. Current position: Principal Statistician, GlaxoSmithKline in Waltham, MA

2018-2020 Ai Ye, Ph.D. student, Department of Psychology and Neuroscience. Current position: Statistical Consultant and Software Developer, RTI International

2016-2020 Eric Van Buren, Ph.D. student, Department of Biostatistics. Current position: Post-doctoral fellow, Harvard University

2017-2019 Huijun Qian, Ph.D. student, Department of Statistics and Operation Research. Current position: Machine Learning Enginee, Meta.

2016-2019 Wujuan Zhong, Ph.D. student, Department of Biostatistics. Current position: Senior scientist in Merck BARDS.

2016-2019 Ruth Huh, Ph.D. student, Department of Biostatistics. Current position: Research Scientist at Eli Lilly and Company.

2016-2017 Evan Kwiatkowski, Ph.D. student, Department of Biostatistics. Current position: Assistant Professor, Department of Biostatistics, The University of Texas MD Anderson Cancer Center at Houston.

2012-2016 Guosheng Zhang, Ph.D. student, Curriculum in Bioinformatics and Computational Biology. Current position: Staff Software Engineer at Google.

2012-2016 Qing Duan, Ph.D. student, Curriculum in Bioinformatics and Computational Biology. Current position: Biostatistician at Cincinnati Children's Hospital Medical Center.

2010-2015 Kuan-Chieh Huang, Ph.D. student, Department of Biostatistics. Current position: Sr. Biostatistician at Gilead Sciences, Inc.

2009-2013 Andrea Byrnes, Ph.D. student, Department of Biostatistics. Current position: Investigator II at Novartis Institutes for BioMedical Research (NIBR)

2009-2013 Yi Liu, Ph.D. student, Department of Computer Science. Current position: Machine Learning Manager at Facebook

Graduate Student Academic Advisor:

2023- Qinghua Li, Ph.D. student, Department of Biostatistics, UNC-CH.

2023- David Lopez, M.S. student, Department of Biostatistics, UNC-CH.

2022- Lin Li, M.S. student, Department of Biostatistics, UNC-CH.

2022-2024 Annie Burgess Page, M.S. student, Department of Biostatistics, UNC-CH. Current position: Health Information Specialist, Carol Woods Retirement Community.

2020-2022 Huaying Qiu, M.S. student, Department of Biostatistics, UNC-CH. Current position: Biostatistician I, Jiang Lab, Beth Israel Deaconess Medical Center

2016-2022 Hillary Heiling, Ph.D. student, Department of Biostatistics. Current position: Scientist, Dana-Farber Cancer Institute.

2016-2021 Kayla Kilpatrick, Ph.D. student, Department of Biostatistics. Current position: Biostatistician III, Duke University

2013-2015 Yinghao Pan, Ph.D. student, Department of Biostatistics. Current position: Assistant Professor, Mathematics and Statistics Department, UNC-Charlotte

2012-2014 Xiaoqiang Xue, Dr.PH., Department of Biostatistics. Current position:Vice President of Biostatistics at Syneos Health.

Graduate Rotation Students:

2024 Spring Katelyn McInerney
2023 Fall Archishma Kavalipati
2023 Fall Muqing Zhou
2023 Fall Yiyan Zhang
2023 Spring Deontae Pharr
2020 Fall Le Huang
2019 Fall Yuriko Harigaya
2016 Winter Angel Wei Huang
2015 Winter Dan Liang
2014 Spring Shengjie Chai
2013 Spring Greg Keele
2012 Spring Guosheng Zhang
2011 Fall Qing Duan

Postdoctoral Scientist Advisor:

2022- Ruyue Zhang, Ph.D. in Medical Science.
2018- Jia Wen, Ph.D. in Statistical Genomics
2022-2023 Laura Zhou, Ph.D. in Biostatistics. Fall 2023 Position: Assistant Professor, Indiana University, School of Medicine
2022-2023 Minzhi Jiang, Ph.D. in Applied Physical Sciences
2017-2020 Yuchen Yang, Ph.D. in Biochemistry and Molecular Biology. Current position: Assistant Professor, Sun Yat-Sen University
2016-2020 Laura Raffield, Ph.D. in Molecular Genetics and Genomics. Current position: Assistant Professor, UNC-CH
2018-2020 Munan Xie, Ph.D. in Botany. Current position: Director, Department of precision medicine at Yilifang Biotechnology Co., Ltd
2016-2017 Josh Martin, Ph.D. in Theoretical Physics. Current position: Bioinformatics II at Duke University School of Medicine
2016-2017 Qing Duan, Ph.D. in Bioinformatics and Computational Biology. Current position: Biostatistician at Cincinnati Children's Hospital Medical Center
2012-2016 Zheng Xu, Ph.D. in Statistics. Current position: Assistant professor, Wright State University
2012-2015 Song Yan, Ph.D. in Statistics. Latest position: Software engineer at Google.

Faculty Mentoring:

2023- Xihao Li, Assistant Professor, Department of Biostatistics, UNC-CH
2020- Anna Bauer, Assistant Professor, Department of Psychiatry, UNC-CH
2020- Misa Graff, Associate Professor, Department of Epidemiology, UNC-CH
2020-2021 Paola Guisti -Rodríguez, Current Position: Assistant Professor, Department of Psychiatry, University of Florida
2019- Matt Halvorsen, Assistant Professor, Department of Genetics, UNC-CH

2020- Chantel Martin, Assistant Professor, Department of Epidemiology, UNC-CH
2020- Rebekah Nash, Assistant Professor, Department of Psychiatry, UNC-CH
2020- Jesse Raab, Assistant Professor, Department of Genetics, UNC-CH
2020- Laura Raffield, Assistant Professor, Department of Genetics, UNC-CH
2018- Dan Schrider, Assistant Professor, Department of Genetics, UNC-CH
2018- Hyejung Won, Assistant Professor, Department of Genetics, UNC-CH
2018-2023 Xiaojing Zheng, Associate Professor, Department of Pediatrics, UNC-CH
2018-2023 Yuchao Jiang, Assistant Professor, Department of Biostatistics, UNC-CH
2017-2023 Michael I. Love, Associate Professor, Department of Biostatistics, UNC-CH
2016-2017 Xianyong Yin, Assistant Professor, Department of Genetics, UNC-CH, Current Position: Senior Research Specialist, Department of Biostatistics, University of Michigan

Visiting Scholar:
2013-2014 Wei Chen, Chief Physician in Community Health, Beijing Maternal and Child Health Care Hospital
2014-2015 Suhua Chang, Assistant Professor in Institute of Psychology, Chinese Academy of Sciences

Programmer:
2012-2013 Yunfei Wang

Statistician:
2013-2014 Yurong Lu

Temporary Data Scientist:
2020 Zihao Liu, M.S. in Biomedical Engineering, University of Connecticut Current position: PhD Student, Molecular, Cellular and Developmental Biology, Ohio State University
2019 Huijun Qian, Ph.D. in Statistics, UNC-CH. Current position: Sr Quantitative Analyst, Enterprise Risk Management, Exelon
2019 Madeline Kowalski, M.S. in Biostatistics, UNC-CH. Current position: MD/PhD student at New York University School of Medicine
2019 Ye Su, M.S. in Bioinformatics, George Washington University
2018 Tong Shan, M.S. in Statistics, UNC-CH. Current position: PhD Student, Statistics, University of South Carolina
2016 Yimeng Tianyao, M.S. in Statistics and Operations Research, UNC-CH. Current position: Senior Quantitative Analyst, Capital One

Graduate Student Thesis Advisory Committees:
2024- Pradham Tanikella, Ph.D. student, Curriculum in Bioinformatics and Computational Biology (committee chair)
2023- Madeline Gillman, Ph.D. student, Curriculum in Bioinformatics and Computational Biology (committee chair)
2023- Micah Hysong, Ph.D. student, Curriculum in Genetics and Molecular Biology
2023- Sool Lee, Ph.D. student, Curriculum in Bioinformatics and Computational Biology

2023-	Brian Gural, Ph.D. student, Curriculum in Bioinformatics and Computational Biology
2023-2024	Bridget Lin, Ph.D. student, Department of Biostatistics
2022-	Jayna Nicholas, Ph.D. student, Curriculum in Genetics and Molecular Biology (committee chair)
2022-	Anna Goddard, Ph.D. student, Pathobiology and Translational Science program
2022-	Kai Xia, Ph.D. student, Department of Biostatistics
2022-2024	Haidong Yi, Ph.D. student, Department of Computer Science
2022-	Nina Nishiyama, Ph.D. student, Curriculum in Bioinformatics and Computational Biology (committee chair)
2021-	Yuriko Harigaya, Ph.D. student, Curriculum in Bioinformatics and Computational Biology (committee chair)
2021-2023	Anthony Abrantes, Dr.Ph. student, Department of Biostatistics
2020-2023	Nil Aygun, Ph.D. student, Curriculum in Bioinformatics and Computational Biology
2019-2023	Sarah Brotman, Ph.D. student, Curriculum in Genetics and Molecular Biology
2018-2023	Darius Bost, Ph.D. student, Curriculum in Bioinformatics and Computational Biology (committee chair)
2020-2021	Kevin Donovan, Ph.D. student, Department of Biostatistics
2020-2021	John Kidd, Ph.D. student, Department of Biostatistics
2020-2021	Rujin Wang, Ph.D. student, Department of Biostatistics
2018-2022	Mike Lafferty, Ph.D. student, Curriculum in Bioinformatics and Computational Biology
2018-2020	Dayne Filer, Ph.D. student, Curriculum in Bioinformatics and Computational Biology
2018-2020	Scott Van Buren, Ph.D. student, Department of Biostatistics
2018-2020	Arjun Bhattacharya, Ph.D. student, Department of Biostatistics
2018-2020	Sarah Reifeis, Ph.D. student, Department of Biostatistics
2018-2020	Pedro Baldoni, Ph.D. student, Department of Biostatistics
2017-2020	Yanwei Cai, Ph.D. student, Curriculum in Bioinformatics and Computational Biology
2017-2020	Kevin Currin, Ph.D. student, Curriculum in Bioinformatics and Computational Biology
2018-2019	Yue Jiang, Ph.D. student, Department of Biostatistics
2018-2019	Anqi Zhu, Ph.D. student, Department of Biostatistics
2017-2019	Wes Crouse, Ph.D. student, Curriculum in Bioinformatics and Computational Biology
2016-2019	Chelsea Raulerson, Ph.D. student, Curriculum in Bioinformatics and Computational Biology
2017-2018	James Xenakis, Ph.D. student, Department of Biostatistics
2016-2018	Vasyl Zhabotynsky, Ph.D. student, Department of Biostatistics
2014-2018	Xiaolei Zhou, Ph.D. student, Department of Biostatistics
2014-2018	Robert Corty, Ph.D. student, Curriculum in Bioinformatics and Computational Biology
2016-2017	Rachel Nethery, Ph.D. student, Department of Biostatistics
2015-2017	Christopher Bryant, Ph.D. student, Department of Biostatistics

2015-2016 Matthew Psioda, Ph.D. student, Department of Biostatistics
2015-2016 Matthew Holt, Ph.D. student, Department of Computer Science
2015-2016 Wei Xue, Dr.PH student, Department of Biostatistics
2015-2016 Ran Tao, Ph.D. student, Department of Biostatistics
2014-2016 Hojin Yang, Ph.D. student, Department of Biostatistics
2015 Thomas Conrad, M.S. student, Department of Biostatistics
2014-2015 Pratyaydipta Rudra, Ph.D. student, Department of Biostatistics
2013-2015 Jin Li, Ph.D. student, Curriculum in Bioinformatics and Computational Biology
2012-2015 Martin Buchkovich, Ph.D. student, Curriculum in Bioinformatics and Computational Biology
2013-2014 Shuai Yuan, Ph.D. student, Computer Science and Informatics, Emory University
2013-2014 Yunfei Wang, Dr.Ph. student, Department of Biostatistics
2013-2014 Ni Zhao, Ph.D. student, Department of Biostatistics
2013-2014 Zhengzheng Tang, Ph.D. student, Department of Biostatistics
2013-2014 Gene Urrutia, Ph.D. student, Department of Biostatistics
2012-2014 TingHuei Chen, Ph.D. student, Department of Biostatistics
2010-2014 Gabi Griffin, Ph.D. student, Curriculum in Genetics and Molecular Biology
2012-2013 Gregory Mayhew, Ph.D. student, Department of Biostatistics
2012-2013 Ni Zhao, M.S. student, Department of Biostatistics
2010-2012 Damien Croteau-Chonka, Ph.D. student, Curriculum in Genetics and Molecular Biology and Bioinformatics and Computational Biology Training Program
2010-2012 Yihui Zhou, Ph.D. student, Department of Biostatistics
2009-2010 Lindsey Ho, Dr.Ph. student, Department of Biostatistics
2009-2010 John Schwatz, Ph.D. student, Department of Biostatistics

Mentor on K99/R00 of Postdoctoral Fellows:
2023+ Jungkyun Seo, Department of Epidemiology

GRANTS

ACTIVE

R01AG079291 Li/Shen/Gan (PI) 04/01/23-03/31/28
NIH/NIA $6,583,070 10% Effort
Study of Selective Cell and System Vulnerability in Alzheimer's Disease
The goal of this study is to develop computational methods and bioinformatics tools to analyze bulk and single cell RNA-seq data, GWAS, array genotyping, whole genome sequencing and functional genomic data to systematically identify and functionally characterize cell-type-specific noncoding variants associated with Alzheimer’s disease (AD) in iPSC-derived cells and brain organoids.
Role: contact PI

U01HG011720 Li/Cox/Reiner (PI) 06/08/21-03/31/26
NIH/NHGRI $4,938,811 20% Effort
Polygenic risk scores and health disparities: the role of blood cells immune response and evolutionary adaptation

The goal of this study is to leverage existing biomarker data to derive new polygenic risk scores (PRS) to improve prediction of disease across ancestrally diverse populations, particularly focusing on inflammation and hematological measures under selective pressure from differential infectious disease exposures.
Role: contact PI

R01 R01HL163972 Franceschini/Li (PI) 05/01/22-04/30/26
NIH/NHGRI $1,881,747 10% Effort
Genetics of Cardiovascular Disease in Chronic Kidney Disease
The goal of this study is to study the genetics underlying cardiovascular disease among individuals affected with CKD.
Role: MPI

R01HL165061 Reiner (PI) 07/01/23-06/30/27
NIH/NHLBI $3,062,484 5% Effort
Structural Variation and Hematological Traits
This project will examine the role of structural variants in the genetic architecture of hematologic traits and contribute to a better understanding of hematopoiesis and pave the way for new research into Precision Medicine for blood diseases.
Role: Co-Investigator, subcontract PI

P50HD103573 Piven (PI) 07/01/20-06/30/25
NIH/NICHD $1,271,070 10% Effort
Clinical Translational Research Center for Neurodevelopmental Disorders
Intellectual and Developmental Disabilities Research Center.
Role: Director for the Data Science Core

U01 DA052713 Shen/Kriegstein (PI) 09/01/20-08/31/25
NIH/NIA $3,230,375 8% Effort
Charting the 3D epigenome in human brain development and diseases
The goal of the project is to systematically profile the 3D epigenome in various cell types and conditions relevant to human brain development and diseases.
Role: Co-Investigator, subcontract PI

R01 HL146500 Reiner (PI) 02/01/20-01/31/24
NIH/NHLBI $2,648,812 8% Effort
Next generation functional genomics of hematology traits
The goal of the project is to discover, fine-map, and investigate causal variants, elements and genes that underlie red blood cell traits and hematological disorders.
Role: Co-Investigator, subcontract PI

R01AG075884 Raffield (PI) 03/01/22-11/30/26
NIH/NIA $3,755,399 2% Effort
Immune Cells in Alzheimer's Disease and Related Dementias in the Jackson Heart Study
The proposed work will assess specific innate and adaptive immune cells, and genes expressed in these cells, and determine whether they are associated with mild cognitive

impairment (MCI) and dementia risk among African Americans from the population-based Jackson Heart Study, as well as target genes and biological mechanisms in immune cells for genetic variants previously associated with dementia.
Role: Co-Investigator

R01MH130671 Sullivan (PI) 09/01/22-08/31/27
NIH/NIMH $3,725,284 10% Effort
1/3 Sequencing and Trans-Diagnostic Phenotyping of Severe Mental Illness in Diverse Populations
The goal of this study is to further knowledge of the genetic architecture of mental illness.
Role: Co-Investigator

UM1HG012003 Won/Mohlke/Love (PI) 09/01/21-05/31/26
NIH/NHGRI $8,318,924 5% Effort
Systematic In Vivo Characterization of Disease-Associated Regulatory Variants
The goal of this study is to systematically characterize the impact of human genetic variation on gene regulation to understand how genomic variation impacts human health and disease.
Role: Co-Investigator

R01 NR019245 Santos (PI) 07/01/20-06/30/25
NINR/NIH $1,917,272 10% Effort
Genetic and Epigenetic Effects on Childhood Cognitive Trajectories
The goal of the project is to advance our understanding of genetic and epigenetic factors related to preterm children's neurodevelopment.
Role: Co-Investigator

R01 MH123724 Sullivan (PI) 06/10/20-03/31/25
NIMH/NIH $4,401,278 5% Effort
A Trans-Nordic Study of Extreme Major Depression
The goal of the project is to conduct a trans-Nordic genetic study for extreme major depression.
Role: Co-Investigator

R01 R01MH125236 Crawford/Gersbach/Sullivan (PI) 04/01/21-01/31/26
NIMH/NIH $1,653,935 10% Effort
Beyond GWAS: High Throughput Functional Genomics & Epigenome Editing to Elucidate the Effects of Genetic Associations for Schizophrenia
The goal of the project is to to drive targeted genetic and functional investigation into regulatory mechanisms relevant for schizophrenia.
Role: Co-Investigator

U24AR076730 LaVange, Ivanova (PI) 09/26/19-05/31/24
NIH $ 51,781,303 3% Effort
HEAL Initiative: Back Pain Consortium (BACPAC) Research Program Data Integration, Algorithm Development and Operations Management Center

The goal of this project is to set the stage for technology assessments, solicitation of patient input and utilities, and the evaluation of high-impact interventions through the innovative design and sound execution of clinical trials, leading to effective personalized treatment approaches for patients with chronic lower back pain.
Role: Co-Investigator, Leader of System Biology Group

R01MH118349 Stein/Love (PI) 12/10/18-11/30/23
NIH $493,569 4% Effort
PathQTL: Integrative Multi-Omics Causal Inference of Molecular Mechanisms Leading to Neuropsychiatric Illness
The goal of this study is to prioritize causal molecular pathways, to identify the relevant cell-type and developmental stage, and to shed light on mechanisms of neuropsychiatric disorders in an unbiased manner.
Role: Co-Investigator

PENDING

omitted

COMPLETED

R01MD013349 Aiello/Harris (PI) 08/14/18-03/31/23
NIH $678,479 5% Effort
The Add Health Epigenome Resource: Life course stressors and epigenomic modifications in adulthood
The overall goals of this project are to investigate the influence of life course psychosocial stressors on DNA methylation and gene expression that may influence cardiometabolic health and depression in a US representative study of young adults.
Role: Co-Investigator

R01GM105785 Sun (PI) 01/17/19-12/31/22
Fred Hutchinson/NIH $105,267 (Subcontract) 0% Effort
Statistical Methods for RNA-Seq Data Analysis
The goal of this study is to develop statistical/computational methods to study cell type composition or cell type-specific gene expression using bulk RNA-seq data, scRNA-seq data, or both bulk RNA-seq and scRNA-seq data.
Role: Co-Investigator

2R01DK093757 Mohlke (PI) 08/01/17-07/31/22
NIH/NIDDK $627,100 8% Effort
Genetic epidemiology of rare and regulatory variants for metabolic traits
The goal of this project is to identify novel genes for metabolic traits, discover pathogenic regulatory variants, and learn how environmental context can influence the dynamic range of gene regulation and the development of disease.
Role: Co-Investigator

R21AR075996 Sayed/Li/Mohlke (PI) 07/01/20-06/30/22

NIAMS/NIH $309,790 5% Effort
Evaluation of the Genetics of Hidradenitis Suppurativa
The goal of the project is to evaluate the genetics underlying Hidradenitis Suppurativa.
Role: MPI

R01HL129132 Li/Reiner (PI) 07/15/16-02/29/22
NIH/NHLBI $621,504 1% Effort
Genetic Studies of Blood Cell Traits in Multi-Ethnic Cohorts
The goal of this study is to map, annotate and validate genes for blood cell traits in multi-ethnic cohorts to increase our knowledge of blood cell trait genetics.
Role: contact PI

1R01MD011609 Manuck (PI) 08/08/17-03/31/22
NIH/NIMHHD $759,176 4% Effort
The Pharmacoepigenomics of recurrent preterm birth in non-Hispanic black women
The goal of this study is to provide immediate and sustained clinical and public health impact to reduce disparities in PTB outcomes in NH black women and infants, thereby reducing neonatal mortality and lifelong morbidity.
Role: Co-Investigator

CCF(5110544) Knowles (PI) 06/01/18-11/30/21
Cystic Fibrosis Foundation $711,233 20% Effort
Discovery of CF modifiers using whole genome sequencing-UNC
The overall goal of this project is to identify genetic modifiers for Cystic Fibrosis using whole genome sequencing data.
Role: Co-Investigator

U54 HD079124 Piven (PI) 09/24/13-05/31/20
NIH/NICHD $1,271,070 10% Effort
Clinical Translational Research Center for Neurodevelopmental Disorders
Intellectual and Developmental Disabilities Research Center.
Role: Core Director

R01HL130733 Lange/Reiner (PI) 08/01/17-04/30/20
University of Colorado Denver/NIH $146,284 (Subcontract) 10% Effort
Sequence analysis of hematological traits in African Americans
The goal is to use sequence and genotyping data in African Americans to discover and functionally characterize novel genetic associations for blood cell traits.
Role: Co-Investigator

5216282-5500000980 Meigs (PI) 05/01/17-10/30/18
Broad Institute/NIH/NIDDK
TOPMed Whole Genome Sequence Analysis of Type 2 Diabetes and Related Traits
The goal of this project is to test the association of common, rare, and structural variation with type 2 diabetes and related traits using TOPMed Whole Genome Sequence data.
Role: Subcontract PI

5U01HL120393 Psaty (PI) 03/01/18-08/31/18
Rare variants and NHLBI traits in deeply phenotyped cohorts
The goal of this project is to leverage the deeply phenotyped cohort in NHLBI TOPMed cohorts to better understand biological pathways that may identify therapeutic targets.
Role: Subcontract PI

1R01DK101855 (NCE) North (PI) 08/15/14-7/31/18
Leveraging ancestral diversity to map adiposity loci in Hispanics
The goal of this project is to identify novel variants that influence traits related to obesity and related metabolic traits in under-represented Hispanic/Latino populations.
Role: Co-Investigator

5R01ES020836 (NCE) Whitsel (PI) 08/06/12-04/30/18
Epigenetic Mechanisms of PM-Mediated CVD risk
The goal of this project is to advance the understanding of epigenetic mechanisms underlying susceptibility to PM-mediated CVD risk in post-menopausal women.
Role: Co-Investigator

1R01DK093757 Mohlke (PI) 09/05/11-7/31/17
Genetic epidemiology of rare and regulatory variants for metabolic traits
The goal of this project is to identify novel variants that influence traits related to diabetes, obesity and the metabolic syndrome and mechanisms by which DNA variants influence gene expression and disease.
Role: Co-Investigator

1R01HG006292 Li (PI) 08/23/11-05/31/17
NIH/NHGRI $250,000 30% Efforts
Design and Analysis of Sequencing-based Studies for Complex Human Traits
The goal of this study is to establish a comprehensive statistical framework for the design and analysis of sequencing-based studies for complex human traits.
Role: PI

1R01 DA030976-01 Wilhelmsen (PI) 09/30/10-05/31/16
NIH $2,729,715 10% Effort
Deep Sequencing Studies for Cannabis and Stimulant Dependence
The goal of this proposal is to identify genes that affect susceptibility to stimulant and cannabis dependence using whole genome sequencing with genotype imputation.
Role: Co-Investigator

1R01HG006703-01 Li (PI) 05/16/12-02/28/16
NIH/NHGRI $224,285 20% Effort
Imputation and Analysis of Rare Variants in Admixed Populations
The goal of this study is to develop statistical methods and computational tools for the imputation of rare genetic variants in admixed populations.
Role: PI

Subcontract No. 3001352222 Li (PI) 12/01/09-12/11/14
GlaxoSmithKline/UMichigan $54,593 3% Effort
The goal of this project is to develop and apply imputation based methodology to genome wide association and sequencing datasets.
Role: Subcontract PI

5P01HD031921-15 Whitsel (PI) 08/01/10-03/15/13
NIH $493,201 8% Effort
Modification of PM-mediated Arrhythmogenesis in Populations
The goal of the project is to examine susceptibility to the arrhythmogenic effects of particulate matter (PM) air pollution contributed by common genetic variation.
Role: Co-Investigator

R01 MH090936-02 Rusyn (PI) 9/17/10-7/31/12
NIH/NIMH $220,904 4% Effort
Facilitating GTEx, Disease, and GxE Analyses Via Fast Expression (e)QTL Mapping
The goal of this project is to develop new statistical tools and graphical user-friendly software to facilitate the analysis of eQTL studies.
Role: Co-Investigator

1RC2HL102924-01(NCE) Jackson, North (PI) 09/30/09-07/31/12
WHI Sequencing Project (WHISP)
NIH/Ohio State Univ. Sub $397,899 16% Effort
The overall goal of this project submitted in response to NHLBI RC2 Topic 'Large-scale DNA Sequencing and Molecular Profiling of Well-phenotyped NHLBI Cohorts' (RFA-OD-09-004) is to identify putative functional variants for high-priority heart lung and blood phenotypes among American post-menopausal women from diverse ancestral and geographic backgrounds.
Role: Co-Investigator

5R01 HL095396-02 Knowles (PI) 09/24/08-07/31/12
NIH/NHLBI $515,788 10% Effort
Molecular Phenotypes for Cystic Fibrosis Lung Disease
The goal of this project is to define a molecular phenotype for CF lung disease, which relates to prognosis, and new targets for therapy.
Role: Co-Investigator

U01 DA024413 Costello (PI) 09/01/07-06/30/12
NIDA/Duke sub (Sullivan, UNC PI) $297,458 8% Effort
A developmental model of gene-environment interplay in SUDs
The major goal of this study is to investigate genetic main effects and gene-environment interactions using GWAS data in longitudinal studies of substance initiation and progression.
Role: Co-Investigator

3R01 DK078150-04 Mohlke (PI) 04/01/07-03/31/12
NIH/NIDDK $389,802 20% Effort

Genetic Epidemiology of Body Mass Index, Adiposity, and Weight Gain
The goals of this study are to test candidate genes for association with obesity-related traits and weight gain across 22 years in women from the Cebu Longitudinal Health and Nutrition Survey and to evaluate interactions with diet composition and physical activity.
Role: Co-Investigator

3R01 CA082659-11S1	Lin (PI)	08/01/09-07/31/11
NIH/NCI	$163,841	20% Effort

Statistical Methods in Cancer Research
The goal of this project is the development of statistical methods for the designs and analysis of clinical and epidemiological cancer studies.
Role: Co-Investigator

PROFESSIONAL SERVICE

Service to Discipline:

Regular Reviewer:

Jul 2017 - 2021:	Genomics, Computational Biology and Technology (GCAT) Study Section
Sep 2023 -	Center for Inherited Disease Research (CIDR)
Sep 2023 -	a Special Government Employee, Endocrinology Subcommittee, Joint Biomedical Laboratory Research and Development (BLRD) and Clinical Science Research and Development (CSRD) Services Scientific Merit Review Board, Department of Veterans Affairs (VA)

Ad Hoc Reviewer for NIH Study Sections:

May 2023:	VA Endocrinology ENDA panel
Spring 2023:	Arthritis, Connective Tissue and Skin (ACTS) Study Section
Spring 2023:	NCI SPORE NCI SPORE (P50) Special Emphasis Panel
Winter 2022:	VA Endocrinology ENDA panel
Jun 2022:	National Institute of Diabetes and Digestive and Kidney Diseases Special Emphasis Panel
Spring 2022:	VA Endocrinology ENDA panel
Spring 2022:	NIDDK Special Emphasis Panel
Spring 2022:	NCI SPORE NCI SPORE (P50) Special Emphasis Panel
Fall 2021:	Arthritis, Connective Tissue and Skin (ACTS) Study Section
Spring 2021:	VA Endocrinology ENDA panel (ad hoc member)
Nov 2020:	NICHD IDDRC Special Emphasis Panel
Nov 2019:	NIEHS Special Emphasis Panel for RIVER R35 Applications
	Oct 2016: Behavioral Genetics and Epidemiology (BGES) Study Section
Jul 2016:	(co-chair) ZRG1 GGG-L (50) Study Section: Novel Genomic Technology Development
	Feb 2016: Genomics, Computational Biology and Technology (GCAT) Study Section
Jun 2014:	NHLBI Special Emphasis Panel ZHL1 CSR-X (O1)

Feb 2014: NHLBI Special Emphasis Panel ZHL1 CSR-X (M1)
Oct 2013: Biodata Management and Analysis (BDMA) Study Section
Feb 2012: Genomics, Computational Biology and Technology (GCAT) Study Section

Other Grant Reviews:
Fall 2023: TOPMed Fellowship Review
Spring 2023: Research Council KU Leuven
November 2022: Medical Research Council, UK
May 2022: Medical Research Council, UK
Jul 2020: Medical Research Council, UK
Feb 2019: Genome Alberta, Canada
Oct 2017: Medical Research Council, UK
Dec 2016: Biomedical Research Fellowship Programme for India
May 2016: Research Grant Counsel, Hong Kong
Mar 2015: Research Grant Counsel, Hong Kong
Jun 2013: ERC (European Research Council) Consolidator Grant Proposals
Jan 2013: Barts and the London Charity Grant Proposals
Apr 2012: Wellcome Trust and Royal Society Sir Henry Dale Fellowship

Editorial Board, Journals:
PLoS Genetics (Associate Editor)
PLoS ONE (Associate Editor)
Genetics (Associate Editor)
Human Genomics (Software section editor)
Frontiers in Statistical Genetics and Methodology
AIMS Genetics

Ad Hoc Reviewer, Journals:
The American Journal of Human Genetics
The American Journal of Public Health
Annals of Applied Statistics
Annals of Neurology
Bioinformatics
Biostatistics
BMC Bioinformatics
BMC Genetics
BMC Genomics
Briefings in Bioinformatics
Cell
Cell Reports
Communications Biology
Epigenetics
European Journal of Human Genetics
Frontiers in Statistical Genetics and Methodology
Frontiers of Medicine
Genetic Epidemiology

Genetics
Genome Biology
Genome Research
Human Heredity
Human Molecular Genetics
International Journal of Biostatistics
JAMA
Journal of American Statistical Association
Journal of Bioinformatics and Computational Biology
Journal of Investigative Dermatology
Nature Communications
Nature Biotechnology
Nature Genetics
Nature Machine Intelligence
Nature Methods
Nature Protocols
Nucleic Acids Research
Pacific Symposium on Biocomputing (*PSB*)
PLoS Computational Biology
PLoS Genetics
PLoS Medicine
PLoS ONE
Proceedings of the National Academy of Sciences of the United States of America
Science Advances
Scientific Reports
Statistical Applications in Genetics and Molecular Biology
Theoretical Population Biology

Others:
Organizing committee, co-chair, 2023 PQG Conference, Boston, MA
Session Organizer, Chair, ICSA 2021, virtual
Session Moderator, the American Society of Human Genetics Annual Meeting, 2017-present
Session Chair, Joint Statistical Meeting Invited Session, Baltimore, MD 2017
Session Chair, Joint Statistical Meeting Invited Session, Chicago, IL 2016
Co-Organizer, Research Triangle Park Statistical Genetics Conference, 2011, 2012, 2013, 2014, 2015, 2016
Session Chair, Joint Statistical Meeting Invited Session, Miami Beach, FL 2011
Member, WIDTH Symposium Planning Committee, Ann Arbor, MI 2008

Services within UNC-Chapel Hill:

2024-	Member, UNC-CH SOM Full Professor APT Committee
2024-	Member, Biostatistics Kuebler Award Committee
2022-2024	Member, tenure-track assistant professor faculty search committee, joint between Biostatistics and Genetics
2022-2023	Chair, tenure-track associate professor faculty search committee, Biostatistics
2022	Creativity Hubs Review

2022 UNC SURF Review
2021 Gillings Study Section
2021 Center of Research Translation Specific Aims (CORT) Review
2018- Biostatistics Graduate Student Recruitment Committee
2013- BBSP Recruitment Committee
2013- Research Computing Advisory Committee
2017-2019 Genetics Department Advisory Committee
2016-2018 Data Science Initiative Committee
2014,2015,2016 Search Committee for Statistical Genetics Faculty Position
2012-2015 Course Organizing Committee: Statistical Software Development
2010-2016 Department of Biostatistics Computing committee
2010-2015 Bioinformatics and Computational Biology Curriculum advisory committee
2014 Search Committee for Computational Genomics Position
2014 Biostatistics Qualifying Exam Committee
2013-2014 Quantitative Sub Committee, Recruitment Committee for Biological and Biomedical Sciences Program (BBSP)
2013-2014 School of Public Health Awards Committee
2013-2014 Doctoral Examinations Committee, Department of Biostatistics
2013-2014 Award Committee, Department of Biostatistics
2013-2014 HHMI International Student Research Fellowship UNC Internal Review Committee
2013 Search Committee for Sequencing Informatics Position
2011-2012 Biostatistics Information Technology Committee, Department of Biostatistics
Spring 2011 BCB Statistics Course Committee,

Memberships in Professional Societies:

International Chinese Statistical Association, 2007-present
American Society of Human Genetics, 2005-present
American Statistical Association, 2002-present
American Association for the Advancement of Science, 2007-2008
American Society for Quality, 2003-2005

RESEARCH STATEMENT

My research interest is in statistical genetics, particularly for the dissection of genetic mechanisms underlying complex human traits. Specifically, my group focuses on the development, implementation, and application of statistical methods and computational tools for an integrative understanding of genetic mechanisms underlying complex human diseases and traits. My research has the approximate 50%-50% split between method development and real data applications.

Methodologically, research in my group has focused on three major areas: (1) the development of integrative genomic methods to more powerfully map genes for complex diseases and traits, and to generate mechanistic hypotheses underlying these traits, in both genetically homogeneous populations as well as recently admixed populations including African Americans and individuals of Hispanic/Latino ancestry. Efforts along this line have resulted in 16 publications[1-16]; (2) proposing rigorous methods and tools for the analysis and visualization of genome-wide chromatin interactome data, resulting in another 16 publications on which I am the last author[17-32], and contributing to an additional of four methods and tools[33-36]; and (3) developing efficient methods for single cell RNA sequencing (scRNA-seq) and spatial transcriptomics data, on which topic my team has published 11 papers[37-47]. Most of the work, albeit recent, has received attention from the community, partly manifested by the citations. For example, SAME-clustering[39] has been cited 48 times since 2020, imputation aided association of blood cell traits[48] 181 times since 2019, SAFE-clustering[37] 92 times since 2018, HUGIn[20] 70 times since 2017, HMRF[18] 51 times since 2016, and MaCH-Admix[2] 156 times since 2012. Below, I will expand on two specific examples from our work mentioned above.

The first example is a recent effort to map genes underlying hematological traits[48]. In this study, we adopted a powerful imputation strategy, which my team has established long-term expertise on, with my original method[49] cited over 2,200 times and the method specifically extended to accommodate admixed populations[2] cited over 150 times. Specifically, for ~21,600 individuals of African ancestry and ~21,700 individuals of Hispanic/Latino ancestry, we started with genotype information measured, by commercially available DNA arrays, at ~1 million genetic markers. With our imputation strategy and latest resources obtained from the NHLBI funded Trans-Omics of Precision Medicine (TOPMed) Program, we were able to directly evaluate genetic association with hematological traits at up to 30-60 million variants, substantially improving genome coverage. The strategy offers a cost-effective way to study the minority populations in the United States without having to rely on still expensive whole genome sequencing approach. Using this approach, we were able to identity associations with two rare variants (with the minor form appearing at the frequency of 0.03% or 1.14% respectively) in the hemoglobin beta gene associated with total white blood cell counts, or hematocrit and hemoglobin levels. These variants have not been detected from studies of primary European ancestry (despite the large sample sizes of over half million individuals in those studies) and would not have been identified without our imputation strategy. Such an approach will be readily adopted by many other researchers studying the genetics of almost any complex traits. The second example is our SAFE-clustering method for single cell RNA-seq clustering[37]. Single cell profiling of the transcriptome has been transforming the field in

many aspects. For most of the purposes, one almost indispensable component is to identify the number and nature of cell types in the data. Despite quite a few methods developed for clustering single cell RNA-seq data, there is surprisingly low concordance among them. As a matter of fact, using standard concordance metrics that range from 0 to 1 (with 1 indicating complete concordance and 0 complete discordance), most of the popular methods result in an average concordance of 0.2-0.4 in 12-14 real datasets we evaluated! This motivated the development of our ensemble method, SAFE-clustering, which has been shown to be among the best performing method from an independent research group[50].

In terms of applications, my team has been focusing on collaborative efforts to study hematological traits, neuropsychiatric disorders and traits, as well as cardio-metabolic traits. For all these traits, the genetic basis has been well established with many being highly heritable. Recent genetic association studies have identified tens to tens of thousands of genetic variants reproducibly associated with these traits. However, the underlying mechanisms remain elusive. My group has been making serious efforts to address several major challenges in terms of biological interpretation of results from genomic studies, prioritization and functional validation of top candidates, as well as clinical translation of genetic association findings. Our efforts have lead to >100 publications since 2015, many in high profile journals, including **three in *Nature*** (where I contributed variant and genotype calling to the 1000 Genomes Project[51], supervised analysis of cell-type-specific 3D epigenomic profiles in the developing human cortex[52], and actively participated in the TOPMed project[53]), **four in *Science*** (where I contributed data and analysis to the PsychENCODE consortium for integrative functional dissection of human brain development and neuropsychiatric disorders[54], co-supervised heart and brain imaging genetics projects[55,56], and examined the implications for building polygenic scores using base-pair mammalian constraint in the zoonomia project[57]), **two in *Cell*** where I participated in the blood cell consortium[58,59], and **five in *Nature Genetics*** on genetics of metrics derived from brain imaging data[60,61], neural cell type specific epigenetic profiling[62], and genetic association of major depressive disorders[63] and type 2 diabetes[64] respectively, just to name a few.

The above research has received multiple NIH awards. These include five grants I have served as the sole principal investigator (PI), contact PI, or MPI: (1) completed R01HG006703 (sole PI) on “Imputation and Analysis of Rare Variants in Admixed Populations”, and (2) completed R01HG006292 (sole-PI) on “Design and Analysis of Sequencing-based Studies for Complex Human Traits”, (3) completed R01HL129132 (contact PI) on “Genetic Studies of Blood Cell Traits in Multi-Ethnic Cohorts”, (4) ongoing U01HG011720 (contact PI) on “Polygenic risk scores and health disparities: the role of blood cells immune response and evolutionary adaptation”, (5) ongoing R01HL163972 (MPI) on “Genetics of Cardiovascular Disease in Chronic Kidney Disease”, and (6) ongoing R01 AG079291 (contact PI) on “Study of Selective Cell and System Vulnerability in Alzheimer's Disease”. Moreover, for at least three projects where I am the co-investigator, I have been playing leadership roles: serving as the Director of Data Science Core in the Intellectual and Developmental Disabilities Research Center (IDDRC); serving as the Group Leader of the System Biology Group for the HEAL Initiative: Back Pain Consortium (BACPAC) Research Program Data Integration, Algorithm Development and Operations Management Center; and serving as the co-chair for the Predictive Modeling Working Group within the 4D Nucleome (4DN) Program, each of which is

a multi-million project. In addition, I have actively participated, if not helped conceived, many other funded projects pertinent to either my methodological or application research.

Finally, I am putting in multiple R01 grant proposals on (1) Genetics of mammalian chromatin interactome where we aim to generate and analyze populations of mammalian (in collaborative cross mice, and in human lymphoblastoid cell lines) interactome, transcriptome and epigenome, to study genetics of a full spectrum of chromatin interactomic phenotypes, and to elucidate and validate contributions of iQTLs to target gene expression; (2) Model-based methods, analysis and applications of chromatin interactome data where we propose to develop model-based statistical methods to map chromatin interactions at kilobase resolution, to identify cell-type-shared and cell-type-specific chromatin interactions in diverse cell types, and to study temporal dynamics of chromatin interactions across different stages of cellular differentiation and/or disease development; and (3) Uncovering genetic mechanisms underlying Alzheimer's disease where we will first aquire and harmonize various in-house, protected and public data, encompassing bulk and single cell RNA-seq data, GWAS summary statistics, array genotyping and whole genome sequencing data, as well as myriads of functional genomic data, then analyze them using a suite of computational methods and bioinformatics tools to generate cell-type-specific mechanistic hypotheses, and finally validate top findings in iPSC-derived neural cells (particularly excitatory neurons and microglia), as well as in iPSC-derived forebrain organoids involving diverse cell types.

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TEACHING STATEMENT

I love teaching, which is one major reason behind my decision to pursue an academic career. Teaching is not just a flow of knowledge from a teacher to students. Rather, it involves two-way learning, communication and interactions. A teacher is supposed to deliver knowledge to students, to encourage students to become motivated and learn independently, and to learn from students. In the following, I first describe my teaching experiences and then present my teaching philosophy.

(1) Teaching Experiences at UNC

After joining UNC, I have given guest lectures in several graduate level courses including BIOS 740 (Statistical Methods for Genetic Association Studies), BIOS735 (Statistical Computing and Software Development), EPID743 (Genetic Epidemiology), EPI889 (Advanced Genetic Epidemiology – High Throughput Data Analysis), and BCB710 (Bioinformatics Colloquium). It has been essential to design the lectures to cater the needs of students in each class. For example, for the epidemiology students, I try to teach the key concepts into context and focus more on interpretation; for the Biostatistics students, I give the mathematical and modeling details so that they can use similar models in other research problems; for the BCB students, I teach about implementation of the methods using different algorithms.

Besides guest lectures, I am the course director for several courses after joining UNC. First, I offered a new course together with Dr. Ethan Lange: BCB725, Introduction to Statistical Genetics, which was well attended with 9-17 students registered when we taught it. Second, after tenure in 2015 and after Dr. Lange moved out of UNC, I develop a new module with Dr. Fei Zou: BCB723, Topics in Statistical Genetics and Genomics. The course has attracted a diverse audience when first taught in Spring 2018 when we had 9 students and 1 auditor, and since then ~10 students every year. We have designed the course to cater the needs of the diverse audience. In particular, (1) we have one lecture covering basic genetics and basic statistics related to the course at the beginning; (2) we provide knowledge that is beneficial only to some audiences (for example, mathematical derivations for Biostatistics students; source codes for BCB students) through the class website but do not attempt to cover in the lectures; (3) we have made some homework problems optional extra credits problems so that motivated students from relevant background are encouraged to tackle more challenging problems; and (4) give students flexible options for their final project. Third, I have been co-directing a full 3-credit course BIOS782 (Statistical Methods in Genetic Studies) with Dr. Danyu Lin where we mainly teach advanced doctoral students in Biostatistics, Statistics, Bioinformatics and Computational Biology, as well as Computer Science students statistical methods underlying commonly used genetic tools, allowing them to master the methods behind as well as encouraging them to develop new or modify existing methods for their purposes. Last but not the least, I have co-directed EPID889 with Dr. Kari North on “Advanced Genetic Epidemiology – High Throughput Data Analysis” where we teach hands-on skills to analyze high throughput big and complex genetic data to students in Genetic Epidemiology, many of whom had no or limited exposure to high throughput computing when entering the class.

All courses have been quite well received even with other potential competing courses such as BCB720, BIOS740, BIOS735, BIOS781, BIOS784, BIOS785, EPID743 that have certain degree of overlap at least when judged solely based on topics covered.

In addition to the regular teaching, I was also invited to teach in short courses, including the Statistical Genetics Short Course at Chapel Hill, North Carolina, in the summer of 2010; the 7th Course “SNP’s and Human Diseases”, Erasmus MC, Rotterdam, in the Netherlands, 2010; the short course on the Analyses of Next Generation Sequencing Studies, in Boston, 2012; the 2nd Annual Short Course on Next Generation Sequencing: Technology and Statistical Methods, UAB in Birmingham, Alabama; 2013 Short Course on Genetic Epidemiology, Nanjing Medical University, Nanjing, China; 2014 Joint Statistical Meeting (JSM) Professional Development Continuing Education Course on Analysis of Genome-Wide Sequencing Association Studies; and the 2019 BIRS Workshop on "Frontiers in Single-cell Technology, Applications and Data Analysis".

(2) Teaching Philosophy

I view learning as the responsibility of the student as well as the instructor. As an instructor, I would like to focus primarily on the responsibility on my side. The teacher serves a guide in students’ pursuit of knowledge. The teacher has already traveled the intellectual ground that the students are covering. Because of this, he or she knows many of the pitfalls and dangers that exist. The teacher is also aware of many of the interesting and wonderful aspects that can be seen along the way. It is the responsibility of the teacher to point out as many of these as possible to the students.

When necessary, the teacher is also responsible for encouraging students to continue this quest beyond the course he or she is teaching. The teacher must be equipped with a myriad of techniques to accomplish this goal. The teacher must be willing to use both rewards and punishments to help the students continue. A teacher can encourage and inspire, but not force knowledge upon a student. A teacher should try his or her best to make the class instructive as well as full of fun. For the above reasons, I always try my best (1) to give a lecture focused on intuitions and concepts, rather than the technical details; (2) to clearly explain and deeply explore less/selected material rather than skimming over everything; and (3) to know my students well through in-class and out-of-class interactions so that I can work out different study plans for different students.

Finally, a teacher must be willing to learn more. Just because the teacher has traveled this intellectual ground before does not mean that he or she knows everything about it. The teacher must be willing to learn and adapt. The teacher should not only keep broadening his/her knowledge, but also keep sharpening his/her teaching techniques from students and peer evaluations.

In conclusion, a teacher is a guide who can aid and encourage students in their quest for knowledge. Teachers cannot force them to continue this quest, but can and should take great efforts to encourage them. Teachers must also be willing to learn from what his or her students are willing to teach them.