Weichen Zhou, Ph.D.

Research Investigator

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Education and Employment

10/2020 - present	Research Investigator,
08/2021 - present	and LEO Lecturer,
	Department of Computational Medicine and Bioinformatics,
	University of Michigan Medical School, Ann Arbor, MI, USA.
11/2015 - 09/2020	Research Fellow,
	Ryan E. Mills Lab, Department of Computational Medicine and Bioinformatics,
	University of Michigan Medical School, Ann Arbor, MI, USA.
07/2014 - 10/2015	Research Associate,
	Jin Lab, Ministry of Education Key Laboratory of Contemporary Anthropology,
	Fudan University, Shanghai, PRC.
09/2009 - 06/2014	Ph.D., Genetics,
	supervisor: Prof. Li (Felix) Jin, Fudan University, Shanghai, PRC
	Thesis: Mutation, function, and evolution of structural variations in human genome.
09/2005 - 07/2009	B.S.E., Bioinformatics,
	Huazhong University of Science and Technology, Wuhan, Hubei, PRC.

Services and Teaching

Editorial Board

2020 - present	*Frontiers in Genetics*
2020 - present	*Frontiers in Bioengineering and Biotechnology*

Teaching Activity

08/2021 - present	Lecturer.
	BIOINF527. Computational Medicine and Bioinformatics, University of Michigan.
09/2021 - 05/2022	Mentor,
	Visiting student (Yanming Gan). Mills Lab, University of Michigan.
07/2019 - 08/2019	Mentor,
	Visiting students (Thomas Chang, Steven Kim). Mills Lab, University of Michigan.
09/2012 - 01/2013	Teaching Assistant.
	Human Evolution. School of Life Science, Fudan University.
02/2011 - 06/2013	Teaching Assistant.
	Human Evolutionary Genetics. School of Life Science, Fudan University.
09/2010 - 01/2011	Teaching Assistant.

Journal club of Human Evolution. School of Life Science, Fudan University.

Service

10/2021	Mentor, Career Paths in Genetics Networking Session: Perfect Your Elevator Speech, Professional Development and Industry Technology Forum, the American Society of Human Genetics.
10/2021	Volunteer, ASHG Connect and Shared Interest Groups, the American Society of Human Genetics.
03/2018	Judger, Forsythe Science Expo, Ann Arbor, MI.

Peer-Reviews (Ad Hoc)

American Journal of Human Genetics
Nature Communication
Bioinformatics
GigaScience
PLOS One
Molecular Biology Report
Computational Biology and Chemistry
Cell Genomics
Frontiers in Genetics

Other Experience and Professional Memberships

2015 - present	American Society of Human Genetics
2018 - present	Association of Chinese Geneticists in America

Honors and Awards

2019	Charles J. Epstein Trainee Awards for Excellence in Human Genetics Research, Semifinalist, the 69th Annual Meeting of the American Society of Human Genetics.
2019	OGPS Postdoctoral Travel Award, University of Michigan Medical School.
2016	Outstanding Dissertation of Ph.D. (2015), Shanghai Municipal Education Commission.
2014	Shanghai Outstanding Graduates, Shanghai Municipal Education Commission.
2013 - 2014	The 4th Research Funding of National Key Disciplines, Grantee, Ministry of Education of People's Republic of China
2013	National Scholarship for Graduate Students, Ministry of Education of People's Republic of China
2013	Outstanding Graduate Students, Fudan University.
2010 - 2012	Academic Scholarships, Fudan University.

Grants

Current Grants

3R21HG011493-02S1 Mills, Boyle (PI) $ 230,098 06/2022-11/2022

New technologies for accurate capture and sequencing of repeat-associated regions

Role: Co-Investigator

MADC developmental project Zhou, Weichen (PI) $ 50,000 07/2022-06/2024

Explore the functional impact of transposable elements in Alzheimer's disease and related dementias

Role: Principal Investigator

2U24HG007497-05 Lee (PI) $2,867,579 08/2019-05/2023

Identifying and Characterizing the Full Spectrum of Haplotype-resolved Structural Variation in Human Genomes

Role: Key Personnel with Effort

1R21HG011493-01 Mills, Boyle (PI) $390,349 12/2020-11/2022

New technologies for accurate capture and sequencing of repeat associated regions

Role: Key Personnel with Effort

Submitted Grants

22-PAF02223 Zhou (PI) $ 416,696 09/2022-08/2024

A multi-omics framework for detection and functional analysis of germline and somatic transposable elements in human tissues

Role: Principal Investigator (Turned Down)

Past Grants

NIH-DHHS-US- 14-PAF07285 Moran (PI) $4,998,681 04/2015-03/2020

2/3 Schizophrenia Genetics and Brain Somatic Mosaicism

Role: Key Personnel with Effort

5R01HG007068-04 Mills (PI) $1,526,575 09/2013-07/2017

Discovery and analysis of structural variation in whole genome sequences

Role: Key Personnel with Effort

Presentations & Abstracts

Speaker

1. Zhou W, PALMER: Identification and characterization of occult mobile element insertions using long-read sequencing technology. *DCMB Tools and Technology Seminar Series*, University of Michigan, 2020.
2. Zhou W, Mills RE. Refining polymorphic retrotransposon insertions in human genomes. *The American Society of Human Genetics*, 2019.
3. Zhou W, Jin L. Whole genome functional traits and evolutionary clues between Copy Number Variations and Segmental Duplications in human genome. *The Annual Meeting of Shanghai Genetics Society*, 2013.

Abstract

1. Zhou W, McDonald TL, Boyle AP, Mills RE. Cas9 targeted enrichment of mobile elements using nanopore sequencing. *The American Society of Human Genetics*, 2021.
2. Zhou W, McDonald TL, Boyle AP, Mills RE. Refining polymorphic retrotransposon insertions in human genomes. *The Biology of Genomes*, 2020.
3. Zhou W, Emery SB, Flasch DA, Wang Y, Kwan KY, Moran JV, Kidd JM, Mills RE. Refining the ability to detect human-specific LINE-1 insertions using long-read sequencing technology. *The American Society of Human Genetics*, 2018.
4. Zhou W, Chapman MR, Yeh G. Stress-induced Alzheimer's disease. *The 16th Annual Pathology Research Symposium*, 2017.
5. Zhou W, Emery SB, Flasch DA, Wang Y, Kwan KY, Moran JV, Kidd JM, Mills RE. PALMER: A novel pre-masking method for detecting mobile element insertions using long-read sequencing technology. *The American Society of Human Genetics*, 2017. Reviewers' Choice Abstract.
6. Zhou W. Predictive model for inflammation grades of chronic hepatitis B: large-scaled analysis on clinical parameters and gene expressions. *The 26th Conference of The Asian Pacific Association for The Study Of*

The Liver (APASL), 2017.

7. Zhou W, Jin L, Zhang F. Increased genome instability in human DNA segments with closely spaced repeats. *The Annual Meeting of Shanghai Genetics Society*, 2012. 1st Poster Award.
8. Zhou W, Zhang F, Jin L. Increased genome instability in human DNA segments with short low-copy repeats. *The 13th International Meeting on Human Genome Variation and Complex Genome Analysis*, 2012.

Peer-Reviewed Publications

1. Porubsky D, Höps W, Ashraf H, Hsieh PH, Rodriguez-Martin B, Yilmaz F, Ebler J, Hallast P, Maggiolini FAM, Harvey WT, Henning B, Audano PA, Gordon DS, Ebert P, Hasenfeld P, Benito E, Zhu Q, Lee C, Antonacci F, Steinrücken M, Beck CR, Sanders AD, Marschall T, Eichler EE, Korbel JO, Human Genome Structural Variation Consortium: Recurrent inversion polymorphisms in humans associate with genetic instability and genomic disorders. ***Cell***. doi: https://doi.org/10.1016/j.cell.2022.04.017.
2. Breuss MW, Yang X, Schlachetzki J, Antaki D, Lana AJ, Xu X, Chung C, Chai G, Stanley V, Song Q, Newmeyer TF, Nguyen A, O'Brien S, Hoeksema MA, Cao B, Nott A, McEvoy-Venneri J, Pasillas MP, Barton ST, Copeland BR, Nahas S, Kraan LV, Ding Y, NIMH Brain Somatic Mosaicism Network, Glass CK, Gleeson JG: Somatic mosaicism reveals clonal distributions of neocortical development. ***Nature***. doi: https://doi.org/10.1038/s41586-022-04602-7.
3. Bao Y, Wadden J, Erb-Downward JR, Ranjan P, **Zhou W**, McDonald TL, Mills RE, Boyle AP, Dickson RP, Blaauw D, Welch JD: SquiggleNet: real-time, direct classification of nanopore signals. ***Genome Biology***. 2021. https://doi.org/10.1186/s13059-021-02511-y.
4. MacDonald TL*, **Zhou W***, Castro CP, Mumm C, Switzenberg JA, Mills RE, Boyle AP: Cas9 targeted enrichment of mobile elements using nanopore sequencing. ***Nature Communication***. 2021. doi.org/10.1038/s41467-021-23918-y. (*****Co-first authors)
5. Ebert P, Audano PA , Zhu Q, Rodriguez-Martin B, Porubsky D, Bonder MJ, Sulovari A, Ebler J, **Zhou W**, Mari RS, Yilmaz F, Zhao X, Hsieh P, Lee J, Kumar S, Lin J, Rausch T, Chen Y, Ren J, Santamarina M, Höps W, Hufsah Ashraf H, Chuang NT, Yang X, Munson KM, Lewis AP, Fairley S, Tallon LJ, Clarke WE, Basile AO, Byrska-Bishop M,Corvelo A, Chaisson MJP, Chen J,Li C, Brand H, Wenger AM, Ghareghani M, Harvey WT, Raeder B, Hasenfeld P, Regier A, Abel H, Hall I, Flicek P, Stegle O, Gerstein MB, Tubio JMC, Mu Z, Li YI, Shi X, Hastie AR, Ye K, Chong Z, Sanders AD, Zody MC, Talkoski ME, Mills RE, Devine SE, Lee C, Korbel JO, Marschall T, Eichler EE, Human Genome Structural Variation Consortium: Haplotype-resolved diverse human genomes and integrated analysis of structural variation. ***Science***. 2021. 10.1126/science.abf7117.
6. Zhao X, Collins RL, Lee WP, Weber AM, Jun Y, Zhu Q, Weisburd B, Huang Y, Audano PA, Wang H, Walker M, Lowther C, Fu J, Human Genome Structural Variation Consortium, Gerstein MB, Devine SE, Marschall T, Korbel JO, Eichler EE, Chaisson MJP, Lee C, Mills RE, Brand H, Talkowski ME: Expectations and blind spots for structural variation detection from long-read assemblies and short-read genome sequencing technologies. ***Am J Hum Genet***. 2021 May 6;108(5):919-928. doi: 10.1016/j.ajhg.2021.03.014.
7. Wang Y, Bae T, Thorpe J, Sherman M, Jones A, Cho S, Daily K, Dou Y, Ganz J, Galor A, Lobon I, Pattni R, Rosenbluh C, Tomasi S, Zhou B, Ball L, Emery SB, Fasching L, Juan D, Lizano E, Narurkar R, Oetjens MT, Shin JH, Soriano E, **Zhou W**, Chess A, Gleeson J, Marques T, Moran JV, Park PJ, Peters M, Pevsner J, Walsh CA, Weinberger D, Brain Somatic Mosaicism Network, Vaccarino F, Urban AE, Kidd JM, Mills RE, Alexej A: Comprehensive identification of somatic point mutations in brain tissue. ***Genome Biology***. 2021. doi.org/10.1186/s13059-021-02285-3.
8. Oleksyk TK, Wolfsberger WW, Weber AM, Shchubelka K, Oleksyk OT, Levchuk O, Patrus A, Lazar N, Castro-Marquez SO, Hasynets Y, Boldyzhar P, Neymet M, Urbanovych A, Stakhovska V, Malyar K, Chervyakova S, Podoroha O, Kovalchuk N, Rodriguez-Flores JL, **Zhou W**, Medley S, Battistuzzi F, Liu R, Hou Y, Chen S, Yang H, Yeager M, Dean M, Mills RE, Smolanka V: Genome diversity in Ukraine. ***GigaScience***. 2021. doi.org/10.1093/gigascience/giaa159.
9. Lin J, Yang X, Kosters W, Xu T, Jia Y, Wang S, Zhu Q, Ryan M, Guo L, Zhang C, Lee C, Devine SE, Eichler

EE, Ye K, Human Genome Structural Variation Consortium: Mako: a graph-based pattern growth approach to detect complex structural variants. ***Genomics, Proteomics & Bioinformatics***. 2021. doi.org/10.1016/j.gpb.2021.03.007.

10. Rodin RE, Dou Y, Kwon M, Sherman MA, D'Gama AM, Doan RN, Rento LM, Girskis KM, Bohrson CL, Kim SN, Nadig A, Luquette LJ, Gulhan DC, Brain Somatic Mosaicism Network, Park PJ, Walsh CA: The landscape of somatic mutation in cerebral cortex of autistic and neurotypical individuals revealed by ultra-deep whole-genome sequencing. ***Nature Neuroscience***. 2021. doi.org/10.1038/s41593-020-00765-6.
11. Zhu X, Zhou B, Pattni R, Gleason K, Tan C, Kalinowski A, Sloan S, Fiston-Lavier A, Mariani J, Petrov D, Barres BA, Duncan L, Abyzov A, Vogel H, Brain Somatic Mosaicism Network, Moran JV, Vaccarino FM, Tamminga CA, Levinson DF, Urban AE: Machine learning reveals bilateral distribution of somatic L1 insertions in human neurons and glia. ***Nature Neuroscience***. 2021. doi.org/10.1038/s41593-020-00767-4.
12. Dayama G, **Zhou W**, Prado-Martinez J, Marques-Bonet T, Mills RE: Characterization of nuclear mitochondrial insertions in the whole genomes of primates. ***NAR Genomics and Bioinformatics***. 2020. http://doi.org/10.1093/nargab/lqaa089.
13. Zook JM, Hansen NF, Olson ND, Chapman LM, Mullikin JC, Xiao C, Sherry S, Koren S, Phillippy AM, Boutros PC, Sahraeian SME, Huang V, Rouette A, Alexander N, Mason CC, Hajirasouliha IC, Ricketts CC, Lee J, Tearle R, Fiddes IT, Barrio AM, Wala J, Carroll A, Ghaffari N, Rodriguez OL, Bashir A, Jackman S, Farrell JJ, Wenger AM, Alkan C, Soylev A, Schatz MC, Garg S, Church G, Marschall T, Chen K, Fan X, English AC, Rosenfeld JD, **Zhou W**, Mills RE, Sage JM, Davis JR, Kaiser MD, Oliver JS, Catalano AP, Spies N, Chaisson MJP, Sedlazeck FJ, Salit M, and Genome in a Bottle Consortium: A robust benchmark for detection of germline large deletions and insertions. ***Nature Biotechnology***. 2020. doi.org/10.1038/s41587-020-0538-8.
14. **Zhou W**, Emery SB, Flasch DA, Wang Y, Kwan KY, Kidd JM, Moran JV, and Mills RE: Identification and characterization of occult human-specific LINE-1 insertions using long-read sequencing technology. ***Nucleic Acid Research***. 2020. doi.org/10.1093/nar/gkz1173.
15. Li Y, Liu X, Ma Y, Wang Y, **Zhou W**, Hao M, Yuan Z, Liu J, Xiong M, Shugart YY, Wang J, Jin L: knnAUC: an open-source R package for detecting nonlinear dependence between one continuous variable and one binary variable. ***BMC Bioinformatics***. 2018. doi.org/10.1186/s12859-018-2427-4.
16. **Zhou W**, Wang Y, Fujino M, Shi L, Jin L, Li X, Wang J: A standardized fold change (SFC) method for microarray differential expression analysis used to reveal genes involved in acute rejection in murine allograft models. ***FEBS Open Bio***. 2018. doi: 10.1002/2211-5463.12343.
17. McConnell MJ, Moran JV, Abyzov A, Akbarian S, Bae T, Cortes-Ciriano I, Erwin JA, Fasching L, Flasch DA, Freed D, Ganz J Jaffe AE, Kwan KY, Kwon M, Lodato MA, Mills RE, Paquola ACM, Rodin RE, Rosenbluh C, Sestan N, Sherman MA, Shin JH, Song S, Straub RE, Thorpe J, Weinberger DR, Urban AE, Zhou B, Gage FH, Lehner T, Senthil G, Walsh CA, Chess A, Courchesne E, Gleeson JG, Kidd JM, Park PJ, Pevsner J, Vaccarino FM, and Brain Somatic Mosaicism Network: Intersection of diverse neuronal genomes and neuropsychiatric disease: The Brain Somatic Mosaicism Network. ***Science***. 2017. doi: 10.1126/science.aal1641.
18. **Zhou W**, Ma Y, Zhang J, Hu J, Zhang M, Wang Y, Li Y, Wu L, Pan Y, Zhang Y, Zhang X, Zhang X, Zhang Z, Zhang J, Li H, Lu L, Jin L, Wang J, Yuan Z, Liu J: Predictive model for inflammation grades of chronic hepatitis B: Large-scale analysis of clinical parameters and gene expressions. ***Liver International***. 2017. doi: 10.1111/liv.13427.
19. Zhang L, Wang J, Zhang C, Li D, Carvalho C, Ji H, Xiao J, Wu Y, **Zhou W**, Wang H, Jin L, Luo Y, Wu X, Lupski JR, Zhang F, Jiang Y: Efficient CNV breakpoint analysis reveals unexpected structural complexity and correlation of dosage-sensitive genes with clinical severity in genomic disorders. ***Human Molecular Genetics***. 2017. doi: 10.1093/hmg/ddx102.
20. Chen L*, **Zhou W***, Zhang C, Lupski JR, Jin L, Zhang F: CNV instability associated with DNA replication dynamics: evidence for replicative mechanisms in CNV mutagenesis. ***Human Molecular Genetics***. 2015. doi: 10.1093/hmg/ddu572. (*****Co-first authors)
21. Peng Z, **Zhou W**, Fu W, Du R, Jin L, Zhang F: Correlation between frequency of non-allelic homologous

recombination and homology properties: evidence from homology-mediated CNV mutations in the human genome. ***Human Molecular Genetics***. 2015. doi: 10.1093/hmg/ddu533.

22. Wu N, Ming X, Xiao J, Wu Z, Chen X, Shinawi M, Shen Y, Yu G, Liu J, Xie H, Gucev ZS, Liu S, Yang N, Al-Kateb H, Chen J, Zhang J, Hauser N, Zhang T, Tasic V, Liu P, Su X, Pan X, Liu C, Wang L, Shen J, Shen J, Chen Y, Zhang T, Zhang J, Choy KW, Wang J, Wang Q, Li S, **Zhou W**, Guo J, Wang Y, Zhang C, Zhao H, An Y, Zhao Y, Wang J, Liu Z, Zuo Y, Tian Y, Weng X, Sutton VR, Wang H, Ming Y, Kulkarni S, Zhong TP, Giampietro PF, Dunwoodie SL, Cheung SW, Zhang X, Jin L, Lupski JR, Qiu G, Zhang F: TBX6 Null Variants and a Common Hypomorphic Allele in Congenital Scoliosis. ***New England Journal of Medicine***. 2015. doi: 10.1056/NEJMoa1406829.
23. Chen L, **Zhou W**, Zhang L, Zhang F: Genome architecture and its roles in human copy number variation. ***Genomics & Informatics***. 2014, 12(4):136-144.
24. Chen Y, Guo L, Chen J, Zhao X, **Zhou W**, Zhang C, Wang J, Jin L, Pei D, Zhang F: Genome-wide CNV analysis in mouse induced pluripotent stem cells reveals dosage effect of pluripotent factors on genome integrity. ***BMC Genomics***. 2014. doi:10.1186/1471-2164-15-79.
25. **Zhou W**, Zhang F, Chen X, Shen Y, Lupski JR, Jin L: Increased genome instability in human DNA segments with self-chains: homology-induced structural variations via replicative mechanisms. ***Human Molecular Genetics***. 2013. doi: 10.1093/hmg/ddt113.
26. Lin R, Wang X, **Zhou W**, Fu W, Wang Y, Huang W, Jin L: Association of polymorphisms in the solute carrier organic anion transporter family member 1B1 gene with essential hypertension in the Uyghur Population. ***Annals of human Genetics***. 2011. doi: 10.1111/j.1469-1809.2010.00622.x.
27. Lin R, Fu W, **Zhou W**, Wang Y, Wang X, Huang W, Jin L: Association of heme oxygenase-1 gene polymorphisms with essential hypertension and blood pressure in the Chinese Han population. ***Genetic Testing and Molecular Biomarkers***. 2011. doi: 10.1089/gtmb.2010.0103.
28. Lin R, Wang X, **Zhou W**, Fu W, Wang Y, Huang W, Jin L: Association of a BLVRA common polymorphism with essential hypertension and blood pressure in Kazaks. ***Clinical and Experimental Hypertension***. 2011. doi: 10.3109/10641963.2010.531854.
29. **Zhou W**, Tan J: Dental anthropology suggests southeast Asian origins amongst the Jomon people of Japan. ***Communication on Contemporary Anthropology***. 2010. doi: 10.4236/coca.2010.41012.
30. **Zhou W**, Genetic and environmental factors of pathogeny: a population genetics view. ***Communication on Contemporary Anthropology***. 2010. doi: 10.4236/coca.2010.41021.

Non-Peer-Reviewed Publications

1. Byrska-Bishop M, Evani US, Zhao X, Basile AO, Abel HJ, Regier AA, Corvelo A, Clarke WE, Musunuri R, Nagulapalli K, Fairley S, Runnels A, Winterkorn L, Lowy-Gallego E, Flicek P, Germer S, Brand H, Hall IM, Talkowski ME, Narzisi G, Zody MC, Human Genome Structural Variation Consortium: High coverage whole genome sequencing of the expanded 1000 Genomes Project cohort including 602 trios. *bioRxiv*. doi: doi.org/10.1101/2021.02.06.430068.