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RESEARCH INTEREST	Population genetics, statistical genetics/genomics, disease gene mapping, integrative genomics, next-generation sequencing data analysis, high dimensional data analysis	
PROFESSIONAL APPOINTMENTS	08/2018-Now: <b>Professor</b> , Epidemiology & Biostatistics School of Public Health, Tongji Medical College Huazhong University of Science and Technology, Wuhan, China  01/2015-08/2018: <b>Principal Investigator</b> , Computational & Systems Biology Genome Institute of Singapore, A*STAR, Singapore  05/2016-08/2018: <b>Adjunct Assistant Professor</b> , Centre for Computational Biology Duke-NUS Medical School, Singapore  09/2012-12/2014: <b>Research Fellow</b> , Department of Biostatistics Harvard T.H. Chan School of Public Health, Harvard University, Boston, Massachusetts, USA • Postdoctoral research on statistical genetics with <i>Xihong Lin</i> and <i>Liming Liang</i>	
EDUCATION	08/2012: <b>Ph.D. in Bioinformatics</b> University of Michigan, Ann Arbor, Michigan, USA • Ph.D. advisor: <i>Noah Rosenberg</i> (Stanford University since 07/2011) • Thesis: Statistical methods for analyzing human genetic variation in diverse populations • 01/2012-08/2012: “Post”-doctoral research on statistical genetics with <i>Gonçalo Abecasis</i>  04/2011: <b>M.A. in Statistics</b> and <b>M.S. in Bioinformatics</b> University of Michigan, Ann Arbor, Michigan, USA  07/2008: <b>B.S. in Physics</b> Peking University, Beijing, China	
SELECTED AWARDS	- Charles J. Epstein Trainee Award semifinalist, American Society of Human Genetics, 2013 - Stellar Abstract Award in the 6th Annual PQG Conference, Harvard University, 2012 - HHMI International Student Research Fellowship, Howard Hughes Medical Institute, 2011-2012 - Rackham Predoctoral Fellowship, University of Michigan, 2011-2012 (declined) - DeLill Nasser Award, Genetics Society of America, 2011 - Fellowship (Program in Biomedical Sciences), University of Michigan, 2008-2009 - May Fourth Scholarship, Peking University, 2006	
TEACHING EXPERIENCE	06/2014 & 12/2014: Sequence Analysis Workshop Instructor, University of Michigan Lecture and hands-on practical on Estimates of Genetic Ancestry  10/2013: PQG Short Course Lecturer, Harvard School of Public Health Statistical methods for ancestry inference with applications to disease gene mapping  01/2011-04/2011: Graduate Student Instructor, University of Michigan BIOSTAT 646 - High throughput molecular genomic and epigenomic data analysis	
PUBLICATIONS	# indicates corresponding author; * indicates co-first author.  H Chen, BE Cade, KJ Gleason, AC Bjornes, AM Stilp, ..., <b>C Wang</b> , ..., X Zhu, SR Sunyaev, R Saxena, X Lin, S Redlin. Multi-ethnic meta-analysis identifies RAI1 as a possible obstructive sleep apnea related quantitative trait locus in men. <i>American Journal of Respiratory Cell and</i>	

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J Liu, X Wan, **C Wang**, C Yang, X Zhou, C Yang (2017). LLR: A latent low-rank approach to colocalizing genetic risk variants in multiple GWAS. *Bioinformatics*, **33**: 3878-3886.

J Dou\*, B Sun\*, X Sim, JD Hughes, DF Reilly, ES Tai, J Liu, **C Wang**# (2017). Estimation of kinship coefficient in structured and admixed populations using sparse sequencing data. *PLOS Genetics*, **13**: e1007021.

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Z Wang, BC Henn, **C Wang**, Y Wei, L Su, R Sun, H Chen, PJ Wagner, Q Lu, X Lin, R Wright, D Bellinger, M Kile, M Mazumdar, MM Tellez-Rojo, L Schnaas, DC Christiani (2017). Genome-wide gene by lead exposure interaction analysis identifies UNC5D as a candidate gene for neurodevelopment. *Environmental Health*, **16**: 81.

X Wang, Z Zhang, M Nathan, T Cai, S Lee, **C Wang**, TW Yu, CA Walsh, X Lin (2017). Rare variant association test in family based sequencing studies. *Briefings in Bioinformatics*, **18**: 954-961.

BE Cade, H Chen, AM Stilp, KJ Gleason, T Sofer, ..., **C Wang**, PC Zee, CL Hanis, SR Sunyaev, SR Patel, CC Laurie, X Zhu, R Saxena, X Lin, S Redline (2016). Genetic Associations with Obstructive Sleep Apnea Traits in Hispanic/Latino Americans. *American Journal of Respiratory and Critical Care Medicine*, **194**: 886-897.

H Chen\*, **C Wang**\*, MP Conomos, AM Stilp, Z Li, T Sofer, AA Szpiro, W Chen, JM Brehm, JC Cledon, S Redline, GJ Papanicolaou, TA Thornton, CC Laurie, K Rice, X Lin (2016). Control for population structure and relatedness for binary traits in genetic association studies via logistic mixed models. *American Journal of Human Genetics*, **98**: 653-666.

X Lin, S Lee, M Wu, **C Wang**, H Chen, Z Li, X Lin (2016). Test for rare variants by environment interactions in sequencing association studies. *Biometrics*, **72**: 156-164.

**C Wang**#, X Zhan, L Liang, GR Abecasis, X Lin (2015). Improved ancestry estimation for both genotyping and sequencing data using projection Procrustes analysis and genotype imputation. *American Journal of Human Genetics*, **96**: 926-937.

**C Wang**##, X Zhan\*, J Bragg-Gresham, HM Kang, D Stambolian, E Chew, K Branham, J Heck-enlively, The FUSION Study, RS Fulton, RK Wilson, ER Mardis, X Lin, A Swaroop, S Zöllner, GR Abecasis# (2014). Ancestry estimation and control of population stratification for sequence-based association studies. *Nature Genetics*, **46**: 409-415.

X Zhan\*, DE Larson\*, **C Wang**\*, DC Koboldt, Y Sergeev, 52 other coauthors, ER Mardis, A Swaroop, GR Abecasis (2013). Identification of a rare coding variant in Complement 3 associated with age-related macular degeneration. *Nature Genetics* **45**: 1375-1379.

**C Wang**#, KB Schroeder, NA Rosenberg (2012). A maximum-likelihood method to correct for allelic dropout in microsatellite data with no replicate genotypes. *Genetics* **192**: 651-669.

**C Wang**<sup>#</sup>, S Zöllner, NA Rosenberg (2012). A quantitative comparison of the similarity between genes and geography in worldwide human populations. *PLOS Genetics* **8**: e1002886. [Featured in *Science* 337: 1151, 2012]

TJ Pemberton, **C Wang**, JZ Li, NA Rosenberg (2010). Inference of unexpected genetic relatedness among individuals in HapMap Phase III. *American Journal of Human Genetics* **87**: 457-464. [Featured in *Am J Hum Genet* 87: 447-448, 2010 and *Genetics* 186(2): NP, 2010]

**C Wang**, ZA Szpiech, J Degnan, M Jakobsson, TJ Pemberton, JA Hardy, AB Singleton, NA Rosenberg (2010). Comparing spatial maps of human population-genetic variation using Procrustes analysis. *Statistical Applications in Genetics and Molecular Biology* **9**: 13.

JT Mosher, TJ Pemberton, K Harter, **C Wang**, EO Buzbas, P Dvorak, C Simon, SJ Morrison, NA Rosenberg (2010). Lack of population diversity in commonly used human embryonic stem-cell lines. *New England Journal of Medicine* **362**: 183-185. [Featured in *Nature* 462: 945, 2009]

NM Kopelman, L Stone, **C Wang**, D Gefel, MW Feldman, J Hillel, NA Rosenberg (2009). Genomic microsatellites identify shared Jewish ancestry intermediate between Middle Eastern and European populations. *BMC Genetics* **10**: 80.

L Huang, **C Wang**, NA Rosenberg (2009). The relationship between imputation error and statistical power in genetic association studies in diverse populations. *American Journal of Human Genetics* **85**: 692-698. [Featured in *Am J Hum Genet* 85: 539-540, 2009 & *Nat Rev Genet* 10: 817, 2009]

**CL Wang**, KW Au, CK Chan, HW Lau, KY Szeto (2008). Detecting hierarchical organization in complex networks by nearest neighbor correlation. *Studies in Computational Intelligence* **129**: 487-494 (Conference Proceedings of NICSO 2007).

#### SOFTWARE DEVELOPED

**SEEKIN**: a C++ program for estimating pairwise genetic relatedness in structured and admixed populations using sparse sequencing data. (Dou *et al.* 2017, *PLOS Genet*)  
**LASER**: a package written in C++ for estimating individual ancestry using either sequencing reads or genotyping data. (Wang *et al.* 2014, *Nat Genet*; Wang *et al.* 2015, *Am J Hum Genet*)  
**LASER Server**: a web server based on the LASER method to estimate individual ancestry. (<https://laser.sph.umich.edu>; Taliun *et al.* 2017, *Bioinformatics*)  
**GMMAT**: an R package to perform efficient genome-wide association tests based on generalized linear mixed models. (Chen\*, Wang\* *et al.* 2016, *Am J Hum Genet*)  
**MicroDrop**: a C++ program for estimating and correcting for allelic dropout in microsatellite data without replicated genotyping. (Wang *et al.* 2012, *Genetics*)

#### MEMBERSHIP

American Society of Human Genetics (ASHG)  
 International Genetic Epidemiology Society (IGES)

#### PROFESSIONAL ACTIVITIES

2015-Now: **Member**, Committee for the GIS Research Pipeline Development Team  
 2013-2014: **Member**, Organizing Committee of the HHMI Alumni Network in Boston Region  
 2012-2013: **Organizer**, PQG Short Courses, Harvard School of Public Health  
 2017: **Reviewer** for Student Paper Award Competition, American Statistical Association (ASA) Section on Statistics in Genomics and Genetics  
 2009-Now: **Reviewer** for *Annals of Human Genetics*, *Bioinformatics*, *Biometrics*, *BMC Bioinformatics*, *BMC Genetics*, *Clinical Chemistry*, *Gene*, *Genetics*, *Genome Biology*, *Genome Research*, *Human Biology*, *Human Heredity*, *Journal of Human Genetics*, *Molecular Biology and Evolution*, *Molecular Ecology*, *PLoS ONE*, *Proceedings of the National Academy of Sciences (PNAS)*, *Scientific Reports*