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PERSONAL INFORMATION	Citizenship: People's Republic of China Languages: English, Chinese Mandarin, Cantonese, Hokkien (Min Nan)	
RESEARCH INTEREST	Population genetics, statistical genetics/genomics, disease gene mapping, integrative genomics, next-generation sequencing data analysis, high dimensional data analysis	
PROFESSIONAL APPOINTMENTS	01/2015-Now: Principal Investigator , Computational & Systems Biology Genome Institute of Singapore, A*STAR, Singapore 09/2012-12/2014: Research Fellow , Department of Biostatistics Harvard University, Boston, Massachusetts, USA <ul style="list-style-type: none">• Postdoctoral research on statistical genetics in <i>Dr. Xihong Lin's</i> group	
EDUCATION	08/2012: Ph.D. in Bioinformatics University of Michigan, Ann Arbor, Michigan, USA <ul style="list-style-type: none">• Advisor: <i>Dr. Noah Rosenberg</i>• Thesis: Statistical methods for analyzing human genetic variation in diverse populations 04/2011: M.A. in Statistics and M.S. in Bioinformatics University of Michigan, Ann Arbor, Michigan, USA 07/2008: B.S. in Physics Peking University, Beijing, China	
MEMBERSHIP	2009-Now: American Society of Human Genetics	
HONORS & AWARDS	Selected Awards <ul style="list-style-type: none">• 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• Rackham Predoctoral Fellowship, University of Michigan, 2011 (declined)• DeLill Nasser Award, Genetics Society of America, 2011• Departmental Fellowship (Biomedical Sciences), University of Michigan, 2008• May Fourth Scholarship, Peking University, 2006• Dean's List, Hong Kong University of Science & Technology, 2005	
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	
MANUSCRIPTS SUBMITTED	H Chen*, C Wang* , MP Conomos, AM Stilp, Z Li, T Sofer, AA Szpiro, W Chen, JM Brehm, JC Celedon, SS Redline, GJ Papanicolaou, TA Thornton, CC Laurie, K Rice, X Lin. Control for population structure and relatedness for binary traits in genetic association studies using logistic mixed models. Submitted. (* Co-first author)	

X Lin, S Lee, M Wu, **C Wang**, H Chen, Z Li, X Lin. Test for rare variants by environment interactions in sequencing association studies. In revision.

- PUBLICATIONS** **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*, in press.
- 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). Estimating individual ancestry using next generation sequencing. *Nature Genetics*, 46:409-415. (* Co-first author)
- 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. (* Co-first author)
- 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**, 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 and *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** **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, *AJHG*)
- MicroDrop**: a C++ program for estimating and correcting for allelic dropout in microsatellite data without replicated genotyping. (Wang *et al.* 2012, *Genetics*).
- CONFERENCE PRESENTATIONS** **C Wang**, Han Chen, X Lin. Control of population stratification in family data using pedigree information and ancestry principal components. *The American Society of Human Genetics 64th Annual Meeting*, San Diego, USA, October 2014. (**Poster**)

C Wang, L Liang, GR Abecasis, X Lin. Tracing individual ancestry in a principal components space. *The American Society of Human Genetics 63rd Annual Meeting*, Boston, USA, October 2013. (**Platform talk, Trainee Award Semifinalist**)

C Wang, X Zhan, S Zöllner, GR Abecasis. Estimating individual ancestry using next generation sequencing. *CSHL Meeting “The Biology of Genomes”*, Cold Spring Harbor, New York, USA, May 2013. (**Poster**)

C Wang, X Zhan, S Zöllner, GR Abecasis. Estimating individual ancestry using next generation sequencing. *HHMI Janelia Conference “Biological Sequence Analysis and Probabilistic Models”*, Ashburn, Virginia, USA, March 2013. (**Poster and blitz talk**)

C Wang, X Zhan, S Zöllner, GR Abecasis. Estimating individual ancestry from extremely low-coverage sequencing data. *The 6th Annual PQG Conference “Sequencing and Complex Traits: beyond 1000 Genomes”*, Boston, Massachusetts, USA, November 2012. (**Platform talk, Stellar Abstract Award**)

C Wang, NA Rosenberg. A quantitative comparison of the similarity between genes and geography in worldwide human populations. *The 12th International Congress of Human Genetics & The American Society of Human Genetics 61st Annual Meeting*, Montreal, Canada, October 2011. (**Poster**)

C Wang, KB Schroeder, NA Rosenberg. A maximum likelihood genotype imputation method to correct for allelic dropout in microsatellite data. *ENAR 2011 Spring Meeting*, Miami, Florida, USA, March 2011. (**Platform talk**)

C Wang, KB Schroeder, NA Rosenberg. A genotype imputation method for allelic dropout in microsatellite data. *The American Society of Human Genetics 60th Annual Meeting*, Washington DC, USA, November 2010. (**Poster**)

C Wang, NA Rosenberg. Comparing spatial maps of genetic variation and geographic locations using Procrustes analysis. *EMBO/EMBL Symposium “Human Variation: Cause and Consequence”*, Heidelberg, Germany, June 2010. (**Poster**)

C Wang, ZA Szpiech, J Degnan, M Jakobsson, TJ Pemberton, JA Hardy, AB Singleton, NA Rosenberg. Comparing spatial maps of population-genetic variation using Procrustes analysis. *The American Society of Human Genetics 59th Annual Meeting*, Honolulu, Hawaii, USA, October 2009. (**Poster**)

PROFESSIONAL ACTIVITIES	2013-2014: Member , Organizing Committee of the HHMI Alumni Network in Boston Region 2012-2013: Organizer , PQG Short Courses, Harvard School of Public Health 2009-Now: Referee for peer-reviewed journals, including <i>Annals of Human Genetics</i> , <i>BMC Bioinformatics</i> , <i>BMC Genetics</i> , <i>Clinical Chemistry</i> , <i>Genetics</i> , <i>Human Biology</i> , <i>Journal of Human Genetics</i> , <i>Molecular Biology and Evolution</i> , <i>PLoS ONE</i> , <i>PNAS</i> , <i>Scientific Reports</i>
COMPUTING SKILLS	Programming: C/C++, Perl, R, MATLAB, Shell Scripting Operating Systems: Linux/Unix, Mac OS X, Microsoft Windows Applications: L ^A T _E X, Microsoft Office, Adobe Illustrator, HTML
REFERENCES	Available upon request.