

CONTACT INFORMATION	Genome Institute of Singapore 60 Biopolis Street, Genome 02-01 Singapore 138672, Singapore	Phone (office): (+65) 6808 8341 Email: wangcl@gis.a-star.edu.sg Website: http://chaolongwang.github.io
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 with <i>Dr. Xihong Lin</i>	
EDUCATION	08/2012: Ph.D. in Bioinformatics University of Michigan, Ann Arbor, Michigan, USA <ul style="list-style-type: none">• Ph.D. advisor: <i>Dr. Noah Rosenberg</i> (now at Stanford University)• Thesis: Statistical methods for analyzing human genetic variation in diverse populations• 01/2012-08/2012: "Post"-doctoral research on statistical genetics with <i>Dr. Gonçalo Abecasis</i> 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	
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, 2011-2012- 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. <i>American Journal of Human Genetics</i> , 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. <i>Nature Genetics</i> , 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. <i>Nature Genetics</i> 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. <i>Genetics</i> 192 : 651-669.
	C Wang , S Zöllner, NA Rosenberg (2012). A quantitative comparison of the similarity between genes and geography in worldwide human populations. <i>PLoS Genetics</i> 8 : e1002886. [Featured in <i>Science</i> 337: 1151, 2012]
	TJ Pemberton, C Wang , JZ Li, NA Rosenberg (2010). Inference of unexpected genetic relatedness among individuals in HapMap Phase III. <i>American Journal of Human Genetics</i> 87 : 457-464. [Featured in <i>Am. J. Hum. Genet.</i> 87: 447-448, 2010 and <i>Genetics</i> 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. <i>Statistical Applications in Genetics and Molecular Biology</i> 9 : 13.
SOFTWARE DEVELOPED	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. <i>New England Journal of Medicine</i> 362 : 183-185. [Featured in <i>Nature</i> 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. <i>BMC Genetics</i> 10 : 80.
	L Huang, C Wang , NA Rosenberg (2009). The relationship between imputation error and statistical power in genetic association studies in diverse populations. <i>American Journal of Human Genetics</i> 85 : 692-698. [Featured in <i>Am. J. Hum. Genet.</i> 85: 539-540, 2009 and <i>Nat. Rev. Genet.</i> 10: 817, 2009]
CONFERENCE PRESENTATIONS	CL Wang , KW Au, CK Chan, HW Lau, KY Szeto (2008). Detecting hierarchical organization in complex networks by nearest neighbor correlation. <i>Studies in Computational Intelligence</i> 129 : 487-494 (Conference Proceedings of NICSO 2007).
	LASER : a package written in C++ for estimating individual ancestry using either sequencing reads or genotyping data. (Wang <i>et al.</i> 2014, <i>Nat. Genet.</i> ; Wang <i>et al.</i> 2015, <i>AJHG</i>)
	MicroDrop : a C++ program for estimating and correcting for allelic dropout in microsatellite data without replicated genotyping. (Wang <i>et al.</i> 2012, <i>Genetics</i>).
	C Wang , Han Chen, X Lin. Control of population stratification in family data using pedigree information and ancestry principal components. <i>The American Society of Human Genetics 64th Annual Meeting</i> , San Diego, USA, October 2014. (Poster)
	C Wang , L Liang, GR Abecasis, X Lin. Tracing individual ancestry in a principal components space. <i>The American Society of Human Genetics 63rd Annual Meeting</i> , 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**)

MEMBERSHIP	2009-Now: American Society of Human Genetics American Statistical Association (2010-2011) International Biometric Society, ENAR (2010-2011)
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.