Chaolong Wang, Ph.D.

Curriculum Vitae updated on February 16, 2016

Contact Information

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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

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
- Postdoctoral research on statistical genetics with *Dr. Xihong Lin*

Education

08/2012: **Ph.D. in Bioinformatics**
University of Michigan, Ann Arbor, Michigan, USA
- Ph.D. advisor: *Dr. Noah Rosenberg* (at 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 *Dr. Gonçalo Abecasis*

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

- 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
- 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

Publications

 # indicates corresponding author; * indicates co-first author.

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 (2016). Control for population structure and relatedness for binary traits in genetic association studies using logistic mixed models. *American Journal of Human Genetics*, in press.

X Lin, S Lee, M Wu, **C Wang**, H Chen, Z Li, X Lin (2015). Test for rare variants by environment interactions in sequencing association studies. *Biometrics*, in press.

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 Heckenlively, 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[#], 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

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*)
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*)
MicroDrop: a C++ program for estimating and correcting for allelic dropout in microsatellite data without replicated genotyping. (Wang *et al.* 2012, *Genetics*)

Membership

2009-Now: American Society of Human Genetics

Professional Activities

2009-Now: **Reviewer** for *Annals of Human Genetics*, *Bioinformatics*, *BMC Bioinformatics*, *BMC Genetics*, *Clinical Chemistry*, *Genetics*, *Human Biology*, *Human Heredity*, *Journal of Human Genetics*, *Molecular Biology and Evolution*, *Molecular Ecology*, *PLoS ONE*, *PNAS*, *Scientific Reports*