Chaolong Wang, Ph.D.

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CONTACT INFORMATION

Tongji Medical College
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RESEARCH INTEREST

Population genetics, statistical genetics/genomics, integrative genomics, next-generation sequencing analysis, epidemiology, infectious disease modelling

PROFESSIONAL APPOINTMENTS

04/2022-Now: **Vice Dean** (Research)
08/2018-Now: **Professor**, Epidemiology & Biostatistics
School of Public Health, Tongji Medical College
Huazhong University of Science and Techology, Wuhan,Hubei, China

01/2015-08/2018: **Principal Investigator**, Computational & Systems Biology
Genome Institute of Singapore, A*STAR, Singapore

05/2016-08/2018: **Adjunct Assistant Professor**, Centre for Computational Biology
Duke-NUS Medical School, Singapore

09/2012-12/2014: **Research Fellow**, Department of Biostatistics
Harvard T.H. Chan School of Public Health, Harvard University, Boston, Massachusetts, USA
- Postdoctoral research on statistical genetics with *Xihong Lin* and *Liming Liang*

EDUCATION

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

- Top 10 Bioinformatics Advances of 2020 in China, 2021
- Hoong-Chien Lee Young Bioinformatician Prize, Bioinformatics Society of Hubei, China, 2020
- HUST Academic Advances of 2020, Huazhong University of Science and Technology, 2020
- PQG Postdoc Travel Award, Program in Quantitative Genomics, Harvard University, 2014
- 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
- Rackham Conference Travel Grant, University of Michigan, 2009, 2010, 2011
- Fellowship (Program in Biomedical Sciences), University of Michigan, 2008-2009
- May Fourth Scholarship, Peking University, 2006

SOFTWARE PACKAGES

This section lists bioinformatics software packages we developed.

CLoMAT: an R package to perform rare-variant association tests for matched case-control data under the conditional logistic regression framework. (Cheng*, Lyu* *et al.* 2022, *Brief Bioinform*)
WEScall: a genotype calling pipeline that utilizes off-target seqeuncing data and linkage disequilibrium information to improve genotying accuracy of both target and off-target variants in whole-exome seqeuncing studies. (Dou *et al.* 2020, *Brief Bioinform*)

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*)

Selected Publications

This section includes first (*) and/or corresponding (#) author papers.

Zhu Z, Wang K, Hao X, Chen L, Liu Z, **Wang C**# (2022). Causal graph among serum lipids and glycemic traits: a Mendelian randomization study. *Diabetes*, in press.

Liu Q, Wu D, **Wang C**# (2022). Identification of genomic regions distorting population structure inference in diverse continental groups. *Quantitative Biology*, in press.

Wang K, Shi X, Zhu Z, Hao X, Chen L, Cheng S, Foo RSY, **Wang C**# (2022). Mendelian randomization analysis of 37 risk factors and coronary artery disease in East Asian and European populations. *Genome Medicine*, **14(1)**: 63.

Ma J*, Hao X*, Nie X, Yang S, Zhou M, Wang D, Wang B, Cheng M, Ye Z, Xie Y, **Wang C**#, Chen W# (2022). Longitudinal relationships of polycyclic aromatic hydrocarbons exposure and genetic susceptibility with blood lipid profiles. *Environment International*, **164**: 107259.

Cheng S*, Lyu J*, Shi X, Wang K, Wang Z, Deng M, Sun B#, **Wang C**# (2022). Rare variant association tests for ancestry-matched case-control data based on conditional logistic regression. Briefings in Bioinformatics, **23(2)**: bbab572.

Wu P*, Ding L*, Li X*, Liu S*, Cheng F*, He Q*, Xiao M, Wu P, Hou H, Jiang M, Long P, Wang H, Liu L, Qu M, Shi X, Jiang Q, Mo T, Ding W, Fu Y, Han S, Huo X, Zeng Y, Zhou Y, Zhang Q, Ke J, Xu X, Ni W, Shao Z, Wang J, Liu P, Li Z, Jin Y, Zheng F, Wang F, Liu L, Li W, Liu K, Peng R, Xu X, Lin Y, Gao H, Shi L, Geng Z, Mu X, Yan Y, Wang K, Wu D, Hao X, Cheng S, Qiu G, Guo H, Li K, Chen G, Sun Z, Lin X, Jin X# , Wang F# , Sun C# , **Wang C**# (2021). Trans-ethnic genome-wide association study of severe COVID-19. *Communications Biology*, **4(1)**: 1034.

Wu D, Li PY, Pan B, Tiang Z, Dou J, Williantarra I, Pribowo AY, Nurdiansyah R; SG Peranakan Project, Foo RSY#, **Wang C**# (2021). Genetic admixture in the culturally unique Peranakan Chinese population in Southeast Asia. *Molecular Biology and Evolution*, **38(10)**: 4463-4474.

Dou J*, Wu D*, Ding L, Wang K, Jiang M, Chai X, Reilly DF, Tai ES, Liu J, Sim X, Cheng S#, **Wang C**# (2021). Using off-target data from whole-exome sequencing to improve genotyping accuracy, association analysis, and polygenic risk prediction. *Briefings in Bioinformatics*, **22(3)**: bbaa084.

Yonova-Doing E*, Zhao W*, Igo RP Jr*, **Wang C***, Sundaresan P, Lee KE, Jun GR, Alves AC, Chai X, Chan ASY, Lee MC, Fong A, Tan AG, Khor CC, Chew EY, Hysi PG, Fan Q, Chua J, Chung J, Liao J, Colijn JM, Burdon KP, Fritsche LG, Swift MK, Hilmy MH,Chee ML, Tedja M, Bonnemaijer PWM, Gupta P, Tan QS, Li Z, Vithana EN, Ravindran RD, Chee SP, Shi Y, Liu W, Su X, Sim X, Shen Y, Wang YX, Li H, Tham YC, Teo YY, Aung T, Small KS, Mitchell P, Jonas JB, Wong TY, Fletcher AE, Klaver CCW, Klein BEK, Wang JJ, Iyengar SK, Hammond CJ#, Cheng CY# (2020). Common variants in SOX-2 and congenital cataract genes contribute to age-related nuclear cataract. *Communications Biology*, **3(1)**: 755.

X Hao*, S Cheng*, D Wu*, T Wu#, X Lin#, **C Wang**# (2020). Reconstruction of the full transmission dynamics of COVID-19 in Wuhan. *Nature*, **584**: 420-424. [Cover Article] [ESI Highly Cited Paper]

A Pan*, L Liu*, **C Wang***, H Guo*, X Hao*, Q Wang, J Huang, N He, H Yu, X Lin#, S Wei#, T Wu# (2020). Association of public health interventions with the epidemiology of the COVID-19 outbreak in Wuhan, China. *Journal of the American Medical Association*, **323**: 1915-1923. [Featured in *JAMA* 323: 1908-1909, 2020] [ESI Highly Cited Paper]

D Wu*, J Dou*, X Chai*, C Bellis, A Wilm, CC Shih, WWJ Soon, N Bertin, CB Lin, CC Khor, M DeGiorgio, S Cheng, L Bao, N Karnani, WYK Hwang, S Davila, P Tan, A Shabbir, A Moh, EK Tan, JN Foo, LL Goh, KP Leong, RSY Foo, CSP Lam, AM Richards, CY Cheng, T Aung, TY Wong, HH Ng, SG10K Consortium, J Liu#, **C Wang**# (2019). Large-scale whole-genome sequencing of three diverse Asian populations in Singapore. *Cell*, 179(3): 736-749. [Cover Article]

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.

D Taliun#, S Chothani, S Schönherr, L Forer, M Boehnke, GR Abecasis, **C Wang**# (2017). LASER server: ancestry tracing with genotypes or sequence reads. *Bioinformatics*, **33**: 2056-2058.

H Chen*, **C Wang***, MP Conomos, AM Stilp, Z Li, T Sofer, AA Szpiro, W Chen, JM Brehm, JC Celedon, 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.

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]

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.

Professional Activities

2009-Now: **Member** of the American Society of Human Genetics (ASHG)
2016-Now: **Member** of the International Genetic Epidemiology Society (IGES)
2021-Now: **Associate Editor** of *Molecular Genetics and Genomics*
2021-Now: **Review Editor** of *Frontiers in Genetics*
2017: **Reviewer** for Student Paper Award Competition, American Statistical Association (ASA) Section on Statistics in Genomics and Genetics

2009-Now: **Reviewer** for *American Journal of Human Genetics*, *Annals of Human Genetics*, *Bioinformatics*, *Biometrics*, *BMC Bioinformatics*, *BMC Genetics*, *BMC Medicine*, *BMJ*, *Briefings in Bioinformatics*, *Cell Genomics*, *Clinical Chemistry*, *Communications Biology*, *Gene*, *Genetics*, *Genome Biology*, *Genome Research*, *Human Biology*, *Human Heredity*, *Journal of Human Genetics*, *Molecular Biology and Evolution*, *Molecular Ecology*, *Molecular Oncology*, *PLoS Computational Biology*, *PLoS Genetics*, *PLoS ONE*, *PNAS*, *Science*, *Scientific Reports*