Chaolong Wang, Ph.D.

Curriculum Vitae updated on March 17, 2021

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

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, *GPB* (journal), 2021
- Young Bioinformatian Award, Hubei Provincial Bioinformatics Society, 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.

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

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

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]

J Dou*, D Wu*, L Ding, K Wang, M Jiang, X Chai, DF Reilly, ES Tai, J Liu, X Sim, S Cheng#, **C Wang**# (2020). Using off-target data from whole-exome sequencing to improve genotyping accuracy, association analysis, and polygenic risk prediction. *Briefings in Bioinformatics*, **doi**:10.1093/bib/bbaa084.

K Yu*, J Lv*, G Qiu*, C Yu, Y Guo, Z Bian, L Yang, Y Chen, **C Wang**, A Pan, L Liang, FB Hu, Z Chen, L Li#, T Wu# for the China Kadoorie Biobank Study (2020). Cooking fuels and risk of all-cause and cardiopulmonary mortality in urban China: a prospective cohort study. *Lancet Global Health*, **8(3)**: e430-e439.

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]

K Huang*, T Yang*, J Xu*, L Yang*, J Zhao*, X Zhang*, C Bai*, J Kang*, P Ran*, H Shen*, F Wen*, W Yao*, T Sun*, G Shan*, Y Lin*, G Xu*, S Wu*, **C Wang**, ..., T Wu, KF Chung, J He, Chen Wang# for the China Pulmonary Health Study Group (2019). Prevalence, risk factors and management of asthma in China: a national cross-sectional study. *Lancet*, **394**: 407-418. [ESI Highly Cited Paper]

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.

Other Publications

Shen M, Xu X, Liu X, Wang Q, Li W, You X, Peng R, Yuan Y, Long P, Niu R, Yang H, Cheng X, Pan A, Tanguay RM, Zhang X, He M, **Wang C**, Liang L, Wu T (2021). Prospective study on plasma microRNA-4286 and incident acute coronary syndrome *Journal of the American Heart Association*, **10(6)**: e018999

Tu Y, Yang P, Zhou Y, Wen X, Li Q, Zhou J, Wang J, Hu J, He N, Wang K, **Wang C**, Tian X, Luo A, Gao F (2021). Risk factors for mortality of critically ill patients with COVID-19 receiving invasive ventilation. *International Journal of Medical Sciences*, **18(5)**:1198-1206.

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.

Fu Y[*], Li Y[*], Guo E[*], He L[*], Liu J, Yang B, Li F, Wang Z, Li Y, Xiao R, Liu C, Huang Y, Wu X, Lu F, You L, Qin T, **Wang C**, Li K, Wu P[#], Ma D[#], Sun C[#], Chen G[#] (2020). Dynamics and correlation among viral positivity, seroconversion, and disease severity in COVID-19: a retrospective study. *Annals of Internal Medicine*, **doi**: 10.7326/M20-3337.

K Wang, L Ding, C Yang, X Hao[*], **C Wang**[*] (2020). Exploring the relationship between psychiatric traits and the risk of mouth ulcers using bi-directional Mendelian randomization. *Frontiers in Genetics*, **11**: 608630.

JF Chai[*], SL Kao[*], **C Wang**, VJ Lim, IW Khor, J Dou, AI Podgornaia, S Chothani, CY Cheng, C Sabanayagam, TY Wong, RM van Dam, J Liu, DF Reilly, AD Paterson, X Sim[#] (2020). Genome-wide association for HbA1c in Malay identified deletion on SLC4A1 that influences HbA1c independent of glycemia. *Journal of Clinical Endocrinology & Metabolism*, **doi**:10.1210/clinem/dgaa658.

X Hao[#], K Wang, C Dai, Z Ding, W Yang, **C Wang**, S Cheng[#] (2020). Integrative analysis of scRNA-seq and GWAS data pinpoints periportal hepatocytes as the relevant liver cell types for blood lipids. *Human Molecular Genetics*, **29(18)**: 3145-3153.

A Leong[*#], VJY Lim[*], **C Wang**, JF Chai, R Dorajoo, CK Heng, RM van Dam, WP Koh, JM

Yuan, JB Jonas, YX Wang, WB Wei, J Liu, DF Reilly, TY Wong, CY Cheng, X Sim# (2020). Association of G6PD variants with hemoglobin A1c and impact on diabetes diagnosis in East Asian individuals. *BMJ Open Diabetes Research & Care*, **8(1)**: e001091.

K Wang, Y Xu, **C Wang**, M Tan, P Chen (2020). A corrected goodness-of-fit index (CGFI) for model evaluation in structural equation modeling. *Structural Equation Modeling*, **27**: 735-749.

A Teumer, Y Li, S Ghasemi, BP Prins, M Wuttke, T Hermle, ..., **C Wang**, ..., AS Butterworth, AM Hung, C Pattaro, A Köttgen (2019). Genome-wide association meta-analyses and fine-mapping elucidate pathways influencing albuminuria. *Nature Communications*, **10(1)**: 4130.

M Wuttke, Y Li, M Li, KB Sieber, MF Feitosa, M Gorski, A Tin, L Wang, ..., **C Wang**, ..., K Stefansson, AM Hung, IM Heid, M Scholz, A Teumer, A Köttgen, C Pattaro (2019). A catalog of genetic loci associated with kidney function from analyses of a million individuals. *Nature Genetics*, **51(6)**: 957-972. [ESI Highly Cited Paper]

H Chen, JE Huffman, JA Brody, **C Wang**, S Lee, ..., CC Laurie, AC Morrison, KM Rice, X Lin (2019). Efficient variant set mixed model association tests for continuous and binary traits in large-scale whole genome sequencing studies. *American Journal of Human Genetics*, **104(2)**: 260-274.

F Takeuchi, M Akiyama, N Matoba, T Katsuya, M Nakatochi, ..., **C Wang**, ..., T Nabika, M Yokota, Y Kamatani, M Kubo, N Kato (2018). Interethnic analyses of blood pressure loci in populations of East Asian and European descent. *Nature Communications*, **9(1)**: 5052.

H Chen, BE Cade, KJ Gleason, AC Bjonnes, AM Stilp, ..., **C Wang**, ..., X Zhu, SR Sunyaev, R Saxena, X Lin, S Redlin (2018). Multi-ethnic meta-analysis identifies RAI1 as a possible obstructive sleep apnea related quantitative trait locus in men. *American Journal of Respiratory Cell and Molecular Biology*, **58**: 391-401.

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.

H Liu, Z Wang, Y Li, G Yu, X Fu, ..., **C Wang**, ..., S Chen, J Liu, F Zhang (2017). Genome-wide analysis of protein-coding variants in leprosy. *Journal of Investigative Dermatology*, **137**: 2544-2551.

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.

W Dai, M Yang, **C Wang**, T Cai (2017). Sequence robust association test (SRAT) for familial data. *Biometrics*, **73**: 876-884

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.

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.

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.

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]

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]

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: **Review Editor** of *Frontiers in Genetics*
2009-Now: **Reviewer** for *American Journal of Human Genetics*, *Annals of Human Genetics*, *Bioinformatics*, *Biometrics*, *BMC Bioinformatics*, *BMC Genetics*, *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*, *Scientific Reports*
2017: **Reviewer** for Student Paper Award Competition, American Statistical Association (ASA) Section on Statistics in Genomics and Genetics