Gao T. Wang

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Education

2009 - 2014	PhD	Structural and Computational Biology & Molecular Biophysics program, Baylor College of Medicine, Houston, Texas, USA
2009 - 2013	Visiting PhD student, Department of Statistics, Rice University, Houston, Texas, USA	
2005 - 2009	BSc	Biological Sciences program, Beijing Forestry University, Beijing, China

Research Training

2015 - present	Postdoctoral scholar	Matthew Stephens' group at University of Chicago
2014 - 2015	Postdoctoral associate	Center for Statistical Genetics at Baylor College of Medicine
2008 - 2009	Research assistant	Jürg Ott's group at Beijing Institute of Genomics

Awards and Honors

2018 *Reviewer's Choice Abstract,* American Society of Human Genetics
2014 *Williams Awards Finalist,* International Genetic Epidemiology Society
2010 *Professor John J. Trentin Award for Scholastic Excellence,* Baylor College of Medicine
2009 *Distinguished College Graduate of Beijing,* Beijing Forestry University
2009 *Outstanding Undergraduate Thesis Award,* Beijing Forestry University

Professional Activities

Scientific Communities

2011 - present	Member	American Society of Human Genetics
2010 - 2016	Associate faculty	FACULTY *of* 1000, Bioinformatics section
2011 - 2014	Member	International Genetic Epidemiology Society

Journal Referee

Since 2016 Scientific Reports
Since 2015 GENE, Bioinformatics
Since 2014 American Journal of Human Genetics, PLOS ONE

Teaching

Short Courses

2014.09	Instructor	*Integrated Analysis of Next Generation Sequence Data,* Tutorial workshop at the 5th ACM Conference on Bioinformatics, Computational Biology and Health Informatics, Los Angeles, California, USA
2014.04	Instructor	*Analysis of Next Generation Sequence Data Workshop,* Perelman School of Medicine, University of Pennsylvania, Philadelphia, USA
2013.06	Instructor	*Annual Advanced Topics in Genome-Wide Association Studies Course,* Ontario Institute for Cancer Research, Toronto, Canada

Invited Talks

Conferences

2018.07 Annual conference of International Society for Computational Biology, Chicago, Illinois, USA
2015.10 Annual conference of American Society of Human Genetics, Baltimore, Maryland, USA
2014.08 Annual conference of International Genetic Epidemiology Society, Vienna, Austria
2012.10 Annual conference of International Genetic Epidemiology Society, Stevenson, Washington, USA

Fellowship and Grants

2009.12 National Human Genome Research Institute fellowship for *Advanced Gene Mapping Course*, New York City, New York, USA

Publications

† *indicates first authored papers*

Preprint

1. **Wang G**†, Sarkar A, Carbonetto P, Stephens M. A simple new approach to variable selection in regression, with application to genetic fine-mapping. *Under review at Journal of the Royal Statistical Society: Series B* doi:10.1101/501114

2. **Wang G**†, Peng B. Script of Scripts: a pragmatic workflow system for daily computational research. *To appear in PLoS Computational Biology*

Journal Articles

3. Peng B, **Wang G**, Ma J, Leong MC, Wakefield C, Melott J, Chiu Y, Du D *et al.*, SoS Notebook: an interactive multi-language data analysis environment. *Bioinformatics* 34:3768–3770 (2018)

4. Urbut SM, **Wang G**, Carbonetto P and Stephens M, Flexible statistical methods for estimating and testing effects in genomic studies with multiple conditions. *Nature Genetics* 51:187–195 (2018)

5. He Z, Zhang D, Renton AE, Li B, Zhao L, **Wang G**, Goate AM, Mayeux R *et al.*, The Rare-Variant Generalized Disequilibrium Test for Association Analysis of Nuclear and Extended Pedigrees with Application to Alzheimer Disease WGS Data. *The American Journal Of Human Genetics* 100:193–204 (2017)

6. Zhang D, Zhao L, Li B, He Z, **Wang G**, Liu DJ and Leal SM, SEQSpark: A Complete Analysis Tool for Large-scale Rare Variant Association Studies Using Whole-Genome and Exome Sequence Data. *Am J Hum Genet* 101:115–122 (2017)

7. Kan M, Auer PL, **Wang G**†, Bucasas KL, Hooker S, Rodriguez A, Li B, Ellis J *et al.*, Rare variant associations with waist-to-hip ratio in European-American and African-American women from the NHLBI-Exome Sequencing Project.. *European Journal Of Human Genetics* 10.1038/ejhg.2015.272 (2016)

8. Auer PL, Reiner AP, **Wang G**, Kang HM, Abecasis GR, Altshuler D, Bamshad MJ, Nickerson DA *et al.*, Guidelines for Large-Scale Sequence-Based Complex Trait Association Studies: Lessons Learned from the NHLBI Exome Sequencing Project. *The American Journal Of Human Genetics* 99:791–801 (2016)

9. vant Hof FN *et al.*, Shared Genetic Risk Factors of Intracranial, Abdominal, and Thoracic Aneurysms. *Journal Of The American Heart Association* 5:e002603 (2016)

10. Li B, **Wang G** and Leal SM, Generation of sequence-based data for pedigree-segregating Mendelian or Complex traits.. *Bioinformatics* 31:3706–8 (2015)

11. Santos-Cortez RLP, Chiong CM, Reyes-Quintos MRT, Tantoco MLC, Wang X, Acharya A, Abbe I, Giese AP, Smith JD, Allen EK, Li B, Cutiongco-de la Paz EM, Garcia MC, Llanes EGDV, Labra PJ, Gloria-Cruz TLI, Chan AL, **Wang G**

et al., Rare A2ML1 variants confer susceptibility to otitis media.. *Nature Genetics* 47:917–20 (2015)

12. Rehman AU, Santos-Cortez RLP, Drummond MC, Shahzad M, Lee K, Morell RJ, Ansar M, Jan A, Wang X, Aziz A, Riazuddin S, Smith JD, **Wang G** *et al.*, Challenges and solutions for gene identification in the presence of familial locus heterogeneity.. *European Journal Of Human Genetics* 23:1207–15 (2015)

13. **Wang G**†, Zhang D, Li B, Dai H and Leal SM, Collapsed haplotype pattern method for linkage analysis of next-generation sequence data.. *European Journal Of Human Genetics* 23:1739–43 (2015)

14. He Z, O'Roak BJ, Smith JD, **Wang G**, Hooker S, Santos-Cortez RLP, Li B, Kan M *et al.*, Rare-variant extensions of the transmission disequilibrium test: application to autism exome sequence data. *American Journal Of Human Genetics* 94:33–46 (2014)

15. **Wang G**†, Li B, Santos-Cortez RLP, Peng B, Leal SM, Lyn Santos-Cortez RP, Peng B and Leal SM, Power analysis and sample size estimation for sequence-based association studies. *Bioinformatics* 30:2377–2378 (2014)

16. Cecchi AC, Guo D, Ren Z, Flynn K, Santos-Cortez RLP, Leal SM, **Wang G**, Regalado ES *et al.*, RNF213 Rare Variants in an Ethnically Diverse Population With Moyamoya Disease. *Stroke* 45:3200–3207 (2014)

17. **Wang G**†, Peng B and Leal SM, Variant association tools for quality control and analysis of large-scale sequence and genotyping array data. *American Journal Of Human Genetics* 94:770–783 (2014)

18. Li B, **Wang G** and Leal SM, PhenoMan: phenotypic data exploration, selection, management and quality control for association studies of rare and common variants. *Bioinformatics* 30:442–444 (2014)

19. Wiszniewski W, Hunter JV, Hanchard NA, Willer JR, Shaw C, Tian Q, Illner A, Wang X, Cheung SW, Patel A, Campbell IM, Gelowani V, Hixson P, Ester AR, Azamian MS, Potocki L, Zapata G, Hernandez PP, Ramocki MB, Santos-Cortez RLP, **Wang G** *et al.*, TM4SF20 ancestral deletion and susceptibility to a pediatric disorder of early language delay and cerebral white matter hyperintensities. *American Journal Of Human Genetics* 93:197–210 (2013)

20. Auer PL, **Wang G** and Leal SM, Testing for rare variant associations in the presence of missing data. *Genetic Epidemiology* 37:529–538 (2013)

21. Li B, **Wang G** and Leal SM, SimRare: a program to generate and analyze sequence-based data for association studies of quantitative and qualitative traits. *Bioinformatics* 28:2703–2704 (2012)

22. Cheung YH, **Wang G**, Leal SM and Wang S, A fast and noise-resilient approach to detect rare-variant associations with deep sequencing data for complex disorders. *Genetic Epidemiology* 36:675–685 (2012)

23. San Lucas FA, **Wang G**, Scheet P and Peng B, Integrated annotation and analysis of genetic variants from next-generation sequencing studies with variant tools. *Bioinformatics* 28:421–422 (2012)

24. **Wang G**†, Yang Y and Ott J, Genome-Wide Conditional Search for Epistatic Disease-Predisposing Variants in Human Association Studies. *Human Heredity* 70:34–41 (2010)

Consortia Authorship

Genotype Tissue Expression (GTEx) Consortium

25. Aguet F *et al.*, Genetic effects on gene expression across human tissues. *Nature* 550:204–213 (2017)

The NHLBI Exome Sequencing Project

26. Auer PL *et al.*, Rare and Coding Region Genetic Variants Associated With Risk of Ischemic Stroke. *Jama Neurology* 72:781 (2015)

27. Tabor HK *et al.*, Pathogenic variants for Mendelian and complex traits in exomes of 6,517 European and African Americans: implications for the return of incidental results. *American Journal Of Human Genetics* 95:183–193

(2014)

28. Gordon AS *et al.*, Quantifying rare, deleterious variation in 12 human cytochrome P450 drug-metabolism genes in a large-scale exome dataset. *Human Molecular Genetics* 23:1957–1963 (2014)

29. Lange LA *et al.*, Whole-exome sequencing identifies rare and low-frequency coding variants associated with LDL cholesterol. *American Journal Of Human Genetics* 94:233–245 (2014)

30. Rosenthal EA *et al.*, Joint linkage and association analysis with exome sequence data implicates SLC25A40 in hypertriglyceridemia. *American Journal Of Human Genetics* 93:1035–1045 (2013)

31. Guo D *et al.*, Recurrent gain-of-function mutation in PRKG1 causes thoracic aortic aneurysms and acute aortic dissections. *American Journal Of Human Genetics* 93:398–404 (2013)

32. Johnsen JM *et al.*, Common and rare von Willebrand factor (VWF) coding variants, VWF levels, and factor VIII levels in African Americans: the NHLBI Exome Sequencing Project. *Blood* 122:590–597 (2013)

33. Norton N *et al.*, Exome sequencing and genome-wide linkage analysis in 17 families illustrate the complex contribution of TTN truncating variants to dilated cardiomyopathy. *Circulation Cardiovascular Genetics* 6:144–153 (2013)

34. Fu W *et al.*, Analysis of 6,515 exomes reveals the recent origin of most human protein-coding variants. *Nature* 493:216–220 (2013)

35. O'Connor TD *et al.*, Fine-scale patterns of population stratification confound rare variant association tests. *plos One* 8:e65834 (2013)

36. Emond MJ *et al.*, Exome sequencing of extreme phenotypes identifies DCTN4 as a modifier of chronic Pseudomonas aeruginosa infection in cystic fibrosis. *Nature Genetics* 44:886–889 (2012)

37. Boileau C *et al.*, TGFB2 mutations cause familial thoracic aortic aneurysms and dissections associated with mild systemic features of Marfan syndrome. *Nature Genetics* 44:916–921 (2012)

University of Washington Center for Mendelian Genomics

38. Shahzad M *et al.*, Molecular outcomes, clinical consequences and genetic diagnosis of Oculocutaneous Albinism in Pakistani population. *Scientific Reports* 7:44185 (2017)

39. Heimer G *et al.*, MECR Mutations Cause Childhood-Onset Dystonia and Optic Atrophy, a Mitochondrial Fatty Acid Synthesis Disorder. *The American Journal Of Human Genetics* 99:1229–1244 (2016)

40. Ansar M *et al.*, Expansion of the spectrum of ITGB6-related disorders to adolescent alopecia, dentogingival abnormalities and intellectual disability. *European Journal Of Human Genetics* 10.1038/ejhg.2015.260 (2015)

41. Ansar M *et al.*, Mutation of ATF6 causes autosomal recessive achromatopsia. *Human Genetics* 134:941–950 (2015)

42. Chong J *et al.*, De Novo Mutations in NALCN Cause a Syndrome Characterized by Congenital Contractures of the Limbs and Face, Hypotonia, and Developmental Delay. *The American Journal Of Human Genetics* 96:462–473 (2015)

43. Chong J *et al.*, Autosomal-Dominant Multiple Pterygium Syndrome Is Caused by Mutations in MYH3. *The American Journal Of Human Genetics* 96:841–849 (2015)

Scientific Software

A list of companion software for methods papers in statistical genetics and computational biology can be found at http://tigerwang.org/software