

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

- 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

- 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. S M Uribut, **G Wang**, M Stephens. Flexible statistical methods for estimating and testing effects in genomic studies with multiple conditions. *bioRxiv* doi:10.1101/096552.

Journal Articles

2. He Z, Zhang D, Renton AE, Li B, Zhao L, **Wang GT**, 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)
3. Zhang D, Zhao L, Li B, He Z, **Wang GT**, 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)
4. Kan M, Auer PL, **Wang GT**[†], Bucayas 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)
5. Auer PL, Reiner AP, **Wang GT**, 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)
6. vant Hof FN *et al.*, Shared Genetic Risk Factors of Intracranial, Abdominal, and Thoracic Aneurysms. *Journal Of The American Heart Association* 5:e002603 (2016)

7. Li B, **Wang GT** and Leal SM, Generation of sequence-based data for pedigree-segregating Mendelian or Complex traits.. *Bioinformatics* 31:3706–8 (2015)
8. 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 GT et al.**, Rare A2ML1 variants confer susceptibility to otitis media.. *Nature Genetics* 47:917–20 (2015)
9. 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 GT et al.**, Challenges and solutions for gene identification in the presence of familial locus heterogeneity.. *European Journal Of Human Genetics* 23:1207–15 (2015)
10. **Wang GT**[†], 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)
11. He Z, O’Roak BJ, Smith JD, **Wang GT**, 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)
12. **Wang GT**[†], 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)
13. Cecchi AC, Guo D, Ren Z, Flynn K, Santos-Cortez RLP, Leal SM, **Wang GT**, Regalado ES *et al.*, RNF213 Rare Variants in an Ethnically Diverse Population With Moyamoya Disease. *Stroke* 45:3200–3207 (2014)
14. **Wang GT**[†], 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)
15. Li B, **Wang GT** 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)
16. 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 GT 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)
17. Auer PL, **Wang GT** and Leal SM, Testing for rare variant associations in the presence of missing data. *Genetic Epidemiology* 37:529–538 (2013)
18. Li B, **Wang GT** 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)
19. Cheung YH, **Wang GT**, 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)
20. San Lucas FA, **Wang GT**, 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)
21. **Wang GT**[†], Yang Y and Ott J, Genome-Wide Conditional Search for Epistatic Disease-Predisposing Variants in Human Association Studies. *Human Heredity* 70:34–41 (2010)

Consortium Projects Publications

The NHLBI Exome Sequencing Project

22. 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)

23. 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)
24. 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)
25. 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)
26. 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)
27. 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)
28. 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)
29. Fu W *et al.*, Analysis of 6,515 exomes reveals the recent origin of most human protein-coding variants. *Nature* 493:216–220 (2013)
30. O'Connor TD *et al.*, Fine-scale patterns of population stratification confound rare variant association tests. *plos One* 8:e65834 (2013)
31. 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)
32. 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

33. 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)

SCIENTIFIC SOFTWARE

Methods I develop / co-develop in the fields of statistical genetics and computational biology typically result in polished software aimed to aid in various research projects in relevant fields. You can find them at <http://tigerwang.org/software>