

# Hua Tang

## CONTACT INFORMATION

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## CURRENT POSITION

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12/01/2016–Present	Professor Department of Genetics Stanford University School of Medicine
12/01/2016–Present	Professor (by courtesy) Department of Statistics Stanford University

## EDUCATION

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1993-1997	Harvard University, Cambridge, MA	AB	Biology
1997-2002	Stanford University, Stanford, CA	PhD	Statistics (minor Genetics)

## PROFESSIONAL EXPERIENCE

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1996-1997	Undergraduate thesis research, Advisor: Richard C. Lewontin. Department of Biology, Harvard University, Cambridge, MA.
1996-1997	Research Assistant, Department of Health Care Policy, Harvard Medical School, Cambridge, MA.
1997-2002	Graduate Student, Advisors: David Siegmund & Marc Feldman, Department of Statistics, Stanford University, Stanford, CA.
06/2002-08/2002	Summer Intern, Genome Therapeutics Corporation, Waltham, MA.
2002-2006	Assistant Member, Division of Public Health Sciences, Fred Hutchinson Cancer Research Center, Seattle, WA.
2003-2006	Affiliate Assistant Professor, Department of Biostatistics, University of Washington, Seattle, WA.
2006-2009	Associate Member, Division of Public Health Sciences, Fred Hutchinson Cancer Research Center, Seattle, WA.

2007-2009	Assistant Professor of Genetics, Stanford University, CA.
2009-2016	Associate Professor of Genetics, Stanford University, CA.
2010-2016	Associate Professor of Statistics (by courtesy), Stanford University, CA.

## HONORS & AWARDS

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1994-1997	John Harvard Scholarship and Elizabeth Cary Agassiz Scholarship. Harvard University.
1997	AB <i>summa cum laude</i> , Harvard University.
1997	Phi Beta Kappa, Harvard University.
1997	Gertrude Cox Scholarship. American Statistical Association.
1998-2002	Howard Hughes Medical Institute Predoctoral Fellowship.
1998	National Science Foundation Predoctoral Fellowship ( <i>declined in favor of HHMI</i> ).
2008-2010	Sloan Research Fellow in Computational Biology.
2015	Stanford-PKU Faculty Fellowship.

## PUBLICATIONS

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1. **Tang H** and Lewontin RC (1999) Locating Regions of Differential Variability in DNA and Protein Sequences. *Genetics* **153**: 485-495.
2. Ettner SL, Hermann RC, and **Tang H** (1999) Differences Between Generalists and Mental Health Specialists in the Psychiatric Treatment of Medicare Beneficiaries. *Health Services Research* **34**: 737-760.
3. **Tang H**, Siegmund DO, Shen P, Oefner PJ and Feldman MW (2002) Frequentist Estimation of Coalescence Times from Nucleotide Sequence Data using a Tree-Based Partition. *Genetics* **161**: 447-459.
4. Risch NJ, Burchard E, Ziv E and **Tang H** (2002) Categorization of humans in biomedical research: genes, race and disease. *Genome Biology* **3**:1-12.
5. Burchard EG, Ziv E, Coyle N, Gomez SL, **Tang H**, Karter AJ, Mountain JL, Pérez-Stable EJ, Sheppard D, and Risch NJ (2003) The Importance of Race and Ethnicity in Biomedical Research and Clinical Practice. *New England Journal of Medicine* **348**:12.
6. Risch NJ, **Tang H**, Katzenstein H, and Ekstein J (2003) Geographic Distribution of Disease Mutations in the Ashkenazi Jewish Population Supports Genetic Drift over Selection. *Am J Hum Genet* **72**:812-822.
7. Risch NJ, **Tang H** (2003) Selection in the Ashkenazi Jewish Population Unlikely-- Reply to Zlotogora and Bach. *Am J Hum Genet* **73**:440-441
8. Varon R, Gooding R, Steglich C, Marns L, **Tang H**, et al. (2003) Partial deficiency of the C-terminal-domain phosphatase of RNA polymerase II is associated with

- congenital cataracts facial dysmorphism neuropathy syndrome. *Nat Genet.* **35**:185-9. PMID: 14517542
9. Jorgenson E, **Tang H**, Gadde M, Province M, Leppert M, Kardia S, Schork N, Cooper R, Rao DC, Eric Boerwinkle E, and Risch N (2005) Ethnicity and human genetic linkage maps. *Am J Hum Genet.* **76**:276-90. PMID: 15627237. PMCID: PMC1196373.
  10. Zhu X, Luke A, Cooper RS, Quertermous T, Hanis C, Mosley T, Gu CC, **Tang H**, Rao DC, Risch N, Weder A (2005) Genome-wide Admixture Mapping for Hypertension Loci: The NHLBI Family Blood Pressure Program. *Nat Genet.* **37**:177-81.
  11. **Tang H**, Quertermous T, Rodriguez B, Kardia SL, Zhu X, Brown A, Pankow JS, Province MA, Hunt SC, Boerwinkle E, Schork NJ, Risch NJ (2005) Genetic Structure, Self-Identified Race/Ethnicity and Confounding in Case-Control Association Studies. *Am J Hum Genet.* **76**:268-75. PMID: 15712363
  12. **Tang H**, Peng J., Wang P., and Risch N. (2005) Estimation of Individual Admixture: Analytical and Study Design Considerations. *Genet Epidemiol.* **28**:289-301.
  13. Salari K, Choudhry S, **Tang H**, Naqvi H, Lind D *et al.* (2005) Genetic Admixture and Asthma Related Phenotypes in Mexican American and Puerto Rican Asthmatics. *Genetic Epidemiology* **29**:76-86.
  14. Kalaydjieva L, Morar B, Chaix R, **Tang H** (2005) A newly discovered founder population: the Roma/Gypsies. *BioEssays.* **27**:1084-94.
  15. Hsu L, Yu X, Houwing-Duistermaat JJ, Uh HW, Elgelta R, Lebec JJP, **Tang H** (2005). Locally weighted transmission/disequilibrium test for genetic association analysis. *BMC genetics, Suppl 1*:S60.
  16. **Tang H**, Coram M, Wang P, Zhu X, Risch NJ. (2006) Reconstructing Genetic Ancestry Blocks in Admixed Individuals. *Am J Hum Genet.* **79**:1-12. PMID: 16773560. PMCID: PMC1474129.
  17. **Tang H**, Jorgenson E, Gadde M, Kardia SLR, Rao DC, Zhu X, Schork NJ, Hanis CL, Risch NJ (2006) Racial Admixture and its Impact on BMI and Blood Pressure in African and Mexican Americans. *Human Genetics*, **119**:624-33.
  18. Choudhry S, Burchard EG, Borrell LN, **Tang H**, Gomez I, Naqvi M, Nazario S, Torres A, Casal J, Martinez-Cruzado JC, Ziv E, Avila PC, Rodriguez-Cintron W, Risch NJ. (2006) Ancestry-Environment Interactions and Asthma Risk among Puerto Ricans. *Am J Respir Crit Care Med.* **174**:1088-93. PMCID: PMC2648109.
  19. Piening BD, Wang P, Bangur CS, Whiteaker J, Zhang H, Feng L, Keane JF, Eng JK, **Tang H**, Prakash A, McIntosh MW, Paulovich A. (2006) Quality Control Metrics for LC-MS Feature Detection Tools Demonstrated on *Saccharomyces cerevisiae* Proteomic Profiles. *J. Proteomics Res.* **5**:1527-34.
  20. Ronald J, **Tang H**, Brem R. (2006) Genome-wide Evolutionary Rates in Laboratory and Wild Yeast. *Genetics*, **174**:541-4.
  21. Zhu X, Zhang S., **Tang H**, Cooper R. A (2006) Classical Likelihood Based Approach for Admixture Mapping: Method and Comparison with a Bayesian Approach. *Hum Genet*, **120**:431-45.

22. Choudhry S, Coyle NE, **Tang H**, Salari K, Lind D, Clark SL, Tsai H, Naqvi M, Phong A, Ung N, Matallana H, Avila PC, Casal J, Torres A, Nazario S, Castro R, Battle NC, Perez-Stable EJ, Kwok P, Sheppard D, Shriver MD, Rodriguez-Cintron W, Risch N, Ziv E, Burchard EG (2006) Population Stratification Confounds Genetic Association Studies among Latino Americans. *Human Genetics* 18:652-64.
23. Wang P, **Tang H**, Zhang H, Whiteaker J, Paulovich AG, McIntosh M (2006) Normalization Regarding Non-Random Missing values in High-throughput Mass Spectrometry Data. In Altman R, Dunker A, Hunter L, Murray T and Klein T, eds. *Proceedings of Pacific Symposium for Biocomputing* 315-326.
24. Hershberg R, **Tang H**, Petrov D. (2007) Reduced Selection Leads to Accelerated Gene Loss in *Shigella*. *Genome Biology* 8:R164.
25. **Tang H**, Choudhry S, Mei R, Morgan M, Rodriguez-Cintron W, Burchard EB, Risch NJ. (2007) Recent Genetic Selection in the Ancestral Admixture of Puerto Ricans. *Am J Hum Genet* 81:626-33.
26. Coram M, **Tang H**. (2007) Improving population-specific allele frequency estimates by adapting supplemental data: an empirical Bayes approach. 459-479. PMC3065192
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29. **Tang H**, Peng J, Wang P, Coram M, Hsu L. (2007) Combining Multiple Family-based Association Studies. *BMC Proceedings* 1:S162
30. Peng J, Wang P, **Tang H**. (2007) Controlling for false positive findings of trans-hubs in expression quantitative trait loci mapping. *BMC Proceedings* 1:S157.
31. Wang P\*, **Tang H**, Fitzgibbon MP, Coram M\*, Zhang H, Yi E, Aebersold R, McIntosh M. (2007) A statistical method for chromatographic alignment of LC-MS data. *Biostatistics* 8:357-67.
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40. Yu X, Randolph TW, **Tang H**, Hsu L. (2009) Detecting Genomic Aberrations Using Products in a Multiscale Analysis. *Biometrics*.
41. Silander K, **Tang H**, Myles S, Jakkula E, Timpson N, Cavalli-Sforza L, Peltonen L. (2009) Worldwide patterns of haplotype diversity at 9p21.3, a locus associated with type 2 diabetes and coronary heart disease. *Genome Med.* 1:51.
42. Basu A, **Tang H**, Lewis CE, North K, Curb JD, Quertermous T, Mosley TH, Boerwinkle E, Zhu X, Risch NJ. (2009) Admixture mapping of quantitative trait loci for blood lipids in African-Americans. *Hum Mol Genet.* 2009 18:2091-8. PMID: 19304782. PMCID: PMC2722229.
43. Peralta CA, Risch N, Lin F, Shlipak MG, Reiner A, Ziv E, **Tang H**, Siscovick D, Bibbins-Domingo K. (2010) The Association of Genetic African Ancestry and Kidney Function among Young African Americans- The CARDIA Study. *Am J Nephrol.* **31**:202-8.
44. Assimes TL, Hólm H, Kathiresan S, Reilly MP, Thorleifsson G, et al. (2010) Lack of association between the Trp719Arg polymorphism in kinesin-like protein-6 and coronary artery disease in 19 case-control studies. *J Am Coll Cardiol* **56**:1552-63.
45. **Tang H**, Siegmund DO, Johnson NA, Romieu I, London SJ. (2010) Joint testing of genotype and ancestry association in admixed families. *Genet Epidemiol.* **34**:783-91. PMID: 21031451. PMCID: PMC3103820.

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49. Carty CL, Johnson NA, Hutter CM, Reiner AP, Peters U, **Tang H**, Kooperberg C. (2011) Genome-wide association study of body height in African-Americans: the Women's Health Initiative SNP Health Association Resource (SHARe). *Hum Mol Genet.* PMID: 22021425. PMCID: PMC3259012.
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51. Chen R, Mias GI, Li-Pook-Than J, Jiang L, Lam HY, Chen R, Miriami E, Karczewski KJ, Hariharan M, Dewey FE, Cheng Y, Clark MJ, Im H, Habegger L, Balasubramanian S, O'Huallachain M, Dudley JT, Hillenmeyer S, Haraksingh R, Sharon D, Euskirchen G, Lacroute P, Bettinger K, Boyle AP, Kasowski M, Grubert F, Seki S, Garcia M, Whirl-Carrillo M, Gallardo M, Blasco MA, Greenberg PL, Snyder P, Klein TE, Altman RB, Butte AJ, Ashley EA, Gerstein M, Nadeau KC, **Tang H**, Snyder M. (2012) Personal omics profiling reveals dynamic molecular and medical phenotypes. *Cell.* 148:1293-307. PMID: 22424236. PMCID: PMC3341616.
52. Thornton T, **Tang H**, Hoffmann TJ, Ochs-Balcom H, Cann B, and Risch NJ. (2012) Estimating Kinship in Admixed Populations. *Am J Hum Genet* 91:122-38. PMID: 22748210. PMCID: PMC3397261.
53. Auer PL\*, Johnsen JM\*, Johnson AD\*, LoAgston BA\*, Lange LA\*, Nalls MA, Franceschini N, Fox K, Lange EM, Rich SS, O'Donnell CJ, Jackson RD, Wallace RB, Chen Z, Graubert TA, Wilson JG, **Tang H\***, Lettre G\*, Reiner AP\*, Ganesh SK\*, Li Y\*, on behalf of the NHLBI GO. (2012) Imputation of exome sequence variants into population-based samples identifies blood cell trait-associated loci in African Americans: the NHLBI GO Exome Sequencing Project. *Am J Hum Genet* 91:794-808. PMID: 23103231. PMCID: PMC3487117.
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55. Shetty PB, **Tang H**, Tayo BO, Morrison AC, Hanis CL, Rao DC, Young JH, Fox ER, Boerwinkle E, Cooper RS, Risch NJ, Zhu X; Candidate Gene Association Resource (CARE) Consortium. (2012) Variants in CXADR and F2RL1 are associated with

- blood pressure and obesity in African-Americans in regions identified through admixture mapping. *J Hypertens.* 30:1970-6. PMID: 22914544. PMCID: PMC3575678.
56. Candille SI, Absher DM, Beleza S, Bauchet M, McEvoy B, Garrison NA, Li JZ, Myers RM, Barsh GS, **Tang H**, Shriver MD. (2012) Genome-wide association studies of quantitatively measured skin, hair, and eye pigmentation in four European populations. *PLoS One.* 7:e48294. PMID 23118974. PMCID: PMC3485197.
  57. Ochs-Balcom HM, Preus L, Wactawski-Wende J, Nie J, Johnson NA, Zakharia F, **Tang H**, Carlson C, Carty C, Chen Z, Hoffman T, Hutter CM, Jackson RD, Kaplan RC, Li L, Liu S, Neuhauser ML, Peters U, Robbins J, Seldin MF, Thornton TA, Thompson CL, Kooperberg C, Sucheston LE. (2013) Association of DXA-derived bone mineral density and fat mass with African ancestry. *J Clin Endocrinol Metab.* 98:E713-7. PMID: 23436924.
  58. Chen Z, **Tang H**, Qayyum R, Schick UM, Nalls MA, Handsaker R, Li J, Lu Y, Yanek LR, Keating B, Meng Y, van Rooij1 FJA, Okada Y, Kubo M, Rasmussen-Torvik L, Keller MF, Lange L, Evans M, Bottinger EP, Linderman MD, Ruderfer DM, Hakonarson H, Papanicolaou H, Zonderman AB, Gottesman O, BioBank Japan Project, CHARGE Consortium, Thompson C, Ziv E, Singleton AB, Loos RJF, Sleiman PMA, Ganesh S, McCarroll S, Becker DM, Wilson JC, Lettre G, Reiner AP (2013) Genome-wide association analysis of red blood cell traits in African Americans: the COGENT Network. *Hum Mol Genet*, 22:2529-38. PMID: 23446634; PMCID: PMC3658166.
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  62. Wu L#, Candille SI#, Choi Y, Xie D, Jiang L, Li-Pook-Than J, **Tang H\***, Snyder M\*. (2013) Variation and genetic control of protein abundance in humans. *Nature*, 499(7456):79-82. PMCID: PMC3789121
  63. Franceschini N, Fox E, Zhang Z, Edwards TL, Nalls MA, et al.. (2013) Genome-wide Association Analysis of Blood-Pressure Traits in African-Ancestry Individuals Reveals Common Associated Genes in African and Non-African Populations. *Am J Hum Genet.* 93:545-54. PMC3769920.

64. Perez MV, Hoffmann TJ, **Tang H**, Thornton T, Stefanick ML, Larson JC, Kooperberg C, Reiner AP, Caan B, Iribarren C, Risch N. (2013) African-American race but not genome-wide African ancestry is negatively associated with atrial fibrillation among postmenopausal women. *Am Heart J*, 166:566-72.
65. Logsdon BA, Dai JY, Auer PL, Johnsen JM, Ganesh SK, Smith NL, Wilson JG, Tracy RP, Lange LA, Jiao S, Rich SS, Lettre G, Carlson CS, Jackson RD, O'Donnell CJ, Wurfel MM, Nickerson DA, **Tang H**, Reiner AP, Kooperberg C; NHLBI GO Exome Sequencing Project. (2014) A variational Bayes discrete mixture test for rare variant association. *Genet Epidemiol*. 38(1):21-30. PMID: PMC4030763
66. Claes P, Liberton DK, Daniels K, Rosana KM, Quillen EE, Pearson LN, McEvoy B, Bauchet M, Zaidi AA, Yao W, **Tang H**, Barsh GS, Absher DM, Puts DA, Rocha J, Beleza S, Pereira RW, Baynam G, Suetens P, Vandermeulen D, Wagner JK, Boster JS, Shriver MD. (2014) Modeling 3D facial shape from DNA. *PLoS Genet*. 10(3):e1004224. (PMCID: PMC3961191)
67. Hoffmann TJ, **Tang H**, Thornton TA, Caan B, Haan M, Millen AE, Thomas F, Risch N. (2014) Genome-wide association and admixture analysis of glaucoma in the Women's Health Initiative. *Hum Mol Genet*. 23(24):6634-43.
68. Keller MF, Reiner AP, Okada Y, van Rooij FJ, Johnson AD, Chen MH, Smith AV, Morris AP, Tanaka T, Ferrucci L, Zonderman AB, Lettre G, Harris T, Garcia M, Bandinelli S, Qayyum R, Yanek LR, Becker DM, Becker LC, Kooperberg C, Keating B, Reis J, **Tang H**, Boerwinkle E, Kamatani Y, Matsuda K, Kamatani N, Nakamura Y, Kubo M, Liu S, Dehghan A, Felix JF, Hofman A, Uitterlinden AG, van Duijn CM, Franco OH, Longo DL, Singleton AB, Psaty BM, Evans MK, Cupples LA, Rotter JI, O'Donnell CJ, Takahashi A, Wilson JG, Ganesh SK, Nalls MA; for the CHARGE Hematology, COGENT, and BioBank Japan Project (RIKEN) Working Groups. (2014) Trans-ethnic Meta-analysis of White Blood Cell Phenotypes. *Hum Mol Genet*. 23:6944-60. PMID: PMC4245044.
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70. Wang YJ, Tayo BO, Bandyopadhyay A, Wang H, Feng T, Franceschini N, **Tang H**, Gao J, Sung YJ; COGENT BP consortium, Elston RC, Williams SM, Cooper RS, Mu TW, Zhu X. (2014) The Association of the Vanin-1 N131S Variant with Blood Pressure is Mediated by Endoplasmic-Reticulum-Associated Degradation and Loss of Function. *PLoS Genet*. 10(9):e1004641. PMID: PMC4169380
71. Zaitlen N\*, Pasaniuc B, Sankararaman S, Bhatia G, Zhang J, Gusev A, Young T, Tandon A, Pollack S, Vilhjálmsson BJ, Assimes TL, Berndt SI, Blot WJ, Chanock S, Franceschini N, Goodman PG, He J, Hennis AJ, Hsing A, Ingles SA, Isaacs W, Kittles RA, Klein EA, Lange LA, Nemesure B, Patterson N, Reich D, Rybicki BA, Stanford JL, Stevens VL, Strom SS, Whitsel EA, Witte JS, Xu J, Haiman C, Wilson JG, Kooperberg C, Stram D, Reiner AP, **Tang H\***, Price AL\*. (2014) Leveraging

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  73. Coram\* MA, Candille\* SI, Duan Q, Chan KHK, Li Y, Kooperberg C, Reiner AP, **Tang H**. (2015) Leveraging Multi-ethnic Evidence for Mapping Complex Traits in Minority Populations: An Empirical Bayes Approach. *Am J Hum Genet* 96:740-52.
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81. Wang H, Choi Y, Tayo B, Wang X, Morris N, Zhang X, Broeckel U, Hanis C, Kardia S, Redline S, Cooper RS, **Tang H**, Zhu X. (2017) Genome-wide survey in African Americans demonstrates potential epistasis of fitness in the human genome. *Genet Epidemiol.* 2017 41:122-135. PMC5226866
82. Liang J, Le TH, Edwards DV, Tayo B, Gaulton KJ, et al. (2017) Single-trait and multi-trait genome-wide association analyses identify novel loci for blood pressure in African-ancestry populations. *PLoS Genet.* 13:e1006728. PMC5446189
83. Lloyd-Jones LR, Robinson MR, Moser G, Zeng J, Beleza S, **Tang H**, Barsh GS, Visscher PM. (2017) Inference on the Genetic Basis of Eye and Skin Colour in an Admixed Population via Bayesian Linear Mixed Models. *Genetics.* 206:1113-1126. PMC5499166
84. Choi Y, Coram M, Peng J, **Tang H** (2017) A Poisson Log-Normal Model for Constructing Gene Co-variation Network Using RNA-seq Data. *J Comput Biol.* 24:721-731. PMC5510689
85. Szulc P, Bogdan M, Frommlet F, **Tang H** (2017) Joint Genotype- and Ancestry-based Genome-wide Association Studies in Admixed Populations. *Genet Epidemiol.* In press. [PMC in progress]
86. Cannon ME, Duan Q, Wu Y, Zeynalzadeh M, Xu Z, Kangas AJ, Soininen P, Ala-Korpela M, Civelek M, Lusi AJ, Kuusisto J, Collins FS, Boehnke M, **Tang H**, Laakso M, Li Y, Mohlke KL. (2017) Trans-ancestry Fine Mapping and Molecular Assays Identify Regulatory Variants at the ANGPTL8 HDL-C GWAS Locus. *G3 (Bethesda).* 7:3217-3227. PMC5592946
87. eGTEx. (2017) Enhancing GTEx by bridging the gaps between genotype, gene expression, and disease. *Nat Genet.* 49:1664-1670.
88. Coram MA, Fang H, Candille SI, Assimes TL, **Tang H**. (2017) Leveraging Multi-Ethnic Evidence for Risk Assessment of Quantitative Traits in Minority Populations. *Am J Hum Genet.* 97:30278-1 PMC5630193

## INVITED PRESENTATIONS

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### National and International Meetings

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| 2001 | NHLBI Family Blood Pressure Program Analysis Workshop. Stanford, CA.                          |
| 2003 | Joint Statistical Meetings, San Francisco, CA.  |
| 2004 | MSRI workshop on Genetics of Complex Disease, UC Berkeley, CA.                                |
| 2004 | Taipei Symposium on Statistical Genomics, Taipei, December 2004.                              |
| 2005 | Joint Statistics Meeting, Minneapolis, MN.  |
| 2005 | Joint meeting of CSPS/IMS. Beijing, China.  |
| 2006 | NCI Workshop on Cancer Epidemiology and Genomics Variation in Hispanic/Latinos, Bethesda, MD. |
| 2006 | Congress of Epidemiology, Seattle, WA.  |
| 2006 | Joint Statistics Meeting, Seattle, WA.  |

- 2007 RECOMB SNP meeting, Los Angeles, CA.
- 2007 International Symposium and ICSA International Conference, Taipei, ROC.
- 2007 Symposium on Recent Development of Statistics in Biological Sciences. Zhunan, ROC.
- 2007 International Conference on the Frontiers of Statistics, Kunming, China.
- 2008 West Northern American Region of the International Biometrics Society Annual Meeting. Davis, CA.
- 2009 Summer school on Statistical Genomics. Singapore.
- 2009 American Society of Human Genetics Meeting. Honolulu, HI.
- 2009 International Chinese Statistical Association Meeting. San Francisco, CA.
- 2010 Joint Statistics Meeting. Vancouver, Canada.
- 2011 IMS-China International Conference on Statistics and Probability. Xi'an, China.
- 2011 Workshop on high-dimensional data analysis. Taipei, ROC.
- 2011 Taipei Symposium of Statistics. Taipei, ROC.
- 2012 ICSA Applied Statistics Symposium, Boston, MA.
- 2012 NIH Symposium "A Grand Opportunity: Developing a Resource for Genetic Epidemiology Research in Adult Health and Aging, Washington DC.
- 2013 ICSA-ISBS Joint Statistics Conference. Bethesda, MD.
- 2013 WNAR 2013 Conference. Los Angeles, CA.
- 2013 SFASA Biostatistics Symposium. Stanford, CA.
- 2013 ICSA International Conference. Hong Kong, China.
- 2014 Joint Applied Statistics Symposium of ICSA-KISS. Portland, OR.
- 2014 International Biometric Conference, Florence Italy.
- 2014 International Genetic Epidemiology Society Meeting. Vienna, Austria.
- 2015 ICSA Applied Statistics Symposium, Fort Collins, CO. June 15, 2015.
- 2015 First EMBL/Stanford Conference: Personalised Health. Heidelberg, Germany.
- 2015 Workshop on complex and high-dimensional data analysis. Kaohsiung, ROC.
- 2016 Computational and Methodological Statistics, Seville, Spain. (Upcoming, December 9)
- 2017 ICSA Applied Statistics Symposium, Chicago, IL. June 27, 2017.

### **Invited Seminars**

- 2007 Statistics and Genomics Seminar, UC Berkeley.
- 2007 Biostatistics Seminar, University of Pennsylvania.
- 2008 National Institute of Genomic Medicine, Mexico.
- 2008 Kaiser Permanente Division of Research, Oakland, CA

2008	Chinese Academy of Sciences - Max Plank Society Partner Institute for Computational Biology, Shanghai, China.
2008	Human Genetics Seminar, University of California, Los Angeles, CA.
2011	Department of Genome Science, University of Washington, Seattle, WA.
2011	Public Health Sciences Seminar, Fred Hutchinson Cancer Research Center, Seattle, WA.
2014	Biostatistics seminar, University of California, Davis, CA.
2014	Biostatistics seminar, Michigan State University. Lansing, MI.
2014	Biostatistics Seminar, Case Western Reserve University. Cleveland, OH.
2015	Bioinformatic Seminar, NorthShore University HealthSystem. Chicago, IL.
2015	Biostatistics Seminar, Harvard University School of Public Health.
2015	Visiting faculty seminar, Stanford Center at Peking University, Beijing, China.
2016	Genetics, Bioinformatics and Systems Biology Seminar, University of California, San Diego, CA.
2016	Statistics and Genomics Seminar, University of California, Berkeley, CA.
2016	Penn Bioinformatics Forum, University of Pennsylvania, Philadelphia, PA.
2016	Bioinformatics Seminar, Yale University, New Haven, CT.
2017	Bioinformatics Seminar, University of California, Los Angeles, CA.

## PROFESSIONAL SERVICE

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### Editorial Board

2010-present	Frontiers in Genetics, Review Editor.
2015-present	PLoS Genetics, Section Editor of Natural Variation.

### Manuscript Review

2002-present	Genetics, Nature Genetics, American Journal of Human Genetics, Genome Research, Human Genetics, Biometrics, Evolutionary Biology, BMC Genetics, Cancer Epidemiology, Biomarkers and Prevention, PLoS Genetics, PLoS Computational Biology, Genetic Epidemiology, American Journal of Epidemiology, ISMB, JASA, Statistica Sinica; Statistical Applications in Genetics and Molecular Biology, PNAS, Bioinformatics, Human Molecular Genetics, Annals of Applied Statistics.
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2008-2015 Guest Associate Editor for PLoS Genetics.  
2008-present Guest Associate Editor for PLoS Computational Biology.

### **Grant Review**

10/2010 NIH FIRCA study section, *ad hoc* reviewer  
02/2014 NIH BDMA study section, *ad hoc* reviewer  
04/2014 NIH DP5, mail-in reviewer  
06/2014 NIH BDMA study section, *ad hoc* reviewer  
2015- NIH BDMA study section, regular member

### **Conference Organization**

2007 ISMB/ECCB, Co-chair for Population Genetics Session of PLoS Track.  
2013 WNAR invited session organizer.  
2013-2015 ICSA invited session organizer.  
2014 JSM, topic-contributed session organizer.  
2015 ENAR invited session organizer.  
2014-present Annual Meeting of the American Society of Human Genetics,  
Scientific Program Committee.  
2016 14th Asia Pacific Bioinformatics Conference, scientific program  
committee and local co-chair.