CURRICULUM VITAE of Wenyi Wang

CONTACT

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Mailing address	Department of Bioinformatics and Computational Biology 1400 Pressler St Houston, TX 77030
Website:	http://odin.mdacc.tmc.edu/∼wwang7

EDUCATION

2003-2007 JOHNS HOPKINS BLOOMBERG SCHOOL OF PUBLIC HEALTH Baltimore, MD
PhD, Biostatistics

2001-2003 COLUMBIA UNIVERSITY COLLEGE OF PHYSICIANS AND SURGEONS
MA, Human nutrition New York City, NY

1997-2001 FUDAN UNIVERSITY Shanghai, China
BS, Honor Science Program, Biology

PROFESSIONAL EXPERIENCE

9/2015 - present *Tenured Associate Professor*
Department of Bioinformatics and Computational Biology,
University of Texas M. D. Anderson Cancer Center

9/2010 - 8/2015 *Tenure-track Assistant Professor*
Department of Bioinformatics and Computational Biology,
University of Texas M. D. Anderson Cancer Center

9/2014 - present *Program co-Director*
Biostatistics, Bioinformatics and Systems Biology,
The University of Texas Graduate School of Biomedical Sciences at Houston

6/2013 - present *Adjunct faculty member*
Department of Statistics,
Texas A&M University

8/2007 - 8/2010 *Postdoctoral Fellow*
Professor Terry Speed, Department of Statistics, University of California at Berkeley
Professor Ron Davis, Stanford Genome Technology Center, Stanford University

10/2008 - 12/2008 *Statistical consultant*
Counsyl, on software for newborn genetic counseling, Palo Alto CA

PROFESSIONAL ACTIVITIES

Institutional activities: Member of the Clinical Research Advisory Committee (approve internal funding for clinical research including clinical trials), Member of the Rice-MDACC joint biostatistics program admission committee, Member of the GSBS (graduate school) membership committee, Member of the Task Force to develop the new core curriculum for GSBS.

Membership: American Statistics Association, ENAR/International Biometric Society,
International Mathematical Society, International Society for Computational Biology,
American Society of Human Genetics, International Chinese Statistical Association,
International Society of Bayesian Analysis, American Association for Cancer Research,
ERCIM Working Group on Computational and Methodological Statistics,
Candidate for Program Chair 2017: ASA Section in Statistical Genetics and Genomics.

Journal referee for: Nature Genetics, Science, Journal of Clinical Oncology,
Proceedings of the National Academy of Sciences, Genome Research,
European Journal of Human Genetics, Nucleic Acids Research,
Cancer Research, Statistical Applications in Genetics and Molecular Biology,
IEEE/ACM Transactions on Computational Biology and Bioinformatics,
Journal of Biomedicine and Biotechnology, Molecular Carcinogenesis,
Annals of Applied Statistics, Bayesian analysis, Clinical Genetics,
British Journal of Dermatology, British Journal of Cancer,
Journal of Applied Statistics, Bioinformatics, PLOS Computation Biology,
BMC Research Notes

Grant referee for: The Netherlands Organization for Health Research and Development,
The American Cancer Society,
NIH Cancer, Heart, and Sleep Epidemiology (CHSA) Study Section (Feb 2016)

Conference program committee: American Association for Cancer Research (subcommittee on Bioinformatics and Computational Biology 2015), RECOMB2015 Satellite Workshop on Cancer Computational Biology and Sequencing, Bayesian Biostatistics and Bioinformatics Conference 2014

Consortium membership: LiFE consortium for Li-Fraumeni studies; the Cancer Genome Atlas projects; ICGC-TCGA DREAM Mutational Calling Challenge (Wang-Wheeler-HGSC team ranked #2 in round 2 and tied with the Broad Institute as #2 in round 3); ICGC PanCanAtlasWorkingGroup (PCAWG) evolution and heterogeneity working group. MuSE is one of the 3 major mutation callers for the PanCanAtlas projects (NCI-sponsored post-TCGA), currently running through all 2,000+ whole-exome sequencing data generated from the TCGA project. Concurrently MuSE is running through all 2,000+ whole-genome sequencing data for the ICGC PCAWG projects.

GRANT SUPPORT

FUNDED

Co-Investigator (20%)
4/1/2016-3/31/2021
Consisten variable selection in $p >> n$ settings.
NIH/NCI
PI: Valen Johnson

Principal Investigator (25%)
09/24/2014-8/31/2019
Statistical methods for genomic analysis of heterogeneous tumors
1R01CA183793 ($1,275,421, $255,084/year);
NIH/NCI

Principal Investigator (40%)
06/01/2013-5/31/2016 (NCE)
Personalized risk assessment for families with Li-Fraumeni syndrome
RP130090 ($460,154, $230,077/year)
Cancer Prevention & Research Institute of Texas (CPRIT)

PI of the MDACC subcontract (11%)
02/01/2013-01/31/2018
Bioinformatics tools for genomic analysis of tumor and stromal pathways in cancer
1R01CA174206-01 ($1,248,881, subcontract $276,870, $55,374/year)
NIH/NCI
PI - Giovanni Parmigiani

Co-Principal Investigator
01/01/2015-12/31/2016
Cancer risk in Li Fraumeni syndrome (LFS) kindreds in regions of high founder mutation prevalence and regions of low prevalence in absence of founder as determined by LFSpro
The Sister Institution Network Fund ($100,000, $50,000/year)
MD Anderson Cancer Center
PI - Strong/Wang

PI of the MDACC subcontract (Postdoctoral fellowship awarded to Yu Fan)
5/1/2014-4/30/2016
GCC/Keck Center's Computational Cancer Biology Training Program
RP140113 ($108,278)
Cancer Prevention Institute of Research (subcontract from University of Houston)
PI - Rathindra Bose

Co-Investigator (4%)
9/1/2014-8/31/2019
Developing New Rational, Personalized Medicine for Lung Cancer Based on Understanding of Lung Cancer Molecular and Cellular Biology
$770,090 ($97,480/year)

NIH/NCI (Subcontract from University of Texas Southwestern Medical Center)
PI - John Minna

PENDING

Principal Investigator (20%)
4/1/2016-3/31/2021
Quantitative characterization and prediction of cancer outcomes in families with Li-Frameni Syndrome
1R01CA201449-01 ($1,250,000, $250,000/year)
NIH/NCI

PUBLICATIONS

Articles

1. Fan Y, Xi L, Hughes DST, Zhang J, Zhang J, Futreal AP, Wheeler DA, **Wang W**✉. Accounting for tumor heterogeneity using a sample-specific error model improves sensitivity and specificity in mutation calling for sequencing data. *Genome Biology, under revision*

2. Li J, Fu C, Speed TP, **Wang W**✉, Symmans F✉. Translating gene-expression profiling for archival tumor tissues with RNA-seq. *Genome Medicine, under revision*

3. Peng G, Bojadzieva J, Ballinger ML, Li J, Savage S, Mai P, Thomas DM, Strong LC, **Wang W**✉. Estimating TP53 mutation carrier probability in families with Li-Fraumeni Syndrome using LFSPRO. *under review*

4. Ahn J, Morita S, **Wang W**✉and Yuan Y✉. Bayesian shared-parameter models for longitudinal dyadic data with informative missing data. *Annals of Applied Statistics, under revision*

5. Shin SJ, Peng G, **Wang W**✉, Ying Yuan✉. Bayesian semiparametric estimation of cancer-specific age-at-onset penetrance with application to Li-Fraumeni Syndrome. *JASA, under revision*

6. Nikooienejad A, **Wang W**✉, Johnson VE✉. Bayesian variable selection for binary outcomes in high dimensional genomic studies using non-local priors. *Bioinformatics, accepted*

7. Palculict TB, Ruteshouser EC, Fan Y, **Wang W**, Strong L, Huff V. Identification of germline DICER1 mutations and loss of heterozygosity in familial Wilms tumor using whole genome sequencing. *Journal of Medical Genetics* Nov 13. pii: jmedgenet-2015-103311. doi: 10.1136/jmedgenet-2015-103311.

8. Zheng S, et al., The Cancer Genome Atlas Research Network, Hammer GD*, Giordano TJ*, Verhaak RGW*. Comprehensive Pan-Genomic Characterization of Adrenocortical Carcinoma. *Nature Genetics, under revision*

9. Lefterova MI*, Shen P*, Odegaard JI*, Fung E, Chiang T, Peng G, Davis RW, **Wang W**, Schrijver I, Scharfe C. Next-generation molecular testing of newborn dried blood spots for cystic fibrosis. *Journal of Molecular Diagnostics, accepted*

10. The Cancer Genome Atlas Research Network. The molecular taxonomy of primary prostate cancer. *Cell* 2015 Nov 5;163(4):1011-25. doi: 10.1016/j.cell.2015.10.025.

11. Fang LT, Afshar PT, Chhibber A,Mohiyuddin M, Fan Y, Mu J, Gibeling G, Barr S, Asadi NB, Gerstein M, Koboldt D, **Wang W**, Wong WH, Lam H. An ensemble approach to accurately detect somatic mutations using SomaticSeq. *Genome Biology*. 2015 Sep 17;16:197. doi: 10.1186/s13059-015-0758-2.

12. Ewing AD, Houlahan KE, Hu Y, Ellrott K, Caloian C, Yamaguchi TN, Bare JC, P'ng C, Waggott D, Sabelnykova VY; ICGC-TCGA DREAM Somatic Mutation Calling Challenge participants, Kellen MR, Norman TC, Haussler D, Friend SH, Stolovitzky G, Margolin AA, Stuart JM, Boutros PC. Combining tumor genome simulation with crowdsourcing to benchmark somatic single-nucleotide-variant detection. *Nat Methods.* 2015 Jul;12(7):623-30. doi: 10.1038/nmeth.3407. Epub 2015 May 18.

13. Peng G, Fan Y, **Wang W**✉. FamSeq: a variant calling program for family-based sequencing data using graphics processing units. *PLOS Computational Biology* 2014 Oct 30;10(10):e1003880. doi: 10.1371/journal.pcbi.1003880.

14. Davis CF, et al.; Cancer Genome Atlas Research Network, Chin L, Meyerson M, Kucherlapati R, Park WY, Robertson AG, Laird PW, Henske EP, Kwiatkowski DJ, Park PJ, Morgan M, Shuch B, Muzny D, Wheeler DA, Linehan WM, Gibbs RA, Rathmell WK, Creighton CJ. The somatic genomic landscape of chromophobe renal cell carcinoma. *Cancer Cell.* 2014 Sep 8;26(3):319-30. doi: 10.1016/j.ccr.2014.07.014. Epub 2014 Aug 21. PMID: 25155756

15. Cancer Genome Atlas Research Network. Comprehensive molecular characterization of urothelial bladder carcinoma. *Nature* 507(7492):315-22, 3/2014. e-Pub 1/2014.

16. Ahn J, Liu S, **Wang W**✉, Yuan Y✉. Bayesian latent-class mixed-effect hybrid models for dyadic longitudinal data with non-ignorable dropouts. *Biometrics* 2013 Dec;69(4):914-24. doi: 10.1111/biom.12100. Epub 2013 Nov 6

17. The Cancer Genome Atlas Research Network. The Cancer Genome Atlas Pan-Cancer analysis project. *Nature Genetics* 2013 Oct;45(10):1113-20. doi: 10.1038/ng.2764.

18. Srivastava S, **Wang W**, Zinny PO, Colen RR, Baladandayuthapani V. Integrating multi-platform genomic data using hierarchical bayesian relevance vector machines. *EURASIP Journal on Bioinformatics and Systems Biology* 2013 Jun 28;2013(1):9. doi: 10.1186/1687-4153-2013-9.

19. Shen P*, **Wang W***, Chi AK, Fan Y, Davis RW, Scharfe C. Target capture using double-stranded DNA probes. *Genome Medicine* 2013, 5:50 doi:10.1186/gm454. *authors contributed equallly

20. Ahn J, Yuan Y, Parmigiani G, Suraokar MB, Diao L, Wistuba II, and **Wang W**✉. DeMix: deconvolution for mixed cancer transcriptomes. *Bioinformatics* 2013 doi: 10.1093/bioinformatics/btt301.

21. Peng G, Fan Y, Palculict TB, Shen P, Ruteshouser EC, Chi A, Davis RW✉, Huff V, Scharfe C, **Wang W**✉. Rare variant detection using family-based sequencing analysis. *Proceedings of the National Academy of Sciences.* ePub, February 20, 2013, doi: 10.1073/pnas.1222158110.

22. Zhang N, Xu Y, O'Hely M, Speed TP, Scharfe C, **Wang W**✉. SRMA: an R package for sequence based calling in candidate genes with custom resequencing microarrays. *Bioinformatics.* e-Pub 05/2012.

23. Hua Y, Gorshkov K, Yang Y, **Wang W**, Zhang N, Hughes DPM. Slow down to stay live: HER4 protects against cellular stress and confers chemoresistance in neuroblastoma. *Cancer.* e-Pub 03/2012.

24. Rubio JP, Wilkins EJ, Kostchet K, Cowie TC, O'Hely M, Burfoot R, **Wang W**, Speed TP, Stankovich J, Horne M. A DNA resequencing array for genes involved in Parkinson's Disease. *Parkinsonism & Related Disorders.* e-Pub 01/2012.

25. Shen P*, **Wang W***, Krishnakumar S, Palm C, Chi AK, Enns GM, Davis RW, Speed TP, Mindrinos MN, Scharfe C. High-quality DNA sequence capture of 524 disease candidate genes. *Proceedings of the National Academy of Sciences.* 2011, Apr 19;108(16):6549-54. Epub 2011 Apr 5.

    *authors contributed equally

26. Lin S*, **Wang W***, Palm C, Davis RW, Juneau K. A Molecular inversion probe assay for detecting alternative splicing. *BMC Genomics* Dec 2010, 11:712.

    *authors contributed equally

27. **Wang W**✉, Shen P, Thyagarajan S, Lin S, Palm C, Horvath R, Klopstock T, Cutler D, Pique L, Schrijver I, Davis RW, Mindrinos M, Speed TP, Scharfe C✉. Identification of rare DNA variants in mitochondrial disorders with improved array-based sequencing. *Nucleic Acids Research* 2011 Jan;39(1):44-58. Epub 2010 Sep 15.

28. **Wang W**, Niendorf KB, Patel D, Blackford A, Marroni F, Sober AJ, Parmigiani G and Tsao H. Estimating *CDKN2A* Carrier probability and personalizing cancer risk assessments in hereditary melanoma using MelaPRO. *Cancer Research.* Jan 2010 doi:10.1158/0008-5472.

29. **Wang W**, Carvalho B, Miller N, Pevsner J, Chakaravarti A and Irizarry RA. Estimating genome-wide copy number using allele specific mixture models. *Journal of Computational Biology.* 2008, 15:857-66.

30. **Wang W**, Chen S, Brune KA, Hruban RH, Parmigiani G and Klein AP. Development and validation of a risk assessment tool for individuals with a family history of pancreatic cancer: PancPRO. *Journal of Clinical Oncology*. 2007;25:1417-22.

31. Nicodemus KK, **Wang W** and Shugart YY. Stability of variable importance scores and rankings using statistical learning tools on single nucleotide polymorphisms (SNPs) and risk factors involved in gene-gene and gene-environment interactions. *BMC Proceedings.* 2007;1 Suppl 1:S58.

32. Chen S, **Wang W**, Lee S, Nafa K, Lee J, Romans K, Watson P, Gruber SB, Euhus D, Kinzler KW, Jass J, Gallinger S, Lindor N, Casey G, Ellis N, Giardiello FM, the Colon Cancer Family Registry, Offit K, Parmigiani G. Prediction of germline mutations and cancer risk in the Lynch syndrome. *Journal of the American Medical Association* 2006;296:1479-87.

33. Gonzalez JR, **Wang W**, Ballana E and Estivill X. A recessive Mendelian model to predict carrier probabilities of DFNB1 for non-syndromic deafness. *Human Mutation* 2006;27:1135-42.

34. Chen S, **Wang W**, Broman K and Parmigiani G. BayesMendel: An R environment for Mendelian risk prediction. *Statistical Application in Genetics and Molecular Biology* 2004;3: Article 21.

Book Chapters

35. **Wang W**, Fan Y, Speed TP. DNA variant calling in targeted sequencing data. In *Advances in statistical bioinformatics: Models and Integrative Inference for High-Throughput Data* (Editors: Do KA, Qin ZS, Vannuci M). Cambridge University Press. June 2013

PRESENTATIONS

Invited Talks

1. Accounting for tumor heterogeneity using a sample-specific error model improves sensitivity and specificity in mutation calling for sequencing data. KU Leuven Center for Human Genetics, Leuven, Belgium, 04/14/2016

2. Gene expression deconvolution of heterogeneous tumor samples: DeMix-Bayes. The Francis Crick Institute. London, UK, 12/15/2015

3. Bayesian variable selection for binary outcomes in high dimensional settings. 8th International Conference of the ERCIM WG on Computational and Methodological Statistics. London, UK, 12/12/2015

4. Gene expression deconvolution in heterogeneous tumor samples using DeMix-Bayes. NCI DCCPS New Grantee Workshop, 11/5/2015

5. Bayesian variable selection for binary outcomes in high dimensional settings. Joint Statistics Meeting. Seattle, WA, 8/9/2015

6. Cancer-specific characterization of the Li-Fraumeni syndrome. A.C. Carmargo Cancer Center, Sau Paulo, Brazil, 7/28/2015

7. Statistical methods for analysis of genomic data from heterogeneous cancer samples. BioC 2015, Seattle, WA, 7/21/2015

8. Statistical methods for analysis of genomic data from heterogeneous cancer samples. International Bioinformatics Workshop. Harbin, China, 7/10/2015

9. Statistical methods for analysis of genomic data from heterogeneous cancer samples. University of Evry, Essonne, France, 5/19/2015

10. Statistical methods for analysis of genomic data from heterogeneous cancer samples, Johns Hopkins University, Department of Biostatistics, Baltimore, MD, 4/6/2015

11. LFSpro: a risk assessment tool to estimate TP53 mutation status in families with Li-Fraumeni Syndrome, The University of Texas School of Public Health, Human Genetics Center, Houston, TX, 2/9/2015

12. DeMix-Bayes: a Bayesian model for the deconvolution of mixed cancer transcriptomes in microarray and RNA sequencing data, Baylor College of Medicine, Computational and Integrative Biomedical Research Center, Houston, TX, 1/14/2015

13. Cancer-specific characterization of the Li-Fraumeni Syndrome, Worcester Polytechnic Institute, Biomedical Engineering, Worcester, MA, 11/6/2014

14. DeMix-Bayes: a Bayesian model for the deconvolution of mixed cancer transcriptomes in microarray and RNA sequencing data, *TCGA Face-to-face network meeting*, Bethesda, MD, 2014.10.28

15. MuSE: somatic evolution estimation for mutation calling in sequencing data of matched tumor-normal samples, The Joint Statistical Meetings, *The Joint Statistical Meetings*, Boston, MA, 2014.8.4

16. Bayesian variable selection for binary outcomes in high dimensional settings, *The International Society of Bayesian Analysis World Meeting*, Cancun, Mexico, 2014.7.17

17. Somatic Mutation Calling and Gene Expression Deconvolution in Heterogeneous Tumor Samples, University of Oxford, Department of Oncology, Oxford, United Kingdom, 2014.6.12

18. Discussant for Keynote Speaker: Two Aspects in Tumor Heterogeneity: Subclonal Mutations and Stromal Expression, *The Southern Regional Council on Statistics Summer Research Conference*, Galveston, TX, 2014.6.3

19. Gene expression deconvolution in heterogeneous tumor samples, Texas A&M Unversity, Department of Statistics, College Station, TX, 2014.2.21

20. Gene expression deconvolution in heterogeneous tumor samples, *7th Annual Bayesian Biostatistics and Bioinformatics Conference*, Houston, TX, 2014.2.13

21. Gene expression deconvolution in heterogeneous tumor samples. *The 9th ICSA International Conference*, HongKong, China, 2013.12.23

22. Personalized risk assessment for families with Li-Fraumeni Syndromes. *The LiFE Consortium Meeting*. Boston, MA, 2013.10.26

23. Gene expression deconvolution in heterogeneous tumor samples. *The Joint Statistics Meetings*. Montreal, Canada, 2013.8.3

24. Rare variant detection using family-based sequencing analysis. Washington University Department of Genetics. St. Louis, MO, 2012.11

25. Determining probability of rare variants: implications for designs of family-based sequencing studies. *The Joint Statistical Meetings*. San Diego, CA, 2012.08

26. Determining probability of rare variants in sequencing studies for familial cancer syndromes. *The International Workshop on Cancer Systems Biology*. Changchun, China, 2012.07

27. Determining probability of rare variants: implications for designs of family-based sequencing studies. *The Southern Regional Council on Statistics: Summer Research Conference*. Jekyll Island, GA, 2012.06

28. Determining probability of rare variants: implications for designs of family-based sequencing studies. *International Conference on Risk Assessment and Evaluation of Predictions*. Silver Spring, MD, 2011.10

29. Determining probability of rare variants: implications for designs of family-based sequencing studies. UT School of Public Health Human Genetics Center, 2011.9

30. Determining probability of germline mutations in family-based sequencing studies. The First Wuxi International Statistics Forum, Wuxi, China, 2011.7

31. Validating risk prediction models using family registries, *Fourth Annual Bayesian Biostatistics Conference*, Houston, TX, 2011.1

32. Statistical methods for DNA resequencing analysis in disease-gene studies, Rice University, Department of Statistics, Houston, TX, 2011.1

SOFTWARE

1. `BayesMendel` (co-author): a comprehensive environment for prediction of inherited cancer susceptibility

   - R package, http://bcb.dfci.harvard.edu/BayesMendel

2. `SRMA`: Sequence robust multi-array analysis for resequencing arrays

   - R package, http://odin.mdacc.tmc.edu/ wwang7/SRMAIndex.html

3. `FamSeq`: Analysis of family-based sequencing data

   - C++ based, GPU based http://bioinformatics.mdanderson.org/main/FamSeq

4. `DeMix`: Deconvolution of mixed cancer genomes

   - R and C code, http://odin.mdacc.tmc.edu/ wwang7/DeMix.html

5. `LFSPRO`: Personalized risk assessment for families with Li-Fraumeni syndromes

   - R package, http://bioinformatics.mdanderson.org/main/LFSPRO
   - R function in BayesMendel, http://bcb.dfci.harvard.edu/BayesMendel

6. `MuSE`: Mutation somatic evolution estimation for sequencing data from matched tumor-normal pairs.

   - C++ based, http://bioinformatics.mdanderson.org/main/MuSE

   Under construction:

7. `iMOMLogit`: Bayesian model selection using non-local priors in logistic models for binary outcomes (R package).

8. `MPC`: Multi-platform variant caller for DNA sequencing data (C++ based).

9. `LFSPRO.cs`: cancer specific risk prediction for families with Li-Fraumeni Syndrome (R package)
10. `LFSPRO.mp`: multiple primary cancer specific risk prediction for families with Li-Fraumeni Syndrome (R package)
11. `Rclone`: identification of subclonal structure using sequencing data from tumor samples. (R package)

TEACHING EXPERIENCE

The UNIVERSITY OF TEXAS MD ANDERSON CANCER CENTER

POSTDOC

2015.8-present Xuedong Pan (joint with Val Johnson, PhD in Genetics, Fudan University)
2015.5-present Nilotpal Sanyal (joint with Val Johnson, PhD in Statistics, University of Missouri)
2012.4-present Yu Fan (PhD in Evolution and Ecology, University of Connecticut)
2013.7-2015.2 Seung Jun Shin (joint with Ying Yuan, PhD in Statistics,
North Carolina State University)
Current position: Tenure-track Assistant Professor in Statistics,
Korea University, Seoul, South Korea
2011.9-2013.8 Jaeil Ahn (joint with Ying Yuan, PhD in Biostatistics, University of Michigan)
Current position: Tenure-track Assistant Professor in Biostatistics and Bioinformatics,
Georgetown University, Washington DC

PHD STUDENT

2014.1-present Zeya Wang (joint with Jeff Morris, Rice Statistics)
2013.5-present Jialu Li (GSBS Biostatistics)
2011.1-2015.8 Gang Peng (GSBS Biostatistics, AAAS/Science Program for Excellence in Science)

RESEARCH ASSISTANT

2014.8-present Elissa Dodd
2013.9-2015.5 Amir Nikooienejad (Texas A&M Statistics)

ROTATION STUDENT

2015.9-2015.12 Yichi Zhang (GSBS)
2012.3-2012.5 Yihua Liu (GSBS)

INTERN

2013.6-2013.8 Emily Johnson (Bellaire high school, Houston TX)
2012.11-2013.7 Sara Algeri (Texas A&M Statistics)
2012.5-2012.8 Ling Chen (Rice statistics)
2012.5-2012.8 Sanvesh Srivastava (Purdue statistics)
2011.1-2011.9 Yan Huang (Rice statistics)
2011.1-2011.5 Yulun Liu (UT SPH Biostat)

THE GRADUATE SCHOOL OF BIOLOGICAL SCIENCES AT HOUSTON

2015.12 Lecturer, Introduction to Bioinformatics GS0011062
2014.11 Lecturer, Introduction to Bioinformatics GS0011062
2013.10 Lecturer, Introduction to Bioinformatics GS0011062

RICE UNIVERSITY, DEPARTMENT OF STATISTICS
2013.1 Lecturer, Biostatistics/Bioinformatics STAT453/553

FUDAN UNIVERSITY, SCHOOL OF LIFE SCIENCES, SHANGHAI, CHINA
2015.6.24-6.28 Statistical Genomics Workshop
Instructor: Drs.Terry Speed, Wenyi Wang, Andrew Teschendorff
Level: Graduate students
Enrollment: 200

TONGJI UNIVERSITY, DEPARTMENT OF BIOINFORMATICS, SHANGHAI, CHINA
2012.7 Invited short course: Assessing risk in familial cancer syndromes
Enrollment: 30

SHANGHAI INSTITUTE OF BIOLOGICAL SCIENCES, CHINESE ACADEMY OF SCIENCES
2011.7 Invited short course: Biostatistics/Bioinformatics
Instructor: Drs. Jun Liu, Wenyi Wang
Level: first-year graduate students
Enrollment: 400

VISITING SCHOLARSHIP
01.2013-12.2014 Fudan University Key Laboratory Senior Visiting Scholarship, Fudan University, School of Computer Science, Shanghai, China

HONORS AND AWARDS

2014	Outstanding service to graduate education The University of Texas Graduate School of Biomedical Sciences at Houston
2011	The Stellar Abstract Award, the 5th Annual Program in Quantitative Genomics, Harvard School of Public Health
2008	Phi Beta Kappa, Delta Omega Alpha
2008	The Jane and Steve Dykacz Award for best student paper in medical statistics, Johns Hopkins Biostatistics
2007	Travel Award, the 11th International Conference on Research in Computational and Molecular Biology
2006	Travel Award, the International Genetic Epidemiology Society 15th Annual Meeting
2005	The June B. Culley Award for best performance in the qualifying oral exam, Johns Hopkins Biostatistics