

# CURRICULUM VITAE of Wenyi Wang

## CONTACT

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## 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*  
Counsel, on software for newborn genetic counseling, Palo Alto CA

## PROFESSIONAL ACTIVITIES

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

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

Grant referee for: The Netherlands Organization for Health Research and Development, The American Cancer Society

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.

## GRANT SUPPORT

### FUNDED

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%)

06/01/2013-11/31/2015

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 (5%)

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%)

9/1/2015-8/31/2020

Quantitative characterization and prediction of cancer outcomes in families with Li-Fraumeni Syndrome

1R01CA201449-01 (\$1,250,000, \$250,000/year)

NIH/NCI

Principal Investigator

11/1/2015-10/30/2017

CUDA-based Parallelization to Accelerate Computation for Cancer Risk Assessment and A Few Analytical Challenges in Cancer Genomic Studies

Compute the cure cancer research grant (\$200,000, \$100,000/year)

NVIDIA Foundation

## PUBLICATIONS

### Articles

1. 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 review*
2. Nikooienejad A, **Wang W**, Johnson VE. Bayesian Variable Selection for Binary Outcomes in High Dimensional Genomic Studies Using Non-Local Priors. *Bioinformatics, 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. *Journal of Clinical Oncology, 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 review*
5. 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, under review*
6. Zheng S, Cherniack AD, Dewal N, Moffitt RA, Danilova L, Murray BA, Lerario AM, Else T, Knijnenburg TA, Ciriello G, Kim S, Assie G, Morozova O, Akbani R, Shih J, Hoadley KA, Choueiri TK, Waldmann J, Mete O, Robertson AG, Raphael BJ, Meyerson M, Demeure MJ, Beuschlein F, Gill AJ, Latronico AC, Fragoso MC, Cope LM, Kebebew E, Habra MA, Whitsett TG, Bussey KJ, Rainey WE, Asa SL, Bertherat J, Fassnacht M, Wheeler DA, The Cancer Genome Atlas Research Network, Hammer GD\*, Giordano TJ\*, Verhaak RGW\*. Comprehensive Pan-Genomic Characterization of Adrenocortical Carcinoma. *Nature Genetics, under revision*
7. The Cancer Genome Atlas Research Network. The molecular taxonomy of primary prostate cancer. *Cell, accepted*
8. 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, in press*
9. 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.
10. 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.

11. Davis CF, Ricketts CJ, Wang M, Yang L, Cherniack AD, Shen H, Buhay C, Kang H, Kim SC, Fahey CC, Hacker KE, Bhanot G, Gordenin DA, Chu A, Gunaratne PH, Biehl M, Seth S, Kaiparettu BA, Bristow CA, Donehower LA, Wallen EM, Smith AB, Tickoo SK, Tamboli P, Reuter V, Schmidt LS, Hsieh JJ, Choueiri TK, Hakimi AA; 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
12. Cancer Genome Atlas Research Network. Comprehensive molecular characterization of urothelial bladder carcinoma. *Nature* 507(7492):315-22, 3/2014. e-Pub 1/2014.
13. 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
14. 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.
15. 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.
16. 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 equally
17. 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.
18. 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.
19. 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.
20. 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.
21. 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.
22. 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

23. 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
24. **Wang W**✉, Shen P, Thyagarajan S, Lin S, Palm C, Horvath R, Klopstock T, Cutler D, Pique L, Schrijver I, Davis RW, Mindrinis 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.
25. **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.
26. **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.
27. **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.
28. 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.
29. 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.
30. 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.
31. 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

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

2. Cancer-specific Characterization of the Li-Fraumeni Syndrome. A.C. Carmargo Cancer Center, Sau Paulo, Brazil, 7/28/2015
3. Statistical methods for analysis of genomic data from heterogeneous cancer samples. BioC 2015, Seattle, WA, 7/21/2015
4. Statistical methods for analysis of genomic data from heterogeneous cancer samples. International Bioinformatics Workshop. Harbin, China,
5. Statistical methods for analysis of genomic data from heterogeneous cancer samples. University of Evry, Essonne, France, 5/19/2015
6. Statistical methods for analysis of genomic data from heterogeneous cancer samples, Johns Hopkins University, Department of Biostatistics, Baltimore, MD, 4/6/2015
7. 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
8. 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
9. Cancer-specific characterization of the Li-Fraumeni Syndrome, Worcester Polytechnic Institute, Biomedical Engineering, Worcester, MA, 11/6/2014
10. 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
11. 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
12. Bayesian variable selection for binary outcomes in high dimensional settings, *The International Society of Bayesian Analysis World Meeting*, Cancun, Mexico, 2014.7.17
13. Somatic Mutation Calling and Gene Expression Deconvolution in Heterogeneous Tumor Samples, University of Oxford, Department of Oncology, Oxford, United Kingdom, 2014.6.12
14. 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
15. Gene expression deconvolution in heterogeneous tumor samples, Texas A&M University, Department of Statistics, College Station, TX, 2014.2.21
16. Gene expression deconvolution in heterogeneous tumor samples, *7th Annual Bayesian Biostatistics and Bioinformatics Conference*, Houston, TX, 2014.2.13
17. Gene expression deconvolution in heterogeneous tumor samples. *The 9th ICSA International Conference*, HongKong, China, 2013.12.23

18. Personalized risk assessment for families with Li-Fraumeni Syndromes. *The LiFE Consortium Meeting*. Boston, MA, 2013.10.26
19. Gene expression deconvolution in heterogeneous tumor samples. *The Joint Statistics Meetings*. Montreal, Canada, 2013.8.3
20. Rare variant detection using family-based sequencing analysis. Washington University Department of Genetics. St. Louis, MO, 2012.11
21. Determining probability of rare variants: implications for designs of family-based sequencing studies. *The Joint Statistical Meetings*. San Diego, CA, 2012.08
22. Determining probability of rare variants in sequencing studies for familial cancer syndromes. *The International Workshop on Cancer Systems Biology*. Changchun, China, 2012.07
23. 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
24. 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
25. Determining probability of rare variants: implications for designs of family-based sequencing studies. UT School of Public Health Human Genetics Center, 2011.9
26. Determining probability of germline mutations in family-based sequencing studies. The First Wuxi International Statistics Forum, Wuxi, China, 2011.7
27. Validating risk prediction models using family registries, *Fourth Annual Bayesian Biostatistics Conference*, Houston, TX, 2011.1
28. 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. MOMLogit: 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)

## TEACHING EXPERIENCE

The UNIVERSITY OF TEXAS MD ANDERSON CANCER CENTER  
POSTDOC

- |                |   |
|----------------|---|
| 2015.8-present | Xuedong Pan (PhD in Genetics, Fudan University)   |
| 2012.4-present | Yu Fan (PhD in Evolution and Ecology, University of Connecticut)  |
| 2013.7-2015.2  | Seung Jun Shin (PhD in Statistics, North Carolina State University)   |
|                | Current position: Tenure-track Assistant Professor in Statistics,<br>Korea University, Seoul, South Korea                       |
| 2011.9-2013.8  | Jaeil Ahn (PhD in Biostatistics, University of Michigan)  |
|                | Current position: Tenure-track Assistant Professor in Biostatistics and Bioinformatics,<br>Georgetown University, Washington DC |

PHD STUDENT

- |                |  |
|----------------|--|
| 2014.1-present | Zeya Wang (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

- |               |                  |
|---------------|------------------|
| 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

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