

Yu Zhang
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Department of Statistics
The Pennsylvania State University
University Park, PA 16802

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(814) 867-0780 (office)
(814)-863-7114 (fax)

CURRICULUM VITAE

RESEARCH INTEREST

Statistical method development, Bayesian modeling, Computational Biology

PROFESSIONAL CAREER

2012- present	Associate Professor of Statistics, The Pennsylvania State University
2006- 2012	Assistant Professor of Statistics, The Pennsylvania State University

POST-DOCTORAL TRAINING

2004-2006	Department of Statistics, Harvard University, Cambridge, MA, USA Advisor: Jun S. Liu
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EDUCATION

2000-2004	Department of Mathematics, University of Southern California, Los Angeles, CA, USA Ph.D. in Applied Mathematics Advisor: Michael S. Waterman
1996-2000	Department of Physics, Peking University, Beijing, China B.S. in Physics

AWARD AND HONORS

2000-2004	Graduate Merit Award, University of Southern California
2001 Summer	Steed Fellowship, University of Southern California

PAPERS SUBMITTED

1. **Zhang Y**, Tian L, Sleiman P, Ghosh S, Hakonarson H. Reanalysis of genome-wide association data sets reveals novel inflammatory bowel disease loci. *Revision submitted to Euro J Hum Genet. Aug 16, 2017*

PUBLICATIONS

1. **Zhang Y**, Ross C Hardison. (2017) Accurate and reproducible functional maps in 127 human cell types via 2D genome segmentation. *Nucleic Acids Res.* gkx659. DOI: <https://doi.org/10.1093/nar/gkx659>
2. **Zhang Y**. (2017) Epigenetic Combinatorial Patterns Predict Disease Variants. *Front. Genet.* 8:71 <https://doi.org/10.3389/fgene.2017.00071>
3. **Zhang Y**. (2016) On the use of p-values in genome wide disease association mapping. *J Biom Biostat*, 7:3.

4. **Zhang Y**, An L, Yue F, Hardison RC (2016). Jointly characterizing epigenetic dynamics across multiple human cell types. *Nucleic Acids Res*, 44(14):6721-31.
5. Chen KB, Hardison RC, **Zhang Y**. (2014) dCaP: detecting differential binding events in multiple conditions and proteins. *BMC Genomics*, **15**(Suppl 9):S12.
6. **Zhang Y**, Ghosh S, Hakondarson H. (2014) Dynamic Bayesian testing of sets of variants in complex diseases. *Genetics*, 98(3):867-78.
7. Lee Y, Ghosh D, **Zhang Y** (2014) Regression hidden Markov modeling reveals heterogeneous gene expression regulation: a case study in mouse embryonic stem cells. *BMC Genomics*, **15**:360 doi:10.1186/1471-2164-15-360
8. Lee Y, Ghosh D, Hardison RC, **Zhang Y**. (2014) MRHMMs: Multivariate Regression Hidden Markov Models and the variantS. *Bioinformatics*, 30(12):1755-6.
9. Ding Y, Tang Y, Kwok CT, **Zhang Y**, Bevilacqua PC, Assmann SM (2013) In vivo genome-wide profiling of RNA secondary structure reveals novel regulatory features. *Nature*. doi:10.1038/nature12756
10. Lee Y, Ghosh D, **Zhang Y** (2013) Association testing to detect gene–gene interactions on sex chromosomes in trio data. *Front. Genet.* 13 November 2013, 4:239
11. **Zhang Y** (2013) *De novo* inference of stratification and local admixture in sequencing studies. *BMC Bioinformatics*, 14(Suppl 5): S17. PMID: PMC3622634.
12. **Zhang Y** (2013) A dynamic Bayesian Markov model for phasing and characterizing haplotypes in next generation sequencing. *Bioinformatics*, 29(7):878-85 PMID: 23407359
13. **Zhang Y** (2013) Detecting interacting mutation clusters in HIV-1 drug resistance. *Proceedings of BIOINFORMATICS 2013 – International Conference on Bioinformatics Models, Methods and Algorithms*. (competitive acceptance, 14%)
14. Song G, Riemer C, Dickins B, Kim HL, Zhang L, **Zhang Y**, Hsu CH, Hardison RC, NISC Comparative Sequencing Program, Green ED, Miller W (2012) Revealing Mammalian Evolutionary Relationships by Comparative Analysis of Gene Clusters. *Genome Bio Evol*, 4:586-601.
15. Xu J, **Zhang Y** (2012) A Generalized Linear Model for Peak Calling in ChIP-Seq Data. *J Comp Biol*. 19:826-838
16. **Zhang Y** (2012) A Novel Bayesian Graphical Model for Genome-Wide Multi-SNP Association Mapping. *Genet Epi*, 36:36-37. PMID: 22127647
17. Wu W, Cheng Y, Keller CA, Ernst J, Kumar SA, Mishra T, Morrissey C, Dorman CM, Chen KB, Drautz D, Giardine B, Shibata Y, Song L, Pimkin M, Crawford GE, Furey TS, Kellis M, Miller W, Taylor J, Schuster SC, **Zhang Y**, Chiaromonte F, Blobel GA, Weiss MJ, Hardison RC (2011) Dynamics of the Epigenetic Landscape During Erythroid Differentiation after GATA1 Restoration. *Genome Res*. 21:1659–1671.
18. **Zhang Y**, Zhang J, Liu JS (2011) Block-Based Bayesian Epistasis Association Mapping with Application to WTCCC Type 1 Diabetes Data. *Ann Appl Stat*. 5:2052-2077.

19. **Zhang Y** and Liu JS (2011) Fast and Accurate Approximation to Significance Tests in Genome-Wide Association Studies. *J Am Stat Assoc*, 106:846-857.
20. Miller W, Hayes VM, Ratan A, Petersen DC, Wittekindt NE, Miller J, Walenz B, Knight J, Qi J, Zhao F, Wang Q, Bedoya-Reina OC, Katiyar N, Tomsho LP, Kasson LM, Hardie RA, Woodbridge P, Tindall EA, Bertelsen MF, Dixon D, Pyecroft S, Helgen KM, Lesk AM, Pringle TH, Patterson N, **Zhang Y**, Kreiss A, Woods GM, Jones ME, Schuster SC. (2011) Genetic diversity and population structure of the endangered marsupial *Sarcophilus harrisii* (Tasmanian devil), *Proc Natl Acad Sci*. 108:12348-53
21. Song G, Hsu CH, Riemer C, **Zhang Y**, Kim HL, Hoffmann F, Zhang L, Hardison R, NISC Comparative Sequencing Program, Green E, Miller W (2011). Conversion Events in Gene Cluster. *BMC Evol Biol*. 11:226
22. **Zhang Y**, Jiang B, Zhu J, and Liu JS (2011) Bayesian Models for Detecting Epistatic Interactions from Genetic Data. *Ann Hum Genet*. 75:183-193.
23. **Zhang Y** (2011) Bayesian Epistasis Association Mapping via SNP Imputation. *Biostatistics*, 12:211-222.
24. **Zhang Y**, Book chapter: False Positive Control for Genome-Wide ChIP-Chip Tiling Arrays. (2010) *Frontiers in Computational and System Biology*. Feng J., Fu W, Sun F (eds.), Springer.
25. Chen KB, **Zhang Y** (2010) A Varying Threshold Method for ChIP Peak-Calling Using Multiple Sources of Information. *Bioinformatics*, 26:i504-i510.
26. Schuster SC, Miller W, Ratan A, Tomsho LP, Giardine B, Kasson LR, Harris RS, Petersen DC, Zhao F, Qi J, Alkan C, Kidd JM, Sun Y, Drautz DI, Bouffard P, Muzny DM, Reid JG, Wang Q, Nazareth LV, Burhans R, Riemer C, Wittekindt NE, Moorjani P, Tindall EA, Taliwal V, Hubisz MJ, Danko CG, Teo WS, Buboltz A, Zhang Z, Oosthuysen A, Steenkamp A, Oostuisen H, Venter P, Gajewski J, **Zhang Y**, Pugh BF, Makova K, Nekrutenko A, Mardis ER, Patterson N, Pringle T, Chiaromonte F, Mullikin J, Eichler EE, Hardison RC, Gibbs RA, Siepel A, Harkins TT, Hayes VM (2010) Complete Khoisan and Bantu Genomes from Southern Africa. *Nature*, 463: 943-947
27. Hsu CH, **Zhang Y**, Hardison RC, NISC Comparative Sequencing Program, Green ED, and Miller W (2010) An Effective Method for Detecting Gene Conversion Events in Whole Genomes, *J Comp Biol*. 17:1281-1297.
28. Ratan A, **Zhang Y**, Hayes VM, Schuster SC, Miller WC (2010) Calling SNPs without a Reference Sequence. *BMC Bioinformatics*, 11:130
29. Miller WC, Wright S, **Zhang Y**, Schuster SC, Hayes VM. (2010) Optimization Methods for Selecting Founder Individuals for Captive Breeding or Reintroduction of Endangered Species. *Pac. Symp. Biocomput*, 15:43–53
30. Hsu CH, **Zhang Y**, Hardison R, Miller W (2009) Whole-Genome Analysis of Gene Conversion Events. *RECOMB-CG*, 181-192
31. Cheng Y, Wu W, Kumar SA, Yu D, Deng W, Tripic T, King DC, Chen KB, Zhang Y, Drautz D, Giardine B, Schuster SC, Miller W, Chiaromonte F, **Zhang Y**, Blobel GA, Weiss MJ and Hardison RC (2009) Erythroid GATA1 function revealed by

- genome-wide analysis of transcription factor occupancy, histone modifications and mRNA expression. *Genome Res.* 19: 2172-2184.
32. **Zhang Y**, Song GT, Vinar T, Green ED, Siepel A, Miller W (2009) Evolutionary History Reconstruction for Mammalian Complex Gene Clusters. *J Comp Biol*, 16:1051-1070.
 33. **Zhang Y**, Song GT, Hsu CH, Miller W (2009) Simultaneous History Reconstruction for Complex Gene Clusters in Multiple Species. *Pac. Symp. Biocomput* 14:162-173.
 34. **Zhang Y**, Niu T (2009) *Handbook on Analyzing Human Genetics Data – Computational Approaches and Software*. Chapter2: Haplotype Structure. Edited by Lin SL and Zhao HY, Springer.
 35. **Zhang Y** (2008) Poisson Approximation for Significance in Genome-wide ChIP-chip Tiling Arrays. *Bioinformatics*, 24(24):2825-2831.
 36. **Zhang Y** (2008) Tree-guided Bayesian inference of population structures. *Bioinformatics*, 24:965-971.
 37. **Zhang Y**, Song GT, Vinar T, Green ED, Siepel A, Miller W (2008) Reconstructing the evolutionary history of complex human gene clusters. *Proceedings of RECOMB* 2008, 29-49.
 38. **Zhang Y**, Liu J (2007) Bayesian inference of epistatic interactions in case-control studies. *Nat Genet.* 39:1167-1173.
 39. **Zhang Y**, Niu T, Liu J (2006) A coalescence-guided hierarchical Bayesian method for haplotype inference. *Am J Hum Genet*, 79(2):313-322.
 40. Valouev A*, **Zhang Y***, Schwartz DC, Waterman MS (2006) Refinement of optical map assemblies. *Bioinformatics*. 22:1217-1224. (*equal contribution)
 41. Valouev A, Li L, Liu Y, Schwartz DC, Yang Y, **Zhang Y**, Waterman MC (2006) Alignment of optical maps. *J. Comp. Biol.* 13(2):442-462.
 42. **Zhang Y**, Waterman MS (2005) An Eulerian path approach to local multiple alignment for DNA sequences. *Proc Natl Acad Sci.* 102(5):1285-1290.
 43. **Zhang Y**, Waterman MS (2003) An Eulerian path approach to global multiple alignment for DNA sequences. *J. Comp. Biol.*, 10(6): 803-819.
 44. **Zhang Y**, Waterman MS (2003) DNA sequence assembly and multiple DNA sequence alignment by an Eulerian path approach. *Cold Spring Harb Symp Quant Biol.*, 68:205-212.
 45. Waterman MS, **Zhang Y** (2003) Eulerian path methods for multiple sequence alignment. *Proceedings of the 2003 IEEE Bioinformatics Conference, CSB 2003*, IEEE Computer Society, Order Number PR02000, Aug 11-14.

INVITED TALKS

2017:

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|-------|---|
| 10/18 | American Society of Human Genetics Annual Meeting 2017. Orlando, FL. Invited platform presentation (8% rate). “New IDEAS for GWAS loci: Using genome segmentation to identify causal variants and tissues driving disease associations” |
| 09/09 | 2017 Bioinformatics and Genomics Retreat. Pennsylvania State |

	University. TBD
07/01	IMS-China, Guilin, Guanxi, China. Invited but rejected due to schedule conflict.
06/25	WNAR meeting in Santa Fe, New Mexico. Invited but rejected due to schedule conflict.
06/25	ICSA Applied Statistics Symposium. Chicago, IL. "Leveraging incomplete information across cell types to identify functional elements and impute missing marks"
02/14	GSK Target Sciences seminar, GlaxoSmithKline, King of Prussia, PA. "2D Genome Functional Annotation in 127 Human Cell Types"
2016:	
09/30	GSK Geminator Presnetations, GlaxoSmithKline, Collegeville, PA. "Integrating genetic and (epi)omics data to identify functional causal variants in complex disease"
08/02	Joint Statistical Meeting, Chicago, IL. "A novel 2D genome segmenta1on method for modeling epigenetic landscapes in multiple cell lines"
05/25	Department of Probability and Statistics, Peking University, Beijing, China. "Scalable computational methods for exploiting multi-cellular epigenomics dynamics"
05/23	Center of Statistical Science, Tsinghua University, Beijing, China. "Scalable computational methods for exploiting multi-cellular epigenomics dynamics"
03/21	Department of Biostatistics and Epidemiology, University of Pennsylvania, Philadelphia, PA. "Jointly characterizing epigenetic landscapes in multiple human cell types"
02/17	Presentation at Dr. Barbara Wold lab, Department of Molecular Biology, California Institute of Technology, CA. "Jointly characterizing epigenetic landscapes in multiple human cell types"
2015:	
11/18	Department of Biology, Howard University, Washington DC. "Jointly characterizing epigenetic landscapes in multiple human cell types"
08/29	2015 Bioinformatics and Genomics Retreat, Penn State University, University Park, PA. "New IDEAS for joint genome segmentation across many cell types"
04/28	Department of Biostatistics and Epidemiology, University of Pennsylvania, Philadelphia, PA. "Bayesian modeling of epigenetic variation in many human cell types"
01/14	Center for Applied Genomics, the Children's Hospital of Philadelphia, Philadelphia, PA. "Novel IDEAS for detecting differential regulation in multiple cell types"

2014:

07/31-08/02 International Conference on Bioinformatics, 2014, Sydney, Australia. "dCaP: detecting differential binding events in multiple conditions and proteins" by Kuan-Bei Chen

2013:

06/30-07/04 IMS-China International Conference on Statistics and Probability, 2013, Chengdu, China.

04/11-04/12 3rd Annual RECOMB Satellite Workshop on Massively Parallel Sequencing, Beijing, China. "De novo inference of population structure and admixture in sequencing studies."

03/28 Department of Biostatistics, University of Pittsburg, PA

03/01 Department of Statistics, Duke University, Durham, NC

02/11-02/13 4th International Conference on Bioinformatics Models, Methods and Algorithms Barcelona, Spain. "Detecting interacting mutation clusters in HIV-1 drug resistance."

2012:

07/14 Mini-Symposium on Statistical Genetics. Beijing Forestry University. Beijing, China

07/08-07/09 Second Joint Biostatistics Symposium. Beijing China. "A new algorithm for detecting mutation clusters in HIV-1 drug resistance".

07/02-07/04 The 2nd Institute of Mathematical Statistics Asia Pacific Rim Meeting. Tsukuba, Japan. "A new Bayesian graphical model for detecting joint mutations in genome-wide association studies".

03-29-04/01 Thirty Years of Computational Biology and Bioinformatics at USC: A symposium in honor of Professor Michael Waterman's 70th and Simon Tavaré's 60th birthdays. "A new Bayesian graphical model for detecting joint mutations in genome-wide association studies".

2011:

10/19 Department of Biostatistics, University of Minnesota, Twin Cities, MN.

10/10-10/15 The 12th International Congress of Human Genetics, the 61st Annual Meeting of the American Society of Human Genetics, Montreal, QC Canada.

10/03 BionanoMatrix Inc. San Diego, CA, USA.

09/30 Department of Statistics, Temple University, Philadelphia PA, USA.

08/29-09/01 The 7th International Conference on Multiple Comparison Procedures, Washington, DC, USA.

07/30-08/04 Joint Statistical Meeting 2011, Invited session, Miami, USA.

06/26-06/29 The 20th Annual ICSA Applied Statistics Symposium. New York City, NY USA.

05/26	Department of Statistics, Peking University, Beijing, China.
02/28	Department of Statistics, Yale University, New Haven, CT USA.
<u>2010:</u>	
09/26-09/29	European Conference on Computational Biology 2010, Ghent, Belgium.
07/10-07/12	International Conference on Statistics and Society, the 4 th International Forum on Statistics, Renmin University, Beijing, China.
07/04-07/06	Probability and Statistics – an International Conference in Honor of PL Hsu’s 100 th Birthday. Peking University, Beijing, China.
<u>2009:</u>	
06/28-07/01	The 1 st Institute of Mathematical Statistics-Asia Pacific Rim Meeting, Seoul, Korea.
06/26-06/28	International Workshop on Probability Theory, Statistics and Their Application to Biology. Peking University, Beijing, China.
04/16-04/17	Current Topic Workshop: Systems Biology of Biological Processes and Diseases: Biological Problems and Statistical Solutions, Mathematical Biosciences Institute. Ohio State University, Ohio, OH USA.
01/06	The Pacific Symposium on Biocomputing (PSB) 2009, Big Island, Hawaii, USA.
<u>2008:</u>	
10/16	Department of Statistics, University of Illinois Urbana Champaign. Urbana, IL USA.
10/10	Krishnaiah and Khatri Lecture Series: Frontiers of Evolutionary Biology. Department of Statistics, Penn State University, University Park, PA USA.
04/18	Center of Bioinformatics, George Washington University. Washington, DC, USA.
03/30	The 12 th Annual International Conference on Research in Computational Molecular Biology (RECOMB) 2008, Singapore.
01/02	Department of Statistics, Peking University, Beijing, China.
<u>2007:</u>	
02/07	Department of Biostatistics, Penn State University Hershey Medical School. Hershey, PA USA.
<u>2006:</u>	
03/01	Center of Genomics, University of Wisconsin Madison, Madison, WI USA.
02/27	Department of Computer Science, University of Minnesota. Twin Cities, MN USA.
02/14	Department of Biostatistics, Johns Hopkins University. Baltimore, MD USA.
02/07	Department of Statistics, University of California Davis. Davis, CA USA.

01/26	Department of Biostatistics, Boston University. Boston, MA.
01/19	Department of Statistics, Penn State University. University Park, PA USA.

GRANTS

ACTIVE

NIH 1R01 GM121613-01A1 PI: Zhang 08/01/2017 – 07/31/2020
 Total Anticipated Amount: \$1,028,042
 Role: PI Effort: 25% of 12 months
 Title: A 2D segmentation method for jointly characterizing epigenetic dynamics in multiple cell lines.
 Co-I: Ross Hardison

ECoS Lab Bench to Commercialization (LB2C) Grant PI: Zhang
 08/01/2017 – 07/31/2018
 Total amount: \$75,000
 Role: PI Effort: 0%
 New From Functions to Disease: New IDEAS to Predict Causal Variants, Effector Genes and Tissues Driving Disease Association.

NIH R24 DK106766-01A1 MPI: Hardison RC (contact), Blobel G, Bodine D, Taylor J, Weiss M, Zhang Y 07/01/2016 – 06/30/2021
 Total Anticipated Amount: \$6,162,391
 Role: PI Effort: 25% of 12 months
 Title: VISION: Validated Systematic IntegratiON of epigenomic data
 Co-I: Berthold Göttgens, Douglas Higgs, James Huges, Feng Yue, Cheryl Keller

NIH 1R01CA178393-01 PIs: Loughran TP (Contact PI), Hardison RC 09/01/2015-08/31/2020
 Total Anticipated Amount: \$1,294,620
 Role: Co-I Effort: 5% of 12 months
 Title: Genomic Architecture of LGL Leukemia

COMPLETED

NIH R01 HG004718-04A1 PI: Zhang Y 08/17/2012-06/30/2017
 Effort: 25% of 12 months
 Role: PI
 Title: New Bayesian Algorithms for Genome-wide Association Mapping

BioStrategy/GSK Partners PI: Zhang Y 12/01/2016-05/31/2017
 Effort: 14% of 12months
 Role: PI
 Title: Integrating Genetic and (Epi)omics Data to Identify Functional Causal Variants in Complex Disease

NIH R01

NIH 1UL1RR033184-01 PI: Sinoway L 06/01/2011-02/29/2016

Effort: 16.7% of 12 months

Role: Investigator

Title: Penn State Clinical and Translational Science Institute

NIH R01 DK065806-06 PI: Hardison R 02/01/2004-03/31/2014

Effort: 5% of 12 months

Multi-PI: Hardison RC, Schuster SC, Miller WC, Chiaromonte F, Zhang Y, Taylor J

Average Annual Support: \$706,720

Title: Global Predictions and Tests of Erythroid Regulation

NIH R01 HG004718-01 PI: Zhang Y 08/15/2008 –06/30/2012

Effort: 25% of 12 months

Role: PI

Average Annual Support: \$141,595

Title: Bayesian Methods for Epistasis Association Mapping

NIH/NHGRI R01 HG02238-18S1 PI: Webb M 08/15/2008-06/30/2012

Effort: 16.7% of 12 months

Role: Co-PI

Average Annual Support: \$709,718

Title: Software for Analyzing Biosequence Data

NIH R01 1RC2HG0055573-01 09/26/2009-07/31/2011

Multi-PI: Hardison RC, Schuster SC, Miller WC, Chiaromonte F, Zhang Y, Taylor J

Title: ARRA: Enhance Human ENCODE by Function Comparisons to Mouse

SCHOLARSHIPS

2013- Associate Editor for *Annals of Applied Statistics*

2012- Associate Editor for *BMC Genetics*

Invited Reviewer for Mathematical Review

2011- Associate Editor for *PLoS One*

Review Editor for *Frontiers in Genetics*

Review Editor for *Frontiers in Statistical Genetics and Methodology*

2011-2014 Review Editor for *Frontiers in Genetic Architecture*

2010- Associate Editor for *Journal of Biometrics & Biostatistics*

PROFESSIONAL SERVICES

2017 Reviewer for NIH IRG/SRG: ZDE1 (to occur in November 2017)

Session chair, ICSA Applied Statistics Symposium 2017, Chicago, IL

Reviewer for NIH IRG/SRG: GCAT

Reviewer for NIH IRG/SRG: ZDE1 GZ16

2016 Reviewer for NIH IRG/SRG: GCAT

	Mail reviewer for NIH ZRG1 RPHB-W 53 R
2015	Reviewer for NIH IRG/SRG: ZDE1 GZ06
	Reviewer for NIH IRG/SRG: ZDE1 GZ07
	Reviewer for NIH IRG/SRG: ZDE1 JR09
2014	Reviewer for NIH IRG/SRG: ZRG1 GGGR-80A
2011	Session organizer and chair, the 20th annual ICSA applied statistics symposium, New York, USA, 06/26-06/29
	Program committee, the international conference on information science and technology, Nanjing, China, 03/26-03/28
2010	Program committee, CISP'10-BMEI, Yantai, China, 10/16-10/18
2009	Session chair, the international workshop on probability theory, statistics and their application to biology, Peking University, Beijing, China, 06/26-06/28
	Session chair, the 1 st institute of mathematical statistics-Asia Pacific rim meeting, Souel, Korea, 06/28-07/01

PROFESSIONAL MEMBERSHIPS

American Statistical Association
 American Society of Human Genetics
 International Chinese Statistical Association
 International Society of Computational Biology

JOURNAL REFERRING (SELECTED)

American Journal of Human Genetics
 Annals of Applied Statistics
 Bioinformatics
 Biometrics
 Genome Research
 Journal of American Statistical Association
 Nature Biotechnology
 Nucleic Acids Research
 PLoS Genetics
 Proceedings of the National Academy of Sciences, USA

UNIVERSITY/DEPARTMENT SERVICES

2017	ICS coordinating committee member (University)
	Chair of PhD qualifying exam
	Hiring committee
	Undergraduate advisor
2016	Promotion and tenure committee
	Safety committee
	Qualifying exam committee
	Undergraduate advisor
2015	College sabbatical review committee chair

	Undergraduate advisor
2014	Faculty search committee member
	Undergraduate advisor
2013	Graduate master's exam committee
	Undergraduate advisor
2012	Graduate master's exam committee chair
	Graduate admission committee
	Undergraduate advisor
2011	Department colloquium chair
	Graduate admission committee
	Undergraduate advisor
2010	Graduate admission committee
	Undergraduate advisor
2009	Department colloquium chair
	Undergraduate committee
2008	Clifford C. Clogg memorial lecture series chair
	Graduate master's exam committee chair
	Undergraduate advisor
2007	Department colloquium chair
	Graduate master's exam committee
	Undergraduate advisor
2006	Library committee chair

TEACHING

The Pennsylvania State University

Fall 2017	Stat500: Applied Statistics
	Stat555.WD: Statgenomics
Spring 2017	Stat500: Applied Statistics
Fall 2016	Stat/Math416: Stochastic Modeling
Spring 2016	Stat500.WD: Applied Statistics
Fall 2015	Stat/Math418: Introduction to Probability and Stochastic Processes for Engineering
	MCIBS541: Critical Analysis of Literature in Bioinformatics and Genomics
Fall 2014	Stat/Math415: Introduction to Mathematical Statistics
Spring 2014	Stat/Math418: Introduction to Probability and Stochastic Processing for Engineers
Fall 2013	Stat500.WD: Applied Statistics
Spring 2013	Stat/CSE/BIOL597B: Bioinformatics II
Fall 2012	Stat511: Regression Analysis and Modeling
Spring 2012	Stat/CSE/BIOL598B: Bioinformatics II
Fall 2011	Stat/Math415: Introduction to Mathematical Statistics
Spring 2011	Stat416: Stochastic Modeling
Fall 2010	Stat/Math415: Introduction to Mathematical Statistics

Spring 2010	Stat/CSE/BIOL597E: Bioinformatics II
Fall 2009	Stat/Math415: Introduction to Mathematical Statistics
Spring 2009	Stat/CSE/BIOL598B: Bioinformatics II
Fall 2008	Stat511: Regression Analysis and Modeling
Spring 2008	Stat/Math415: Introduction to Mathematical Statistics
Fall 2007	Stat544: Categorical Data analysis I
Spring 2007	Stat/Math415: Introduction to Mathematical Statistics
Fall 2006	Stat/Math414: Introduction to Probability

University of Southern California

Fall 2001	Math 108: Introductory College Mathematics
Summer 2001	Math 118x: Fundamental Principles of the Calculus

ADVISING AND MENTORING

Postdoctoral Fellows

Kuan-bei Chen, in 2014

Yeonok Lee, 2010-2014 (Joint with Debashis Ghosh)

PhD Thesis Advisor

Guanjue Xiang, current since 2017 (3rd year)

An Lin, current since 2016 (4th year)

Kuan-bei Chen, PhD in Computer Science, graduated in 2013 (her official chair is Webb Miller because I am not a CSE associated faculty, but her thesis is with me)

Tyler Malys, PhD in IBIOS, 2011-2014 (dropped out)

Jialin Xu, PhD in Statistics, graduated in 2012

PhD Committee Member

Current:

Naomi Yamada, PhD in BMB

Yiafei Lv, PhD in IBIOS

Tao Yang, PhD in IBIOS

Akshay Kakumanu, PhD in BMB

Yin Tang, PhD in IBIOS

Han Zheng, PhD in BMB

Past:

Rohit Reja, PhD in BMB, graduated in 2016

Yurong Guo, PhD in Neuroscience, graduated in 2015

Yang Liu, PhD in Statistics, graduated in 2015

Xiang Zhan, PhD in Statistics, graduated in 2015

Luyi Wo, PhD in IBIOS, dropped out

Wenyu Hua, PhD in Statistics, graduated in 2014

Jayaram Raghuram, PhD in Computer Science, graduated in 2014

Marcus Nunes, PhD in Statistics, graduated in 2013

Venkatesh Muktali, PhD in IBIOS, graduated in 2013
Giltae Song, PhD in Computer Science, graduated in 2013
Gue Su Chang, PhD in IBIOS, graduated in 2013
Lu Zhang, PhD in Health and Human Development, graduated in 2013
Jing Chen, PhD in Veterinary and Biomedical Sciences, graduated in 2013
Liye Zhang, PhD in IBIOS, graduated in 2012
Zhenhai Zhang, PhD in IBIOS, graduated in 2011
Chih-Hao Hsu, PhD in Computer Science, graduated in 2010
Pannapa Changpetch, PhD in Statistics, graduated in 2010
Xianyun Mao, PhD in Statistics, graduated in 2010
Katerina Sinclair, PhD in Human Development and Family Study, graduated in 2010

Master Committee Member

Venkatesh Muktali, MS in IBIOS, 2013
Seyed Safa Eslanbolchi, MS in Energy and Mineral Engineering, graduated in 2010
Yueping Zhang, MS in Biology, graduated in 2007

Advisor for Minor in Statistics

Yin Tang, PhD in BMB, Current
Naomi Yamada, PhD in BMB, Current

Graduate Academic Advisor

Chandra, Saksham; Hao, Han; in 2012
Shen, Frank; Peng Jiayu; Xu Zhanxiong; Constantinou Panayiotis; in 2013

Undergraduate Research Advisor

Heaton Connor (Aug 2017 – present)

Undergraduate Academic Advisor

Current: Byrne, Matthew; Erickson, Matthew P; Li, Xiaohan; Liang, Qihan; Liu, Xiqing;
Sabeen, Aaron L; Zhang, Ruiqi; Zhou, Yubaihe; Jersild, Elliot; Liu, Sitong; Gao, Zibin;

Past: Heckman, Eric A; Khan, Hassen; Knoll, Spencer R; Levert, Emma L; Ma, Brian;
Mathews, Megan E; McGarry, Brynne M; Moatz, Taylor C; Momyer, Ross D; Novak,
Andrew J; Oshie, Jacob M; Sanzo, Alexandra M; Shi, Keyi; Spotts, Kevin D; Wong,
Esteban; Wong, Ho Kit; Cao, Xukun; Fang, Haijiao; Huang, Xiaoping; Jean-Louis,
Kevin M; Kaplan, Joshua B; Kwiatkoski, Andrew R; Lee, Han Joo; Li, Yangying; Lu,
Tong; Maher, James P; Mao, Xian; Mi, Yang; Oung, Teran B; Park, Inchul; Pencille,
Christopher P; Su, Di; Xie, Yunfei; Zhang, Jingwen; Zhang, Tianyang;