UNIVERSITY OF MIAMI
CURRICULUM VITAE

Date: 5 /18/2022

I. PERSONAL

2. Name: Lily Wang, Ph.D.
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4. Address: 1120 NW 14th Street, Miami, FL 33136
5. Current Academic Rank: Associate Professor
5A. Current Track of Appointment: Tenure
6. Primary Department: Public Health Sciences
7. Secondary or Joint Appointment: Human Genetics

II. HIGHER EDUCATION

8. Institutional:

1998	BA in Mathematics, *summa cum laude* School of Arts and Sciences, Temple University, Philadelphia, PA
2000	MS in Biostatistics School of Public Health, the University of North Carolina at Chapel Hill, Chapel Hill, NC
2004	Ph.D. in Biostatistics School of Public Health, the University of North Carolina at Chapel Hill, Chapel Hill, NC

9. Non-Institutional: N/A

10. Certification and Licensure: N/A

III. EXPERIENCE

11. Academic:

2004 – 2012	Assistant Professor (tenure-track) Department of Biostatistics, Vanderbilt University School of Medicine
2012 – 2015	Associate Professor (with tenure) Department of Biostatistics, Vanderbilt University School of Medicine
2015 – 2022	Associate Professor (with tenure) Division of Biostatistics, Department of Public Health Sciences, University of Miami Miller School of Medicine

2017 – 2022 Associate Professor
Dr. John T. Macdonald Foundation Department of Human Genetic
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12. Hospital Appointments: N/A

13. Non- Academic: N/A

14. Military: N/A

IV. PUBLICATIONS

15. Books and Monographs Published: N/A

16. Juried or Refereed Journal Articles or Exhibitions:

** and__ indicates corresponding author*

1. Silva TC, Young JI, Martin ER, Chen X, **Wang L*** (2022) MethReg: estimating the regulatory potential of DNA methylation in gene transcription. *Nucleic Acids Research*, https://doi.org/10.1093/nar/gkac030 [IF: 16.971]

2. Jacobsen GE FI, Quintero MA, Santander AM, Pignac-Kobinger J, Damas OM, Deshpande AR, Kerman DH, Ban Y, Gao Z, Silva TC, Wang L, Beecham AH, McCauley JL, Burgueño JF, Abreu MT (2022). Lamina propria phagocyte profiling reveals targetable signaling pathways in refractory inflammatory bowel disease. Gastro Hep Advances. In Press [IF: NA]

3. Moro A, Gao Z, Wang L, Yu A, Hsiung S, Ban Y, Yan A, Sologon CM, Chen XS, Malek TR (2022) Dynamic transcriptional activity and chromatin remodeling of regulatory T cells after varied duration of IL-2R signaling. Nature Immunology. In Press [IF: 25.61]

4. Gardner OK, Van Booven D, Wang L, Gu T, Hofmann NK, Whitehead PL, Nuytemans K, Hamilton- Nelson KL, Adams LD, Starks TD, Cuccaro ML, Martin ER, Vance JM, Bush WS, Byrd GS, Haines JL, Beecham GW, Pericak-Vance MA, Griswold AJ (2022) Genetic Architecture of RNA Editing Regulation in Alzheimer Disease across Diverse Ancestral Populations, Human Molecular Genetics, ddac075. [IF: 6.15]

5. Zhang L, Young JI, Gomez L, Silva TC, Schmidt MA, Cai J, Chen X, Martin ER, **Wang L*** (2021) Sex-specific DNA methylation differences in Alzheimer's disease pathology. *Acta Neuropathologica*

Communications. 9:77 [IF: 7.801]

6. Odom JO, Colaprico A, Silva TC, Chen XS, **Wang L*** (2021) PathwayMultiomics: An R Package for Efficient Integrative Analysis of Multi-Omics Datasets with Matched or Un-matched Samples. *Frontiers in Genetics* 12: 783713 [IF: 4.599]

7. Lehmann BD, Colaprico A, Silva TC, Chen J, An H, Ban Y, Huang H, Wang L, James JL, Balko JM, Gonzalez-Ericsson PI, Sanders ME, Zhang B, Pietenpol JA, Chen XS (2021) Multi-omics analysis identifies therapeutic vulnerabilities in triple-negative breast cancer subtypes. *Nature Communications* 12, 6276 [IF: 14.919]

8. Lu M, Sha Y, Silva TC, Colaprico A, Sun X, Ban Y, Wang L, Lehmann BD, Chen XS (2021) LR Hunting: A Random Forest Based Cell–Cell Interaction Discovery Method for Single-Cell Gene Expression Data. *Frontiers in Genetics* 12:708835 [IF: 4.599]

9. Caunca MR, Wang L, Cheung YK, Alperin N, Lee SH, Elkind MSV, Sacco RL, Wright CB, Rundek T. (2021) Machine learning-based estimation of cognitive performance using regional brain MRI markers: the Northern Manhattan Study. Brain Imaging and Behavior. 15(2):1270-1278 [IF: 3.418]

10. Zhang L, Silva TC, Young JI, Gomez L, Schmidt MA, Hamilton-Nelson KL, Kunkle BW, Chen X, Martin ER, **Wang L*** (2020). Epigenome-wide meta-analysis of DNA methylation differences in prefrontal cortex implicates the immune processes in Alzheimer's disease. *Nature Communications*. 11, 6114 [IF:14.92]

11. Odom GJ, Ban Y, Colaprico A, Liu L, Silva TC, Sun X, Pico AR, Zhang B, **Wang L***, **Chen X*** (2020) pathwayPCA: An R package for integrative pathway analysis with modern PCA methodology and gene selection. *Proteomics*. 20, 1900409. [IF: 3.106]

12. Silva TC, Young JI, Martin ER, Chen X, **Wang L*** (2020). MethReg: estimating regulatory potential of DNA methylation in gene transcription. R package version 1.0.0. DOI: 10.18129/B9.bioc.MethReg

13. Zhang L, Odom G, Silva T, Gomez L, **Wang L*** (2020). rnaEditr: Statistical analysis of RNA editing sites and hyper-editing regions. R package version 1.0.0. DOI: 10.18129/B9.bioc.rnaEditr

14. Benatar M, Zhang L, Wang L, Granit V, Statland J, Barohn R, Swenson A, Ravits J, Jackson C, Burns TM, Trivedi J, Pioro EP, Caress J, Katz J, McCauley JL, Rademakers R, Malaspina A, Ostrow LW, Wuu J (2020) Validation of serum neurofilaments as prognostic and potential pharmacodynamic biomarkers for ALS. Neurology, 95(1):e59-e69 [IF: 8.320]

15. Burgueno JF, Reich A, Hazime H, Quintero MA, Fernandez I, Fritsch J, Santander AM, Brito N, Damas OM, Deshpande A, Kerman DH, Zhang L, Gao Z, Ban Y, Wang L, Pignac-Kobinger J, Abreu MT (2020) Expression of SARS-CoV-2 Entry Molecules ACE2 and TMPRSS2 in the Gut of Patients With IBD. Inflammatory Bowel Diseases, 26 (6) 797–808 https://doi.org/10.1093/ibd/izaa085 [IF: 4.005]

16. Mallik S, Odom G, Gao Z, Gomez L, **Chen X***, **Wang L*** (2019) An Evaluation of Supervised Methods for Identifying Differentially Methylated Regions in Illumina Methylation Arrays. Briefings in Bioinformatics, 20 (6), 2224-2235 PMID: 30239597 [IF: 9.101]

17. Gomez L, Odom GJ, Young JI, Martin ER, Liu L, Chen X, Griswold AJ, Gao Z, Zhang L, **Wang L*** (2019) coMethDMR: Accurate identification of co-methylated and differentially methylated regions in epigenome-wide association studies with continuous phenotypes. Nucleic Acids Research, 47 (177): e98 [IF: 11.147]

18. Gardner OK, Wang L, Booven DV, Whitehead PL, Hamilton-Nelson KL, Adams LD, Starks TD, Hofmann NK, Vance JM, Cuccaro ML, Martin ER, Byrd GS, Haines JL, Bush WS, Beecham GW, Pericak-Vance MA, Griswold AJ (2019) RNA editing alterations in a multi-ethnic Alzheimer disease cohort converge on immune and endocytic molecular pathways. Human Molecular Genetics, ddz110, https://doi.org/10.1093/hmg/ddz110 [IF: 4.544]

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apnea. *J Oral Maxillofac Surg* 71:743-751

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104. Glowa P, Frasier PY, Wang L, Eaker K, Osterling W (2003) What happens after we identify intimate partnerviolence. *Fam Med* 35: 730-736.

105. Sloane PD, Zimmerman S, Suchindran C, Reed P, Wang L, Boustani M, Sudha S (2002) The public health impact of Alzheimer's disease, 2000-2050: potential implication of treatment advances. Annu Rev Public Health 23: 213-231.

106. Herman-Giddens ME, Wang L, Koch G (2001) Secondary sexual characteristics in boys: estimates from the national health and nutrition examination survey III, 1988-1994. Arch Pediatr Adolesc Med 155: 1022-1028.

17. Other Works, Publications and Abstracts: N/A

18. Other Works Accepted for Publication: N/A

V. PROFESSIONAL

19. Grants

Current

1R01AG061127-01 (Wang) 02/1/19 – 1/31/2024 4.14 cal. months (34.5%)
NIH/NIA $1,918,750
Building blood-based DNA methylation signatures for AD that are reflective of CNS changes
Role: Principal Investigator

R01 (Martin, Wang, Kunkle) 05/15/19 – 02/29/2024 2.4 cal. months (20%)
NIH $3,806,592
Integrative Genomic Approaches for Understanding Sex Differences in Alzheimer's Disease
Role: Principal Investigator

7BC03 (Thomas) 03/17/17 – 04/30/22 1.2 cal. months (10%)
Bankhead Coley Research Prog. $1,866,436
Identifying Infection and Molecular Determinants of Health Disparities in HCV infected Minority Populations for the Prevention and Early Detection of HCC
Role: Co-investigator

Pending

1R01 NS128145-01 (Wang) 07/1/22 –6/30/2027 4.14 cal. months (34.5%)
NIH/NIA $3,577,351
New computational tools for understanding and predicting AD via age-associated DNA methylation changes
Role: Principal Investigator
This grant received an impact score of 24 at recent scientific review study section meeting.

Past

1R21AG060459-01 (Wang) 08/15/18 – 05/31/2021 1.2 cal. months (10%)
NIH/NIA $422,125
New statistical strategies for comprehensive analysis of epigenome-wide methylation data
Role: Principal Investigator

1U54NS092091 (Benatar) 09/30/14 - 06/30/2019 1.8 cal. months (15%)
NIH/NINDS $5,167,529
Clinical Research in ALS & Related Disorders for Therapeutic Development
Role: Biostatistician

1U01NS107027-01 (Benatar) 5/15/2018 – 3/31/2023 0.6 cal. months (5%)
NINDS/NCATS $3,662,906
Multi-Center ALS Biomarker Validation Study (CReATe Biomarkers)
Role: Statistician

1R21ES028397-01 (Robbins) 08/01/17 – 07/31/19 0.6 cal. months (5%)
NIEHS
Elucidating the Effects of Arsenic Exposure on Human Fetal Development
Role: Co-investigator

2P50NS071674-06 (Vance) 09/01/11 -08/31/17 1.2 cal. months (10%)
NIH/NINDS $1,718,820
Morris K. Udall Parkinson Disease Center of Excellence - Genetics of Parkinsonism
Role: Co-investigator

4UL1TR000460-05 (Sacco) 07/1/2012 – 06/30/2017 1.2 cal. months (10%)
NIH $2,614,379
Miami Clinical and Translational Science Institute
Role: Co-Investigator

1R21 HG006037-01A1 (Wang, Zhao) 05/01/2013 – 04/30/2016 2.4 cal. months (20%)
NHGRI $445,160

Integrative Statistical Models for Pathway Analysis of GWAS Data
Role: Principal Investigator

1R03CA167695-01A1 (Zhao) 09/01/2013-08/31/2016 0.6 cal. months (5%)
NIH/NCI $154,186
Investigating MicroRNAs and Their Regulatory Networks in Glioblastoma
Role: Co-Investigator

1R01 LM011177-01 (Wang, Zhao) 05/01/2012 – 04/30/2016 2.4 calendar (20%)
NLM $1,044,708
Mapping the Genetic Architecture of Complex Disease via RNA-Seq and GWAS Data
Role: Principal Investigator

1P50MH096972-01 (Blakely) 07/01/2012 - 06/30/2017 1.2 calendar (10%)
NIH/NIMH $6,627,257
Enduring Effects of Early-Life Serotonin Signaling
Role: Co-Investigator

1R03DE022093-01 (Wang, Zhao) 09/1/2011 – 8/31/2014 1.2 calendar (10%)
NIDCR $245,986
Understanding Genetic Basis of Dental Caries via Integrative Genomic Approaches
Role: Principal Investigator

20. Editorial Responsibilities

Editorial Board

2011 – Present *Genes, Frontiers in Neurogenomics*
2012 – Present *Annals of Biometrics & Biostatistics*

Journal Reviewer

American Journal of Human Genetics (2021)	*Bioinformatics* (2013,2019, 2020)	*Neurology* (2008)
Behavioral Sleep Medicine (2009)	*Cephalagia* (2007)	*Pattern Recognition* (2012)
BMC Bioinformatics (2014)	*PLoS One* (2015)	*Psychiatry Research* (2012)
BMC Genomics (2014)	*Genome Biology* (2020)	*Statistics in Medicine* (2011)

21. Professional and Honorary Organizations

2004 - Present	Member, American Statistical Association
2015 - Present	Member, American Society of Human Genetics
2015 – Present	Member, John P. Hussman Institute for Human Genomics, University of Miami
2015 – Present	Member, Sylvester Cancer Center, University of Miami
2019 – Present	Member, Cancer Epigenetics Program, Sylvester Cancer Center, University of Miami

22. Honors and Awards

1994–1998	Outstanding Achievement Scholarship, Temple University
1994–1998	Temple University Honors Program
1994	The President's Award, Temple University
1995	Howard Hughes Medical Institute Research Fellowship
1997	Most Promising Mathematics Major Award, College of Arts and Sciences, Temple University
2004	Student Travel Award, University of North Carolina Graduate School
2006	Travel Award for Young Investigator's Workshop, Spring Meeting of the Eastern North American Region of the International Biometric Society

23. Post-Doctoral Fellowships: N/A

24. Other Professional Activities:

NIH Study section

Nov 8, 2021	*Grant Reviewer*, for Gabriella Miller Kids First (Kids First) Pediatric Research Program, Center for Scientific Review, NIH
June 29-30, 2020	*Grant Reviewer*, for Genetics of Health and Disease Study Section (GHD), Center for Scientific Review, NIH
Dec 12, 2019	*Grant Reviewer*, for NIH Director's Early Independence Award program
June 8-9, 2016	*Grant Reviewer*, for Biodata Management and Analysis Study Section (BDMA), Center for Scientific Review, NIH
Nov 19, 2015	*Grant Reviewer*, for special initiative *Clinical Studies of Mental Illness Not Involving Treatment Development, Efficacy, or Effectiveness Trials (Collaborative R01)* ZRG1 GGG-S (60) C, Center of Scientific Review, NIH
June 24-25, 2014	*Grant Reviewer*, for special initiative *New Computational Methods for Understanding the Functional Role of DNA Variants that are Associated with Mental Disorders (R01)*, ZRG1

IMST-D (55), Center of Scientific Review, NIH

June 12-15, 2014 *Session Chair*, Environmental / Spatial Statistics session, *The 8th International useR! Conference*, Nashville, TN

Feb 23, 2012 Grant Reviewer, for special initiative *Predictive Multiscale Models for Biomedical, Biological, Behavioral, Environmental and Clinical Research (U01),* National Institute of Biomedical Imaging and Bioengineering

Selected Poster and Oral Presentations

July 31, 2022 Sex-specific DNA methylation differences associated with Alzheimer's disease. *Alzheimer's Association International Conference*

May 13, 2022 DNA methylation changes in Alzheimer's disease. *The Florida Consortium on the Neurobiology of Cognition Annual Meeting* (Invited)

Mar 15, 2022 Distinct sex-specific DNA methylation differences in Alzheimer's disease. *Annual meeting of the Alzheimer's Disease Genetics Consortium* (Invited)

Oct 18, 2021 Integrative meta-analysis of blood and brain epigenome-wide association studies of Alzheimer's disease. *American Society of Human Genetics Annual Meeting*

Feb 25, 2021 Sex-specific DNA methylation changes in Alzheimer's Disease pathology. *Annual meeting of the Alzheimer's Disease Genetics Consortium.* (invited)

Oct 28, 2020 Epigenome-wide meta-analysis of DNA methylation differences in prefrontal cortex implicates the immune processes in Alzheimer's disease. *The American Society of Human Genetics Annual Meeting*

July 28, 2020 Meta-analysis of genomic regions in epigenome-wide association studies. *The Bioconductor Annual Conference*

Nov 7, 2019 DNA methylation biomarkers in colon cancer. *Cancer Epigenetics faculty meeting.*

Dec 11, 2017 Moving beyond tip of the iceberg – statistical strategies for identifying differentially methylated regions. *Department of Public Health Sciences Biostatistics Seminar Series.*

April 17, 2017 Statistical models for biomarker analysis of DNA methylation data. *Human Genetics and Genomics Seminar Series, University of Miami*

July 24, 2014 A Generalized Linear Mixed Model for Pathway Analysis of Genome-wide Association Study, *Department of Public Health Sciences, University of Miami, FL*

April 13, 2011 An Efficient Hierarchical Generalized Linear Mixed Model for Pathway Analysis of Genome-wide Association Studies. *Department of Biostatistics seminar, Vanderbilt University School of Medicine, Nashville, TN*

Mar 21, 2010 A Unified Mixed Effects Model for Gene Set Analysis of Time Course Microarray Experiments. *Spring Meeting of the Eastern North American Region of the International Biometric Society (ENAR),* New Orleans, LA

Feb 6, 2007 Critical Review of Published Microarray Studies for Cancer Outcome. *Biostatistics clinic, joint*

presentation with Constantine Aliferis

Aug 15, 2006 On Methods for Gene Function Scoring as a Means of Facilitating the Interpretation of Microarray Results. Vanderbilt University *Biostatistics clinic, joint presentation with Bing Zhang*

Dec 2, 2005 Some Statistical Aspects of Analysis of Genomic Sequences. *Twelfth Annual International Conference on Statistics, Combinatorics, Mathematics and Applications*, Auburn, Alabama

April 15, 2005 Pharmacogenetics and Drug Development, *Computational Genetics Journal Club, VUMC*

Mar 20, 2005 Approximating Pairwise Alignment Score Distributions, *Spring Meeting of the Eastern North American Region of the International Biometric Society (ENAR),* Austin, TX

April 15, 2004 Some Statistical Aspects of the Analysis of Genomic Sequences, *Division of Epidemiology and Biostatistics, University of Illinois at Chicago, Chicago, IL*

Mar 28, 2004 Some Statistical Aspects of Analysis of Genomic Sequences, *Spring Meeting of the Eastern North American Region of the International Biometric Society (ENAR),* Pittsburgh, PA

VI. TEACHING

25. Teaching Awards Received: N/A

26. Teaching Specialization

Graduate School Courses

Spring 2017 - 2022 Instructor for *Epidemiology 705 Advanced Statistical Methods II*

Fall 2002 Teaching Assistant for *Categorical Data Analysis,* UNC School of Public Health

Fall 2003 Teaching Assistant for *Health Informatics: Use of Large Health Care Databases,* UNC Schoolof Public Health

Lectures and workshops

Oct 22, 2020 MethReg: estimating regulatory potential of CpG methylations in gene transcription, at *Cancer Epigenetics Colloquium*

April 3, 2019 Generalized additive models. Invited guest lecture for *BST 691 High Dimensional and Complex Data*

April 18, 2018 Generalized additive models. Invited guest lecture for *BST 691 High Dimensional and Complex Data*

Dec 6, 2017 DNA methylation data analysis, Part II. Invited guest lecture for *HGG 621: Design and Analysis of Genomic Studies*

Dec 4, 2017 DNA methylation data analysis, Part I. Invited guest lecture for *HGG 621: Design and Analysis of Genomic Studies*

Nov 27, 2017 Strategies for analyzing DNA methylation data at *University of Miami Epigenomics Working Group meeting.*

July 14, 2017 Strategies for analyzing DNA methylation data, Part II. *Sylvester Comprehensive Cancer Center Biostatistics and Bioinformatics Shared Resource Mini Lecture.*

May 24, 2017	Strategies for analyzing DNA methylation data, Part I. *Sylvester Comprehensive Cancer Center Biostatistics and Bioinformatics Shared Resource Mini Lecture*.
June 12, 2017	Statistical models for biomarker analysis of DNA methylation data. Invited guest lecture for *BST 692 Case Studies in Biostatistics*
Feb 29, 2016	Some Statistical Considerations on Gene Set Enrichment Analysis. *Sylvester Comprehensive Cancer Center (SCCC) Bioinformatics Workshop*
Feb 24, 2016	Some Statistical Issues in Pathway Analysis of Genome-wide Studies. *Biostatistics Collaboration and Consulting Core (BCCC) Roundtable*
Sept 17, 2012	Data management and analysis for successful clinical research. *Department of Neurology, VUMC*
Mar 26, 2012	Some statistical issues in pathway analysis of genome-wide studies, *Vanderbilt Kennedy Center Methodology Workshops*
July 22, 2010	Pathway analysis for genome-wide association studies. *Continuing Education Series for MS Biostatisticians, Department of Biostatistics, VUMC*
May 18, 2010	Data management and analysis for successful clinical research. *Department of Neurology, VUMC*
Sept 26, 2008	Gene set enrichment analysis of microarray experiments, *Vanderbilt Kennedy Center Methodology Workshops*
Jan 17, 2007	Pathways to the analysis of microarray data, *Vanderbilt Kennedy Center Methodology Workshops*
Oct 12, 2006	Design of clinical studies. *Department of Neurology, VUMC*
Aug 21, 2006	Remote homology detection for biological sequences: theory and applications, *Vanderbilt Kennedy Center Methodology Workshops*
April 17, 2006	Planning microarray experiments, *Vanderbilt Kennedy Center Methodology Workshops*
Sept 30, 2005	How to approach genetic sequencing database: a primer, *Vanderbilt Kennedy Center Methodology Workshops*
Sept 28, 2005	Making sense of DNA and protein sequences. *Biostatistics seminar series, Department of Biostatistics, VUMC*
Oct 21, 2004	Statistical modeling. *Statistical Thinking in Biomedical Research Short Course, IGP Program, VUMC*
Oct 15, 2004	How to conduct statistical modeling. *Research Skills Workshops, Vanderbilt University Medical Center*

27. Thesis and Dissertation Advising/Post-doctoral Student Supervision:

Mentoring

2019 – Present	Tiago Chedraoui Silva, Assistant Scientist. *Integrative analysis of genomics and epigenomics data*
2018 – Present	Gabriel Odom, Postdoctoral Fellow/Assistant Professor. *Statistical methods and software for integrative analysis of genomics data*
2018 – 2021	Lanyu Zhang, Research Analyst. *Meta-analysis for epigenome-wide association studies*
2018 – 2019	Lizhong Liu, Research Analyst. *Prediction modeling in epi-genomics research*
2017 - 2018	Saurav Mallik, Postdoctoral Fellow. *Evaluation of statistical methods for identifying DMRs*

in epigenome-wide association studies.

Graduate Student Rotations in Lab

2020	Luz Ruiz, graduate student in Human Genetics and Genomics Ph.D. program. *Sex-specific gene regulation in Alzheimer's disease*
2021	Jiaming Hu, graduate student in Human Genetics and Genomics Ph.D. program. *Tissue-specific gene regulation in Alzheimer's disease*

Thesis Committee

In progress	Gillian Jacobsen. *Interrogating phagocytes to discover pathobionts in Crohn's disease.*
In progress	Sarah Fazal. *Identification and characterization of structural variants in neurological disorders*
In progress	Beronica Ocasio. (Chair of thesis committee) *Facilitating the Rational Development of Novel Cancer Therapeutics using Big Data and Artificial Intelligence*
2020	Yifan Sha. *High order interaction hunting.*
2020	Mengying Li. *New methods on classified mixed model prediction: theory and applications*
2019	Michelle Caunca. *A population neuroscience approach for analyzing regional structural brain MRI data in cognitive aging*
2019	Yalda Zarnegarnia. *Methods used for estimating the Receiver Operating Characteristic curve from clustered data and case-control studies*
2017	Chun Wu. *Human brain transcriptome profiles in obesity*
2017	Amol Pande. *Boosting method for longitudinal data.*
2016	Hongmei Liu. *Weighted maximum frequency selection and precision small molecule screening for cancer*
2016	Jie Fan. *On classified mixed model prediction*
2015	Fei Tang. *Random forest missing data approaches.*

Other Teaching activities

2016 – Present	Chair, Biostatistics Exam committee for Epidemiology Ph.D. students

VII. SERVICE

28. University Committee and Administrative Responsibilities:

University of Miami

2021 – 2022	Member, Faculty search committee, Department of Public Health Sciences (Prevention Sciences)
2020 – Present	Member, University of Miami Medical Faculty Council

2015 – 2020	Co-Director, Statistical and Bioinformatics Consulting Core, Hussman Institute for Human Genomics
2018 – 2019	Member, Committee to Review Criteria of Appointment, Promotion and Tenure

Vanderbilt University

2004 – 2015	Biostatistics Group Leader, Neurology collaboration plan, Department of Neurology, VUMC
2004 – 2014	Biostatistics and Genetics Coordinator, Statistics and Methodology Services Core, Vanderbilt Kennedy Center
2004 - 2006 & 2011 - 2015	Member, Biostatistics faculty search committee, Department of Biostatistics, VUMC
2006 - 2007	Member, Projects Allocations Committee, Department of Biostatistics, VUMC
2007 – 2015	Member, Promotions Committee, Department of Biostatistics, VUMC
2007 – 2015	Member, Bioinformatics and Biostatistics Core, Vanderbilt Conte Center for Neuroscience Research
2007 – 2010	Secretary, DSMB for clinical trial *Safety and Tolerability of Neurostimulation in Early State Parkinson's Disease*
2010 – 2015	Member, Strategic Planning Committee, Department of Biostatistics, VUMC
2010 – 2015	Secretary, DSMB for clinical trial *Long-term follow-up of deep brain stimulation for early stage Parkinson's disease*

29. Community Activities: N/A