Curriculum Vitae

SHILI LIN
Department of Statistics
The Ohio State University

Education

1989-1993	Ph. D.	Statistics	University of Washington, Seattle, Washington
1987-1989	M. A.	Mathematics	Bowling Green State University, Ohio
	M. S.	Computer Science	Bowling Green State University, Ohio
1979-1983	B. S.	Mathematics	South China Normal University, Guangzhou, China

Professional Experience

2004-	Professor, Department of Statistics, Ohio State University.
2018-2021	Faculty Co-Director, Computational Health and Life Sciences Community of Practice (CoP), Translational Data Analytics Institute, Ohio State University (Founding Director of the CoP).
2009-2014	Professor, Division of Biostatistics, College of Public Health, Ohio State University.
2005-2015	Guest Professor, Mathematical Sciences Institute, South China Normal University, Guangzhou, China.
2004-2017	Visiting Professor, Mathematical Biosciences Institute, Ohio State University.
2015	Visiting Professor, Statistical and Applied Mathematical Sciences Institute.
2014	Visiting Professor, Shanghai Center for Mathematical Sciences.
1999-2004	Associate Professor, Department of Statistics, Ohio State University.
1995-1999	Assistant Professor, Department of Statistics, Ohio State University.
1993-1995	Neyman Visiting Assistant Professor, Department of Statistics, University of California at Berkeley.
1983-1986	Lecturer, Department of Mathematics, South China Normal University, Guangzhou, China.

Other Professional Appointments/Elected Officer/National Commitee

2020-Present	Board of Director, Canadian Statistical Sciences Institute (CANSSI)
2020-Present	Management Committee, International Statistical Institute (ISI) Committee on Women in Statistics
2019-Present	Chair, Social Program Committee, International Biometric Society (IBS)
2019-Present	Institute of Mathematical Statistics (IMS) representative to the Joint Committee on Women in the Mathematical Sciences
2020-Present	Member, IMS Committee on Equality and Diversity
2021-2022	Chair, Member Engagement Committee, American Statistical Association (ASA) Section on Statistics in Genomics and Genetics (SSGG)
2018	Ex officio, ASA Committee on Women
2017-2020	President Elect, President, Past President, and Past Past President, Caucus for Women in Statistics
2017-2018	Chair, Interdisciplinary Ph.D. Program in Biostatistics, The Ohio State University
2016-2020	Regular member, National Institute of Health Biostatistical Methods and Research Design (BMRD) Study Section
2015-2017	Associate Editor, Statistics in Biosciences (SIBS)

2015-2017	Internal Advisory Board, Center for Pharmacogenomics, The Ohio State University
2014-2016	Regular member, National Institute of Health Genomics, Computational Biology and Technology (GCAT) Study Section
2011-2015	ASA Committee of Representatives to American Association for the Advancement of Science (AAAS) (Section N – Medical Sciences)
2011-present	Editorial Board Member, Genetic Epidemiology
2006-present	Associate Editor, Biometrics
2005-2018	Local Scientific Advisory Committee, Mathematical Biosciences Institute (MBI), The Ohio State University.
2004-2012	Associate Editor, Journal of Statistical Planning and Inference.
2004-2006	Associate Editor, Journal of the American Statistical Association.
2003-present	Associate Editor, Statistical Applications in Genetics and Molecular Biology.
1996-1998	Secretary, Caucus for Women in Statistics.

Honors and Awards

2014	Elected Member of the International Statistical Institute
2009	Elected Fellow of the American Association for the Advancement of Science
2007	Delivered the Iowa State University Women in Mathematical Sciences 2007 Distinguished Lecture
2004	Elected Fellow of the American Statistical Association
2002	Research featured in the Ohio State University College of Mathematical and Physical Sciences 2002-2003 Science Calendar
1992	Z. W. Birnbaum Prize for outstanding work as a graduate student, Department of Statistics, University of Washington
1985	Outstanding Teacher Award for excellence in teaching and research, South China Normal University
1980	Second Prize in the first Mathematics Competition, South China Normal University
1979-1983	Outstanding Student Awards, South China Normal University

Professional Society Memberships

1992-present	American Statistical Association
1992-present	Caucus for Women in Statistics
1998-present	International Genetic Epidemiology Society
2006-present	International Chinese Statistical Association
2008-present	American Association for the Advancement of Science
2009-present	International Biometric Society - ENAR

NATIONAL/INTERNATIONAL PROFESSIONAL SERVICES

NIH Grant Review Panels

Special Emphasize Panel, October 2002.

Genome Study Section (the finale!), June 2004.

Special Review Committee for three National Institute of Mental Health cooperative agreement applications (U01's), March, 2005.

Special Emphasis Panel for grant proposals for collaborations with the National Centers for Biomedical Computing (U01's), December 2005

National Cancer Institute Special Emphasis Panel, November 2007

National Cancer Institute Special Emphasis Panel, April 2008

National Cancer Institute Special Emphasis Panel, November 2008

National Cancer Institute Special Emphasis Panel, April 2010

National Center for Biosciences Computing Special Emphasis Panel, June 2010

National Cancer Institute Special Emphasis Panel, April 2011

Genomics, Computational Biology and Technology (GCAT), February 2012.

National Institute of Child Health and Human Development NGS Newborn Screening Panel, April 2013.

Genomics, Computational Biology and Technology (GCAT), October 2014.

Genomics, Computational Biology and Technology (GCAT), June 2015.

Genomics, Computational Biology and Technology (GCAT), October 2015.

Biostatistical Methods and Research Design (BMRD) Study Section, June 2016.

Biostatistical Methods and Research Design (BMRD) Study Section, October 2016.

Biostatistical Methods and Research Design (BMRD) Study Section, February 2017.

Biostatistical Methods and Research Design (BMRD) Study Section, June 2017.

Biostatistical Methods and Research Design (BMRD) Study Section, February 2018.

Biostatistical Methods and Research Design (BMRD) Study Section, June 2018.

Biostatistical Methods and Research Design (BMRD) Study Section, October 2018.

Biostatistical Methods and Research Design (BMRD) Study Section, June 2019.

Biostatistical Methods and Research Design (BMRD) Study Section, October 2019.

Biostatistical Methods and Research Design (BMRD) Study Section, June 2020.

Early Stage Investigator Maximizing Investigator Research Award (ESI MIRA), March 2021

NSF Grant Review Panels

Joint NSF/NIGMS Review Panel in Mathematical Biology, Arlington, VA, February 4-6, 2002.

Division of Mathematical Sciences Screening Panel, February 2003.

Division of Mathematical Sciences Screening Panel, February 2004.

Research Experience for Undergraduates (REU), November 2006.

Division of Mathematical Sciences Screening Panel, February 2009.

Division of Mathematical Sciences Screening Panel, February 2013.

Ad Hoc Grant Reviewer

National Science Foundation (mail reviewer several times).

Wellcome Trust (mail reviewer).

Canadian Centres of Excellence, January 2006.

Canadian Centres of Excellence, January 2008.

Ohio Super Computing Center, March 2009.

Ohio Super Computing Center, August 2009.

Research Grants Council of Hong Kong, March 2017.

Natural Sciences and Engineering Research Council of Canada, January 2018

CANSSI Collaborative Research Team Projects Program (LOI), August 2020

Natural Sciences and Engineering Research Council of Canada, January 2023

External Examiner of Ph.D. Thesis

Hong Kong University, Hong Kong2007.
Hong Kong University, Hong Kong2009.
University for Health Sciences, Medical Informatics and Technology, Astria, 2011.

Journal Referee

American Journal of Human Genetics,
Annals of Applied Statistics
Annals of Statistics
Bioinformatics
Biometrics
BMC Genetics
BMC Genomics
Briefings in Bioinformatics
Computational Statistics and Data Analysis
European Journal of Human Genetics
Genetics
Genetic Epidemiology
Genome Biology
Human Heredity
Journal of Agricultural, Biological and Environmental Statistics
Journal of American Statistical Association
Journal of Genetics and Genomics
Journal of Human Genetics
PLoS ONE
PLoS Computational Biology
Statistics and Computing
Statistical Science
The American Statistician

Conference/Workshop Organizer/Chair/National Committee

Chair of the Organizing Committee for the Fifth Florence Nightingale Day: A celebration of women in statistics and promoting statistics and data science to 8-12th grade students. Hosted by the Ohio State University and the University of Texas at Dallas, October 29, 2022 (a hybrid event with students attending the in-person event in Columbus and online).

Organizer and Chair of "Women in Statistics Luncheon Meeting," 31st International Biometric Conference, Riga, Latvia, July 2022.

Chair of the Organizing Committee for the Fourth Florence Nightingale Day: A celebration of women in statistics and promoting statistics and data science to 8-12th grade students. Hosted by the Ohio State University and the University of Texas at Dallas, October 23, 2021 (an online international event).

Organizer and host of a webinar in the Webinar Series of the ASA Section on Statistics in Genomics and Genetics. June 2021.

Chair of the Organizing Committee for the Third Florence Nightingale Day: A celebration of women in statistics and promoting statistics and data science to 8-12th grade students. Hosted by the Ohio State University, November 14, 2020 (online event due to COVID-19).

Member of the Joint Statistical Meeting (JSM) 2021 Program Committee.

Member of the Scientific Committee for the 2nd International Conference on Statistics: Theory and Applications (ICSTA'20), Prague, Czech Republic, August 2020 (moved online due to COVID-19).

Member of the International Program Committee, XXX^{th} International Biometric Conference, Seoul, South Korea, July 2020 (moved online due to COVID-19).

Chair of the International Committee on Social Program, XXX^{th} International Biometric Conference, Seoul, South Korea, July 2020 (moved online due to COVID-19). Created the Florence Nightingale Award and selected the inaugural awardee.

Chair of the Organizing Committee for the Second Florence Nightingale Day: A celebration of women in statistics and promoting statistics and data science to 8-12th grade students. The Ohio State University, October 19, 2019.

Member of the Executive Committee of the 2019 Women in Statistics and Data Science Conference, Bellevue, Washington, October 2019.

Organizer of the Special Topics Session (STS) "Statistical analysis of complex data in statistical genetics and bioinformatics," International Statistical Institute World Statistics Congress, Kuala Lumpur, Malaysia, August 2019.

Chair of the Organizing Committee for the inaugural Florence Nightingale Day: Exploring statistics and data science for 8-12th grade female students. The Ohio State University, October 27, 2018. Wrote an article on the event that was published in the March 2019 AMStat News.

Member of the Steering Committee for the Florence Nightingale Day, jointly launched by the Caucus for Women in Statistics and the American Statistical Association, 2018.

Member of the organizing committee, Joint Biostatisitcs Symposium, The Ohio State University, Cleveland Clinic Foundation, and Case Western Reserve University, 2015 – 2022 annually.

Member of the Executive Committee of the 2018 Women in Statistics and Data Science Conference, Cincinnati, OH, October 2018.

Organizer of Panel Session on "Implicit Bias and Power Dynamics: How We Can Change the Culture," 2018 Women in Statistics and Data Science Conference, Cincinnati, OH,

October 2018.

Co-organizer of MBI Fall 2018 Emphasis Semester Workshop "Family-based Genomic Studies," September 2018.

Organizer of Invited Session "Statistical models for estimating and testing causal effects in biomedical studies," Joint Statistics Meetings, July, 2018.

Organizer of "Women in Statistics Luncheon Meeting," XXIXth International Biometric Conference, Barcelona, Spain, July 2018.

Organizer of the Invited Paper Sessions (IPS) "Integrative analysis of complex data - from genomics to bioinformatics," International Statistical Institute World Statistics Congress, Marrakech, Morocco, July 2017.

Organizer of Lunch Roundtable Discussion Group "Empowering Women in Statistics and Data Sciences," International Statistical Institute World Statistics Congress, Marrakech, Morocco, July 2017.

Organizer and Chair of the Invited Session "The 3D Genome - How Statistics Can Help Shape It," Sponsored by the Committee of Representatives to AAAS, Joint Statistics Meetings, 2016.

Organizer of Lunch Roundtable Discussion Group "The Role of Statistics in the Big Data Era of Genomics and Epigenomics Research," 60th World Statistics Congress (ISI 2015), Rio de Janeiro, Brazil, July 2015.

Organizer of Workshop "Bioinformatics: Statistical Modeling and Analysis of Whole Genome Methylation and Chromatin Interaction (Epigenetics)," Statistical and Applied Mathematical Sciences Institute (SAMSI), March 2015.

Organizer of Symposium "Obesity And Microbiome - Concepts And Contradictions," 2015 Annual AAAS Meeting, San Jose, February 2015.

Member of the Organizing Committee of the Second Symposium of Nationwide Children's Hospital and The Ohio State University "Road to Collaboration for the Human Genetics and Genomics Community: Big Data and Big Ideas in Genomic Medicine," Columbus, January 2015.

Member of the Steering Committee of the International Conference on Intelligent Biology and Medicine, December 2014, San Antonio.

Program Leader of 2014-2015 Statistical and Applied Mathematical Sciences Institute (SAMSI) Program "Beyond Bioinformatics: Statistical and Mathematical Challenges," Research Triangle Park, 2014-2015.

Co-organizer on "Beyond Bioinformatics Opening Workshop," Statistical and Applied Mathematical Sciences Institute (SAMSI), September 2014.

Co-organizer of Topic-Contributed Session "Recent advances in the analysis of ranking data," JSM, Boston, 2014.

Co-organizer of Symposium "The Science of Uncertainty in Genomic Medicine," Annual AAAS Meeting, Boston, 2013.

Chair of Invited Session "Powerful statistical models and methods in next generation sequencing" ENAR 2012 Spring Meeting.

Chair of Invited Session of a journal showcase session in the ICSA 2012 Applied Statistics Symposium. Boston, 2012.

Organizer and chair of invited session "Novel Mixture Modeling and Likelihood Methods in Modern Biomedical Applications," XXVI International Biometric Conference, Kobe, Japan, 2012.

Co-organizer of the "Thompson Symposium" in honor of Elizabeth Thompson's 60th Birthday and her election to the National Academy of Sciences, University of Washington, Seattle, 2009.

Co-organizer of Workshop on Statistical System Biology, Mathematical Biosciences Institute, The Ohio State University, 2009.

Co-organizer of Workshop on MicroRNA in Development and Cancer, Mathematical Biosciences Institute, The Ohio State University, 2007.

Organizer of an Biometrics Section Invited Session, JSM 2006.

Organizer of an IMS/WNAR Invited Session, WNAR 2006.

Organizer of an Invited Session, ICSA 2006.

Co-organizer of Workshop on Gene Expression Data Analysis, Mathematical Biosciences Institute, The Ohio State University, 2004.

Organizer of a Special Contributed Session for the Joint Statistics Meetings, Sponsored by the Caucus for Women in Statistics, 1999.

Session Chair for the Joint Statistics Meetings multiple times prior to 1999.

Notable Work Related to Diversity, Equity, and Inclusion (DEI)

During the year serving as president of the Caucus for Women in Statistics:

Helped orchestrate the successful proposal for the establishment of the FN David and EL Scott Lectures at Join Statistical Meetings (JSM) – first major lectures named after women statisticians at JSM.

Worked with ASA to jointly launch the Florence Nightingale Day (FN Day) to promote statistics and data science and to attract middle and high school students — especially women and those from under-represented and disadvantaged groups — to pursue education and a future career in data-related fields. FN Day has since been expanded to be an international event, and we just hosted the 4th Annual FN Day in October 2021.

Worked on various initiatives to advance the mission of CWS, including international membership, establishment of country representatives, endowment, developing country member fund, webinar, and organization of technical session in conferences.

Promote and mentor women and minorities from diverse background:

Act as nominator or write supporting letters for women to receive professional awards and recognitions, including the ASA Fellows Award.

Mentor colleagues from under-represented groups.

Formed and chair the IBS Social Program Committee to address DEI issues:

Fostered the partnership between IBS and CWS and chaired the Social Program Committee (with members from all continents — Africa, Asia, Australia, Europe, North America, and South America) to create the Nightingale Award in 2020 as a celebration of the 200th birth anniversary of Florence Nightingale and the Year of the Women in Statistics.

Continued to work on and successfully established the Nightingale Award as a regular biennial IBS-CWS Award to individuals who have demonstrated successful scholarship as well as care for disadvantaged individuals or groups.

Organize a lunch-time session to address EDI issues for the biennial International Biometric Conference (IBC) in 2018, 2020 (cancelled due to the pandemic), and 2022.

In the process of organizing other events to promote diversity, equity, and inclusion within the international biometric society, including honoring past females and males presidents of the IBS, and recording, preserving, and sharing "citizen" interviews of any individual IBS members with an inspiring story of their career and/or career path.

Chair the Member Engagement Committee of the ASA SSGG to serve its membership:

Organize a webinar series featuring a diverse group of speakers presenting topics of high interest to members in the Section on Statistics in Genomics and Genetics (SSGG).

Organize other activities, including mentoring, career advise, and social interactions to engage the members and to promote equity and a welcoming community environment.

Engage in IMS effort to promote equity and diversity:

Compiled data on Women on Editorial Boards (WEB) of the Institute of Mathematical Statistics (IMS) sponsored journals and presented the results to the Joint Committee on Women in the Mathematical Sciences.

Made a request to the IMS president to collect gender and other information on members so that not only more meaning analysis can be done for the WEB data, but also to better serve the membership; subsequently served as a member on a newly formed Equity and Diversity Committee that surveyed the IBS membership for gender and other information. Continue to serve as a member in the committee to address DEI issues.

Engagement with the Canadian Statistical Sciences Institute (CANSSI) DEI:

Play an instrumental role in CANSSI DEI as a member of the Board of Directors. I have connected CANSSI to IMS for possible collaboration on addressing DEI issues, and I have introduced the Florence Nightingale Day as a significant piece of CANSSI's international and broad outreach portfolio, which is now being included as an important activity of the institute's programs.

TEACHING

Regular Courses

Taught regularly scheduled classes (from introductory statistics to PhD level courses) at Ohio State (and Berkeley) since 1993.

Short Courses

- Summer Institute in Statistical Genetics, North Carolina State University (2000-2005)

- Summer Institute in Statistical Genetics, University of Washington (2006-2009)
- Short Course on Statistical Genetics and Genomics, University of Alabama at Birmingham (2011-2012)
- Short Course on Next Generation Sequencing: Technology & Statistical Methods, University of Alabama at Birmingham (2011-2012)
- Summer Biomedical Big Data Workshop, Purdue University (2016)
- Workshop on Omic Data Analysis, Ohio State University Medical Center and the Mathematical Biosciences Institute (2015-2017)

Supervision of Study Group

Organizer of the Statistical Genetics and Bioinformatics Reading Group/Journal Club at the Ohio State University; mentor for 5-10 students and postdocs per quarter/semester since 1997 (every semester/quarter for 25 years).

STUDENTS, POSTDOCS, AND OTHERS

Ph.D. Advisees

Name	Year	Awards and Honors	First[a]/Current Position[b]
Yuqun Luo	2002	Journal Awards (3 times) OSU PDF Award (2001) Student Travel Award (2001) Hayes Research Forum (2001) Best Consultant Award (2002) Whitney Award (2002)	FDA[b]
Zachary Skrivanek	2002	Journal Award	Eli Lilly[a,b]
Swati Biswas	2003	Student Travel Award (2002) Hayes Research Forum (2003) Teaching Awards (3 times) Best Consultant Award (2003)	Professor, University of Texas at Dallas[b]
Babis Papachristou	2005	Powers Teaching Award (2001) OSU PDF Award (2003, 2005) Best RA Award (2005) Hayes Research Forum (2005) Lindback Award for Teaching	Associate Professor, Rowan University[b]
Shuyan Wan	2006		Merck[a,b]
Jie Ding	2008	Best RA Award (2007) Whitney Award (2008)	Veracyte Inc[b]
Jingyuan Yang	2010	University Fellowship (2005) Travel Award, SISG (2007) Whitney Award (2010)	Statistics Manager, Amgen[a]
Liang Niu	2012	Best RA Award (2011)	Associate Professor, University of Cincinnati[b]

Name	Year	Awards and Honors	First[a]/Current Position[b]
Dao-Peng Chen	2013		Postdoc, Tsing Hua University[a]
Meng Wang	2014		Nationwide Children's Research Institute[a,b]
Shuang Xia	2014		Capital One[a]
Fangyuan Zhang	2015	University Fellowship (2011) Presidential Fellowship (2014) Best RA Award (2014) ASA Biometrics Section Student Travel Award (2015) Whitney Award (2015)	Associate Professor[b] Texas Tech University
Han Zhang	2017		MassMutual[b]
Xiaofei Zhou	2019	Best RA Award (2017) Best TA Award (2018) Whitney Award (2019)	Novartis[a,b]
Chenggong Han	2020		Google[a]
Shuyuan Lou	2021		Incyte[a]
Pei Yang	2021	GlaxoSmithKline[a]	
Qing Xie	2021	Koch Fellowship (two times)	Novartis[a]
Zilu Liu	2022	University Fellowship Best RA Award (2021)	 Amgen[a]
Qiaolan Deng	2022		Wells Fargo[a]
Boyang Zhang*	2022		Illumina[a]
Qingyu Chen	Current		
Yongqi Liu	Current	University Fellowship	

*Department of Animal Science

Masters Students (Thesis Advising)

Name	Year	Awards and Honors	Current Position/Affiliation
Matthew Brems	2015	Best TA Award (2015)	Junior Data Scientist at Optimus Consulting (first position)
Cheng Cao	2020		PhD student at Hong Kong Univ
John Lesniak	Current		

Summer Research Experience for Undergraduate Students

Name	Year	Achievements	Undergraduate University
Emma Rogge	2014	Poster Presentation	Harvard University
Shuyuan Lou	2014	Poster Presentation	Ohio State University

2012 NIGMS Bursary Service (Award) Mentoring

Name	Period	Position/Affiliation at Time of Award
Daniel Enquobahrie	2011-2012	Assistant Professor, University of Washington
Abdus Sattar	2011-2012	Assistant Professor, Case Western Reserve University
Xiaowei Guan	2011-2012	Graduate Student, Case Western Reserve University
Dave Fardo	2012-2013	Assistant Professor, University of Kentucky

Other Students/Visiting Students (supervised leading to joint publications)

Name	Period	Current Position/Affiliation for Visitors
John Lawrence	1996, 1998	Statistician, Food and Drug Administration
Xin Gao	1999-2000	Associate Professor, York University
Jim Rogers	2000-2001	Statistician, Pfizer Pharmaceuticals
Roxana Alexandridis*	2000-2003	Postdoc, University of Wisconsin
Chin-Yuan Liang	2007-2010	MS in Statistics, OSU.
Jiyuan Zhou	2008-2009	Visiting student from Hong Kong University
Katie Thompson	2010-2013	Assistant Professor, University of Kentucky
Degang Zhu	2014-2015	Visiting student from Shanghai University of Finance and Economics
Yuan Gao	2016-2017	PhD in Biostatistics, OSU
Min-Ho Cho	2016-2017	PhD in Statistics, OSU
Hengrui Luo	2016-2017	PhD in Statistics, OSU
Hancong Tang	2016-2018	PhD Program in Pharmacy, OSU

*A poster based on a paper published on Bioinformatics won first prize in the poster competition in the Seventh International Meeting of the Microarray Gene Expression Data Society Toronto, Canada, September 8-10, 2004.

Postdocs Mentored

Name	Period	First Position/Affiliation
Rong Cheng	1999-2000	Statistical Geneticist, Columbia University
Daolong Wang	1999-2002	Research Assistant Professor UT Health Science Center at San Antonio
Zhenqiu Liu	2004-2005	Assistant Professor, University of Maryland
Zailong Wang	2004-2005	Novartis Pharmaceuticals Corporation
Jin Zou	2004-2007	Assistant Professor, Northern Michigan University
Dustin Potter	2005-2008	
Abbas Khalili	2006-2007	Assistant Professor, McGill University, Canada
Wei Guo	2006-2009	NIH
Shuying Sun	2007-2009	Assistant Professor, Case Western Reserve University
Cenny Taslim	2008-2012	OSU Medical Center
Erik Bloomquist	2009-2010	FDA
Jincheol Park	2012-2013	Assistant Professor, Keimyung University, South Korea
Xiangtao Liu	2012-2014	Statistics/Solid Tumor Program
Deepak Ayyala	2013-2016	Jackson Laboratory
Farhad Shokoohi	2014-2017	University of Nevada at Las Vegas

GRANTS

Principal Investigator

1. R01GM114142 "Omics analysis of three-dimensional transcriptional regulation," National Institute of General Medical Sciences, NIH, 04/13/2015-11/30/2024. (MPI)

2. DMS-1208968 "Modeling and Analysis of Genomic Imprinting and Maternal Effects," Division of Mathematical Sciences (Statistics Program), NSF, 09/01/2012-8/31/2019.

3. DMS-1220772 "Collaborative Research: ATD: Statistical and Computational Methods for the Analysis of Metagenomic Count Data," Division of Mathematical Sciences (COFFES - Computational Foundations for Emerging Science Frontiers), NSF, 09/01/2012-8/31/2018.

4. 1R03CA171011-01 "Identifying rare haplotype-environment interactions using Logistic Bayesian Lasso," NCI, 07/01/2012-6/30/2015.

5. DMS-1042946 "ATD: Statistical methods and software for analyzing massively parallel epigenomic sequencing data," Division of Mathematical Sciences, NSF, 10/1/2010-9/30/2014.

6. R01 HG002657-01A1 "Statistical methods for gene mapping - a new paradigm," National Human Genome Research Institute, NIH, 1/20/04-12/31/2008.

7. DMS-0306800 "Statistical methods for gene mapping based on a confidence set approach," Division of Mathematical Sciences, NSF, 8/1/03-7/31/07.

8. DMS-9971770 "Statistical and computational methods in genetic analysis," Division of Mathematical Sciences, NSF, 1999-2002.

9. DMS-9632117 "Statistical methods for summarizing and combining gene maps," Division of Mathematical Sciences, NSF, 1996-1998.

10. "Statistical and computational methods in human genome studies," Ohio State University Seed Grant, 1996-1997.

Co-Principal Investigator

11. U54 CA113001 (Center Director: Tim Huang; Role: Project 2 leader) Project 2: Integrating genomic & epigenomic alterations in cancer and its microenvironment. National Cancer Institute, NIH, 2004-2010.

12. R01 NS46696-01A1 (PI: Yang Liu), "CD24 Polymorphism and Multiple Sclerosis," National Institute of Neurological Disorders & Stroke, NIH, 2004-2009.

13. BRTT (PI: Yang Liu) "A Commercialization Platform for immunotherapeutics of Cancer and Multiple sclerosis," Biomedical Research and Technology Transfer Partnership Awards (Ohio Third Frontier Projects), 2005-2009.

Co-Investigator

14. R01HL164906 (PI: Raymond Benza), "PHORA-Pulmonary Hypertension Outcome Risk Assessment," National Heart, Lung, and Blood Institute, NIH, 09/01/2022 – 08/31/2027.

15. Gates Grant (PI: Larry Schlesinger) "Alveolar macrophage immunobiology and functional genomics: Unlocking human to human variation in host response to M. tuberculosis" Bill & Melinda Gates Foundation, 08/20/2015 - 07/31/2020.

16. NSFC (PI: Yueqing Hu) "Incorporating Structural Features of Genes into Multi-site Association Studies," National Science Foundation of China, 01/01/2016 - 12/31/2019.

17. R01 CA151979 (PI: Qianben Wang) "Regulation of androgen receptor function by H3K4 methylation in prostate cancer" National Cancer Institute, 9/1/2011-8/30/2016.

18. U54 CA113001 (PI: Tim Huang) "Interrogating epigenetic changes in cancer genomes" National Cancer Institute, 3/1/2010-2/28/2015.

19. U01ES015986 (PI: Tim Huang) "Environmental epigenetics and stem/progenitor cell injury," National Institute of Environmental Health Sciences, 2007-2011.

20. R01CA069065 (PI: Tim Huang) "CpG Island Methylator Phenotypes in Breast Cancer". National Cancer Institute, NIH, 2007-2012.

21. 1 R01 HL083478-01 (PI: Phil Diaz) "Alveolar macrophage proteomics in HIV-induced emphysema," National Heart, Lung and Blood Institute, NIH, 2005-2010.

22. P01 DK55546 (PI: Lee Hebert) "Genetic and clinical risk factors for human SLE nephritis," NIH, 2001-2004.

23. (PI: Barbara Licht) "Idiopathic epilepsy in poodles: determining the modes of inheritance," the American Kennel Club Canine Health Foundation and the Poodle Club of America Foundation, Inc. 1997-1999.

24. R01 HG01093-01 (PI: Terry Speed) "Studies in gene mapping," National Human Genome Research Institute, NIH, 1994 - 1997.

Statistician

25. R01HL134673 (PI: Ray Benza) "PHORA: A Clinical Decision Support Tool for Patients with Pulmonary Arterial Hypertension," National Heart, Lung, and Blood Institute, NIH 04/01/2017 – 01/31/2022.

Other/Travel Grants

26. Received a grant for preparation to present a paper in the Genetic Analysis Workshop 13 in New Orleans, November 2002.

27. Received a grant for preparation to present a paper in the Genetic Analysis Workshop 12 in San Antonio, Texas, October 2000.

28. Received a grant for preparation to present a paper in the Genetic Analysis Workshop 11 in Arcachon, France, September 1998.

29. Received a travel award to present a paper in the First Annual International Conference on Computational Biology, Santa Fe, New Mexico, January 1997.

30. Received funding to participate in the Workshop on Map Integration (all expenses paid), funded by the Pittsburgh Supercomputer Center, Pittsburgh, PA, December 1995.

31. Received funding to participate in the Workshop on Statistical Methods in Genetic Mapping (all expenses paid), funded by the Research Foundation of Mental Hygiene, Inc., Tarrytown, NY, September 1995.

32. Received funding to participate in IMA Summer Program in Molecular Biology for two weeks (all expenses paid), funded by the Institute of Mathematics and its Applications, University of Minnesota, July 1994.

33. Received a travel award to participate in the Pathway to Future Workshop for women statisticians (all expenses paid), funded by the IMS, Chapel Hill, NC, June 1994.

34. Received a travel award to present a paper in the WNAR Student Paper Competition, Corvallis, OR, June 1992.

INVITED TALKS

1. "Challenges inHigh-Dimensional Genomics — Statistical Inference with Sparse Single CellHi-C Data," The 4th International Conference on Statistical Distributions and Applications (ICOSDA). Huntington, WV, October 2022

2. "Celebrating the Legacy of Florence Nightingale: Information about the Florence Nightingale Day," International Day of Women in Statistics & Data Science (IDWSDS), Virtual, October 2022.

3. "Challenges in High-Dimensional Genomics—Statistical Inference with Sparse Single Cell Hi-C Data," Special Invited Session in the Sixth International Webinar on "Recent Trends in Statistical Theory and Applications - 2022) (WSTA-2022). July 2022.

4. "CaTCHing TADs by Random Walks on Single-Cell Hi-C Data: Reality or Fiction?" 6th International Conference on Mathematical and Computational Medicine (Virtual Participation). June, 2022.

5. "CWS: Nurturing and Empowering Women in Statistics," Korean Statistical Society Conference, November 2021 (participated through Zoom).

6. "Sparsity in Single Cell Hi-C Data – Not All Zeros Are Created Equal," International Chinese Statistical Association Applied Statistics Symposium, Zoom Conference, September 2021.

7. "Florence Nightingale Day: Inspiring and passing the 'lamp' to the next generation statisticians," Western North American Regional of the International Biometric Society, Zoom Conference, June 2021 (postponed from 2020 meeting scheduled in Anchorage, AK, June 2020, due to COVID-19).

8. "Sparsity in Single Cell Hi-C Data – Not All Zeros Are Created Equal," 5th International Conference on Mathematical and Computational Medicine, Zoom Conference, June 2021.

9. "Bayesian Lasso for detecting common and rare genetic variants associated with survival traits," International Indian Statistical Association, Zoom Conference, May 2021 (postponed from 2020 meeting scheduled in Chicago, IL, May 2020, due to COVID-19).

10. "Random Effect Modeling of Whole Genome Chromatin 3D Structure: From Bulk to Single Cell Data," Department of Statistics, University of South Carolina, Columbia, SC, April 2021 (Zoom seminar).

11. "Detecting Differentially Methylated Regions Using Bayesian Credible Bands," International Biometric Conference, Seoul, South Korea, July 2020 (talk was delivered online due to COVID-19).

12. "Investigating Relationships of Multiomics and their Roles in Complex Traits," Division of Biostatistics, University of Minnesota, Minneapolis, MN, February 2020.

13. "Statistical Inference of Chromatin 3D Structures from DNA Methylation Data," The 11th International Chinese Statistical Association International Conference, Hangzhou, China, December 2019.

14. "Investigating Relationships of Multiomics and their Roles in Complex Traits," Department of Horticulture and Crop Science, Ohio State University, Columbus OH, November 2019.

15. "Partial Likelihood for Detecting Imprinting and Maternal Effects on Complex Diseases," Women in Statistics and Data Science Conference, Bellevue, WA, October 2019.

16. "Detecting Differentially Methylated Regions Accounting for Cell Purity Using Bayesian Credible Bands," 62nd World Statistics Congress of the International Statistical Institute, Kuala Lumpur, Malaysia, August 2019.

17. "Statistical Inference of Chromatin 3D Structures from DNA Methylation Data," Joint Statistical Meetings, Denver, CO, July 2019.

18. "Detecting Differentially Methylated Regions Accounting for Cell Purity Using BCurve," International Chinese Statistical Association, Raleigh, NC, June 2019.

19. "Partial Likelihood for Detecting the Effects of Two Epigenetic Factors on Complex Diseases," 4th International Conference on Mathematical and Computational Medicine, Cancun, Mexico, December 2018.

20. "Partial Likelihood for Detecting the Effects of Two Epigenetic Factors on Complex Diseases," Michigan Technology University, Houghton, MI, October, 2018.

21. "Using Credible Bands for Demarcating Differentially Methylated Regions Based on BS-seq Data," Mini-Conference to Celebrate Elizabeth Thompson's Contributions to Statistics, Genetics and the University of Washington, Seattle, WA, June 2018.

22. "Random Effect Modeling of Whole Genome Chromatin 3D Structure," Penn State University, State College, PA, March 2018.

23. "Random Effect Modeling of Whole Genome Chromatin 3D Structure," Oregon State University, Corvallis, OR, November 2017.

24. "Whole Genome Chromatin 3D Structure Recapitulation," Fred Hutchinson Cancer Research Center, Seattle, WA, September 2017.

25. "tREX: A Statistical Inference Method for Chromatin 3D Structure," The Second International Conference on Computational Genomics and Proteomics, Playa Blanca, Panama, August 2017.

26. "Statistical Methods for Inference of Spatial Gene Regulation," 61st World Statistics Congress of the International Statistical Institute, Marrakech, Morocco, July 2017.

27. "tREX: A Statistical Inference Method for Chromatin 3D Structure," Graybill 2017 Conference, Fort Collins, CO, June 2017.

28. "Chromatin 3D structure recapitulation and long-range gene regulation with application to cancer genomics," MD Anderson Department of Biostatistics, Houston, TX, May 2017.

29. "Modeling and Inference for Spatial Chromatin Interactions," MBI Visitor Seminar Series, Columbus, OH, April 2017.

30. "Detection of Differentially Methylated Regions Using BS-seq Data," International Biometric Society ENAR Meeting, Washington DC, March 2017.

31. "Statistical Inference for Chromatin 3D Structure," International Chinese Statistical Association International Conference, Shanghai, China, December 2016.

32. "Partial Likelihood for Detecting the Effects of Two Epigenetic Factors on Complex Diseases," School of Statistics and Management, Shanghai University of Finance and Economics, Shanghai, China, December 2016.

33. "Opportunities and Statistical Challenges for Women in Genetic Research," Women in Statistics and Data Science Conference, Charlotte, NC, October 2016.

34. "Modeling and Inference for Spatial Chromatin Interactions," Department of Biostatistics, University of North Carolina, NC, September 2016.

35. "Impact of Data Resolution on Three-Dimensional Structure Inference Methods," Joint Statistical Meetings, Chicago, IL, August 2016.

36. "The Power of Statistics and Bioinformatics for Helping to Unlock Epigenetic Secrets," Special Lecture in "Big data training for translational omics research," an NIH-funded workshop hosted at Purdue University, West Lafayette, IN, July 2016

37. "BCurve: Detection of Differentially Methylated Regions Using BS-seq Data Based on Bayesian Credible Bands," The Third Taihu International Statistical Forum, Shanghai, China, July 2016.

38. "Three Dimensional Chromatin Structure and Spatial Gene Regulation," The 4th Institute of Mathemtical Statistics Asia Pacific Rim Meeting, Hong Kong, June 2016.

39. "Addressing the Correlated Feature in Sequencing-Based DNA Methylation Data for Detecting DMR," International Speaker Seminar Series of CIHR STAGE, Toronto, Canada, June 2016.

40. "BCurve: Detection of Differentially Methylated Regions Using BS-seq Data Based on Bayesian Credible Bands". 3rd International Conference on Mathematical and Computational Medicine. Columbus, OH, May 2016.

41. "Addressing the Correlated Feature in Sequencing-Based DNA Methylation Data for Detecting DMR," Department of Biostatistics, University of Pittsburgh, April 2016.

42. "Detecting Associations of Rare Variants with Common Diseases Using SNP Data on Families," International Biometric Society ENAR Meeting, Austin, Texas, March 2016.

43. "Addressing the Correlated Feature in Sequencing-Based DNA Methylation Data for Detecting DMR," Department of Biostatistics, Yale University, CT, February 2016.

44. "Robust partial likelihood approach for detecting imprinting and maternal effects," Department of Environmental Health Biostatistics and Bioinformatics Seminar Series, University of Cincinnati, Cincinnati, OH, October 2015.

45. "Robust partial likelihood approach for detecting imprinting and maternal effects," Joint Statistical Meetings, Seattle, WA. August 2015.

46. "Statistical Challenges in Analyzing Methylation and Long-Range Interaction Data," 2014-15 Program in Bioinformatics: Transition Workshop, Statistical and Applied Mathematical Sciences Institute, May 2015.

47. "Robust partial likelihood approach for detecting imprinting and maternal effects using case-control families," Academia Sinica, Taipei, Taiwan, January 2015.

48. "Robust partial likelihood approach for detecting imprinting and maternal effects using case-control families," International Statistics Conference "Statistics and Society in the New Information Age: Challenges and Opportunities," Colombo, Sri Lanka, December 2014.

49. "Toward the 3D Genome: Chromatin Interaction and Regulation," National Health Research Institute, Zhunan, Taiwan, December 2014.

50. "Toward the 3D Genome: Chromatin Interaction and Regulation," Department of Mathematics, National Chong Cheng University, Chia-Yi, Taiwan, 2014.

51. "Robust partial likelihood approach for detecting imprinting and maternal effect," Department of Biostatistics, University of Minnesota, Minneapolis, MN, December 2014.

52. "Logistic Bayesian LASSO for Identifying Rare and Common Haplotypes and Environmental Factors Associated with Common Diseases," Shanghai Center for Mathematical Sciences, Fudan University, Shanghai, China, April 2014.

53. "Toward the 3D Genome: Chromatin Interaction and Regulation," Institute of Systems Biology, Shanghai Jiao Tong University, Shanghai, China, April 2014.

54. "Logistic Bayesian LASSO for Identifying Rare and Common Haplotypes and Environmental Factors Associated with Common Diseases," Institute of Management, Shanghai Maritime University, Shanghai, China, April 2014.

55. "Three Dimensional Chromatin Structure and Spatial Gene Regulation," Ordered Data Analysis, Models and Health Research Methods: An International Conference in Honor of H.N. Nagaraja for His 60th Birthday. University of Texas at Dallas, March 2014.

56. "Whole Genome 3D Architecture of Chromatin and Regulation," Department of Mathematics and Statistics, McGill University, Montreal, Canada, October 2013.

57. "Whole Genome 3D Architecture of Chromatin and Regulation," Statistics at the Crossroads: Its Multifaceted Impact on the Society, Akron, OH, October 2013.

58. "Logistic Bayesian Lasso for Identifying Rare and Common Haplotypes and Environmental factors Associated with Complex Diseases," IMS-China, Chengdu, China, July 2013.

59. "Reconstruction of Spatial Chromatin Structure of Long-Range Regulation," 2nd Taiwan Epigenomics Symposium, National Chung Cheng University, Chia-Yi Taiwan, July 2013.

60. "Challenges in Modeling and Analyzing DNA Methylation Data," Statistical and Applied Mathematical Sciences Institute (SAMSI), Research Triangle Park, North Carolina, May 2013.

61. "Whole Genome 3D Architecture of Chromatin and Regulation," Biostatistics Center, The Ohio State University, Columbus, Ohio, April, 2013.

62. "Design and Analysis of Several Epigenetic Factors," Biostatistics Branch Seminar, National Institute of Environmental Health Sciences, Research Triangle Park, North Carolina, March 2013.

63. "Whole Genome 3D Regulation Analysis Using Sequencing," 2nd Annual Short Course on Next Generation Sequencing: Technology & Statistical Methods, Birmingham, AL, December 2012.

64. "Bayesian Modeling for Identifying Spatial Interactions of Chromatins". Zing Conference on Mathematical and Computational Medicine, Xcaret, Mexico, December 2012.

65. "Identifying Spatial Interactions of Chromatins Based on Mixture Modeling". XXVI International Biometric Conference, Kobe, Japan, August 2012.

66. "Bayesian Modeling for Identifying Spatial Interactions of Chromatins". Institute of Bioinformatics and Department of Statistics, Seoul National University, August 2012.

67. "Epigenomics methods I". Second Annual Short Course on Statistical Genetics and Genomics, University of Alabama in Birmingham, Birmingham, July 2012.

68. "Epigenomics methods II". Second Annual Short Course on Statistical Genetics and Genomics, University of Alabama in Birmingham, Birmingham, July 2012.

69. "Detecting Rare Haplotype Complex Disease Association Using Triads" International Chinese Statistical Association Applied Symposium, Boston, MA, June, 2012.

70. "Whole Genome Sequencing Based 3D Regulation Analysis". NHGRI Next Generation Sequencing short course, University of Alabama in Birmingham, Birmingham, December 2011.

71. "Assessing the effects of two epigenetic factors on complex genetic traits". Conference on risk assessment and evaluation of predictions. Silver Spring, MD, October, 2011.

72. "Identifying Rare Haplotypes Associated with Common Diseases through Logistic Bayesian LASSO". Joint Statistical Meeting, Miami, FL, August, 2011.

73. "Epigenetics Methods". First Annual Short Course on Statistical Genetics and Genomics, University of Alabama in Birmingham, Birmingham, July 2011.

74. "DNA Methylation Analysis - Microarray and Sequencing". Annual Meeting of the International Chinese Statistical Association, New York, June 2011.

75. "Likelihood Approach for Detecting Imprinting and Maternal Effects in Family-Based Association Studies". Department of Statistics, Yale University, March 2011.

76. "Cancer Epigenetics". ICBP Mathematical Meeting, Berkeley, CA, October 2010.

77. "Space oriented rank based data integration". Joint Statistical Meetings, Vancouver, Canada, August 2010.

78. "Case-parents control-parents design for detecting association and parent-of-origin effects". First Joint Biostatistics Symposium, Beijing, China, July 2010.

79. "Bayesian Analysis of Spatial Interactions in Chromatins with Application to MCF-7 ChIA-PET Data". Institute of Biostatistics, Fudan University, Shanghai, China, July 2010.

80. "Integration of Rank-based Biomedical Information". Department of Biostatistics, Southern Medical University, Guangzhou, China, July 2010.

81. "Space oriented rank based data integration". Interface 2010, Seattle, WA, June 2010.

82. "BASIC: Bayesian analysis of spatial interactions in chromatins with application to MCF-7 ChIA-PET data.". Center for Cancer Systems Biology Annual Workshop, Columbus, OH, June 2010.

83. "Space oriented rank based data integration". Mathematical Biosciences Institute, Columbus, OH, April 2010.

84. "Space oriented rank based data integration". International Conference on Frontiers of Interface between Statistics and Sciences in honor of C. R. Rao's 90th year. Hyderabad, India, December 30, 2009-January 2, 2010.

85. "Genetic imprinting and maternal effects," short course, 14th Summer Institute in Statistical Genetics, University of Washington, Seattle, WA, June 2009.

86. "Normalization and mixture modeling for next generation sequencing data," Illumina Sequencing User Group Meeting, The Ohio State University, Columbus, OH, June 2009.

87. "Modeling and Testing of Imprinting and Heterogeneous Maternal Effects" 4th Canadian Genetic Epidemiology and Statistical Genetics Meeting, Harrison Hot Springs, BC, Canada, May 2009.

88. "Modeling Imprinting and Heterogeneous Maternal Effects" Department of Mathematics, Wright State University, May 2009.

89. "Finite Mixture of Sparse Normal Linear Models in High Dimensional Feature Space with Applications to Genomics Data," ENAR, San Antonio, TX, March 2009.

90. "Modeling Imprinting and Heterogeneous Maternal Effects," Institute of Statistical Sciences, Academia Sinica, Taipei, Taiwan, December 2008.

91. "Robust Gene Pairs for Cross-Study and Cross-Platform Integration and Prediction," 4th World Conference of the International Association in Statistical Computing, Yokohama, Japan, December 2008.

92. "A Robust Unified Approach to Analyzing Methylation and Gene Expression Data," Department of Mathematics and Statistics, Newcastle University, Newcastle, UK, July 2008.

93. "A Robust Unified Approach to Analyzing Methylation and Gene Expression Data," International Biometric Conference, Dublin, Ireland, July 2008.

94. "Analysis of genetic data on related individuals," Summer Institute in Statistical Genetics, University of Washington, June 2008.

95. "Generalized Linear Modeling with Regularization for Detecting Common Disease Rare Haplotype Association," Ohio Collaborative Conference on Bioinformatics, University of Toledo, OH, June 2008.

96. "CSI for linkage and association studies". Department of Mathematics and Statistics, University of Windsor, Windsor, Canada, April 2008.

97. "Regularized logistic regression for detecting common disease rare haplotype association". Division of Biostatistics, University of Maryland Marlene and Stewart Greenebaum Cancer Center, Baltimore, MD, March 2008.

98. "CSI for linkage and association studies". Department of Statistics, North Carolina State University. Raleigh, NC, January 2008.

99. "Genomewide Tagging SNPs with Entropy Based Methods". Workshop on Genomics and DNA Sequence Analysis, National Health Research Institutes, Zhunan, Taiwan, June 2007.

100. "A cross entropy Monte Carlo approach to integrating data from microRNA targets or genomic experiments". Symposium on Recent Development of Statistics in Biological Sciences, National Health Research Institutes, Zhunan, Taiwan, June 2007.

101. "Modeling and analysis of SAGE libraries - the aging Brain". The 2007 Taipei International Statistical Symposium and ICSA International Conference, Academia Sinica, Taipei, Taiwan, June 2007.

102. "Pedigree data analysis". Summer Institute in Statistical Genetics, University of Washington, Seattle, June 2007.

103. "MicroRNA expression profiles for the NCI-60". Bioinformatics Seminars, Texas A&M University, College Station, TX, May 2007.

104. "Cross Entropy Monte Carlo for Aggregating microRNA Targets or Genomic Experiments". Division of Biostatistics, IUPUI, Indianapolis, IN, May 2007.

105. "A cross entropy Monte Carlo approach to integrating data from microRNA targets or genomic experiments". Department of Epidemiology and Biostatistics, Memorial Sloan-Kettering Cancer Center, New York, NY, April 2007.

106. "Modeling and analysis of SAGE libraries - the aging Brain". Department of Statistics, Iowa State University, Ames, IA, April 2007.

107. "Aggregation of ranked lists via cross entropy Monte Carlo". Department of Statistics and Probability, Michigan State University. East Lansing, MI, October 2006.

108. "Rank aggregation of microRNA targets via cross entropy Monte Carlo". XXIII International Biometric Conference, Montreal, Canada, July 2006.

109. "Rank aggregation of microRNA targets via cross entropy Monte Carlo". International Conference on Frontiers of Statistics - Biostatistics and Bioinformatics, Changchun, China, July 2006.

110. "Rank aggregation of microRNA targets via cross entropy Monte Carlo". University of Macau, Macau, June 2006.

111. "Advanced pedigree MCMC". Summer Institute in Statistical Genetics, University of Washington, Seattle, June 2006.

112. "Biomarker detection, prediction, and recapitulation of tumor progression pathways using methylation data". National Cancer Institute ICBP Conference, Nashville, TN, May 2006.

113. "Statistical analysis of "omic" data". The 8th Annual OSU Comprehensive Cancer Center Scientific Meeting. Columbus, OH, February 2006.

114. "Microarray Gene Expression Data Analysis," four lectures for the Mathematical Biosciences Institute 2005 Summer Program, Ohio State University, Columbus, OH, August 1-4, 2005.

115. "Statistical methods and applications in genetics, genomics, proteomics, and bioinformatics." Department of Mathematics, South China Normal University. Guangzhou, China, July 2005.

116. "CSI-Multipoint." Department of Mathematics, South China Normal University . Guangzhou, China, July 2005.

117. "Statistical applications in cancer genetics and cancer genomics". Santou University Medical School. Santou, China, July 2005.

118. "Statistical genetics and genomics". Department of Mathematics, Santou University. Santou, China, July 2005.

119. "Multilocus LD Measure and tagging SNP selection." Annual Meeting of the Statistical Society of Canada, Saskatoon, Saskatchewan, Canada, June 2005.

120. "Class discovery and classification of tumor samples using mixture modeling of gene expression data - a unified approach," 2005 International Biometric Society ENAR Spring Meeting, Austin, TX, March 2005 .

121. "CSI - Multipoint," Department of Epidemiology and Biostatistics, Case Western Reserve University, November 2004.

122. "Multipoint confidence set inference - statistical methods for linkage analysis," Joint Statistical Meetings, Toronto, Canada, August 2004.

123. "Advanced pedigree MCMC," Summer Institute in Statistical Genetics, North Carolina State University, June 2004.

124. "Class discovery and classification of tumor samples using mixture modeling of gene expression data - a unified approach," Annual joint Ohio State University, Cleveland Clinic Foundation, and Case Western Reserve University Biostatistics Symposium, May 2004.

125. "A confidence set approach for gene mapping," Department of Biostatistics, Section on Statistical Genetics, University of Alabama at Birmingham, January 2004.

126. "Statistical genetics and bioinformatics," Mathematical Biosciences Institute, Ohio State University, September 2003.

127. "A confidence set approach for gene mapping," Department of Statistics, Case Western Reserve University, April 2003.

128. "Analysis of data from SLE families," SLE Research Meetings, Division of Nephrology, Ohio State University, July 2002.

129. "Advanced pedigree analysis," Summer Institute in Statistical Genetics, North Carolina State University, June 2002.

130. "Mathematical modeling and statistical analysis in disease gene mapping – mathematics and the genome," Undergraduate Recognition Ceremony, Department of Mathematics, The Ohio State University. May 3, 2002.

131. "An alternative formulation for testing linkage." Joint statistical meetings. Indianapolis, IN, August 2000.

132. "Linkage analysis on pedigrees," Summer Institute in Statistical Genetics, North Carolina State University, June 2000.

133. "Statistical methods for analyzing genetic data," Nephrology Research Conference, Division of Nephrology, Ohio State University, November 1999.

134. "Incorporating crossover interference into human gene mapping using the chi-square models," Joint Ohio State, Cleveland Clinic Foundation, Case Western Reserve University Biostatistics Symposium, CWRU, May 1999.

135. "Incorporating crossover interference into human gene mapping using the chi-square models," Department of Statistics, Carnegie Mellon University, February 1999.

136. "Mapping complex traits: two-locus models, testing procedures, and difficulties," Department of Genetics, University of Pittsburgh, PA, February 1999.

137. "Incorporating crossover interference into human gene mapping using the chi-square models," Department of Mathematics and Statistics, Miami University, OH, November 1998

138. "Monte Carlo methods in genetic analysis," 2nd World Conference of the International Association for Statistical Computing (IASC), Pasadena, CA, February 1997.

139. "Research in statistical genetics," Department of Biostatistics and Epidemiology, University of Southern California, February 1997.

140. "Modeling genetic crossover interference in human gene mapping using chi-square models," Department of Statistics, Purdue University, November 1996.

141. "Multipoint linkage analysis via Metropolis jumping kernels." International Chinese Statistics Association Applied Statistics Symposium. Johns Hopkins University, Baltimore, MD, June 1996.

142. "Modeling genetic crossover interference in human gene mapping with chi-square models," Department of Statistics, Ohio State University, May 1996.

143. "Statistical methods for summarizing and combining genetic map information from independent studies." Map Integration Workshop. Pittsburgh Supercomputer Center. Pittsburgh, PA, December 1995.

144. Invited participant in the Workshop on Statistical Methods in Genetic Mapping, Tarrytown, NY, November 1995.

145. "Monte Carlo methods in genetic epidemiology: opportunities and problems." Joint statistical meetings. Orlando, FL, August 1995.

146. "Monte Carlo methods in genetic epidemiology," Neyman Seminar, Department of Statistics, University of California at Berkeley, March 1995.

147. "Markov chain Monte Carlo analysis on pedigrees." Department of Statistics, Texas A & M University, College Station, TX, February 1995.

148. "Markov chain Monte Carlo analysis on pedigrees." Department of Statistics, Florida State University, Tallahassee, FL, February 1995.

149. "Markov chain Monte Carlo analysis on pedigrees." Department of Biostatistics, University of Minnesota, Minneapolis, MN, February 1995.

150. "Markov chain Monte Carlo analysis on pedigrees." Department of Statistics, Purdue University, West Lafayette, IN, February 1995.

151. "Markov chain Monte Carlo analysis on pedigrees." Department of Statistics, Pennsylvania State University, University College, PA, February 1995.

152. "Markov chain Monte Carlo analysis on pedigrees." Department of Biostatistics, Harvard University, Boston, MA, January 1995.

153. "Markov chain Monte Carlo analysis on pedigrees." Department of Statistics, Ohio State University, Columbus, OH, January 1995.

154. "Monte Carlo methods and computationally challenging problems in genetic epidemiology," Joint Statistical Meetings, Toronto, Canada, August 1994.

155. "Markov chain Monte Carlo linkage analysis on pedigrees." IMA summer program in Molecular Biology held at the University of Minnesota, July 1994.

156. "Markov chain Monte Carlo estimates of probabilities on pedigrees." Department of Mathematics, University of Southern California, Los Angeles, CA, April 1994.

157. "Markov chain Monte Carlo estimates of probabilities on pedigrees." Department of Biostatistics and Epidemiology, University of California, San Francisco, CA, October 1993.

158. "Markov chain Monte Carlo estimates of probabilities on pedigrees." Department of Statistics, Iowa State University, Ames, IA, March 1993.

159. "Markov chain Monte Carlo estimates of probabilities on pedigrees." Department of Mathematics, University of Idaho, Moscow, ID, February 1993.

160. "Markov chain Monte Carlo estimates of probabilities on pedigrees." Department of Statistics, University of California, Berkeley, CA, January 1993.

161. "The Gibbs sampler and other Markov chain Monte Carlo methods in genetic applications." Gibbs Sampling Workshop, Salt Lake City, Utah, July 1992.

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Books

1. **Lin, S.**, Zhao, H. (2009) Handbook on Analyzing Human Genetics Data: Computational approaches and software. Springer, New York.

2. **Lin, S.**, Scholtens, D., Datta, S. (2022) Bioinformatics Methods: From Microarrays to Next-Generation Sequencing. CRC Press.

Refereed Papers in Edited Books / Book Chapters

3. Han, C., Park, J., **Lin, S.** (2022) BCurve: Bayesian Curve Credible Bands Approach for Detection of Differentially Methylated Regions. In *DNA Methylation* (Ed: Weihua Guan), *Methods in Molecular Biology*, **2432**,167-185.

4. Hansen, K., Siegmund, K., **Lin, S.** (2019) Chapter 33: DNA Methylation, 933-948. In: *Handbook of Statistical Genomics (4th Edition).* Ed: David Balding, Ida Moltke, and John Marioni. John Wiley & Sons.

5. Liu, Z., and **Lin, S.** (2018) Sparse Treatment Effect Model for Taxa Identification with High Dimensional Metagenomics Data. In *Microbiome Analysis* (Methods in Molecular Biology), **1849**, 309-318. Ed: Robert G. BeikoWill HsiaoJohn Parkinson, Humana Press.

6. Park, J., **Lin, S.** (2015) Statistical Inference on Three-Dimensional Structure of Genome by Truncated Poisson Architecture Model. In *Ordered Data Analysis, Modeling, and Health Research Methods - In Honor of H. N. Nagaraja's 60th Birthday* Choudhary, P., Nagaraja, C., Ng, T. (Eds.) Springer Proceedings in Mathematics & Statistics, Pages 245-261, Springer, New York.

7. **Lin, S.** (2013) Assessing the Effects of Imprinting and Maternal Genotypes on Complex Genetic Traits. In *Risk Assessment and Evaluation of Predictions.* Lee, M.-L.T., Gail, M., Pfeiffer, R., Satten, G., Cai, T., Gandy, A. (Eds.) Lecture Notes in Statistics, Vol. 210, Pages 285-300, Springer, New York.

8. Taslim, C., Huang, K., Huang, T., **Lin, S.** (2012) Analyzing ChIP-seq data: preprocessing, normalization, differential identification and binding pattern characterization. (Methods in Molecular Biology). Vol 802, 275-291. Ed. J Wang, AC Tan, T Tian. Humana Press.

9. Deatherage, D.E., Potter, D., Yan, P., Huang, T.H.-M., **Lin, S.** (2009) Methylation analysis by microarray. Chapter 9, Microarray Analysis of the Physical Genome: Methods and Protocols (Methods in Molecular Biology). **556**, 117-139. Ed. Jonathan Pollack. Humana Press.

10. Igo, R., Luo, Y., **Lin, S.** (2010) Monte Carlo linkage analysis methods and software packages. In *Handbook on analyzing human genetic data: computational approaches and software*. Lin, S., and Zhao, H.Y. Eds. Springer, New York.

11. Yan, P., Potter, D., Deatherage, D.E., **Lin, S.**, Huang, T.H.-M. (2008) Differential methylation hybridization: profiling DNA methylation in a high-density CpG island microarray. Chapter 8, Methods in Molecular Biology for DNA Methylation Analysis, 2nd edition.

12. Siegmund, K., **Lin. S.** (2007) Chapter 40. Epigenetics. In: *Handbook of Statistical Genetics (3rd Edition).* Ed: David Balding, Martin Bishop and Chris Cannings. John Wiley & Sons.

13. **Lin, S.**, Alexandridis, R. (2003) Classification of tissue samples using mixture modeling of microarray gene expression data. In: *Science and Statistics: A Festschrift for Terry Speed.* IMS Lecture Notes – Monograph Series, Volume 40. Ed: D. R. Goldstein. Beachwood: IMS. pp 419-435.

14. **Lin, S.** (1996) Monte Carlo methods in genetic analysis. In: *Genetic mapping and DNA sequencing.* IMA Volumes in Mathematics and its Applications. Eds: T. P. Speed and M. S. Waterman. New York: Springer-Verlag. pp 15-38.

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15. Xie, Q., Han, C., Jin, V., **Lin, S.** (2022) HiCImpute: A Bayesian Hierarchical Model for Identifying Structural Zeros and Enhancing Single Cell Hi-C Data. *PLOS Computational Biology*, **18** (6), e1010129. doi.org/10.1371/journal.pcbi.1010129.

16. Chen, Q., Song, C., **Lin, S.** (2022) An Adaptive and Robust Test for Microbial Community Analysis. *Frontiers in Genetics*, 19 May 2022. https://doi.org/10.3389/fgene.2022.846258

17. Turkmen, A., **Lin, S.** (2021) Detecting X-linked common and rare variant effects in family-based sequencing studies. *Genetic Epidemiology*, **45**, 36-45.

18. Han, C., Xie, Q., **Lin, S.** (2021) Are dropout imputation methods for scRNA-seq effective for scHi-C data? *Briefings in Bioinformatics*, **22**(4): bbaa289. DOI: 10.1093/bib/bbaa289

19. Kim, M., **Lin, S.** (2020) Characterization of histone modification patterns and prediction of novel promoters using functional principal component analysis. *PLoS ONE*, 5(5):e0233630.

20. Zhou, X., Wang, M., **Lin, S.** (2020) Detecting Rare Haplotypes Associated with Complex Diseases Using Both Population and Family Data: Combined Logistic Bayesian Lasso. *Statistical Methods in Medical Research*, **29**, 3340-3350. https://doi.org/10.1177/0962280220927728

21. Zhang, F., **Lin, S.** (2020) Incorporating Information from Markers in LD with Test Locus for Detecting Imprinting and Maternal Effects. *European Journal of Human Genetics*, **28**, 1087-1097

22. Shokoohi, F., Khalili, A., Asgharian, M., and **Lin, S.** (2019) Capturing heterogeneity of covariate effects in hidden subpopulations in the presence of censoring and large number of covariates. *Annals of Applied Statistics*, **13**, 444-465.

23. Zhang, F., Khalili,A., and **Lin, S.** (2019) Imprinting and Maternal Effect Detection Using Partial Likelihood Based on Discordant Sibpair Data. *Statistica Sinica*, **29**, 1915-1937. doi:10.5705/ss.202016.0114

24. Datta, A., Biswas, S., and **Lin S.** (2019) A Family-Based Rare Haplotype Association Method for Quantitative Traits. *Human Heredity*, 83:175-195.

25. Park, J. and **Lin, S.** (2019) Evaluation and Comparison of Methods for Recapitulation of 3D Spatial Chromatin Structures. *Briefings in Bioinformatics*, **20**, 1205-1214.

26. Ma, V. L., **Lin, S.** (2019) Examining the rare disease assumption used to justify HWE testing with control samples. *Mathematical Biosciences and Engineering*, **17**, 73-91.

27. Chen, D.-P., Zhang, F., **Lin, S.** (2019) AIJ: Joint Test for Simultaneous Detection of Imprinting and Non-imprinting Allelic Expression Imbalance. *Mathematical Biosciences and Engineering*, **17**, 366-386.

28. Luo, H., **Lin, S.** (2018) Evaluation of Classical Statistical Methods for Analyzing BS-Seq Data. *OBM Genetics*, **2** Article 053; doi:10.21926/obm.genet.1804053.

29. Han, C., Tang, H., Lou, S., Goa, Y. Cho, M. H., **Lin, S.** (2018) Evaluation of Recent Statistical Methods for Detecting Differential Methylation Using BS-seq Data. *OBM Genetics*, **2** Article 041; doi:10.21926/obm.genet.1804041.

30. Li, L., Wang, C., Lu, T., **Lin, S.**, and Hu Y-Q. (2018) Indirect effect inference and application to GAW 20 data. *BMC Genetics*, **19**(Suppl 1): 67

31. Zhou, X., Wang, M., Stewart, W.C.L., and **Lin, S.** (2018) Logistic Bayesian LASSO for detecting association combining family and case-control data. *BMC Proceedings*, **12**(Suppl 9): 54.

32. Zhang, Y., Hofmann, J.N., Purdue, M.P., **Lin, S.**, Biswas, S. (2017) Logistic Bayesian LASSO for Genetic Association Analysis of Data from Complex Sampling Designs. *Journal of Human Genetics*, **62**, 819-829.

33. Turkmen, A. and **Lin, S.** (2017) Are Rare Variants Really Independent? *Genetic Epidemiology*, **41**, 363-371.

34. Park, J. and **Lin, S.** (2018) Detection of Differentially Methylated Regions Using Bayesian Curve Credible Bands. *Statistics in Biosciences*, **10**, 20-40.

35. Zhang, F., Ding, J. and **Lin, S.** (2017) Testing for Associations of Opposite Directionality in a Heterogeneous Population. *Statistics in Biosciences*, **9**, 137-159.

36. Zhang, Y., **Lin, S.**, and Biswas, S. (2017) Detecting rare haplotype-environment interaction under uncertainty of gene-environment independence assumption. *Biometrics*, **73**, 344-355.

37. Park, J., **Lin, S.** (2017) A Random Effect Model for Reconstruction of Spatial Chromatin Structure. *Biometrics*, **73**, 52-62.

38. Zhu, D., Hu, Y., and **Lin, S.** (2016) Block-Based Association Tests for Rare Variants Using Kullback-Leibler Divergence. *Journal of Human Genetics*, **61**, 965-975 .

39. Qin, Z. Li, B., Conneely, K.N., Wu, H., Hu, M., Ayyala, D., Park, Y., Jin, V.X., Zhang, F., Zhang, H., Li, L., **Lin, S.** (2016) Statistical challenges in analyzing methylation and long-range chromosomal interaction data. *Statistics in Biosciences*, **8**, 284-309.

40. Park, J., **Lin, S.** (2016) Impact of Data Resolution on Three-Dimensional Structure Inference Methods. *BMC Bioinformatics*, **17**:70.

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SOFTWARE PACKAGES/COMPUTING CODE

https://www.asc.ohio-state.edu/statistics/statgen/ or https://github.com/sl-lin

1. SIMPLE (Sequential Imputation for MultiPoint Linkage Estimation): Calculates linkage statistics, such as LOD scores and NPL statistics by sequential imputation. (Joint work with Skrivanek, Z. and Irwin, M.)

2. START: Finds starting points for MCMC analysis performed on large, complex pedigrees and polymorphic markers. (Joint work with Luo, Y.)

3. MAXPROC: Calculates maximum likelihood estimates of linkage parameters under heterogeneity and their standard errors using EM and SEM algorithms. (Joint work with Biswas, S.)

4. CSI (Confidence Set Inference): Constructs confidence set of markers for a disease locus based on a nonparametric confidence set inference approach. (Joint work with Papachristou, C.)

5. DNC-MIX: Class discovery and classification of tumor samples by modeling the distribution of a gene expression profile as a mixture, with each component characterizing the expression levels in a class. (Joint work with Alexandridis, R. and Irwin, M.)

6. tagSNPFinder: Computes multilocus LD measures and selects tagging SNPs within haplotype blocks. (Joint work with Liu, Z.)

7. Pathway: Use methylation profiles and clinical variables to group tumor samples into clusters and then organize them into a tree to represent tumor progression pathways that conform to strict heritability. (Joint work with Wang, Z.)

8. DE-SAGE: Analyze SAGE library data using a Bayesian hierarchical and mixture modeling approach and RJMCMC computational algorithms. (Joint work with Wang, Z.)

9. miRComp: A filtering step of putative microRNA targets through aggregating the predictions by several algorithms using two composite statistics - composite ranks and composite "p-values". (Joint work with Zou, J., and Qiu, F.)

10. MC-PDT: Perform test of linkage disequilibrium in the presence of linkage using pedigree data based on Monte Carlo samples of complete data given observed data. (Joint work with Ding, J.)

11. TopKCEMC: A rank aggregation tool for integrating data from multiple sources based on ranks. (joint work with Ding, J.)

12. rGLM: Generalized linear modeling with regularization for Case-control association studies; suitable for both common disease/common variants and common disease/rare variance scenarios. (Joint work with Guo, W.)

13. DIME: An ensemble of three mixture models (GNG, NUDGE, iNUDGE) for differential analysis. This package can be used for analyzing ChIP-seq, gene expression, and DNA methylation data. (Joint work with Taslim, C.)

14. LBL: Logistic Bayesian Lasso for finding association of SNP haplotypes with a trait in a case-control setting. (Joint work with Biswas, S., Wang, M., Xia, S., and Zhou, X.)

15. BOG: Performing three statistical tests (hypergeometric, Mann-Whitney, and Gene Set Enrichment Analysis) to find Cluster of Orthologous Groups (COG) that are enriched or depleted among genes that are significantly different (e.g. in their gene expression, protein DNA binding, etc.) under two different conditions. (Joint work with Park, J.)

16. LIME: LIME is a partial Likelihood approach for detecting Imprinting and Maternal Effects using nuclear families with an arbitrary number of affec ted and unaffected children. (Joint work with Yang, J., and Zhang, F.)

17. MDM (formerly MCDIST): R package MDM (formerly MCDIST) provides functions for the analysis of chromatin interactions using MC_DIST model (for one sample problem, i.e., detecting chromatin interactions from noises), Two-Step model and One-Step model (for two-sample problem, i.e., detecting differential chromatin interactions), based on Chromatin Interaction Analysis by Paired-End Tag Sequencing (ChIA-PET) data. (Joint work with Niu, L. and Lou, S.)

18. KL-Rare: We provide the R code for performing four tests based on Kullback-Leibler divergence to assess overall association of a group of common and rare variants with a common disease.

19. tREX: provides two methods, tPAM and tREX, for reconstruction of 3D structure of chromatins using Hi-C data. (Joint work with Park, J.)

20. MethylCapSig: Performs five statistical tests (t, MethMAGE, and three mean vector tests) to find regions that are differentially methylated using MethylCap-Seq data that have been processed by PrEMeR-CG. (Joint work with Ayyala, D.)

21. GrammR: To represent metagenomic samples on the Euclidean space to examine similarity amongst samples by studying clusters in the model. Given the matrix of metagenomic counts for samples, this package (1) quantifies dissimilarity between samples using Kendall's tau-distance, (2) constructs multidimensional models of different dimension, and (3) plots the models for visualization and comparison. (Joint work with Ayyala, D.)

22. ChIASim: An in silico procedure for generating protein-mediated long-range interaction data. The algorithm imitates the experimental procedures that produce real ChIA-PET, Hi-ChIP, or PLAC-seq data. (Joint work with Shuyuan Lou)

23. HiCImpute: An implementation of a Bayesian hierarchy model that improves single cell Hi-C data quality through identification of structural zeros imputation of dropouts. (Joint work with Qing Xie)

24. scHiCSRS: A software package implementing a self-representation-smoothing formulation coupled with a Gaussian mixture modeling for identifying structural zeros and imputing dropouts for single cell Hi-C data (Joint work with Qing Xie)

INVENTION/PATENT

Patent title: Polymorphic CD24 Genotypes that are Predictive of Multiple Sclerosis Risk and Progression.
Inventors: Yang Liu (15% credit), Qunmin Zhou (40% credit), Pan Zheng (15% credit), Kottil Rammohan (15% credit), Shili Lin (15% credit).
IPC8 Class: AC12Q168FI
USPC Class: 435 6