



Hongzhe Lee, PhD

Past ICSA-related activities:

Dr. Li is a lifetime member of ICSA and has contributed to ICSA in multiple capacity. He has served on the Program Committee (2021-2022), Nomination and Election Committee (2017-2019), Publication Committee (2017-present) and multiple ICSA-sponsored conference committees, including the program committees of ICSA Applied Statistics Symposium (2011, 2017), ICSA China Conference (2019) and ICSA International Conference (2010, 2016, 2019). He chaired the Program Committee and co-Chaired the Organizing Committee of the very successful 2019 ICSA 11th International Conference in Hangzhou, China. He has been very active in organizing the IBS-China Joint Biostatistics Meetings.

Dr. Li was the founding Associate Editor of *Statistics in Biosciences (SIBS)*, and since 2017, he has been serving as the joint Editor-in-Chief of the Journal. Since 2014, Dr. Li has been an Associate Editor of *Statistica Sinica*. SIBS is one of the two ICSA sponsored journals, focusing on development and application of statistical methods and their interface with other quantitative methods. During his editorship, the journal has seen increased readerships and submissions and increased the yearly published issues from two to three. He has co-edited special issues for the journal, including the Special issue on *Network Data Analysis* in 2012 and Special issue on *Statistics in Microbiome and Metagenomics* in 2021. Because of his unselfish support of the ICSA, he was awarded the ICSA Outstanding Service Award in 2020.

Draft statement of future ICSA services and commitment:

I am honored and humbled to be a candidate for president of the ICSA. As society embraces data science in all aspects and scales, members of the ICSA are well-positioned to lead in data science innovation and to broaden engagement with the full range of applications and problems in the world. Our members include world leaders who are actively engaging in high impact research in physical, social, economic and life sciences.

I believe areas for the ICSA's immediate attention include: 1) broader engagement in data science, 2) leadership training, and 3) culture of diversity and inclusion.

Broader and deeper engagement in data science: The ICSA must take a leadership role to broaden its engagement in data science by forming partnerships with societies of domains of various applications, including applied mathematics, computer science, informatics, and social and economic sciences, as well as by engaging in industry activities. Fostering interdisciplinary connections can be accomplished through joint seminars, workshops and conferences.

Development of leadership skills: Members of the ICSA have made significant contributions in statistical theory, methods and applications and have trained many promising young statisticians. The ICSA must create opportunities for our members to take leadership roles in ICSA and other professional societies and to foster leadership skills at various levels through a leadership training program, which will include managing a team of scientists and interacting with senior leaders.

Culture of diversity, inclusion and equity:

The cross-disciplinary nature of our field has drawn members from diverse work environments, from various backgrounds. ICSA leaders must strengthen relationships with professional societies to foster a greater community of individuals from diverse backgrounds and to promote, support, and advance equity, diversity and inclusion. Moreover, in response to recent events, ICSA must unite as a community to denounce any hate and discrimination against Asian Americans and Pacific Islanders (AAPIs).

CURRICULUM VITAE

Hongzhe Li/ Hongzhe Lee, Ph.D.

Perelman Professor of Biostatistics, Epidemiology and Informatics
Fellow of ASA, IMS and AAAS

Professor of Biostatistics and Statistics
Vice Chair of Research Integration
Director, Center for Statistics in Big Data
Department of Biostatistics, Epidemiology and Informatics (DBEI)
Graduate Faculty, Genomics and Computational Biology (GCB)
Graduate Faculty, Applied Mathematics and Computational Science (AMCS)

Mailing Address:

Department of Biostatistics, Epidemiology and Informatics
University of Pennsylvania Perelman School of Medicine
215 Blockley Hall, 423 Guardian Drive, Philadelphia, 19104-6021

Phone: (215)573-5038 Fax: (215)573-1050 Cell: (610)952-6133
Email: hongzhe@penncare.upenn.edu, <http://statgene.med.upenn.edu>

PERSONAL INFORMATION

Born on October 11, 1967, US citizen since April 2000, Married with two children
US Passport name: Hongzhe Lee
Academic/working name: Hongzhe Li (all Dr. Li's publications are under Hongzhe Li)

EDUCATION

1995, Ph.D., Statistics, University of Washington, Seattle (Advisor: Elizabeth Thompson)
Dissertation: "*Semiparametric Estimation of Major Gene and Random Environmental Effects for Age of Onset*"

1989, B.S., Mathematics, Peking University, Beijing

ACADEMIC APPOINTMENTS

10/2019, *The Perelman Professor of Biostatistics, Epidemiology and Informatics*,
University of Pennsylvania Perelman School of Medicine

05/2005 – present, *Professor of Biostatistics* (with tenure), *Faculty Member*, Graduate
Group in Genomics and Computational Biology (Since 12/2005), *Faculty Member*,
Graduate Group in Applied Mathematics and Computational Science (Since 07/2013),
University of Pennsylvania

Vice Chair of Research Integration (05/01/2018 – present).
Director, Program in Statistical Evaluation of the Human Microbiome (07/01/2015 – present)
Chair, Graduate Program in Biostatistics (01/01/2016 –12/31/2018)
Director, Center for Statistics in Big Data (07/01/2016 – present)
Department of Biostatistics, Epidemiology and Informatics (DBEI)
University of Pennsylvania Perelman School of Medicine, Philadelphia, Pennsylvania
09/2011 – present, *Professor of Statistics* (secondary appointment)
Department of Statistics, The Wharton School, University of Pennsylvania

07/2001-- 05/2005, *Associate Professor* (with tenure), 09/1998-06/2001, *Assistant Professor* (tenure track), Graduate Faculty Member of the Graduate Groups of Statistics, Biostatistics, Genetics, and Epidemiology, Rowe Program in Human Genetics and Department of Medicine, University of California, Davis.

09/1995--08/1998, *Research Associate Biostatistician*,
Section of Biostatistics, Mayo Clinic, Rochester, Minnesota

OTHER AFFILIATIONS/ACADEMIC VISITS

2001-2005, *Affiliate Member*, Center for Bioinformatics and Molecular Biostatistics, University of California, San Francisco

04-06, 08/2004, *Visiting Associate Professor* (Sabbatical leave), Department of Statistics, Stanford University

HONORS AND AWARDS

2020 *ICSA Outstanding Service Award*
2020 *Biometrics most read paper*, Lu, Shi and Li (2019)
2020 *ASA Philadelphia Chapter Award in Research Excellence*, ASA
2020 *John A. Lynch Lecture*, College of Science, University of Notre Dame
2017 *Elected Fellow*, American Association for Advancement of Science (AAAS)
2017 *Gordon C Ashton Memorial Lecture*, 13th Guelph Annual Biomathematics and Biostatistics Symposium, Canada
2016/2017/2018 *Chair-Elect/Chair/Past Chair*, Section on Statistics in Genomics and Genetics, American Statistical Association (ASA)
2015-2021 *Chartered member*, NIH Genetics of Health and Disease (GHD) Study Section
2014 *Jane M. Glick Graduate Student Teaching Award*, University of Pennsylvania
2013 *Elected Fellow*, Institute of Mathematical Statistics (IMS)
2011-2016 *Member*, Board of Scientific Counselor, Clinical Sciences & Epidemiology, National Cancer Institute, National Institutes of Health
2008-2012 *Chartered member*, NIH Biostatistical Methods and Research Design (BMRD) Study Section.

2010 *Graduate Program in Biostatistics Teaching Award*, Department of Biostatistics and Epidemiology, University of Pennsylvania.
2009 *Myra Samuels Memory Lecturer*, Department of Statistics, Purdue University
2008 *Elected Fellow*, American Statistical Association (ASA)
2008 *Elected member*, International Statistical Institute (ISI)
2000 *University of California Davis Health System Research Award*, UC Davis
1999 ``*Best Paper of the Year*'' Award, International Genetic Epidemiology Society

KEYNOTE/PLENARY LECTURES/PRESENTATIONS

2021 *Keynote Lecture*, Leeds Annual Statistical Research Workshops, University of Leeds
2021 *Public Health Ground Round Speaker Series*, University of Nebraska Medical Center
2019 *Plenary Speaker*, iBRIGHT 2019 Conference, MD Anderson Cancer Center
2019 *Keynote Speaker*, Inaugural Harvard Chan Microbiome Symposium, Harvard University
2019 *Keynote Speaker*, The 8th International Workshop on Compositional Data Analysis (CoDaWork 2019), Barcelona, Spain
2018 *Special Lecture*, Big Data Training for Translational Omics Research, Purdue University
2017 *Invited Mentor*, 2017 Innovation Lab on Quantitative Approaches to Biomedical Data Science Challenges in Our Understanding of the Microbiome
2014 *Keynote Speaker*, Symposium on Personalized Medicine – Emerging Technologies and Microbiome Research, Medical University Graz, Austria
2012 *Keynote Speaker*, Workshop on Data Mining for NGS Analysis, IEEE International Conference on Bioinformatics and Biomedicine (BIBM 2012)
2008 *Keynote Speaker*, ASA Delaware Chapter Meeting of the American Statistical Association
2007 *Science at The Edge Seminar*, Michigan State University.

TRAINEES WITH SPECIAL AWARDS

2018 Jiarui Lu (PhD student), *ENAR Distinguished Student Paper Award*.
2016 Julie Kobie (PhD Student), *ENAR Distinguished Student Paper Award*.
2013 Jun Chen (PhD student), *Saul Winegrad, MD Award for Outstanding Dissertation*, University of Pennsylvania
2012 Jichun Xie (PhD student), *Saul Winegrad, MD Award for Outstanding Dissertation*, University of Pennsylvania
2010 X. Jessie Jeng (Postdoc fellow), *David P. Byar Young Investigator Award*, Biometrics Section, American Statistical Association

EDITORIAL SERVICES

2019 Guest editor, Proceedings of National Academy of Sciences (PNAS)
2017 –2021 *Co-Editors-in-Chief*, Statistics in Biosciences
2015 –present, *Associate Editor*, Biostatistics and Epidemiology
2014 –present, *Associate Editor*, Statistica Sinica

2012 --present, *Associate Editor*, Biometrics
2003 –2011, *Associate Editor*, Journal of the American Statistical Association (Theory and Methods)
2009 – 2016, *Founding Associate Editor*, Statistics in Biosciences (SIBS)
2012 *Guest Editor*, Special issue on network data analysis, *Statistics in Biosciences*

SERVICES TO NATIONAL/INTERNATIONAL COMMITTEES/LEADERSHIP ROLES

2021-2022 *Program Committee member*, ICSA
2017-2022 *Publication Committee member*, ICSA
2018-2022 *Elected Member-at-Large (Steering Group)* of Section on Statistics, AAAS
2017-2019 *Member*, Nomination and Election Committee, ICSA
2015/2016 *Chair-Elect/Chair*, Program Committee, Section on Statistics in Genomics and Genetics, ASA
2015 *Invited Extramural expert*, NIH Microbiome Long-term IRP Research Planning
2015 *Member*, UAB Multidisciplinary Clinical Research Center (MCRC) (NIH P60 AR064172) Advisory Committee
2015 *Co-Chair, Site visit*, Infections and Immunoepidemiology Branch, National Cancer Institute
2015 *Co-Chair, Site visit*, Clinical Genetics Branch, National Cancer Institute
2014-present *Member*, External Advisory Committee, COBRE for the Center for Molecular Epidemiology at Dartmouth Medical School
2014 *Chair, Site visit*, Biostatistics Branch, National Cancer Institute
2013 *Co-Chair, Site visit*, Nutritional Epidemiology Branch, National Cancer Institute.
2012 *Co-Chair, Site visit*, Genetic Epidemiology Branch, National Cancer Institute, NIH
2008-2011 *Member*, Education Committee, International Biometrics Society
2010-2012 *Member*, Committee on International Relations in Statistics of the American Statistical Association
2009 – 2012 *Member*, ENAR Student Award Committee

LEADERSHIP ROLE IN NEW PROGRAM/INITIATIVE/CONFERENCE AT PENN

2019 Founded and Chaired the annual *Conference on Big Data in Population Health Sciences*.
2020 Founded and Chaired monthly mini-series on *Open Insights in Biomedical Data Science*

PROFESSIONAL MEMBERSHIP

Member of American Association for the Advancement of Science (AAAS)
Member of the American Society of Human Genetics (ASHG)
Member of the American Statistical Association (ASA)
Member of the International Biometric Society (ENAR)
Fellowship Member, Royal Statistical Society (RSS)

Lifetime Member, International Chinese Statistical Association (ICSA)
Lifetime Member, Institute of Mathematical Statistics (IMS)
Elected Member, International Statistical Institute

**MAJOR ACTIVE RESEARCH GRANTS AS PRINCIPAL INVESTIGATOR (PI)
(DIRECT COST \$/Year)**

2017-2021 NIH R01-GM123045, Principal Investigator, 25% effort, *Statistical Methods for Microbiome and Metagenomics*.

2018-2022 NIH R01-GM129781, Principal Investigator, 25% effort, *Methods for Integrative Data Analysis*.

2020-2022, NIH P30-DK050306 (Biomedical Data Science Core), Principal Investigator, 10% effort, *Center for Molecular Studies in Digestive and Liver Diseases*.

2019- present, Director, PenNSAM Nutrition Analytic Core, Penn Center for Nutritional Science and Medicine. 10% effort.

**PAST GRANTS AS THE PRINCIPAL INVESTIGATOR (PI)
(Hongzhe Li/Hongzhe Lee Served as PI on the Following Grants)**

2012-2018, NIH R01-CA127334, Principal Investigator, 20% effort, *Statistical Methods for Genomic Data with Graphical Structure*

2012-2016, NIH R01-GM097505, Principal Investigator, 20% effort, *Statistical methods for Analysis of Next Generation Sequencing Data*

2011-2016, NIH T32-EY021451, Principal Investigator, *Training in Ophthalmic Statistical Genetics and Bioinformatics*

2007 – 2012, NIH/R01 CA127334, Principal Investigator, 30% effort, \$190K/yr, *Statistical Methods for Genomic Data with Graphical Structures*

2006 - 2011, NIH/R01 ES009911, Principal Investigator, 30% effort, \$190K/yr, *Survival Analysis Methods in genetic Studies*

2007-2008 NIH/P01 AG025532, Principal Investigator (Biostatistics Core) (PI Gino Cortopassi, UC Davis), \$140K, *A Mitochondrial Longevity Pathway: P66Shc Mechanisms*. Direct Costs: \$140,000 (20% effort)

2005-2007, Principal Investigator of Scientific Opportunity Fund under NIH U19AG023122 (PI Dr. Steven Cummings, UCSF), *Consortium to Study the Genetics of Longevity*. Direct Costs: \$50,000

2002 – 2007, NIH R01 ES009911, Principal Investigator, Direct costs: \$600,000 (35% effort), *Survival models for mapping genes for complex diseases*

2005-2006, Principal Investigator, Pennsylvania Department of Health Research Grant, *Nonparametric pathway-based regression models for integrative analysis of cancer genomic data*. Direct Costs: \$140,000

2000-2003, Principal Investigator of UC Davis Subcontract, NIH/U24 AI049213, Biostatistics core (PI Dr. Glenys Thomson, UC Berkeley), *13th International Histocompatibility Working Group*. Direct costs: ~\$110,000 (15% effort)

2000-2003, Principal investigator, UC Davis Health System Research Award Grant, *Statistical and Computational Methods for Microarray Gene Expression Data*. Direct costs: \$150,000

1998 – 2001, NIH R01 ES009911, Principal Investigator, *Survival models for mapping genes for complex diseases* Direct costs: \$420,000 (30% effort)

MAJOR ACTIVE RESEARCH GRANTS AS CO-INVESTIGATOR (% effort)

08/2018-07/2021, U01-DK108809 (Ganz, P/Deo, R), 10% effort,. *Identifying Modifiable Biomarkers/Mediators for Cardiovascular Disease in Chronic Kidney Disease*.

06/2018-05/2023, R01-HL141408 (Fajgenbaume, D). 5% effort. *mTOR as a Central Regulator of iMCD Pathogenesis and Novel Therapeutic Target*

05/2017 – 04/2022, U54-CA163004 (Wang,T/Rustgi,A) BETRNet Sub w/Columbia Univ, 0.36 month (salary only), *The Role of the Microenvironment in Barrett's Esophagus*

09/2017-07/2022, R01GM123014, *Mediation Analysis Methods to Model Human Microbiome Mediating Disease-leading causal Pathways in Children* (PI: Zhigang Li), 10% effort (subcontract PI).

2015 –present Penn-CHOP Microbiome Program, University of Pennsylvania and Children's Hospital of Philadelphia, 10% effort. *Analytical/Statistical analysis for Various Projects*.

09/2016-06/30/2021, NIH/R01 DK107566 (PI: Dr. Amanda Anderson), 2%-10% effort, *The Gut Microbiome and the Metabolome in Chronic Kidney Disease*

2016-present, Enterome/Intercept Pharmaceuticals (PI: Dr Gary Wu), 5% effort, An Open-Label, Randomized, Single Dose and Multiple Dose Trial to Assess the Pharmacokinetics of Obeticholic Acid (OCA)

2010-present, NIH P30-CA016520, Co-Investigator (PI: Dang, C), 1% effort, *Biostatistics Core, Abramson Cancer Center of the University of Pennsylvania Core Support Grant*

09/2018-06/2023, NIH R01-DE026603 (Graves, D), 5% effort. *Diabetes Reversal and the Subgingival Microbiota*

MAJOR COLLABORATIVE GRANTS/CONTRACTS FINISHED
(Grants with <5% efforts are not listed)

2015-2020 CHOP (PI: Zemel, B, Wu G), 10% effort, *Infant Growth and Microbiome Study (I-Gram2)*

2014-2019, NIH GM113657, Co-investigator (PI: Tishkoff S), 5% effort,
Integrative Genomics and Body Size and Metabolism in Ethnically Diverse Africans

2015-2019, NIH DP3DK108220, Co-investigator (PI: Dr. Katalin Susztak), 10% effort,
Epigenetic Drivers and Biomarkers of Diabetic Kidney Disease.

2016-2019, PCORI/CCFA (PI: James Lewis), 10% effort,
Comparative effectiveness of the Specific Carbohydrate and Mediterranean Diets to Induce Remission in Patients with Crohn's disease

2018-2019, U01DK099924, *Anti-inflammatory therapy in diabetic CKD* (PI: Dominic Raj, George Washington University), 15% effort.

2013- 2018, NIH/R01 CA124709, Co-Investigator (PI: Dr. John Mairs), 10% effort, *The Genetic Basis of Neuroblastoma Tumorigenesis*

2014-2018 NIH GM108600, Co-Investigator (PI: Mingyao Li), 10% effort,
Statistical Methods for Transcriptome Profiling using RNA Sequencing

2012-2016, NIH U54 HL117798, Co-investigator (PI: Fitzgerald G), 7% effort,
Personalization of Therapeutic Efficacy and Risk (GLUE Grant)

2012-2016, NIH GM103591 Co-investigator (PI:Wu G), 5% effort,
Host-Microbial Interactions in the Gut Oxygen Equilibrium

2009-2016 NIH P30- AI45008, Co-Investigator (PI : Hoxie, J), 5% effort,
Biostatistics Core, Center For Aids Research (CFAR)

2011-2015 NIH R01-HL105993 Co-investigator (PI: Margulies/Cappola,T) 10% effort,
Integrative Genomics of Human Heart Failure

2009-2014, NIH U01-HL098957, Co-Investigator (PI: Collman, R), 10% effort, *Human Respiratory Tract Microbiome in Health, HIV Infection and HIV Lung Disease*

2010-2014, NIH R01-GM088566 Co-Investigator, Co-Investigator (PI: Feng, R), 10% effort, *Genome-Wide Association Studies Using Integrated CNV and SNP Information*

2008- 2013, NIH/R01 CA124709, Co-Investigator (PI: Dr. John Mairs), 15% effort, *The Genetic Basis of Neuroblastoma Tumorigenesis*

2009 –2013, NIH UH2-DK083981, Co-Investigator (PI: Lewis/Wu/Bushman), 20% effort,
Diet, Crohn's Disease and the Gut Microbiome

2009-2013, NIH R01-HG005854, Co-Investigator (PI: Li, M) ,10% effort, *Statistical Methods for Gene Mapping Studies in Admixed Populations*

2008 – 2013, NIH/R01ES016626, Co-Investigator (PI: Dr. Jinbo Chen), 10% effort, *Statistical Methods in Genetic Epidemiology Research*

2008-2011, NIH/R01HD056465, Co-Investigator (PI: Dr. Struan Grant), 5% effort, *Genome-Wide Association Study of Childhood Obesity*

2007-2008 NIH/P01CA097323, Co-investigator (Biostatistics Core) (PI Garrett Brodeur, Children's Hospital of Philadelphia), 10% effort. *Neuroblastoma Biology and Therapy*

2005-2007, Co-PI, NIH P20RR020741 (PI Dr. Stephen Kimmel, U Penn), *Transdisciplinary research on genetics of complex traits.* (7% effort)

1999-2004, Co-investigator, NIH U01DK057249, (PI Dr. Sharon Adler, UCLA), *Identification of Diabetic Nephropathy Gene.* Direct costs: ~\$100,000 (15% effort)

1999-2003, Co-Investigator, NIH/R01 AR044804 (PI Dr. Lindsey Criswell, UCSF), *Testing SLE Candidates Loci Using Cases and Their Parents.* Direct costs: ~\$110,000 (15% effort)

FORMAL TEACHING

University of Pennsylvania

Statistical Methods for Genomic Data Analysis (2006S, 2007F, 2009F, 2013F)
(Established this new course at U Penn)

Probability I (Biostatistics PhD Probability Core course at Penn, established this new course in the Department of Biostatistics, Epidemiology and Informatics at Penn) (2010F, 2011F, 2012F, 2018F, 2019F)

Big Data in Biomedical Research (2015F, 2016F, 2017F, 2020F) (Established this new course at U Penn).

Guest lecture (2009-2012, 2019 Penn): *Statistical Computing*

Guest lecture (2016, Penn): *Frontiers: Precision Medicine FRO531*

Stanford University (Sabbatical leave):

Topics in Statistical Genetics and Computational Biology (2004S),
Special Topics in Computational Biology (2004, summer)

University of California, Davis:

Statistical Genetics (2000W)

Probability and Statistics for Engineering (2001S)

Computational functional genomics (2002W)

Statistical methods for Biological sequence analysis (2003S)

(Established new courses in Statistical Genetics, Computational functional genomics, Statistical Methods for Biological Sequence Analysis in the Department of Statistics at UC Davis)

OTHER TEACHING - SHORT COURSES

JSM CE Short Course (07/2019, co-taught with Curtis Huttenhower): *Statistical and computational methods and software for microbiome and metagenomics and applications*. Joint Statistical Meeting of the American Statistical Association, Denver, CO

JSM CE Short Course (07/2018, co-taught with Curtis Huttenhower): *Statistical and computational methods and software for microbiome and metagenomics and applications*. Joint Statistical Meeting of the American Statistical Association, Vancouver, Canada

Penn Causal Inference and Big Data Summer Institute (2017, 2018), University of Pennsylvania

Short course (12/2010): *Statistical Methods for Analysis of Genome-wide Association Studies*, Sun Yat-Sen University, China

JSM CE Short Course (08/2012, co-taught with Wei Pan): *Statistical Methods for Genome-Wide Association, Copy Number Variants and Rare Variants Analysis*. Joint Statistical Meeting of the American Statistical Association, San Diego, CA

5th Annual Short Course on Statistical Genetics and Genomics, University of Alabama, Birmingham, *Microbiome and Metagenomics*.

JUNIOR FACULTY MENTORED AT PENN

Mingyao Li, Jinbo Chen, Yong Chen, Rui Feng, Christopher Brown (Genetics), Kyle Bittinger (CHOP)

PH.D. STUDENTS/POSTDOCTORAL FELLOWS ADVISED/MENTORED

Current PhD Students

Haotian Zheng, Biostatistics

Rong Ma, Biostatistics

Jianqiao Wang, Biostatistics

Rebecca Deek, Biostatistics

Haoshu Xu, Applied Mathematics and Computational Science

Current Postdoc Fellows

Jingru Zhang (PhD, Peking University), 2019-2021

Siyuan Ma (PhD, Harvard University), 2020-2022

**PhD Students Advised/Co-advised, Dissertation and Their Current Positions
(21 PhD students advised)**

Yezheng Li, PhD in Applied Mathematics and Computational Science (AMCS), 11/2020, University of Pennsylvania
Community Membership Testing and Missing Value Imputation: Theory and Methods
Data Scientist, eBay

Jiarui Lu, PhD in Biostatistics, 08/2020, University of Pennsylvania
Statistical Inference for High Dimensional Models in Genomics and Microbiome
Principal Statistical Consultant, Novartis

Lu Huang, PhD in Biostatistics, 10/2020, University of Pennsylvania
Bayesian Balance Regression and Medication Analysis for Analysis of Microbiome Compositional Data
Data Scientist, Uber

Mingyang Liu, PhD in Applied Mathematics and Computational Science, 05/2020, University of Pennsylvania, *New Machine Learning Methods for Genomics and Metagenomics Applications*
Quantitative Researcher, Akuna Capital LLC

Yuanpei Cao, PhD in Applied Mathematics and Computational Science, 09/2016, University of Pennsylvania, *Statistical Methods for High Dimensional Count and Compositional Data with Applications to Microbiome Studies.*
Data Scientist, AirBnB

Zhang (Eric) Chen, PhD in Genomics and Computational Biology, 05/2016, University of Pennsylvania, *Microbiome and Metagenomics: Statistical Methods, Computation and Applications.*
Data Scientist, United Imaging Health Care, Boston

Pixu Shi, PhD in Biostatistics, 05/2016, *Statistical Methods for Compositional and Tree-structured Count Data.*
Assistant Professor, Duke University

Julie Kobie, PhD in Biostatistics, 05/2016, *Sparse Simultaneous Signal Detection with Applications in Genomics.*
Biostatistician, Merck.

Le B Nguyen, PhD in Genomics and Computational Biology, 05/2013, University of Pennsylvania (joint with Dr. John Maris), *Integrative approach identifies predisposition genes in Neuroblastoma.*

Qian Wu, PhD in Biostatistics, 12/2013, University of Pennsylvania, *Statistical methods for multi-sample CNV and ChIP data analysis.*

Assistant Professor, Fred Hutchison Cancer Research Center.

Jun Chen, PhD in Genomics and Computational Biology, 05/2012, University of Pennsylvania, *Statistical Methods for Analysis of Human Microbiome Data*.
Associate Professor, Mayo Medical School/Mayo Clinic

Jichun Xie, PhD in Biostatistics (jointly advised with Tony Cai), 07/2011, University of Pennsylvania, *High-dimensional Statistics in Genomics: Theory and Applications*.
Associate Professor of Biostatistics, Duke University

Jing He, PhD in Biostatistics (jointly advised with Mingyao Li), 07/2011, University of Pennsylvania, *Statistical Methods for Genetics Association Studies*.
Statistician, IMS Health

Shaokun Shannon Chuai, PhD in Biostatistics, 10/2011, University of Pennsylvania, *Statistical Methods for Analysis of Structured Genomic Data*.
Chief Operating Officer (COO), Burning Rock Dx.

Saran Vardhanabhuti, PhD in Biostatistics, 11/2011, University of Pennsylvania, *Statistical Methods for Muti-sample Analysis of Genomic Data*.
Senior Manager, Kite Pharma

Caiyan Li, PhD in Biostatistics, 07/2009, University of Pennsylvania, *Statistical Methods for Analysis of Graph-Constrained Genomic Data*.
Director of Biostatistics – Head of Oncology, Xencor

Zhi Wei, PhD in Genomics and Computational Biology, 05/2008, University of Pennsylvania, *Statistical Methods for Network-based Analysis of Genomic Data*.
Professor, New Jersey Institute of Technology.

Jiang Gui, Ph.D. in Statistics, 2005, UC Davis, *Penalized Estimation in the High-Dimensional Low-Sample Size Settings, with Applications to Genomic Data*
Associate Professor, Dartmouth College School of Medicine.

Fangxin Hong, Ph.D. in Statistics., 2004, UC Davis, *Statistical Methods for Analysis of Microarray Time Course Gene Expression Data*.
Senior Research Scientist, Dana-Farber Cancer Institute

Chun Zhang, Ph.D. in Statistics, 2004, UC Davis, *Hidden Markov Models for Admixture Mapping*.
Head of Exploratory Statistics, Abbvie

Xiaoyun Zhong, Ph.D. in Statistics, 2003, UC Davis, *Survival Models for Mapping Genes for Complex Disease*.
Senior Statistician, Forest Laboratory Inc.

Visiting PhD Students (PhD Research Projects)

Wanlu Deng, PhD – Visiting PhD student from Peking University (08/2010-10/2011),
Lecture, Tsinghua University

Qin Chang, PhD – Visiting PhD student from Shandong University (08/2011-10/2012),
Lecturer, China Petroleum University

Fan Xia, PhD – Visiting PhD student from Hong Kong University (08/2011-10/2012),
Sr. Principal Statistician, BeiGene, Shanghai

Postdoctoral Fellows Trained (years and current positions) (20 postdoc fellows trained)

Sai Li (2018-2021), Assistant Professor, Renmin University of China

Fei Xue (2019-2021), Assistant Professor, Purdue University

Shulei Wang (2018-2020), Assistant Professor, UIUC

Abhishek Chakraborty (2016-2019), Assistant Professor, Texas A & M University

Yuan Gao (2016-2018), Children's Hospital of Philadelphia

Preetam Nandy (2017-2018), Data Scientist, LinkedIn

Michael Sohn (2015-2018), Assistant Professor, University of Rochester

Jing Ma (2015-2017), Assistant Professor, Texas A&M University

Wanjie Wang (2014-2016), Assistant Professor of Statistics, National University of
Singapore.

Wei Lin (2011-2014), Associate Professor, Peking University, China.

Dave Zhao (2012- 2014), Associate Professor of Statistics, University of Illinois, Urbana-
Champaign.

Yinghua Wu (2011-2014), Quantitative Researcher, Elmagin Capital LLC

Xingge Jessie Jeng (2009-2012), Associate Professor of Statistics, North Carolina State
University.

Zhongyin John Daye (2009-2012), Statistical Consultant, Research Triangle Park

Jianxin Yin (2009-2011), Associate Professor, Renmin University of China, Beijing.

Ramon Xulvi-Brunet (2008- 2009), In Europe

Hokeun Sun (2008 – 2011), Associate Professor, Pusan National University (PNU),
Korean

Lifeng Wang (2006 – 2008), Executive Director, JPMorgan Chase & Co

Stefano Monni (2006 – 2008), Assistant Professor, American University of Beirut

Xingxue (Cathy) Liu (2007-2008), Associate Director of Statistics, Pfizer

Wanlong Sun (2002-2004), Lecturer, Peking University

Yihui Luan (2001-2004), Professor, Shandong University, PR China

PhD Dissertation Committees Served:

University of California at Davis: Wei Wang, Lei Zhou, Danh Nguyen, Blyth Durbin,
Nicole Collet.

University of Pennsylvania:

Biostatistics/Statistics: Robert Krafty, Lu Chen, Cheng Jia, Xinglei Chai, Richard Aplec, Yu Hu, Simon Vandekar, Zijian Guo, Linjun Zhang, Lingjiao Zhang

Genomics and Computational Biology (GCB): Nicholas Stong, Zhandong Liu, Serena Dollive, Erik Clarke, Rithun Mukherjee, Scott Norton, Elizabeth Piette.

MD/PhD Joint Degree Program: Rose Yun Li, Michael Loesche, Casey Bartow-McKenney

Epidemiology PhD Program: Emma Zihe Zheng, Richard Aplec.

NIH K-Award Mentorship

Josephine Ni, MD, K08, *Determinants of bacterial biofilm formation at the intestinal mucosal interface and their roles in pathogen exclusion*

Ravy Vajravelu, MD, K08-DK119475, *Evaluation of multiple medication exposures concurrently using a novel algorithm.*

Saar Gill, MD, K08-CA-194256, *Chimeric Antigen Receptor T cell Therapy for Acute Myeloid Leukemia (AML)*

Rennie Rhee, MD, K23-AR071514, *Nasal Microbiome and Host Immunity in Granulomatosis with Polyangiitis*

Sony Tuteja, PharmD, K23-HL143161, *Impact of the gut microbiome on response to lipid lowering therapy*

External Dissertation Reader/Committee Served

Herbert Pang, Biostatistics, Yale University

Fenghai Duan, Biostatistics, Yale University

Li Zeng, Biostatistics, Yale University

Johannes Ostner, Helmholtz Zentrum München

EXTERNAL GRANT REVIEW/STUDY SECTIONS, PROGRAM REVIEW

2021

Reviewer, GHD Study Section

Reviewer, Research Grants Council (RGC)

2020

Reviewer, GHD Study Section

Reviewer BCMB-F (5) Special emphasis panel

2019

Reviewer, GHD Study Section

2018

Reviewer, GHD Study Section

2017

Reviewer, National Cancer Institute (NCI) Outstanding Investigator Award (OIA)
Reviewer, GHD Study Section
Reviewer, ZDK1 GRB-N (M2) 1, Inflammatory Bowel Disease Genetics Consortium
Reviewer, Secretariat of the Research Grants Council (RGC) of Hong Kong

2016

Reviewer, National Cancer Institute (NCI) Outstanding Investigator Award (OIA)
Reviewer, GHD Study Section
Reviewer, NSERC, Mathematical and Statistical Sciences, Canada

2015

Reviewer, National Cancer Institute (NCI) Outstanding Investigator Award (OIA) Initiative
Reviewer, NIH Transformative Research Award
Reviewer, GHD Study Section

2014

Reviewer, ZRG1 GGG-A (03) M, Member Conflict: Genetics and Genomics
Reviewer, Bridging the Gap between Cancer Mechanism and Population Science (U01)
Reviewer, UK Medical Research Council, MRC MRP (DS)
Reviewer, UK Medical Research Council, MRC Strategic Skills
Reviewer, The Netherlands Organization for Scientific Research (NWO)

2013

Reviewer, MRC Biostatistics Unit Research Theme, UK, Medical Research Council
NIH Molecular and Cellular Hematology Study Section (reviewer)
NIH Special Panel, Behavioral Interventions to Address Multiple Chronic Health Conditions in Primary Care (reviewer)
NIH Genetics of Health and Disease (GHD) study Section (reviewer)
NIEHS Microbiome Review Panel (reviewer)
Canadian Statistical Sciences Institute (CANSSI), Reviewer for Collaborative Research Projects.
Reviewer, Research Grants Council (RGC) of Hong Kong

2012

NIH BMRD Study Section (regular member)
NIH Special panel on P01 Statistical Genetics review
INRA (The French National Institute for Agricultural Research) Review
NIH Special panel ZRG1 BST-U(02) review

2011

NIH BMRD Study Section (regular member).
NIH ZRG1 GGG-M (40) Special panel on P01 Statistical Genetics

2010

Reviewer of Biostatistics Branch of the National Cancer Institute Intramural Program (site visit).

NIH BMRD Study Section (regular member)

2009

NIH BMRD Study section (regular member).

ZDK GRB-7(04) Special Review Panel on Center for Integrative Cancer Biology

2008

Methods of statistical analysis of DNA sequence data for studies relating variation to disease (ZMH1 ERB-C(06)S)

National Medical Research Council (Singapore)

BMRD Study section (regular member)

2007

BMRD Study section

NSF Mathematical Sciences (Statistics and Probability)

Special Emphasis Panel (BST-E(50)), Collaborations with NCBCs

2006

SRRB-0 Advanced Proteomic Platforms and Computation Sciences for the NCI Clinical Proteomic Technologies Initiative

BMRD study section

Special Emphasis Panel/SRG 2007/01 ZRG1 BST-E, Collaborations with National Centers for Biomedical Computing

2005

CSR Special Emphasis Panel, Collaborations with National Centers for Biomedical Computing

2004

MITACS-National Center of Excellence, Canada

NCI Review Panel, Integrative Cancer Biology Program

Italian Telethon Foundation, External reviewer

2002-2003

NIH EDC-3 Study Section (regular member)

2002

Austrian Science Fund (FWF), Der Wissenschaftsfonds

2001

Center for Environmental and Toxic Studies, Texas A&M

UC Life Sciences Informatics Program

National Cancer Institute, Member of Special Emphasis Panel

CONFERENCE PROGRAM COMMITTEES AS CHAIR AND MEMBER

2022 Organizer, Banff/BIRS Workshop - Deep Learning for Genetics, Genomics and Metagenomics: Latest developments and New Directions
2020 IBC (International Biometrics Conferences), International Program Committee
2019 Chair/Organizer, First Penn Conference on Big Data in Population Health Sciences
2019 Organizer, Banff workshop – The Role of Genomics and Metagenomics in Human Health: Recent Developments in Statistical and Computational Methods
2019 Chair, Scientific Program Committee, 11th ICSA International Conference
2019 Program Committee, 2019 ICSA-China Conference
2018 Program Committee, 5th IBS-China Joint Biostatistics Meeting
2017 Program Committee, 2017 Graybill’s Conference in Statistical Genomics and Genetics
2017 Program Committee, 2017 ICSA Applied Statistics Symposium, Chicago
2016 Bioinformatics Fall Conference Planning Committee, CHOP and Penn
2016 Program Committee, 4th Joint Biostatistics Symposium, Shanghai, China
2016 Program Committee, 2016 10th ICSA International Conference, Shanghai, China
2016 Program Committee, 2016 Joint Statistics Meeting, Chicago
2013 – 2020 Organizing Committee, Mid-Atlantic Genetic Epidemiology and Statistics (MAGES) Conference
2014 Program Committee, Third Joint Biostatistics Symposium, Chengdu, China
2012 Program Committee, Second Joint Biostatistics Symposium, Beijing China
2011 Program Committee, ICSA Applied Statistics Symposium, New York City
2010 Program Committee, ICSA International Conference, Guangzhou, China
2010 Program Committee, First Joint Biostatistics Symposium in China
2009, Program Committee, Workshop on “Probability and Statistics and their application to Biology”, Beijing, Peking University
2009 Organizer and Program Committee (with Shili Lin and Tim Huang at The Ohio State University), Mathematical Biosciences Institute (MBI) Workshop “*Systems Biology of Biological Processes and Diseases: Biological Problems and Statistical Solutions*”, The Ohio State University
2007 Member, ENAR Program Committee
2006 Organizing/Program Committee, *New Biostatistics Methods Workshop*, National Health Research Institute, Taiwan
2004 Member of Committee, 13th International Histocompatibility Workshop and Conference

PROFESSIONAL SERVICES/MAJOR COMMITTEES SERVED AT LOCAL LEVEL

Major Committee and Service at the University of Pennsylvania, 2005 – present

Member, Executive Committee, Applied Mathematics and Computational Sciences (AMCS) (2021 – present)

Member, Curriculum Committee, Applied Mathematics and Computational Sciences (AMCS) (2021 – present)

Member, Committee on Academic Personals (COAP), DBEI (2005- present)
Biostatistics Faculty Recruitment Committee (2007-present)
Member, Division of Biostatistics Award Committee (2011-present)
Leadership Team, Penn Center for Precision Medicine (PCPM) (2016-present)
Member, Penn Center for Nutritional Science and Medicine (PenNSAM) Steering Committee (2018 -present).
Member, Internal Advisory Board (IAB) for the Penn-CHOP Microbiome Program (2015-present)
Organizer/Leader, Deep Learning in Biomedical Research Working Group, 2018-2019.
Review Committee, University Research Foundation, 2018
DBEI Research Day Planning Committee, 2018-2019
Member, AMCS Admission Committee, 2019
Member, CCEB Seminar Committee (2015- present)
GGEB PhD Biostatistics Qualifying Exam Committee (2019)
GGEB Executive Committee (2016 – 2018)
Chair, CCEB Awards Committee (2015 – 2017)
Member, Biomedical Curriculum and Academic Standards Committee, Biomedical Graduate Studies (2016 –2017).
Member, Review Committee, Cell and Molecular Biology Program, University of Pennsylvania (2015)
Chair, Qualifying Exam Committee, Genomics and Computational Biology Graduate Group (2014)
Member, Search Committee for Chair of Department of Genetics (2013)
Chair, Curriculum Committee (Division of Biostatistics) (2006-2011)
Chair, Admission Committee (Genomics and Computational Biology graduate group (2006-2008)
Member of Executive Committee (Genomics and Computational Biology graduate group (2006- 2010)
Chair, Genomics and Computational Biology Retreat Committee (2006)
Chair of Ad Hoc Committee to review Biostatistics Graduate Curriculum (Task force) (2008)
GCB Admission Committee (2009-2015),
Penn Genome Frontier Institute Recruitment Committee (2008)
Member, Review Committee, Department of Biophysics and Biochemistry, University of Pennsylvania (2010)
Member, Division of Biostatistics Executive Committee (2010-2016)
Seminar Committee, Center for Clinical Epidemiology and Biostatistics (2006 –2013)
Award Committee, Center for Clinical Epidemiology and Biostatistics (2013-2017)

Major Committee, Membership and Service at University of California, Davis, 1998—2005

Served as member of Center for Health Services Research in Primary Care, UC Davis Cancer Center, Shared Microarray Core Facility Committee of the Cancer Center, Executive committee of graduate program in Biostatistics, various faculty Search

Committees, Admission and Awards Committee of Graduate Groups of Statistics and Biostatistics; Graduate Advising Committee, Graduate Group of Biostatistics

Major Committees Served at Mayo Clinic, Rochester, 1995-1998

Member of Obstetrics and Gynecology Research Committee (1995-1998)
Psychiatry and Psychology Research Committee (1995-1998)

INVITED BOOK CHAPTERS (PEER-REVIEWED)

1. Ma R and **Li H** (2020): Estimating Large and Sparse Microbe-Metabolite Network in Microbiome Studies. *Wiley Handbook of Statistical Computing*. Edited by Helen Hao Zhang.
2. **Li H**, Zheng H (2020): Statistical and Computational Methods for Analysis of Shotgun Metagenomics Sequencing Data. *Statistical Analysis of Microbiome Data*, edited by Somnath Datta and Subharup Guba, Springer.
3. Lu Huang and **Li H** (2020): Bayesian Balance Regression in Microbiome Studies Using Stochastic Search. *Festschrift in honor of Professor Vera Pawlowsky-Glahn*, Edited by Peter Filzmoser, Karel Hron, Josep Antoni Martin-Fernandez and Javier Palarea-Albaladejo.
4. **Li H** (2019): Statistical and Computational Methods in Microbiome and Metagenomics. In *Handbook of Statistical Genomics 4th Ed*, Edited by David Balding and John Marioni, pp977-996.
5. **Li H** and Ma J (2019): Graphical Models in Genetics, Genomics and Metagenomics. In *Handbook of Graphical Models*, Edited by Marloes Maathuis, Mathias Drton, Steffen L. Lauritzen and Martin Wainwright. CRC Press, Boca Raton, FL.
6. **Li H** (2014): Isoform Specific Gene Expression Analysis. In *Statistical Analysis of Next Generation Sequencing Data*, Edited by Somnath Datta and Dan Nettleton.
7. Chen J and **Li H** (2013): Kernel Methods for Regression Analysis of Microbiome Compositional Data. *2012 ICSA Applied Statistics Symposium Proceedings*, edited by Yi Liu, Mingxiu Hu and Jianchang Lin, Springer Science.
8. Cai TT, Jeng XJ, and **Li H** (2012): Analysis and Inference of Microarray Data. Invited book chapter, *Advanced Medical Statistics*, Ed: J.Q. Fang, H. Jin, L. Tian and Y. Lu. World Scientific Publishing Company.
9. **Li H** (2012): Genetical Genomics Data: Some Statistical Problems and Solutions. *Advances in Statistical Bioinformatics: Models and Integrative Inference for High-Throughput Data*. Edited by Kim-Anh Do, Steve Qin and Marina Vannucci. Cambridge University Press.

10. **Li H** (2011): Hidden Markov random field models for network-based analysis of genomic data. *Handbook of Computational Statistics: Statistical Bioinformatics*, edited by Henry Lu, Bernhard Scholkopf and Hongyu Zhao, pp 353-368.
11. **Li H** (2010): High dimensional Statistics in Genomics. In *Analysis of High Dimensional Data*, edited by Tony Cai and Xiaotong Shen, pp169-193.
12. **Li H** (2008): Censored data regression in high-dimension and low sample size settings for genomic applications. *Statistical Advances in Biomedical Sciences: State of Art and Future Directions*. edited by A. Biswas, S. Datta, J Fine and M Segal. Wiley and Sons. pp 385-403.
13. **Li H** (2008): Statistical methods for inference of genetic networks and regulatory modules. *Analysis of Microarray Data: Network-based Approaches*. Edited by Emmert-Streid and Dehmer. Wiley VCH. pp 143-167.
14. **Li H** (2007): Survival analysis methods in genetic epidemiology. *Current Topics in Human Genetics: Studies of Complex Diseases*. edited by H-W Deng, H Shen, Y Liu and H Hu. World Scientific Publishing.

PEER-REVIEWED JOURNAL PUBLICATIONS (Listed by Year of Publication. Students/postdocs supervised by Prof Li are marked with *)

2021 Accepted/In Press

1. *Li S, Cai TT and **Li H** (2021): Inference for high-dimensional linear mixed-effects models: A quasi-likelihood approach. *Journal of American Statistical Association*, *accepted*.
2. *Ma R, Cai TT and **Li H** (2020): Global and Simultaneous Hypothesis Testing for High-Dimensional Logistic Regression Models. *Journal of American Statistical Association*, *accepted*.
3. *Ma R, Cai TT and **Li H** (2020): Optimal Permutation Recovery in Permuted Monotone Matrix Model. *Journal of American Statistical Association*, *accepted*.
4. *Wang S, Cai TT and **Li H** (2020): Optimal estimation of Wasserstein distance on a tree with an application to microbiome studies. *Journal of American Statistical Association*, *accepted*.
5. Li Z, Tian L, O'Malley AJ, Karagas MR, Hoen AG, Christensen BC, Madan JC, Wu Q, Gharaibeh RA, Jobin C and **Li H** (2020): IFAA: Robust association identification and inference for absolute abundance in microbiome analyses. *Journal of American Statistical Association*, *accepted*.

6. *Ma R, Cai TT and **Li H** (2020): Optimal estimation of bacterial growth rates based on permuted monotone matrix. *Biometrika*, accepted.
7. *Wang S, Cai TT and **Li H** (2020): Hypothesis Testing for Phylogenetic Composition: A Minimum-cost Flow Perspective. *Biometrika*, accepted.
8. *Ma R, Cai T.,T. and **Li H** (2020): Optimal estimation of simultaneous signal using absolute inner product with applications to integrative genomics. *Statistica Sinica*, accepted.
9. *Lu J, **Li H** (2021): Hypothesis Testing in High-Dimensional Instrumental Variables Regression with an Application to Genomics Data. *Statistica Sinica*, accepted.
10. Cai TT, **Li H** and Ma R (2020): Optimal Structured Principal Subspace Estimation: Metric Entropy and Minimax Rates. *Journal of Machine Learning Research*, accepted.
11. Viles WD, Madan JC, **Li H**, Karagas MR, Hoen AG (2021): Information content of higher-order association of the human microbiota network. *Annals of Applied Statistics*, accepted.
12. *Deek R and **Li H** (2021): A Zero-Inflated Latent Dirichlet Allocation Model for Microbiome Studies. *Frontiers in Genetics*, 11:1844.
13. *Liu M and **Li H** (2021): Estimation of Heterogeneous Restricted Mean Survival Time Using Random Forest. *Frontiers in Genetics*, 11:1727.
14. Sheng Z, Qiu C, Liu H, Gluck C, Hsu J, He J, Hsu CY, Sha D, Weir MR, Isakova T, Raj DS, Ricon-Choles H, Feldman HI, Townsend R, **Li H**, Susztak K (2020): Systematic integrated analysis of genetic and epigenetic variation in diabetic kidney disease. *Proceedings of the National Academy of Sciences*, accepted.
15. Tanes C, Bittinger K, Gao Y, Friedman ES, Nessel L, Paladhi U, Chau L, Panfen E, Fischbach MA, Braun J, Xavier R, Clish C, **Li H**, Bushman FD, Lewis JD, Wu GD (2020): Role of Diet in the Recovery of the Human Gut Microbiome and its Metabolome. *Cell Host & Microbe*, accepted.
16. Wilson N, Zhao N, Zhan X, Koh H, Fu W, Chen J, **Li H**, Wu MC and Plantinga AM (2020): MiRKAT: Kernel Machine Regression-Based Global Association Tests for the Microbiome. *Bioinformatics*, accepted.
17. Rhee RL, Lu J, Bittinger K, Sreih AG, Lee JJ, Mattei LM, Miner JJ, Cohen NA, Kelly BJ, Grayson PC, **Li H**, Collman RG, Merkel PA (2021): Dynamic changes in the nasal microbiome in patients with granulomatosis with polyangiitis. *Arthritis & Rheumatology*, in press.

18. Smith SA, Chau L, Ogawa SA, Whelan KA, Hamilton K, Chen J, Tan L, Chen EZ, Keibaugh S, Fogt F, Bewtra M, Braun J, Xavier RJ, Clish CB, Slaff B, Wiljie A, Bushman F, Lewis JD, **Li H**, Bennett MJ, Nakagawa H and Wu GD (2021): Mitochondrial dysfunction alters intestinal epithelial metabolism of hepatic acylcarnitines. *Journal of Clinical Investigation*, 131(1): e133371.
19. Raj DS, Sohn MB, Dember LM, Charytan DM, Himmelfarb J, T. Alp Ikizler, Rajnish Mehrotra, Ramezani A, Regunathan-Shenk R, Hsu JY, Landis JR, **Li H**, Kimmel PL, Kliger AS, and Dember LM for the Hemodialysis Novel Therapies Consortium (2021): The Microbiome and p-Inulin in Hemodialysis: A Feasibility Study. *Kidney360*, in press.
20. Gershuni V, Li Y, Elovitz M, **Li H**, Wu GD, Compher CW (2021): Maternal gut microbiota reflecting poor diet quality is associated with spontaneous preterm in a prospective cohort study. *American Journal of Clinical Nutrition*, in press.
21. Ma J, Bowen Xing, Yan Cao, Xin He, Kate E. Bennett, Chao Tong, Chiyang An, Taylor Hojnacki, Zijie Feng, Sunbin Ling, Sunbin Ling, Gengchen Xie, Yuan Wu, Yue Ren, Bryson W. Katona, Ming Yu, **Li H**, Ali Naji, Hua X (2021): The menin/JunD/Pbk axis regulates compensatory beta cell proliferation. *EMBO Molecular Medicine*, in press.

2020

22. *Cao Y, Zhang A and **Li H** (2020): Multi-sample estimation of bacterial composition matrix in metagenomics data. *Biometrika*, 107: 75-92.
23. Bushman FD, Conrad M, Ren Y, Zhao C, Gu C, Petucci C, Kim M-S, Abbas A, Downes KJ, Devas N, Mattei LM, Breton J, Kelsen J, Marakos S, Galgano A, Kachelries K, Erlichman J, Hart JL, Moraskie M, Kim D, Zhang H, Hofstaedter CE, Wu GD, Lewis JD, Zackular JP, **Li H**, Bittinger K and Baldassano R (2020): Multi-omic analysis of the interaction between *Clostridioides difficile* infection and pediatric inflammatory bowel disease. *Cell Host & Microbe*, 28(3):422-433.
24. Bittinger K, C Zhao, Y Li, E Ford, E Friedman, J Ni, C Kulkarni, J Cai, Y Tian, Q Liu, A Patterson, D Sarkar, Siu Hung Joshua Chan, C Maranas, A Saha-Shah, P Lund, B Garcia, L Mattei, J Gerber, M Elovitz, A Kelly, P DeRusso, D Kim, C Hofstaedter, M Goulian, **Li H**, F Bushman, B Zemel, Wu G (2020): Bacterial colonization reprograms the neonatal gut metabolome. *Nature Microbiology*, 5:838-847.
25. Cullen CM, Aneja KK, Beyhan S, Cho CE, Woloszynek S, Convertino M, McCoy SJ, Zhang Y, Anderson MZ, Alvarez-Ponce D, Smirnova E, Karstens L, Dorrestein PC, **Li H**, Gupta AS, Cheung K, Powers JG, Zhao Z, Rosen G (2020): Emerging priorities for microbiome research. *Frontiers in Microbiology*, 11:136.
26. Yarmarkovich M, Farrell A, Sison III A, Di Marco M, Raman P, Parris J, Monos DS, **Lee H**, Stevanovic S, Maris JM (2020): Immunogenicity and Immune Silence in Human Cancer. *Frontiers in Immunology*, 11: 69.

2019

27. Cai TT, Li H, *Ma J and Xia Y (2019): Differential Markov random field analysis with an application to detecting differential microbial community networks. *Biometrika*, 106(2): 401-416.
28. Guo Z, Wang W, Cai T, Li H (2019): Optimal estimation of genetic relatedness in high-dimensional linear models. *Journal of American Statistical Association*, 114: 358-369.
29. *Cao Y, Lin W and Li H (2019): Large covariance estimation for compositional data via composition-adjusted thresholding. *Journal of American Statistical Association*, 114 (526): 759-772.
30. *Lu J, Shi P and Li H (2019): Generalized linear models with linear constraints for microbiome compositional data. *Biometrics*, 75: 235-244.
31. *Sohn M and Li H (2019): Compositional mediation analysis for microbiome studies. *Annals of Applied Statistics*, 13: 661-681.
32. Gao B, Liu X, Li H and Cui Y (2019): Integrative analysis of genetical genomics data incorporating network structures. *Biometrics*, 75(4): 1063-1075.
33. Gluck C, Qiu C, Han SY, Palmer M, Oark J, Ko YA, Guan Y, Sheng X, Hanson RL, Huang J, Chen Y, Park ASD, Mantzaris I, Verma A, Li H and Susztak K (2019): Kidney cytosine methylation changes can improve renal function decline estimation in patients with diabetic kidney disease. *Nature Communications*, 10, Article No: 2461.
34. Cordero P, Narikh VN, E Chin, A Erbilgin, M Gloudemans, C Shang, Y Huang, AC. Chang, KS. Smith, F Dewey, K Zaleta, M Morley, J Brandimarto, N Glazer, A Pavlovic, M Zhao, C Moravec, W H. Tang, J Viterna, C Malloy, S Hannenhalli, Li H, S Ritter, M Li, D Bernstein, A Connolly, H Hakonarson, A J. Lusic, K B. Margulies, A A. Depaoli-Roach, S B. Montgomery, M T. Wheeler, T Cappola, and E A. Ashley (2019): Pathologic gene network rewiring implicates PPP1R3A as a central regulator in pressure overload heart failure. *Nature Communications*, 10, Article number: 2760.
35. McGinniss JE, Imai I, Simon-Soro A, Brown MC, Knecht VR, Frye L, Ravindran PM, Dothard MI, Wadell DA, Sohn MB, Li H, Christie JD, Diamond JM, Haas AR, Lanfranco AR, DiBardino DM, Bushman FD, Collman RG. (2019): Molecular analysis of the endobronchial stent microbial biofilm reveals bacterial communities that associate with stent material and frequent fungal constituents. *PLoS One*, 14(5):e0217306.
36. Simon-Soro A, Sohn MB, McGinniss JE, Imai I, Brown MC, Knecht VR, Bailey A, Clarke EL, Cantu E, Li H, Bittinger K, Diamond JM, Christie JD, Bushman FD, Collman RG (2019): Upper Respiratory Dysbiosis with a Facultative-dominated

Ecotype in Advanced Lung Disease and Dynamic Change after Lung Transplant. *Annals of the American Thoracic Society*, 16(11): 1383-1391

37. Park J, Guan Y, Sheng X, Gluck C, Seasock MJ, Hakimi AA, Qiu C, Oullman J, Verma A, **Li H**, Palmer M, Susztak K (2019): Functional methylome analysis of human diabetic kidney disease. *JCI Insight*, 4(11). pii: 128886
38. Lee JW, Moen EL, Punshon T, Hoen AG, Stewart D, **Li H**, Karagas MR, Gui J (2019): An integrated Gaussian graphical model to evaluate the impact of exposures on metabolic networks. *Computers in Biology and Medicine*, 114: 103417.

2018

39. *Gao Y, **Li H** (2018): Quantifying and comparing bacterial growth dynamics in multiple metagenomic samples. *Nature Methods*, 15:1041-1044.
40. Xia Y, Cai TT and **Li H** (2018): Joint testing and false discovery rate control in high-dimensional multivariate response regression model. *Biometrika*, 105: 249-269.
41. *Cao Y, Lin W and **Li H** (2018): Two-sample tests of high dimensional means for compositional data. *Biometrika*, 105:115-132.
42. *Sohn M and **Li H** (2018): A GLM-based latent variable ordination method for microbiome samples. *Biometrics*, 74: 448-457.
43. Vajravelu R, Scott FI, Mamtani R, **Li H**, Moore JH, Lewis JD (2017): Medication class enrichment analysis: a novel algorithm to analyze multiple pharmacologic exposures simultaneously using electronic health record data. *Journal of the American Medical Informatics Association*, 25: 780-789.
44. Li Z, Lee K, Karagas MR, Madan JC, Hoen AG, O'Malley J, **Li H** (2018): A multivariate zero-inflated logistic model for microbiome relative abundance data. *Statistics in Biosciences*, 10(3): 587-608.
45. Friedman ES, Li Y, Shen TC, Jiang J, Chau L, Adorini L, Babakhani F, Edwards J, Shapiro D, Zhao C, Carr RM, Bittinger K, **Li H**, Wu G (2018): FXR-dependent modulation of the human small intestinal microbiome by the bile acid derivative obeticholic acid. *Gastroenterology*, 155(6): 1741-1752.
46. Liao M, Xie Y, Mao Y, Lu Z, Tan A, Wu C, Zhang Z, Chen Y, Li T, Ye Y, Yao Z, Jiang Y, **Li H**, Yang X, Wang Q, Mo Z (2018): Comparative analyses of fecal microbiota in Chinese isolated Yao population, minority Zhuang and rural Han by 16S RNA sequencing. *Scientific Reports*, 8: 1141.
47. Pierson SK, Stonestrom AJ, Shilling D, Ruth J, Nabel C, Singh A, Ren Y, Stone K, **Li H**, van Rhee F and Fajgenbaum DC (2018): Plasma proteomics identifies a 'chemokine

storm' in idiopathic multicentric Castleman disease. *American Journal of Hematology*, 93(7): 902-912.

48. Kofke W, Yue Ren, John G Augoustides, **Li H**, Katherine Nathanson, Robert Siman, Qing Cheng Meng, Weiming Bu, Sukanya Yandrawatthana, Guy Kositratna, Cecelia Kim, Joseph Bavaria (2018): Reframing the biological basis of neuroprotection using functional genomics: differentially weighted, time-dependent multifactor pathogenesis of human ischemic brain damage. *Frontiers in Neurology*, 9: 497.
49. Sinha R, Habibul Ahsan, Martin Blaser, J. Gregory Caporaso, Joseph Russell Carmical, Andrew T Chan, Anthony Fodor, Mitchell H Gail, Curtis C Harris, Kathy Helzlsouer, Curtis Huttenhower, Rob Knight, Heidi H Kong, Gabriel Y Lai, Diane Leigh Smith Hutchinson, Loic Le Marchand, **Li H**, Michael J Orlich, Jianxin Shi, Ann Truelove, Mukesh Verma, Emily Vogtmann, Owen White, Walter Willett, Wei Zheng, Somdat Mahabir, Christian Abnet (2018): Next steps in studying the human microbiome and health in prospective studies, Bethesda, MD May 16 - 17, 2017. *Microbiome*, 6(1): 201.

2017

50. *Zhao SD, Cai TT, Cappola TP, Margulies KB, **Li H** (2017): Sparse simultaneous signal detection for identifying genetically controlled disease genes. *Journal of American Statistical Association*, 112:1032-1046.
51. *Shi P and **Li H** (2017): A model for paired-multinomial data and its application to analysis of data on a taxonomic tree. *Biometrics*, 73(4): 1266-1278.
52. *Zhao SD, Cai TT and **Li H** (2017): Optimal detection of weak positive latent dependence between two sequences of multiple tests. *Journal of Multivariate Analysis*, 160: 169-184.
53. Tang ZZ, Chen G, Alekseyenko A, **Li H** (2017): A general framework for association analysis of microbial communities on a taxonomic tree. *Bioinformatics*, 33(9): 1278-1285.
54. *Chen EZ, Bushman FD, **Li H** (2017): A model-based approach for species abundance quantification based on shotgun metagenomic data. *Statistics in Biosciences*, 9: 13-27.
55. Ni J, Ting-Chin David Shen, Eric Z. Chen, Aubrey Bailey, Manuela Roggiani, Alexandra Sirota-Madi, Elliot S. Friedman, Lillian Chau, Andrew Lin, Ilana, Nissim, Justin Scott, Abigail Lauder, Christopher Hoffmann, Gloriany Rivas, Lindsey Albenberg, Robert N. Baldassano, Jonathan Braun, Ramnik J. Xavier, Clary B. Clish, Marc Yudkoff, **Li H**, Mark Goullian, Frederic D. Bushman, James D. Lewis, Gary D. Wu (2017): A Role for Bacterial Urease in Crohn's Disease and Gut Dysbiosis. *Science Translational Medicine*, 9(416), eaah6888

56. Ko Y, Yi H, Qiu C, Huang S, Park J, Ledo N, Kottgen A, **Li H**, Rader DJ, Pack MA, Brown CD, Susztak K (2017): Genetic-variation-driven gene-expression changes highlight genes with important functions for kidney disease. *American Journal of Human Genetics*, 100(6): 940-953.
57. Schoch H, Kreibich AS, Ferri SL, White RS, D Bohorquez, A Banerjee, RG Port, HC Dow, L Cordero, A Pallathra, H Kim, **Li H**, W Bilker, S Hirano, RT Schultz, K Borgmann-Winter, C-G Hahn, D Feldmeyer, GC Carlson, T Abel and ES Brodtkin (2017): Sociability Deficits and Altered Amygdala Circuits in Mice Lacking Pcdh10, an Autism Associated Gene. *Biological Psychiatry*, 81(3): 193-202.
58. Kamoun M, McCullough KP, Maiers M, Fernandez Vina MA, **Li H**, Teal V, Leichtman AB, Merion RM (2017): HLA amino acid polymorphisms and kidney allograft survival. *Transplantation*, 101(5):e170-e177.

2016

59. Cai T, **Li H**, Liu W and *Xie J (2016): Joint Estimation of Multiple High-dimensional Precision Matrices. *Statistica Sinica*, 26(2), 445-464.
60. *Shi P, Zhang A and **Li H** (2016): Regression Analysis for Microbiome Compositional Data. *Annals of Applied Statistics*, 10(2): 1019-1040.
61. *Chen EZ, **Li H** (2016): A two-part mixed-effects model for analyzing longitudinal Microbiome compositional data. *Bioinformatics*, 32(17): 2611-2617.
62. Wu GD, Compher C, Chen EZ, Smith SA, Shah R, Bittinger K, Chehoud C, Albernberg LG, Nessel L, Gilroy E, Star J, Weijie AM, Flint HJ, Metz DC, Bennett MJ, **Li H**, Bushman FD, Lewis JD (2016): Comparative Metabolomics in Vegans and Omnivores Reveal Constraints on Diet-Dependent Gut Microbiota Metabolite Production. *Gut*, 61(1): 63-72.
63. Madan JC, Hoen AG, Lundgren SN, Farzan SF, Cottingham KL, Morrison H, Sogin M, **Li H**, Moore JH, Karagas MR (2016): Effects of Cesarean delivery and formula supplementation on the intestinal microbiome of six-week old infants. *JAMA Pediatrics*, 11: 1-8.
64. Ferri SL, Kreibich AS, Torre M, Piccoli CT, Dow H, Pallathra AA, **Li H**, Bilker WB, Gur R, Abel T, and Brodtkin ES (2016): Activation of Basolateral Amygdala in Juvenile C57BL/6J Mice During Social Approach Behavior. *Neuroscience*, 335: 184-194.

2015

65. **Li H** (2015): Microbiome, Metagenomics and High Dimensional Compositional Data Analysis. *Annual Review of Statistics and Its Application*, 2:73-94.

66. *Lin W, Feng R and **Li H** (2015): Regularization Methods for High-Dimensional Instrumental Variables Regression With an Application to Genetical Genomics. *Journal of American Statistical Association, Theory and Methods*, 110: 270-288.
67. Zhao N, Chen J, Carroll IM, Ringel-Kulka T, Epstein MP, Zhou H, Zhou JJ, Ringel Y **Li H** and Wu MC (2015): Testing in Microbiome Profiling Studies with the Microbiome Regression-based Kernel Association Test (MiRKAT). *American Journal of Human Genetics*, 96, 797-807.
68. Lewis JD, Eric Z. Chen, R.N. Baldassano, A.R. Otley, A.M. Griffiths, D. Lee, K. Bittinger, A. Bailey, E.S. Friedman, C. Hoffmann, L. Albenberg, R. Sinha, C. Compher, E. Gilroy, L. Nessel, A. Grant, C. Chehoud, **Li H**, G.D. Wu, F.D. Bushman (2015): Inflammation, Antibiotics, and Diet as Environmental Stressors of the Gut Microbiome in Pediatric Crohn's Disease. *Cell Host & Microbe*, 18(4): 489-500.
69. *Wu Q, Won KJ and **Li H** (2015): Nonparametric Tests for Differential Histone Enrichment with ChIP-Seq Data. *Cancer Informatics*, Suppl. 1 11-22. [PMCID:PMC4310510](https://pubmed.ncbi.nlm.nih.gov/26111111/).
70. *Jeng J, *Wu Q and **Li H** (2015): A Statistical Method for Identifying Trait-Associated Copy Number Variants. *Human Heredity*, 79(3-4):147-156.
71. *Kelly BJ, Gross R, Bittinger K, S Sherrill-Mix, JD. Lewis, RG. Collman, FD. Bushman and **Li H** (2015): Power and Sample-Size Estimation for Microbiome Studies Using Pairwise Distances and PERMANOVA. *Bioinformatics*, 31(15): 2461-2468.
72. Chen L, Liu H, Kocher JPA, **Li H**, Chen J (2015): glmgraph: An R Package for Variable Selection and Predictive Modeling of Structured Genomic Data. *Bioinformatics*, 31(24): 3991-3993.
73. Lee D, Baldassano RN, Otley AR, Albenberg L, Griffiths AM, Comphter C, Chen EZ, **Li H**, Gilroy E, Nessel L, Grant A, Chehoud C, Bushman FD, Wu G and Lewis J (2015): Comparative Effectiveness of Nutritional and Biological Therapy in North American Children with Active Crohn's Disease. *Inflammatory Bowel Diseases*, 21(8): 1786-1793.
74. Jaewook Oh, Iryna F. Sanders, Eric Z. Chen, **Li H**, John W. Tobias, R. Benjamin Isett, Sindura Penubarthi, Hao Sun, Don A. Baldwin and Nigel W. Fraser (2015): Genome Wide Nucleosome Mapping for HSV-1 shows Nucleosome Free Regions on many Genes. *PLoS One*, 10(2):e0117471. [PMCID: PMC4339549](https://pubmed.ncbi.nlm.nih.gov/26111111/).
75. *Xie J, Cai T, **Li H** (2015): Correction to the paper "Optimal False Discovery Rate Control for Dependent Data". *Statistics and Its Inference*, 9(1); 33-35.

76. Zsiros E, Duttagupta P, Dangaj D., **Li H**, Frank R, Garrabrant T, Hagemann IS, Levine B, June CH, Zhang L, Wang E, Marincola FM, Bedognetti D, Powell DJ, Tanyi J, Feldman MD, Kandalafi LE, Coukos G (2015): The Ovarian Cancer Chemokine Landscape is Conducive to Homing of Vaccine-primed and CD3/CD28 Costimulated T cells Prepared for Adoptive Therapy. *Clinical Cancer Research*, 21:2840-2850.
77. Li YR, Zhao SD, Li J, JP. Bradfield, M Mohebnasab, L Steel, J Kobie, DJ Abrams, FD. Mentch, JT Glessner, Y Guo, Z Wei, JJ Connolly, CJ Cardinale, M Bakay, D Li, SM Maggadottir, KA Thomas, H Qui, RM Chiavacci, CE Kim, F Wang, J Snyder, B Flatø, Ø Førre, LA Denson, SD. Thompson, ML Becker, SL Guthery, A Latiano, E Perez, E Resnick, C Strisciuglio, A Staiano, E Miele, MS. Silverberg, BA. Lie, M Punaro, RK Russell, DC Wilson, MC. Dubinsky, DS Monos, V Annese, JE Munro, C Wise, H Chapel, C Cunningham-Rundles, JS Orange, EM Behrens, KE Sullivan, S Kugathasan, AM Griffiths, J Satsangi, SFA Grant, PMA Sleiman, T Finkel, C Polychronakos, RN Baldassano, ET Luning Prak, JA Ellis, **Li H**, BJ Keating, H Hakonarson (2015): Genetic Sharing and Heritability of Pediatric Age-of-Onset Autoimmune Diseases. *Nature Communications*, 6:8442 | DOI: 10.1038/ncomms9442.
78. Li YR, J Li, SD Zhao, JP Bradfield, FD Mentch, SM Maggadottir, C Hou, DJ Abrams, D Chang, F Gao, Y Guo, Z Wei, JJ Connolly, CJ Cardinale, M Bakay, JT Glessner, D Li, C Kao, KA Thomas, H Qiu, RM Chiavacci, CE Kim, F Wang, J Snyder, MD Richie, B Flatø, Ø Førre, LA Denson, SD Thompson, ML Becker, SL Guthery, A Latiano, E Perez, E Resnick, RK Russell, DC Wilson, MS Silverberg, V Annese, BA Lie, M Punaro, MC Dubinsky, DS Monos, C Strisciuglio, A Staiano, E Miele, S Kugathasan, JA Ellis, JE Munro, KE Sullivan, C Wise, H Chapel, C Cunningham-Rundles, SFA Grant, JS Orange, PMA Sleiman, EM Behrens, AM Griffith, J Satsangi, TH Finkel, A Keinan, ET Luning Prak, C Polychronakos, RN Baldassano, **Li H**, BJ Keating, H Hakonarson (2015): Meta-analysis of shared genetic architecture across ten pediatric autoimmune diseases. *Nature Medicine*, 21(9): 1018-1027.

2014

79. *Lin W, Shi P, Feng R and **Li H** (2014): Variable selection in regression with compositional covariates. *Biometrika*, 101 (4): 785-797.
80. *Zhao, SD, Cai T and **Li H** (2014): Direct estimation of differential networks. *Biometrika*, 101(2): 253-268. [PMCID: PMC4443936](#)
81. *Sun H, Lin W, Feng R and **Li H** (2014): Network-regularized high dimensional Cox regression for Analysis of Genomic data. *Statistica Sinica*, 24, 1433-1459.
82. Hu Y, Liu Y, Mao X, Jia C, Ferguson J, Xue C, Reilly M, **Li H**, Li M (2014): PennSeq: accurate isoform-specific gene expression quantification in RNA-Seq by Modeling Non-Uniform Read Distribution. *Nucleic Acids Research*, 42(3):e20. [PMCID: PMC3919567](#).

83. *Vardhanabhuti S, Jeng J, Wu Y and **Li H** (2014): Parametric modeling of whole-genome sequencing data for CNV identification. *Biostatistics*, 15(3):427-441. PMCID: PMC4059462.
84. He S, Yin J, **Li H** and Wang X (2014): Graphical model selection and estimation for high dimensional tensor data. *Journal of Multivariate Analysis*, 128, 165-185.
85. *Wang W, **Li H** and Wei Z (2014): A change-point model for identifying 3'UTR switching by next-generation RNA sequencing. *Bioinformatics*, 30(15): 2162-2170. PMCID:PMC4103598.
86. *Zhao SD, Cai T and **Li H** (2014): More powerful genetic association testing via a new statistical framework for integrative genomics. *Biometrics*, 70(4): 881-890. PMCID: PMC4425276.
87. Hu X, Feng Y, Zhang D., Zhao SD, Greshock J, Hu Z, Zhang Y, Yang L, Wang L-P, Jean S, Li C, Huang Q, Katsaros D, Montone K, Tanyi JL, Lu Y, Boyd J, Nathanson KL, **Li H**, Mills H, Lin Z (2014): A Functional genomic approach identifies FAL1 as an oncogenic long noncoding RNA that associates with BMI1 and represses p21 expression in human cancer. *Cancer Cell*, 26: 344-357. PMCID: PMC4159613.
88. Albenberg, LA, Esipova, TV, Judge, CP, Bittinger, K, Chen, J, Grunberg, S, Baldassano, RN, Lewis, JD, **Li H**, Bushman, FD, Vinogradov, SA, and Wu, GD (2014): Oxygen Measurements and Gene Sequencing Reveal a Correlation between Intraluminal Oxygen Gradient and Radial Partitioning of Gut Microbiota. *Gastroenterology*, 147 (5): 1055-1068.e8. PMCID: PMC4252572.
- 2013
89. *Jeng XJ, Cai TT and **Li H** (2013): Simultaneous Discovery of Rare and Common Segment Variants. *Biometrika*, 100(1): 157-172. PMCID: PMC3696347
90. Cai TT, **Li H**, Liu W and Xie J (2013): Covariate-Adjusted Precision Matrix Estimation with an Application in Genetical Genomics. *Biometrika*, 100(1): 139-156.
91. *Chen J and **Li H** (2013): Variable Selection for Sparse Dirichlet-Multinomial Regression with An Application to Microbiome Data Analysis. *Annals of Applied Statistics*, 7(1): 418-442. PMCID: PMC3846354
92. *Deng W, Geng Z and **Li H** (2013): Learning Local Directed Acyclic Graphs Based On Multivariate Time Series Data. *Annals of Applied Statistics*, 7: 1663-1683. PMCID: PMC3898602.
93. *Chen J, Bushman FD, Lewis J, Wu GD and **Li H** (2013): Structure-Constrained Sparse Canonical Correlation Analysis with an Application to Microbiome Data Analysis. *Biostatistics*, 14(2): 244-258. PMCID: PMC3590923.

94. *Fan X, Chen J, Fung WK and **Li H** (2013): A logistic normal multinomial regression model for microbiome compositional data analysis. *Biometrics*, 69:1053-1063.
95. *Vardhanabhuti S, Li M and **Li H** (2013): A Hierarchical Bayesian Model for Estimating and Inferring Differential Isoform Expression for Multi-Sample RNA-Seq Data. *Statistics in Biosciences*, 5(1): 119-137. [PMCID: PMC3669631](#).
96. *Yin J and **Li H** (2013): Adjusting for High-dimensional Covariates in Sparse Precision Matrix Estimation by ℓ_1 -Penalization. *Journal of Multivariate Analysis*, 116: 365-381. [PMCID: PMC3653344](#).
97. *Wei Z, J Minturn, E Rappaport, G Brodeur and **Li H** (2013): Network-Based Analysis of Multivariate Gene Expression Data. *Methods in Molecular Biology*, vol. 972, 121-139. [PMCID: PMC3692268](#)
98. Hoffmann C, Dollive S, Grunberg S, Chen J, **Li H**, Wu, GD, Lew JD, Bushman FD (2013): Archaea and Fungi of the Human Gut Microbiome: Correlations with Diet and Bacterial Residents. *PLoS One*, 8(6): e66019. doi:10.1371/journal.pone.0066019. [PMCID: PMC3684604](#)
99. *Wu Y, Tian L, Pirastu M, Stambolian D and **Li H** (2013): MATCHCLIP: Locate precise breakpoints for copy number variation using CIGAR string by matching soft clipped reads. *Frontiers in Genetics*, 4:157. doi: 10.3389/fgene.2013.00157. [PMCID: PMC3744852](#)
100. **Li H** (2013): Systems Biology Approaches to Epidemiological Studies of Complex Diseases. *WIREs Systems Biology and Medicine*, 5(6): 677-686.
101. Koeth RA, Wang Z, Levison BS, Buffa JA, Org E, Sheehy B, Britt EB, Fu X, Wu Y, Li L, Smith JD, DiDonato JA, Chen J, **Li H**, Wu GD, Lewis JD, Warrier M, Brown JM, Krauss RM, Tang WHW, Bushman FD, Lusis AJ, and Hazen SL (2013): Gut microbiota metabolism of L-carnitine, a nutrient in red meat, promotes atherosclerosis. *Nature Medicine*, 19: 576-585. [PMCID: PMC3650111](#)

2012

102. Cai TT, *Jeng X, **Li H** (2012): Robust Detection and Identification of Sparse Segments in Ultra-High Dimensional Data Analysis. *Journal of the Royal Statistical Society Series B (Statistical Methodology)*, 74(5), 773-797. [PMCID: PMC356306](#).
103. *Daye ZJ, Chen J and **Li H** (2012): High-dimensional heteroscedastic regression with an application to eQTL data. *Biometrics*, 68 (1): 316-326. [PMCID: PMC3218221](#).
104. *Sun H and **Li H** (2012): Robust Gaussian graphical modeling via l_1 penalization, *Biometrics*, 68: 1197-1206. [PMCID: PMC3535542](#).

105. **Li H** (2012): U-statistics in Genetic Association Studies. *Human Genetics*, 131(9): 1395-1401. [PMCID: PMC3419299](#).
106. *Daye J, *Xie J, **Li H** (2012): A sparse structured shrinkage estimator for nonparametric varying-coefficient model with an application in genomics. *Journal of Computational and Graphical Statistics*, 21: 110-133. [PMCID: PMC3419598](#).
107. *He J, **Li H**, Edmondson A, Rader D and Li M (2012): A Gaussian copula approach for the analysis of secondary phenotypes in case-control genetic association studies. *Biostatistics*, 13(3): 497-508. [PMCID: PMC3372941](#).
108. *Yin J and **Li H** (2012): Model selection and estimation in the matrix normal graphical model. *Journal of Multivariate Analysis*, 107: 119-140. [PMCID: PMC3285238](#).
109. *Chen J, Bittinger K, Charlson ES, Hoffmann C, Lewis J, Wu GD, Collman RG, Bushman FD and **Li H** (2012): Associating microbiome composition with environmental covariates using generalized UniFrac distances. *Bioinformatics*, 28(16):2106-2113. [PMCID: PMC3413390](#).
110. Charlson ES, Bittinger K, Chen J, Diamond JM, **Li H**, Collman RG, Bushman FD (2012): Assessing bacterial populations of the lung by comparing replicate samples from the upper and lower respiratory tracts. *PloS One*, 7(9): e42786. [PMCID: PMC3435383](#).
111. Fairless A, Dow HC, Kreibich AS, Torea M, Kuruvilla M, Gordon E, Morton EA, Tan J, Berrettini WH, **Li H**, Abel T and Brodtkin ES (2012): Sociability and brain Development in BALB/cJ and C57BL/6J Mice. *Behavior Brain Research*, 228: 299-310. [PMCID: PMC3474345](#).
112. *Daye J, **Li H** and Wei Z (2012): A Powerful Test for Multiple Rare Variants Association Studies that Incorporate Sequencing Qualities. *Nucleic Acids Research*, Vol. 40 (8): e60. [PMCID: PMC3340416](#).

2011

113. Huang J, Ma S, **Li H** and Zhang CH (2011): The sparse Laplacian shrinkage estimator for high-dimensional regression. *Annals of Statistics*, 39(4), 2021-2046. [PMCID: PMC3217586](#).
114. *Xie J, Cai TT, **Li H** (2011): Sample size and power analysis for sparse signal recovery in genome-wide association studies. *Biometrika*, 98 (2): 273-290. [PMCID: PMC3419390](#).

115. *Chen J, *Xie J and **Li H** (2011): A penalized likelihood approach for bivariate conditional normal models for dynamic co-expression analysis. *Biometrics*, 67(1), 299-308. [PMCID: PMC2902622](#).
116. Wei X, Huang J and **Li H** (2011): Variable selection and estimation in high-dimensional varying-coefficient models. *Statistica Sinica*, 21:1515-1540.
117. *Yin J and **Li H** (2011): A sparse conditional Gaussian graphical model for analysis of genetical genomics data. *Annals of Applied Statistics*, 5(4): 2630-2650. [PMCID: PMC3419502](#).
118. Lu T, Liang H, **Li H**, Wu H (2011): High dimensional ODEs coupled with mixed-effects modeling techniques for dynamic gene regulatory network identification. *Journal of American Statistical Association*, 104: 1242-1258. [PMCID: PMC3509540](#).
119. *Xie J, Cai TT, Maris J and **Li H** (2011): Optimal false discovery rate control for dependent data. *Statistics and Its Interface*, 4(4): 417-430. [PMCID: PMC3415307](#).
120. Wu GD, *Chen J, Hoffmann C, Bittinger K, Chen YY, Keilbaugh SA, Bewtra M, Knights D, Walters WA, Knight R, Sinha R, Gilroy E, Gupta K, Baldassano R, Nessel L, **Li H**, Bushman FD, Lewis JD (2011): Linking long-term dietary patterns with gut microbial enterotypes. *Science*, 334 no. 6052 pp. 105-108. [PMCID: PMC3368382](#).
121. Wang K, Diskin SJ, Attiyeh EF, Winter C, Schnepf RW, Diamon M, Zhang H, Hou C, Bosse K, Mayes PA, Glessner J, Kim C, Frackelton E, Marris M, Wang Q, Glaberson W, Chiavacci W, Nguyen L, Saeki N, Sasaki H, Grant SFA, Mosse YP, Iolascon A, **Li H**, Devoto M, McGrady PW, London WB, Capasso M, Rahman N, Hakonarson H & Maris JM (2010): Integrative genomics identifies *LMO1* as a neuroblastoma oncogene. *Nature*, 469, 216-220. [PMCID: PMC3320515](#).
122. *Winter C, Austin RS, Blanvillain-Baufumé B, Reback MA, Monniaux M, Wu MF, Sang Y, Yamaguchi A, Yamaguchi N, Parker JE, Parcy F, Jensen ST, **Li H** and Wagner D (2011): LEAFY target genes reveal a direct link between biotic stimulus response and flower. *Developmental Cell*, 20(4) 430-443.
123. Dow H, Kaercher K, Sankoorikal G, Pauley E, Lohoff F, Ferraro T, **Li H**, Brodtkin E (2011): Genetic dissection of intermale aggressive behavior in BALB/cJ and A/J mice. *Genes, Brain and Behavior*, 10: 57-68. [PMCID: PMC3017637](#)
124. Fairless AH, Shah RY, Guthrie AJ, **Li H** and Brodtkin ES (2011): Deconstructing sociability, an autism-relevant phenotype, in mouse models. *The Anatomical Record: Advances in Integrative Anatomy and Evolutionary Biology*, 294(10):1713-25. [PMCID: PMC3176979](#).
125. *Nguyen LB, Diskin SJ, Cappasso M, Wang K, Diamond MA, Glessner J, Kim C, Attiyeh EF, Mosse YP, Cole K, Lolascon A, Devoto M, Hakonarson H, **Li H**, Maris

JM (2011): Phenotype restricted genome-wide association study using a gene-centric approach identifies three low-risk Neuroblastoma susceptibility loci. *PLoS Genetics*, 7(3): e1002026. [PMCID: PMC3060064](#).

126. Minot S, Rohini S, *Chen J, **Li H**, Keibaugh S, Wu G, Lewis J and Bushman F (2011): The human gut virome: inter-individual variation and dynamic response to diet. *Genome Research*, 21: 1616-1625. [PMCID: PMC3202279](#).

2010

127. *Jeng J, Cai, TT and **Li H** (2010): Optimal sparse segment identification with application in copy number variation analysis. *Journal of American Statistical Association*, 105 (491): 1156-1166. [PMCID:PMC3610602](#).
128. *Li C and **Li H** (2010): Variable selection and regression analysis for graph-structured covariates with an application to genetics. *Annals of Applied Statistics*, 4 (3): 1498-1516. [PMCID: PMC3423227](#).
129. *Li C, *Wei Z and **Li H** (2010): Network-based empirical Bayes methods for linear models with applications to genomic data, *Journal of Biopharmaceutical Statistics*, 20: 209-222. [PMCID: PMC3422552](#).
130. **Li H**, *Wei Z and Maris J (2010): A hidden Markov random field model for genome-wide association studies. *Biostatistics*, 11: 139-150. [PMCID:PMC2800164](#).
131. *Xulvi-Brunet R and **Li H** (2009): Co-expression networks: graph properties and Topological comparisons. *Bioinformatics*, 26: 205-214. [PMCID: PMC2804297](#).
132. *Sun H, **Li H** (2010): A Bayesian approach for graph-constrained estimation for high-dimensional regression. *International Journal of Systems and Synthetic Biology*, 1(2): 255-272. [PMCID: PMC3422552](#).
133. Wu, GD, Lewis JD, Hoffmann C, Chen YY, Knight R, Bittinger K, Hwang J, Chen J, Berkowsky R, Nessel L, **Li H**, Bushman F (2010): Sampling and pyrosequencing methods for quantifying bacterial communities in the human gut. *BMC Microbiology*, 10:206. [PMCID: PMC2921404](#).
134. Sleiman P, M Imielinski, J. P. Bradfield, K Annaiah, S.A.G. Willis-Owen, N.M. Rafaels, S Michel, K Bønnelykke, C.E. Kim, E.C. Frackelton, J.T. Glessne, C. Hou, J. Flory, F.G. Otieno, E. Santa, K. Thomas, R.M. Smith, W.R. Glaberson, M. Garris, R.M. Chiavacci, T.H Beaty, I. Ruczinski, J. Allen, J.M. Spergel, R. Grundmeier, R.A. Mathias, J.D. Christie, E. von Mutius, W.O.C. Cookson, M. Kabesch, M.F. Moffatt, M.M. Grunstein, **Li H**, K.C. Barnes, M. Devoto, M. Magnusson, S.F.A. Grant, H. Bisgaard and H. Hakonarson (2010): Variants of DENND1B Associated with Asthma in Children. *New England Journal of Medicine*, 362: 36-44.

135. Charlson ES, Jun Chen, Rebecca Custers-Allen, Kyle Bittinger, **Li H**, Rohini Sinha, Jennifer Hwang, Frederic D. Bushman and Ronald G. Collman (2010): Disordered microbial communities in the upper respiratory tract of cigarette smokers. *PLoS One*, 5(12): e15216. [PMCID: PMC3004851](#)

2009

136. Capasso M, Hou C, Asgharzadeh S, Attiyeh EF, Mosse YP, Diskin SJ, Cole K, Bosse K, Diamond M, Laudenslager M, Winter C, Bradfield JP, Scott RH, Jagannathan J, Glessner JT, Kim C, London, WB, Seeger RC, **Li H**, Rahman N, Rappaport E, Hakonarson H, Devoto M, Maris J (2009): Common variations in the BARD1 tumor suppressor gene influence susceptibility to high-risk neuroblastoma. *Nature Genetics*, 41(6): 718-723. [PMCID: PMC2753610](#)
137. Paulson T, Maley C, Li X, **Li H**, Sanchez C, Chao D, Odze R, Vaughan T, Blount P, Reid B (2009): Chromosomal instability and copy number alterations in Barrett's esophagus and esophageal adenocarcinoma. *Clinical Cancer Research*, 15: 3306-3314. [PMCID: PMC2684570](#).
138. Diskin, SJ, C. Hou, J.T. Glessner, E.F. Attiyeh, M. Laudenslager, K. Bosse, K. Cole, Y.P. Mosse, Andrew Wood, Jill E. Lynch, Katlyn Pecor, Maura Diamond, Cynthia Winter, Kai Wang, Cecilia Kim, Elizabeth A. Geiger, Patrick W. McGrady, Alexandra I. F. Blakemore, Wendy B. London, Tamim H. Shaikh, Jonathan Bradfield, Struan F. A. Grant, **Li H**, Marcella Devoto, Eric R. Rappaport, Hakon Hakonarson, John M. Maris (2009): Copy number variation at 1q21.1 associated with neuroblastoma. *Nature*, 459: 987-991. [PMCID: PMC2755253](#).
139. Flory J, P Sleiman, J Christi, K Annaiah, J Bradfield, C Kim, J Glessne, M Imielinski, **Li H**, E Frackelton, H Cuiping, G Otieno, K Thomas, R Smith, W Glaberson, M Garris, R Chiavacci, J Allen, J Spergel, R Grundmeier, M Grunstein, M Magnusson, S Grant, K Bønnelykke, H Bisgaard, H Hakonarson (2009): 17q12-21 variants interact with smoke exposure as a risk factor for pediatric asthma but are equally associated with early versus late onset asthma in North-Americans of European Ancestry. *Journal of Allergy and Clinical Immunology*, 124(3): 605-607.

2008

140. *Monni S and **Li H** (2008): Vertex clustering of graphs using reversible jump MCMC. *Journal of Computational and Graphical Statistics*, 17(2): 388-409.
141. *Wang L, **Li H** and Huang J (2008): Variable selection in nonparametric varying-coefficient models for analysis of repeated measurements. *Journal of the American Statistical Association*, 103: 1556- 1569. [PMCID:PMC2801925](#).
142. *Luan Y, **Li H** (2008): Group additive regression models for analysis of genomic Data. *Biostatistics*, 9:100-113.

143. *Wei Z and **Li H** (2008): A hidden spatial-temporal Markov random field model for network-based analysis of time course gene expression data. *Annals of Applied Statistics*, 2(1), 408-429.
144. *Li C and **Li H** (2008): Network-constraint regularization and variable selection for analysis of genomic data. *Bioinformatics*, 24: 1175-1182.
145. Maris JM, Yael PM, Bradfield JP, Hou C, Monni S, Scott RH, Asgharzadeh S, Attiveh EF, Diskin SJ, Laudenslager M, Winter C, Cole K, Glessner JT, Kim C, Frackelton EC, Casalunovo T, Eckert AW, Capasso M, Rappaport EF, McConville C, London WB, Seeger RC, Rahman N, Devoto M, Grant SFA, **Li H** and Hakonarson H (2008): A genome-wide association study identifies a susceptibility locus to clinically aggressive neuroblastoma at 6p22. *New England Journal of Medicine*, 358: 2585-2593. PMCID: PMC2742373
146. Fairless AH, Dow H, Toledo MM, Kalkus KA, Edelmann M, **Li H**, Talbot K, Arnold SE and Brodtkin ES (2008): Low Sociability is associated with reduced size of corpus callosum. *Brain Research*, 1230: 211-217. PMCID: PMC2629607
147. *Wei Z, Li M, Rebbeck T, **Li H** (2008): U-statistics-based tests for multiple genes in genetic association studies. *Annals of Human Genetics*, 72:821-833. PMCID: PMC2574710
148. Kamoun M, Holmes JH, Israni AK, Kearns JD, Teal V, Yang W, Rosasa SE, Joffe MM, **Li H**, Feldman HI (2008): HLA-A amino acid polymorphism and delayed kidney allograft function. *Proceedings of National Academy of Sciences*, 105(48): 18883-18888. PMCID: PMC2596272

2007

149. *Wei Z, **Li H** (2007): Nonparametric pathways-based regression models for analysis of genomic data. *Biostatistics*, 8(2): 265-284.
150. *Wang L, *Chen G, **Li H** (2007): Group SCAD regression analysis for microarray time course gene expression data. *Bioinformatics*, 23: 1486-1494.
151. *Wei Z and **Li H** (2007): A Markov random field model for network-based analysis of genomic Data. *Bioinformatics*, 23: 1537-1544.

2006

152. *Hong F, **Li H** (2006): Functional hierarchical models for identifying genes with different time-course expression profiles. *Biometrics*, 62: 534-544.

153. **Li H** and Gui J* (2006): Gradient directed regularization for sparse Gaussian concentration graphs, with applications to inference of genetic networks. *Biostatistics*, 7: 302-317.

2005

154. *Gui J, **Li H** (2005): Threshold gradient descent method for censored data regression, with applications in pharmacogenomics. *Pacific Symposium on Biocomputing*, 10, 272-283.
155. *Gui J, **Li H** (2005): Penalized Cox regression analysis in the high-dimensional and low-sample size settings, with applications to microarray gene expression Data. *Bioinformatics*, 21:3001-3008.
156. **Li H**, *Luan Y (2005): Boosting proportional hazards models using smoothing spline, with application to high-dimensional microarray data. *Bioinformatics*, 21:2403-2409.
157. Heit JA, Sobell JL, **Li H**, Sommer SS (2005): The Incidence of venous thromboembolism among Factor V Leiden carriers: a community-based cohort study. *Journal of Thrombosis and Haemostasis*, 3: 305-311.
158. Seldin MF, Shigeta R, Laiho, **Li H**, Saila H, Savolainen A, Leirisalo-Repo M, Tuomilehto-Wolf E, Kaarela K, Kauppi M, Alexander HC, Begovich AB, Tuomilehta J (2005): Finnish case-control and family studies support PTPN22 R620W polymorphism as a risk factor in rheumatoid arthritis, but suggest only minimal or no effect in juvenile idiopathic arthritis. *Genes and Immunity*, 6(8): 720-2.
159. Yang N, **Li H**, Criswell LA, Gregersen PK, Alarcon-Riquelme ME, Kittles R, Shigeta R, Silva G, Patel PI, Belmont JW, Seldin MF (2005): Examination of ancestry and ethnic affiliation using highly informative diallelic DNA markers: application to diverse and admixed populations and implications for clinical epidemiology and forensic medicine. *Human Genetics*, 29: 1-11.

2004

160. *Luan Y, **Li H** (2004): Model-based methods for identifying periodically regulated genes based on the time course microarray gene expression data. *Bioinformatics*, 20:332-339.
161. *Zhong X, **Li H** (2004): Score tests of genetic association in the presence of linkage based on the additive genetic gamma frailty model. *Biostatistics*, 5:307-327.
162. **Li H**, *Gui J (2004): Partial Cox regression analysis for high-dimensional microarray gene expression data. *Bioinformatics*, 20:i208-i215.

163. *Sun W, **Li H** (2004): Ascertainment-adjusted maximum likelihood estimation for the additive genetic gamma frailty models. *Lifetime Data Analysis*, 10: 229-245.
164. Seldin MF, Morii T, Collins-Schramm EC, Chima B, Kittles R, Criswell LA, **Li H** (2004): Putative ancestral origins of chromosomal segments in individual African Americans: Implications for admixture mapping. *Genome Research*, 14:1076-1084.
165. *Li L, **Li H** (2004): Dimension reduction methods for microarrays with application to censored survival data. *Bioinformatics*, 20:3406-3412.
166. *Zhang C, K Chen, Seldin M, **Li H** (2004): A hidden Markov modeling approach for admixture mapping based on case-control data. *Genetic Epidemiology*, 27:225-239.

2003

167. **Li H**, *Luan Y (2003): Kernel Cox regression models for linking gene expression profiles to censored survival data. *Pacific Symposium on Biocomputing*, 8: 65-76.
168. *Luan Y, **Li H** (2003): Clustering of time-course gene expression data using a mixed-effects model with B-splines. *Bioinformatics*, 19: 474-482.
169. Krahn LE, **Li H**, O'Connor MK (2003): Patients who strive to be ill: factitious disorder with physical symptoms. *American Journal of Psychiatry*, 160:6, 1163-1168.

2002

170. **Li H**, *Zhong X (2002): Multivariate survival models induced by genetic frailties, with application to linkage analysis. *Biostatistics*, 3(1): 57-75.
171. **Li H** (2002): The additive genetic gamma frailty model for linkage analysis of diseases with variable age of onset using nuclear families. *Lifetime Data Analysis*, 8: 315-334.
172. **Li H**, *Luan Y, *Hong F, *Li Y (2002): Statistical methods for analysis of time-course gene expression data. *Frontiers in Bioscience*, 7, a90-98, May.
173. Hsu Li, **Li H**, Houwing J (2002): A method for incorporating ages at onset in affected sib pair linkage studies. *Human Heredity*, 54:1-12.
174. *Zhong X, **Li H** (2002): An additive genetic gamma frailty model for two-locus linkage analysis using sibship age of onset data. *Statistical Applications in Genetics and Molecular Biology*, Vol 1, No 1, Article 2.
175. Collins-Schramm HE, Phillips CM, Operario DJ, Lee JS, Webber JL, Hanson RL, Knowler WC, Cooper R, **Li H**, Seldin MF (2002): Ethnic-difference markers for use

in mapping by admixture linkage disequilibrium. *American Journal of Human Genetics*, 70: 737-750.

176. Seligman VA, Lum R, Olson JL, **Li H**, Criswell LA (2002): Demographic differences in the development of lupus nephritis. *American Journal of Medicine*, 112: 726-29.
177. Parsa A, Peden E, Lum RF, Seligman VA, Olson JL, **Li H**, Seldin MF, and Criswell LA (2002): Association of angiotensin converting enzyme polymorphisms with systemic lupus erythematosus and nephritis: analysis of 644 SLE families. *Genes and Immunity*, 3 (supplement 1), S42-S46.

2001

178. **Li H**, *Hong F (2001): Cluster-Rasch models for microarray gene expression data. *Genome Biology*, research0031.1-0031.13.
179. **Li H** (2001): A permutation procedure for the haplotype method for identification of disease-predisposing variants. *Annals of Human Genetics*, 65:189-196.
180. Seligman VA, Suarez C, Lum R, Inda SE, Olson J, **Li H**, Seldin MF, Criswell LA (2001): Ethnic variation in the association of FcgammaRIIIA polymorphism with lupus nephritis. *Arthritis & Rheumatism*, 44: 618-625.
181. Shields RC, McBane RD, Kuiper JD, **Li H**, Heit JA (2001): Efficacy and safety of intravenous phytonadione (Vitamin K1) for correction of chronic oral anticoagulation. *Mayo Clinic Proceedings*, 76:260-266.

2000

182. **Li H**, Hsu L (2000): Effects of ages at onset on the power of the affected sib pair and transmission/disequilibrium tests. *Annals of Human Genetics*, 64:239-254.
183. **Li H**, Fan JJ (2000): A general test of association for complex diseases with variable age of onset. *Genetic Epidemiology*, 19: S43-S49.
184. Collins HE, **Li H**, Inda SE, Anderson J, Laiho K, Tuomilehto J, Seldin MF (2000): A simple and accurate methods for determination of microsatellite total allele content differences between DNA pools. *Human Genetics*, 106(2): 218-226.
185. St. Louis EK, Wijidicks EFM, **Li H**, Atkinson JD (2000): Predictors of poor outcome in patients with a spontaneous cerebellar hematoma. *The Canadian Journal of Neurological Sciences*, 27: 32-36.
186. Yanovski J, Diament AL, Sovik KN, Nguyen TT, **Li H**, Sebring NG, Warden CH (2000): Associations between uncoupling protein 2, body composition, and testing

energy expenditure in lean and obese African American, white, and Asian children. *American Journal of Clinical Nutrition*, 71:1405-1412.

187. Silverman MB, Roche PC, Kho RM, Keeney GL, **Li H**, Podratz KC (2000): Molecular and cytokinetic pretreatment risk assessment in endometrial carcinoma. *Gynecologic Oncology*, 77(1):1-7.
188. Criswell LA, Moser KL, Gaffney PM, Inda S, Lin D, Chen JJ, **Li H**, Gray-McGuire C, Neas BR, Rich SS, Harley JB, Behrens TW, Seldin MF (2000): PARP alleles and SLE: failure to confirm association with disease susceptibility (letter to editor). *Journal of Clinical Investigation*, 105:1501-1502.
189. Zanetta GM; Webb MJ; **Li H**; Keeney, GL (2000): Hyperestrogenism: a relevant risk factor for the development of cancer from endometriosis. *Gynecologic Oncology*, 79(1):18-22.
190. Krahn LE; Gleber E; Rummans TA; Pileggi TS; Lucas DL; **Li H** (2000): The effects of electroconvulsive therapy on melatonin. *Journal of ECT*, 16(4):391-8.
191. Gershwin ME; Leung PS; **Li H**; Seldin MF (2000): Primary biliary cirrhosis and autoimmunity: evaluating the genetic risk. *Israel Medical Association Journal*, 2 Suppl:7-10.

1999

192. **Li H** (1999): The additive genetic gamma frailty model for linkage analysis of age-at-onset variation. *Annals of Human Genetics*, 63:455-468.
193. Therneau TM, **Li H** (1999). Computing the Cox model for case cohort designs. *Lifetime Data Analysis*, 5:99-112.
194. Gould PM; Bonner JA; Sawyer TE; Deschamps C; Lange CM; **Li H** (1999): Patterns of failure and overall survival in patients with completely resected T3 N0 M0 non-small cell lung cancer. *International Journal of Radiation Oncology, Biology, Physics* 45:91-5.
195. Villeneuve JB, Silverman BM, Alderete B, Cliby WA, **Li H**, Croghan Gary, Podratz KC, Jenkins RB (1999): Loss of markers linked to BRCA1 precedes loss at important cell cycle regulatory in epithelial ovarian cancer. *Genes, Chromosomes and Cancer*, 5(1):65-9.
196. Weiner JS, Sherris D, Kasperbauer J, Lewis J, **Li H**, Persing D (1999): Relationship of human papillomavirus to Schneiderian papillomas. *Laryngoscope*, 109(1):21-6.
197. Heit JA, Minor TA, Andrews JC, Larson DR, **Li H**, Nichols WL (1999). Determinants of plasma Fibrin D-Dimer sensitivity for acute pulmonary embolism as defined by

- pulmonary angiography. *Archives of Pathological Laboratory Medicine*, 123(3):235-40.
198. Sawyer TE; Bonner JA; Gould PM; Deschamps C; Lange CM; **Li H** (1999): Patients with stage I non-small cell lung carcinoma at postoperative risk for local recurrence, distant metastasis, and death: implications related to the design of clinical trials. *International Journal of Radiation Oncology, Biology, Physics*, 45(2):315-21.
199. Sawyer TE, Bonner JA, Gould PM, Garces YI, Foote RL, Lange CM, **Li H** (1999): Predictors of subclinical nodal involvement in clinical stages I and II non-small cell lung cancer: implications in the inoperable and three-dimensional dose-escalation settings. *International Journal of Radiation Oncology, Biology, Physics*, 43(5):965-70.
200. Flemming KD, Wijdicks EFM, St. Louis EK, **Li H** (1999): Predicting deterioration in patients with lobar haemorrhages. *Journal of Neurology, Neurosurgery and Psychiatry*, May;66(5):600-5.
201. Gibson GE, **Li H**, Pittelkow MR (1999): Homocysteinemia and livedoid vasculitis. *Journal of the American Academy of Dermatology*, 40(2 Pt 1):279-81.
202. Frias AE Jr., **Li H**, Keeney GL, Podratz KC, Woodruff TK (1999): Preoperative serum levels of inhibin A are independent prognostic factors in postmenopausal women with epithelial ovarian carcinoma. *Cancer*, 15;85(2):465-71.
203. Bonner JA; Garces YI; Sawyer TE; Gould PM; Foote RL; Deschamps C; Lange CM; **Li H** (1999): Frequency of noncontiguous lymph node involvement in patients with resectable nonsmall cell lung carcinoma. *Cancer*, 86:1159-64.
204. Magtibay PM; Perrone JF; Stanhope CR; Katzmann JA; Keeney GL; **Li H** (1999). Flow-cytometric DNA analysis of early stage adenocarcinoma of the cervix. *Gynecol Oncology*, 75(2):242-247.
205. Sawyer TE; Bonner JA; Gould PM; Foote RL; Deschamps C; Lange CM; **Li H** (1999): Factors predicting patterns of recurrence after resection of N1 non-small cell lung carcinoma. *Ann Thorac Surg*, Oct;68(4):1171-6.
- 1998
206. **Li H**, Thompson EA, Wijsman EA (1998): Semiparametric estimation of major gene effects for age of onset. *Genetic Epidemiology*, 15:279-298.
207. **Li H**, Yang P, Schwartz AG (1998): Analysis of age of onset data from case-control family studies. *Biometrics*, 54:1030-1039.
208. **Li H**, Huang J (1998): Semiparametric linkage analysis using pseudolikelihoods on neighbouring Sets. *Annals of Human Genetics*, 62:323-336.

209. Adams KM, **Li H**, Nelson RL, Ogburn PL Jr, Danilenko-Dixon DR (1998): Sequelae of unrecognized gestational diabetes. *American Journal of Obstetrics and Gynecology*, 178(6):1321-32.
210. Erickson D, Grarib H, **Li H**, van Heerden JA (1998): Treatment of patients with toxic multinodular goiter. *Thyroid*, 8: 277-282 .
211. Limburg M, Wijdicks EFM, **Li H** (1998): Ischemic stroke after general surgical procedures: clinical features, neuroimaging and risk factors. *Neurology*, 50(4):895-901.
212. Gould PM, Bonner JA, Sawyer TE, Deschamps C, Lange CM, **Li H** (1998): Bronchial carcinoid tumors: importance of prognostic factors that influence patterns of recurrence and overall survival. *Radiology*, 208(1):181-5.
213. Dinneen S, Maldonado D, Leibson C, Klee G, **Li H**, Melton J, Rizza R (1998): Effects of a change in the diagnostic criteria for diabetes on development of the disease. *Diabetes Care*,21(9): 1408-1413.
214. Shadid GE, Tinsley JA, **Li H**, Offord KP, Agerter DC (1998): A survey of family physicians and psychiatrists: psychotropic prescribing practices and educational needs. *General Hospital Psychiatry, Medicine and Primary Care*, 20:360-367.
215. St. Louis EK, Wijdicks EFM, **Li H** (1998): Predictive neurologic deterioration in patients with cerebellar hematomas. *Neurology*, 51: 1364-1369.
216. Lutz ME, Otley CC, Roenigk RK, Brodland DG, **Li H** (1998): Cutaneous reinnervation of flaps and grafts of the face. *Archives of Dermatology*, 134:1271-1274.

1997

217. **Li H**, Thompson EA (1997): Semiparametric estimation of major gene and random familial effects for age of onset. *Biometrics*,53:282-293.
218. **Li H**, Schaid DJ (1997): GENEHUNTER: Application to analysis of bipolar pedigrees and some extensions. *Genetic Epidemiology*,14:659-663.
219. Schaid DJ, **Li H** (1997): Genotype relative-risks and association tests for nuclear families with missing parental data. *Genetic Epidemiology*, 14:1113-1118.
220. Sawyer TE, Bonner JA, Gould PM, Foote RL, Deschamps C, Trastek VF, Pairolero PC, Allen MS, Lange CM, **Li H** (1997): Effectiveness of postoperative irradiation in stage IIIA cancer based on regression tree analyses of recurrence risks. *Annals of Thoracic Surgery*, 64: 1402-1408.

221. Sawyer T, Bonner J, Gould P, Foote R, Deschamps C, Trastek V, Pairolero P, Allen M, Shaw E, Marks R, Frytak S, Lange C, **Li H** (1997): The impact of surgical adjuvant thoracic radiation therapy for patients with nonsmall cell lung carcinoma with ipsilateral mediastinal lymph node involvement. *Cancer*, 80:1399-408.
222. Tomac TA, Rummans TA, Pileggi TS, **Li H** (1997): Safety and efficacy of electroconvulsive therapy in patients over age 85. *The American Journal of Geriatric Psychiatry*, 5(2):126-30.

INVITED JOURNAL DISCUSSIONS

1. **Li H** (2012): Introduction to Special Issue “Methods for Analysis of Graphs and Networks and Their Applications in Biosciences”, *Statistics in Bioscience*, 4:1-2.
2. **Li H** (2009): Invited Discussion on "A stochastic partitioning method to associate high-dimensional responses and covariates" by Monni and Tadesse, *Bayesian Analysis*, 4:449-552.
3. **Li H** (2006): Invited Discussion of the "Likelihood-based inference on haplotype effects in genetic association studies" by Lin and Zeng. *Journal of the American Statistical Association*, 101:114-115.
4. **Li H** and *Hong F (2006): Invited Discussion of the paper “Hidden Markov models for microarray time course data in multiple experiments” by Yuan and Kendzioriski. *Journal of the American Statistical Association*, 101: 1332-1334.

PUBLICATIONS IN HLA 2004: Immunobiology of the Human MHC

1. Thomson G, **Li H**, JS Dorman, BA Lie, E Migot, A Steenkiste, JM Akey, S McWeeney, R Single(2004): Statistical approaches for analysis of HLA-associated and other complex diseases. *HLA 2004: Immunobiology of the Human MHC. Proceedings of the 13th International Histocompatibility Workshop and Congress*. (Hansen JA and Dupont B, eds), Volume I & II, IHWG Press, Seattle, WA, 2004
2. Mignot E, L Lin, **Li H**, G Thomson, M Lathrop, K Tokunaga, Y Honda, Y Dauvilliers, M Tafti, M Billiard, Gt Mayer, J Montplaisir, G Rouleau, H Temple), M Thorpy, B Martins, Mm Vazquez, C Alaez, C Gorodezky, G Schoch, B Lo, F. Grumet (2004): HLA allele and microsatellite studies in narcolepsy *HLA 2004: Immunobiology of the Human MHC. Proceedings of the 13th International Histocompatibility Workshop and Congress*. (Hansen JA and Dupont B, eds), Volume I & II, IHWG Press, Seattle, WA, 2004.
3. Tamouzal R, S Laoussadi (for EUROAS), C Papasteriades, S Roggero, J Armas, **Li H**, G Thomson, M Lathrop and A Toubert (2004): HLA of Spondyloarthropathies. *HLA 2004: Immunobiology of the Human MHC. Proceedings of the 13th International*

Histocompatibility Workshop and Congress. (Hansen JA and Dupont B, eds), Volume I & II, IHWG Press, Seattle, WA, 2004.

4. Thorsby E, S. Caillat-Zucman, J.F. Eliaou, M. Lathrop, **Li H**, B.A. Lie, C. Mazzilli, E. Mignot, J.L. Nelson, A. Pugliese, J. Reveille, G. Thomson and A. Toubert (2004): Additional disease predisposing genes in the HLA complex A summary of the 13. IHWS Disease component studies. *HLA 2004: Immunobiology of the Human MHC. Proceedings of the 13th International Histocompatibility Workshop and Congress.* (Hansen JA and Dupont B, eds), Volume I & II, IHWG Press, Seattle, WA, 2004.
5. Lie BA, Mora B, Boland A, Thorsby E, Mazzilli MC, Absi L, Arranz E, Bonamico M, Borelli I, Corazza GR, de la Concha EG, Drabek J, Fasano A, Fasano ME, Fernandez L, Garrote JA, Gay C, Greco L, Kerhin-Brkljacic V, Kolek A, **Li H**, Louka AS, Mantovani V, Neuhausen SL, Percopo S, Perez-Bravo F, Pozsonyi E, Rosati R, Rajczyk K, Salvaneschi L, Schoch G, Sollid LM, Testi M, Thomson G, Zonn JJ, Zunec R (2004): Joint Report from the 13. IHWS Celiac Disease Component. *HLA 2004: Immunobiology of the Human MHC. Proceedings of the 13th International Histocompatibility Workshop and Congress.* (Hansen JA and Dupont B, eds), Volume I & II, IHWG Press, Seattle, WA, 2004.
6. Nelson JL, Lambert NC, Brautbar C, El-Gabalaway H, Fraser P, Gorodezky C, **Li H**, Jonas B, Konenkov V, Lathrop M, Martin J, Moxley G, Oen K, Papasteriades C, Schroeder M, Tikly M, Vejabaesya S, Vu C, Yoo B, Agrawal S, Alves H, Charoenwongse P, Deng A, Fainboim L, Haq SA, Liaquat A, Li-Yu J, Mustafa K, Papaioannou-Voniatis D, Park W, Saaibi D, Soeroso J, Torralba T, Zeng Q, Thorsby E, Thomson G, Eliaou JF, McWeeney S. (2004): The 13th International Histocompatibility Working Group for Rheumatoid Arthritis Joint Report. *HLA 2004: Immunobiology of the Human MHC. Proceedings of the 13th International Histocompatibility Workshop and Congress.* (Hansen JA and Dupont B, eds), Volume I & II, IHWG Press, Seattle, WA, 2004.
7. Pugliese, J.S. Dorman, A. Steenkiste, **Li H**, E. Thorsby, M. Lathrop, G. Schoch, G. Thomson, S. Caillat-Zuchman together with the 13th IHWS Type 1 Diabetes Component Participating Investigators (2004): Joint report of the 13th Type 1 Diabetes (T1D) component. *HLA 2004: Immunobiology of the Human MHC. Proceedings of the 13th International Histocompatibility Workshop and Congress.* (Hansen JA and Dupont B, eds), Volume I & II, IHWG Press, Seattle, WA, 2004.

INVITED CONFERENCE/SEMINAR PRESENTATIONS BY YEAR

2021

Conference

The 5th International Workshop on the Statistical Analysis of Multi-outcome Data (SAM2021), Xian, China

9th International Forum on Statistics 2021, Beijing, China

ENAR 2021, Baltimore, Maryland (virtual)

JSM 2021, Seattle

Seminar

Stanford Biomedical Data Science seminar, Stanford University
ASA SSGG webinar
Center for Engineering MechnoBiology, University of Pennsylvania
Department of Biostatistics, University of Nebraska (public health ground rounds lecture)
Columbia Genomics Seminar, Columbia University
Epidemiology and Biostatistics, Memorial Sloan Kettering Cancer Center

2020

Conferences

Data-driven Precision Medicine and Translational Research in the Era of Big Data, St. Jude Children’s Research Hospital, Memphis, TN (virtual)
ENAR Conference, Nashville, TN (virtual)
JSM 2020, Philadelphia, PA (virtual)

Seminar

Notre Dame Science (John Lynch Lecture), University of Notre Dame
Department of Applied Mathematics and Statistics, University of Notre Dame
University of South Florida Initiative on Microbiomes (virtual)
DIPHR, Eunice Kennedy Shriver National Institute of Child Health & Human Development (virtual)

2019

Conferences

ENAR 2019 Conference, Philadelphia, PA
JSM 2019, Denver, CO
ICSA Data Science Conference, Xi Shuang Ban Na, China
ICSA International Conference, Hangzhou, China
Molecular Med TRI-CON, San Francisco, CA
Hangzhou International Conference on Frontiers of Data Sciences, Hangzhou, China
The 8th International Workshop on Compositional Data Analysis, Barcelona, Spain
University of Florida 2019 Statistics Annual Conference, Gainesville, FL
Arrowhead Translational Microbiome Conference, Boston, MA
Inaugural Harvard Chan Microbiome Symposium, Harvard University
iBRIGHT 2019: Integrative Biostatistics Research for Clinical Trials, Statistical Genetics & High-throughput omic Technologies
BIRS Workshop on “Emerging Statistical Challenges & Methods for Analysis of Human Microbiome Data”, Banff, Canada

Seminars

Department of Computational Math, Science and Engineering, Michigan State University
Center of Statistical Science, Tsinghua University, Beijing, China
Department of Biostatistics, Peking University
Department of Biostatistics, Columbia University

2018

Conferences

Joint 2018 IMS Annual Meeting / 12th International Vilnius Conference, Lithuania
XXIX International Biometrics Conference (IBC2018), Barcelona, Spain.
ENAR Conference, Atlanta, GA
Symposium on Microbiome: Hype and Hope, Seattle, WA
Respiratory Pathogens Research Center Symposium, University of Rochester
JSM 2018, Invited discussant, Vancouver, Canada
Hangzhou International Conference on Frontiers of Data Science, Hangzhou, China
10th DIA China Annual Meeting, Beijing, China
The 2nd CMS-Biocodex Microbiota Summit Forum, Shenzhen, China
The 3rd Asian American Assembly of IBD (AAA-IBD), Chengdu, China

Seminars

Department of Biostatistics, University of Washington, Seattle
Department of Global Biostatistics and Data Science, Tulane University
SJTU-Yale Joint Biostatistics Center, Shanghai Jiaotong University, Shanghai, China
Department of Statistics, Fudan University, Shanghai, China
Department of Statistics and Actuarial Science, University of Waterloo, Canada
Department of Statistics, University of Minnesota
Lilly Research Laboratories, Eli Lilly, Indianapolis, IN
Department of Biostatistics, University of Pittsburg

2017

Conferences

ENAR Conference, Washington DC
Joint Statistics Meeting (JSM), Baltimore, Maryland
Graybill Conference, Colorado State University, Fort Collins, CO
The 5th Workshop on Biostatistics and Bioinformatics, Georgia State University
ICSA Applied Statistics Symposium, Chicago, IL
Second Workshop on Statistical and Algorithmic Challenges in Microbiome Data Analysis, Broad Institute, Boston, MA
Perspectives and Analysis Methods for Personalized Medicine, IMS NUS, Singapore
Next Steps in Studying the Human Microbiome and Health in Prospective Studies Workshop, NCI/NIH, DC.
13th Annual Guelph Biomathematics and Biostatistics Symposium, Guelph, Canada
2017 International Conference on Data Science, Fudan University, Shanghai, China
Workshop on Statistical Genetics and Bioinformatics, Tsinghua University, China

Seminars

Department of Biostatistics and Bioinformatics, University of Wisconsin, Madison.
Division of Biostatistics, Northwestern University
Department of Biostatistics, MD Anderson Cancer Center
Department of Biostatistics and Bioinformatics, Duke University

Department of Global Biostatistics and Data Science, Tulane University
Center for Statistical Science, Tsinghua University, Beijing, China
School of Statistics, Renmin University of China, Beijing, China

2016

Conferences

ENAR Conference, Austin, Texas
International Biometric Conference (IBC), Victoria, Canada
Joint Statistics Meeting (JSM), Chicago
1st Workshop on Statistical and Algorithmic Challenges in Microbiome Data Analysis,
Simons Foundation, New York
4th IBS-China International Biostatistical Conference, Shanghai, China
Workshop on Fusion Learning, BFF inferences and Statistical Foundations, Rutgers
University, New Jersey
Fudan International Conference on Data Science, Shanghai, China
The 10th ICSA International Conference, Shanghai, China

Seminars

Lilly Research Laboratories, Eli Lilly, Indianapolis, IN
Takeda Pharmaceuticals, Boston, MA
Johnson and Johnson Pharmaceutical Research & Development, Spring House, PA
Department of Biostatistics, University of Florida
Center of Statistical Science, Peking University, Beijing
Department of Automation/Bioinformatics Division, Tsinghua University, Beijing
School of Statistics, Renmin University of China, Beijing
Department of Statistics, Pennsylvania State University, State College, PA
Department of Biostatistics, Yale University

2015

Conferences

ENAR Conference, Miami, Florida
Statistical Society of Canada Annual Meeting, Dalhousie University, Halifax NS, Canada
Joint Statistics Meeting, Seattle, Washington
Oberwolfach Workshop, Recent Developments in Statistical Methods with Applications
to Genetics and Genomics Workshop, Germany
Midwest Biopharmaceutical Statistics Workshop (MBSW), Bowling Green, Indiana
Informs Annual Meeting, Philadelphia

Seminars

Department of Biostatistics, University of North Carolina at Chapel Hill, North Carolina
Regeneron Genetics Center, Tarrytown, New York
Department of Biostatistics and Bioinformatics, Tulane University, Louisiana
Department of Biostatistics, Johns Hopkins University, Baltimore, Maryland
Department of Biological and Computational Statistics, Cornell University
Department of Statistics, Colorado State University
Division of Biostatistics, University of California at Berkeley

Bin Yu's group, Department of Statistics, University of California at Berkeley
Division of Biostatistics, New York University
Department of Biostatistics, University of Houston Health Center, Houston

2014

Conferences

Banff/BIRS conference on “Statistical and Computational Theory and Methodology for Big Data Analysis”, Banff, Canada
ENAR Conference, Baltimore, Maryland
Joint Statistics Meeting, Boston
Workshop “Mathematical, Statistical and Computational Aspects of the New Science of Metagenomics”, Newton Institute, Cambridge University, UK.
Bayesian Biostatistics & Bioinformatics Conference, MD Anderson Cancer Research Center, Houston
The Second International Forum on Non/Semi-parametric Statistics, Chengdu, China
Third Biostatistics Symposium, Chengdu, China
SAMSI 2014-2015 Bioinformatics Opening Workshop, Research Triangle, North Carolina
10th Anniversary Celebration of the Center for Medical Research, Medical University Graz, Austria (Keynote speaker)
Mid-Atlantic Genetic Epidemiology and Statistics (MAGES) Conference

Seminars

Lane Center for Computational Biology, Carnegie Mellon University
Department of Biostatistics, Harvard University
Department of Biostatistics, Columbia University
MRC Biostatistics Unit, Cambridge University
Section of Statistical Genetics and NORC, University of Alabama, Birmingham
Division of Biostatistics, Geisel School of Medicine, Dartmouth College, NH
Department of Biostatistics and Bioinformatics, Duke University

2013

Conferences

ENAR, Orlando, Florida
Channel meeting of the International Biometric Society, St Andrews, UK
Joint Statistics Meeting (JSM), Montreal, Canada

Seminars

Department of Biostatistics, University of Washington
Division of Public Health, Fred Hutchison Cancer Research Center
Department of Mathematics and Statistics, Boston University
Center for Bioinformatics, Boston University
Dept of Medical Statistics and Bioinformatics, Leiden University Medical Centre, Leiden, Netherlands (two lectures)
Biostatistics Branch, National Cancer Institute, Washington, DC.
Quantitative Biomedical Research Center, UT Southwestern Medical Center, Dallas, TX
Division of Biostatistics, Miami University, FL

Cancer Control Research Seminar Talk, University of Pennsylvania Perelman School of Medicine

2012

Conferences

ENAR, Washington DC

Joint Statistics Meeting, San Diego, CA

ICSA Applied Statistics Symposium, Boston, MA

5th Annual Bayesian Biostatistics Conference, MD Anderson, Houston

8th International Purdue Symposium on Statistics, Purdue University

6th Annual CEET Symposium, Villanova, PA

Workshop on Data Mining for NGS Analysis (keynote speaker), IEEE International Conference on Bioinformatics and Biomedicine (BIBM 2012), Philadelphia, PA

7th Annual MMOC & UM NORC Symposium, Ann Arbor, MI

Seminars:

Department of Statistics, Iowa State University

Division of Biostatistics, Miami University

Department of Biostatistics and Epidemiology, Michigan State University

Department of Statistics, Yale University

The University of Michigan Kidney Epidemiology and Cost Center

Department of Biostatistics and Bioinformatics, University of Wisconsin at Madison

2011

Conferences:

ICSA Applied Statistics Symposium, New York City

IMS-China International Conference on Statistics and Probability, Xian

ENAR Spring Conference, Miami Beach

ASA Joint Statistics Meeting, Miami Beach.

Workshop on High Dimensional Statistics, Massachusetts.

Banff Workshop on Current Challenges in Statistical Learning

UCLA IPAM Workshop IV: Coancestry, Association, and Population Genomics

Seminars:

Department of Biostatistics, Emory University.

Department of Statistics, Penn State University.

Department of Statistics, University of Illinois at Urbana-Champaign

Division of Biostatistics, Dartmouth College

Department of Statistics, The Wharton School, University of Pennsylvania

2010

Conferences

ENAR Conference, New Orleans, LA

ASA Joint Statistical Meeting, Vancouver, BC, Canada.

The 8th ICSA International Conference: Frontiers of Interdisciplinary and Methodological Statistical Research, Guangzhou, China
First Joint Biostatistics Symposium, Beijing
Frontiers of Statistical Decision Making and Bayes Analysis (In honor of James O. Berger), San Antonio, TX.
International Conference on Statistics and Society, Beijing, China
Probability and Statistics: An international conference in honor of P.L. Hsu's 100th Birthday, Beijing.
Frontiers in Statistics and Genetics, Penn State University Medical Center
Global Health and International Relations, Fudan University, Shanghai.
SAMSI Opening Tutorials and Workshop on Complex Networks.

Seminars:

Institute of Genetic Medicine, University of Louisville.
Biostatistics Program, Fred Hutchinson Cancer Research Center.
Department of Biostatistics, University of North Carolina Chapel Hill
Human Genetics Center and Biostatistics, University of Texas at Houston.
Department of Mathematics, Shangdong University
School of Life Science, Fudan University
Department of Health Sciences Research, Mayo Clinic
Department of Statistics, The Wharton School, University of Pennsylvania
Department of Statistics, Temple University
Department of Statistics, Sun Yat-sen University (6 hrs short course)

2009

Conferences:

ENAR conference, San Antonio, TX
ASA Joint Statistical Meeting, Washington, DC
First IMS Asia Pacific Rim Conference, Seoul, Korean
International Chinese Statistical Association Applied Statistics Symposium, San Francisco.
Workshop on “Probability and Statistics and their application to Biology”, Beijing, Peking University.
International Biostatistics Research Conference, University of Sciences and Technology of China, Hefei, China.

Seminar:

Department of Statistics, George Washington University
Department of Statistics, Purdue University (Myra Samuels Lecture)
Department of Biostatistics and Computational Biology, University of Rochester.
Department of Biological Sciences/Program in Computational Biology, University of Southern California
Department of Statistics, University of California, Irvine.

2008

Conferences:

International Biometrics Conference, Dublin, Ireland.

ENAR conference, Washington DC.
IMS-China Conference, Hangzhou
ASA Joint Statistical Meeting, Denver
International Conference on Machine Learning and Data Mining, Beijing
1st Annual Symposium on Integrative Biology, Dartmouth University
International Chinese Statistical Association Applied Statistics Symposium, New Jersey
ASA Delaware Local Chapter Meeting, Wilmington, DE.

Seminars:

Department of Statistics, University of Connecticut
Department of Statistics, University of Chicago
Department of Statistics, North Carolina State University
Department of Statistics, Temple University

2007

Conferences:

ENAR conference, Atlanta
The 2007 Taipei Statistical Symposium and ICSA International Conference, Taipei
International Conference in Bioinformatics, Hangzhou, China
Recent Development of Statistics in Biological Sciences, NHRI, Taipei.
Short Course in Statistical Genetics, ASA Philadelphia local chapter, Philadelphia
Workshop “Statistical Methods in Bioinformatics”, Munich, Germany.

Seminars:

Department of Biostatistics, University of Wisconsin at Madison.
Division of Biostatistics, Thomas Jefferson University
Department of Statistics, Fudan University, Shanghai
Institute of Biostatistics, Fudan University, Shanghai
Center for Theoretical Biology, Peking University
Department of Automation, Tsinghua University, Beijing.
Science at Edge Seminar Series, Michigan State University
Section of Biostatistics and Epidemiology, Dartmouth Medical School.
Department of Statistics, Texas A & M University
Department of Biostatistics, University of Maryland

2006

Conferences:

ENAR conference, Tampa
ICSA Applied Statistics Symposium, Connecticut
Annual Meeting of the Classification Society of North America, New Jersey
International Workshop on Applied Probability, Connecticut
Workshop on New Development of Biostatistics, National Health Research Institute,
Taiwan

Seminars:

Division of Biostatistics, University of Minnesota
Division of Biostatistics, Yale University

2005

Conferences:

Pacific Symposium on Biocomputing (selected for oral presentation), Hawaii
ENAR conference, Austin
Joint Statistical Meeting (invited talk), Minneapolis
Joint Statistical Meeting (Discussant), Minneapolis
Symposium of Longevity Consortium, California

Seminars:

Department of Biostatistics, University of Alabama, Birmingham
Department of Biostatistics, Johns Hopkins University, Baltimore
Division of Biostatistics, UC San Diego

Division of Biostatistics and Bioinformatics, National Health Research Institute, Taiwan
Department of Statistics, University of Hong Kong.
Genetics Graduate Group, University of California at Davis.
Department of Statistics, Rutgers University
Department of Biostatistics, Columbia University

2004

Conferences:

MSRI Workshop on Genetics of Complex Traits, UC Berkeley
International Conference on Analysis of Genomic Data, Boston.
International Biometrics Society Meeting (WNAR) , New Mexico
The 12th International Conference on Intelligent Systems for Molecular Biology (ISMB)
(selected for oral presentation), Glasgow, UK.
Joint Statistical Meeting, Toronto, Canada

Seminars:

Department of Biostatistics, University of Washington
Division of Biostatistics, Stanford University
Department of Biostatistics and Epidemiology, University of Pennsylvania
Statistical Genetics Group, Celera Diagnostic
Biostatistics Section, National Cancer Institute
Center for Theoretical Biology, Peking University

2003

Conferences:

Pacific Symposium on Biocomputing (selected for oral presentation), Hawaii
International Biometrics Meeting (ENAR), Tampa
Royal Statistical Theme Meeting (selected for oral presentation), Belgium
18th International Workshop on Statistical Modeling (Selected for oral presentation),
Belgium
Joint Statistical Meeting, San Francisco

IMA Microarray Data Analysis Workshop, University of Minnesota

Seminars:

Department of Biostatistics and Epidemiology, UCSF
Arcturus Applied Genomics, San Diego
Department of Statistics, Stanford University

2002

Conferences:

13th International Histocompatibility Workshop, Canada
Taipei International Statistical Symposium, Taiwan

Seminars:

Department of Biostatistics, University of Michigan
Department of Biostatistics, University of North Carolina - Chapel Hill
Division of Biostatistics, Stanford University
Department of Statistics, Hong Kong University
Department of Statistics, Chinese University of Hong Kong
Division of Biostatistics and Bioinformatics, Taiwan National Health Research Institutes

2001

Conferences:

International Biometrics meeting (ENAR), Charlotte
School of Mathematics, Peking University, Beijing (Prof Minping Qian): three lectures for
Summer School for Bioinformatics.

Seminars:

Department of Statistics (Terry Speed's Group in Genetics and Biology), University of
California-Berkeley
Department of Biostatistics and Epidemiology, University of Pennsylvania
Division of Biostatistics, University of California-Berkeley

1995-2000

Conferences:

International Symposium on Theoretical Biology – Beijing
13th Sacramento Statistics Institute, Sacramento
NIH Workshop: New Quantitative Methods to Map Genes for Complex Diseases,
California
National Institute of Environmental Health Sciences - Environmental Genome Project
Meeting, NIEHS, NC

Seminars:

Department of Statistics (Terry Speed's Group in Genetics and Biology), University of
California-Berkeley.
Department of Biostatistics, John Hopkins University
Department of Biostatistics and Epidemiology, University of California, San Francisco.

Thomson Lab, Department of Integrative Biology, UC Berkeley
Program in Human Genetics, University of California, Davis
Department of Statistics, University of Iowa
Section of Biostatistics, Mayo Clinic
Department of Biostatistics, Fox Chase Cancer Center
Division of Biostatistics, University of Minnesota