Jiehuan Sun

CONTACT
INFORMATION

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Department of Biostatistics
Yale University
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EDUCATION

Yale Univeristy, New Haven, Connecticut, USA

  PhD., Biostatistics, Expected Graduation: May 2017

Johns Hopkins Bloomberg School of Public Health, Baltimore, Maryland, USA

  ScM., Biostatistics, May 2012

Huazhong University of Science and Technology, Wuhan, Hubei, China

  B.E., Bioinformatics, June 2010

HONORS AND
AWARDS

- Conference Travel Fellowship Award, Yale Graduate Student Assembly, 2016.
- Top 10 candidates nominated by Yale University for HHMI International Student Research Fellowships, 2015.
- Kocherlakota Award from the Department of Biostatistics at Johns Hopkins Bloomberg School of Public Health, 2011.
- Title of Outstanding Student from Huazhong University of Science and Technology, 2009.
- Scholarship for Outstanding Student Leader from the Department of Bioinformatics at Huazhong University of Science and Technology, 2009.
- Scholarship for Outstanding Study Performance from the Department of Bioinformatics at Huazhong University of Science and Technology, 2006-2009.

PUBLICATIONS

Qiongshi Lu, Chentian Jin, **Jiehuan Sun**, Russell Bowler, Katerina Kechris, Naftali Kaminski, and Hongyu Zhao (2016). "Post-GWAS prioritization through data integration provides novel insights on chronic obstructive pulmonary disease." *Statistics in Biosciences, in press.*

Qiongshi Lu, Yiming Hu, **Jiehuan Sun**, Yuwei Cheng, Kei-Hoi Cheung, Hongyu Zhao (2015). "A statistical framework to predict functional non-coding regions in the human genome through integrated analysis of diverse types of annotation data. *Scientific Reports 5: 10576.*

Jiehuan Sun and Hongyu Zhao (2015). "The application of sparse estimation of covariance matrix to quadratic discriminant analysis. *BMC bioinformatics 16(1): 48.*

Jiehuan Sun, Xintao Hu, Xiu Huang, Yang Liu, Kaiming Li, Xiang Li, Junwei Han, Lei Guo, Tianming Liu, and Jing Zhang (2012). "Inferring consistent functional interaction patterns from natural stimulus FMRI data." *NeuroImage 61(4): 987-999.*

Jian Yu, Xiaobin Xing, Lingyao Zeng, **Jiehuan Sun**, Wei Li, Han Sun, Ying He, Jing Li, Guoqing Zhang, Chuan Wang, Yixue Li, and Lu Xie (2012). "SyStemCell: a database populated with multiple levels of experimental data from stem cell differentiation research." *PloS one 7(7): e35230.*

MANUSCRIPTS

*: Co-first author

Jiehuan Sun, Jose D. Herazo-Maya, Xiu Huang, Naftali Kaminski, and Hongyu Zhao. "Distance-correlation based gene set analysis in longitudinal studies". (Under revision at Annals of Applied Statistics)

Jiehuan Sun, Joshua L. Warren, and Hongyu Zhao. "A Bayesian semiparametric factor analysis model for subtype identification". (Under revision at Statistical Applications in Genetics and Molecular Biology)

Jiehuan Sun, Jose D. Herazo-Maya, Naftali Kaminski, Hongyu Zhao, and Joshua L. Warren. "A dirichlet process mixture model for clustering longitudinal gene expression data". (Under review at Journal of the Royal Statistical Society: Series C)

Jose D. Herazo-Maya*, **Jiehuan Sun***, Philip Molyneaux, Julian Villalba-Nunez, Argyrios Tzouvelekis, Qin Li, Heather Lynn, Brenda M. Juan-Guardela, Xiting Yan, George Michel, Nachelle Aurelien, Kathleen O. Lindell, Melinda J. Klesen, Yingze Zhang, Hongyu Zhao, Joe GN Garcia, Imre Noth, Antje Prasse, Ziv Bar-Joseph, Kevin F. Gibson, Erica Herzog, Ivan O. Rosas, Toby Maher, and Naftali Kaminski. "A 52-gene signature in peripheral blood identifies a genomic profile associated with increased risk of mortality and poor disease outcomes in Idiopathic Pulmonary Fibrosis". (Under review at The Journal of the American Medical Association)

Molei Liu*, **Jiehuan Sun***, Jose D. Herazo-Maya, Naftali Kaminski, and Hongyu Zhao. "Joint models for time-to-event data and longitudinal biomarkers of high dimension".

Jiehuan Sun, Tianqi Liu, Jose D. Herazo-Maya, Kuang-Yao Lee, Naftali Kaminski, and Hongyu Zhao. "Sure independence feature screening for longitudinal biomarkers and a survival outcome".

MEMBERSHIP
- American Statistical Association

PRESENTATIONS
- "A Dirichlet Process Mixture Model for Clustering Longitudinal Gene Expression Data", *Joint Statistical Meetings (JSM)* **July 30 - August 4, 2016**.
- (**Invited**) "Discovery of Novel Loci Associated with COPD by Pooling Information from Related Clinical Feature and Functional Annotation", *Eastern North American Region (ENAR) Spring Meeting* **March 6-9, 2016**.
- "Discovery of Novel Loci Associated with COPD by Pooling Information from Related Clinical Feature and Functional Annotation", *Bioinformatics Transition Workshop - SAMSI* **May 11-13, 2015**.
- "The application of sparse estimation of covariance matrix to quadratic discriminant analysis", *The 29th New England Statistics Symposium* **April 24-25, 2015**.
- "Discovery of Novel Loci Associated with COPD by Pooling Information from Case-control status, Related Clinical Feature, and Functional Annotation", *Statistical and Computational Challeges in Omics Data Integration workshop - SAMSI* **Feb. 16-17, 2015**.

TEACHING EXPERIENCE
Yale University, New Haven, Connecticut, USA

Teaching Assistant **Jan. 2015 - May. 2015**
Course: Longitudinal and Multilevel Data Analysis.

Teaching Assistant **Jan. 2015 - May. 2015**
Course: Theory of Survival Analysis.

Teaching Assistant **Sept. 2014 - Dec. 2014**
Course: Categorical Data Analysis.

Teaching Assistant **Sept. 2013 - Dec. 2013**
Course: Categorical Data Analysis.

Johns Hopkins Bloomberg School of Public Health, Baltimore, Maryland, USA

Tutor **Nov. 2011 - Jan. 2012**
Course: Essentials Of Probability And Statistical Inference II: Statistical Inference.

Teaching Assistant **Sept. 2011 - May 2012**
Course: Methods in Biostatistics, 650 series.

Computer Skills
- Statistical Softwares: proficient in R; some experience with SAS and Matlab.
- Languages: proficient in C, C++, Perl, Unix shell script.
- Applications: Office Microsoft, LaTeX, etc.
- Operating Systems: Unix/Linux, Windows.