

ZHIGUANG (CALEB) HUO

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EDUCATION

University of Pittsburgh,

Pittsburgh, PA, US

- Ph.D. in [Biostatistics](#), *April 2017*
 - Dissertation: *Statistical integrative omics methods for disease subtype discovery*
 - GPA: *3.93/4.00*
 - Advisors: [George C. Tseng, ScD](#) and [Yong Seok Park, PhD](#)
- M.S. in [Physics](#), *Apr 2012*
 - GPA: *3.86/4.00*

Harbin Institute of Technology,

Harbin, Heilongjiang, China

- B.S. in [Physics](#), *June 2011*
 - GPA: *90.43/100*

RESEARCH INTEREST

My research interest lies in the intersection between statistical methodology and its applications to genomics and bioinformatics. I am particularly interested in genomic data integration, models and variable selection in high-dimensional data, graphical models, Bayesian methods, optimization and statistical computing. I have collaborated with biologists in the fields of cancer and psychiatry, analyzing a broad range of genomic data. These experiences motivate me to develop methodology and software that are practical, user-friendly and easy to use.

PROFESSIONAL EXPERIENCE

- Assistant Professor *July 2017 ~ Now*
 - Department of Biostatistics, University of Florida

PUBLICATIONS

2018

1. **Zhiguang Huo**, Yun Zhu, Lei Yu, Jingyun Yang, Philip De Jager, David A. Bennett, Jinying Zhao (2018). Altered DNA methylation variability associated with Alzheimer's Disease. (Submitted)
2. Wang, Kai Wen, Xiangrui Zeng, Xiaodan Liang, **Zhiguang Huo**, Eric P. Xing, and Min Xu (2018). Image-derived generative modeling of pseudo-macromolecular structures-towards the statistical assessment of Electron CryoTomography template matching. (Submitted)
3. Cynthia R. Johnson, Kimberly Brown, Susan Hyman, Maria M. Brooks, Courtney Aponte, Lynne Levato, Brianna Schmidt, Victoria Evans, **Zhiguang Huo**, Roxanna Bendixen, Heather Eng, Theresa Sax, Tristram Smith (2018). Parent Training for Feeding Problems in Children with Autism Spectrum Disorder: Initial Randomized Trial. (Submitted)
4. Li Zhu, **Zhiguang Huo**, Tianzhou Ma, George Tseng (2018). Bayesian indicator variable selection to incorporate multi-layer overlapping group structure in multi-omics applications. (Submitted)
5. **Zhiguang Huo***, Li Zhu, Tianzhou Ma, Hongcheng Liu, Song Han, Daiqing Liao, Jinying Zhao and George Tseng* (2018). Two-way Horizontal and Vertical Omics Integration for Disease Subtype Discovery. (Submitted, rejected by *Bioinformatics*, rejected by *Nucleic Acids Research*) (*: co-corresponding author).

⁰Last modified: July 1, 2018

6. Tianzhou Ma[†], **Zhiguang Huo**[†], Anche Kuo[†], Li Zhu, Fang Zhou, Xiangrui Zeng, Chien-Wei Lin, Silvia Liu, Lin Wang, Tanbin Rahman, Lun-Ching Chang, Sunghwan Kim, Jia Li, Yongseok Park, Chi Song and George C. Tseng. (2018). MetaOmics - Comprehensive Analysis Pipeline and Web-based Software Suite for Transcriptomic Meta-Analysis. (Submitted) ([†]: co-first author).
7. **Zhiguang Huo**, Shaowu Tang, Yongseok Park, George Tseng. (2018) P-value evaluation, variability index and biomarker categorization for adaptively weighted Fisher's meta-analysis method in omics applications. (Submitted, rejected by *the Annals of Applied Statistics*, rejected by *Biostatistics*, rejected by *Journal of Computational and Graphical Statistics*)
8. Marianne Seney, **Zhiguang Huo**, Kelly Cahill, Leon French, Rachel Puralewski, Joyce Zhang, Ryan W. Logan, George Tseng, David A Lewis, Etienne Sibille. (2018) Opposite molecular signatures of depression in men and women. *Biological Psychiatry*
9. **Zhiguang Huo**, Chi Song, George C. Tseng. (2018) Bayesian latent hierarchical model for transcriptomic meta-analysis to detect biomarkers with clustered meta-patterns of differential expression signals. *Annals of Applied Statistics* (Accepted).
10. Kelly Cahill[†], **Zhiguang Huo**[†], George Tseng, Ryan W. Logan*, Marianne L. Seney* (2018), Improved identification of concordant and discordant gene expression signatures using an updated rank-rank hypergeometric overlap approach. *Scientific Reports* 8.1 (2018): 9588. ([†]: co-first author, *: co-corresponding author).

2017

11. SungHwan Kim, Dongwan Kang, **Zhiguang Huo**, Yongseok Park, George C. Tseng. (2017) Meta-analytic principal component analysis in integrative omics application. *Bioinformatics*, 1, 8.
12. Enwright, John, **Zhiguang Huo**, Dominique Arion, John Corradi, Aiqing He, George Tseng, and David Lewis. (2017) Transcriptome alterations of prefrontal cortical parvalbumin neurons in schizophrenia. *Molecular Psychiatry*.
13. **Zhiguang Huo**, George C. Tseng. (2017) Integrative Sparse K -means with overlapping group lasso in genomic applications for disease subtype discovery. *The Annals of Applied Statistics*, 11(2), 1011-1039.
14. Dominique Arion, **Zhiguang Huo**, John F. Enwright, John P. Corradi, George Tseng and David A. Lewis. (2017) Transcriptome alterations in prefrontal pyramidal neurons distinguish schizophrenia from bipolar and major depressive disorders. *Biological Psychiatry*.

2016

15. **Zhiguang Huo**, Ying Ding, Silvia Liu, Steffi Oesterreich, and George Tseng. Meta-Analytic Framework for Sparse K -Means to Identify Disease Subtypes in Multiple Transcriptomic Studies. *Journal of the American Statistical Association*, 111, no. 513 (2016): 27-42.
16. Zhu, Li, Ying Ding, Cho-Yi Chen, Lin Wang, **Zhiguang Huo**, SungHwan Kim, Christos Sotiriou, Steffi Oesterreich, and George C. Tseng. "MetaDCN: meta-analysis framework for differential co-expression network detection with an application in breast cancer." *Bioinformatics* (2016): btw788.

2015 and before

17. Silvia Liu, Wei-Hsiang Tsai, Ying Ding, Rui Chen, Zhou Fang, **Zhiguang Huo**, SungHwan Kim, Tianzhou Ma, Ting-Yu Chang, Nolan Michael Priedigkeit, Adrian V. Lee, Jianhua Luo, Hsei-Wei Wang, I-Fang Chung, George C. Tseng. (2015). Comprehensive evaluation of fusion transcript detection algorithms and a meta-caller to combine top performing methods in paired-end RNA-seq data. *Nucleic Acids Research*, 10.1093/nar/gkv1234.
18. Tiffany A. Katz, Serena G. Liao, Vincent J. Palmieri, Robert K. Dearth, Thushangi Pathiraja, **Zhiguang Huo**, Patricia Shaw, Sarah Small, Nancy E. Davidson, David G. Peters, George C. Tseng, Steffi Oesterreich, Adrian V. Lee. (2015) Targeted DNA Methylation Screen in the Mouse Mammary Genome Reveals a Parity-Induced Hypermethylation of IGF1R That Persists Long after Parturition. *Cancer Prevention Research* 8, no. 10 (2015): 1000-1009.

19. Yan P. Yu, Silvia Liu, **Zhiguang Huo**, Amantha Martin, Joel B. Nelson, George C. Tseng and Jian-Hua Luo. (2015) Genomic copy number variations in the genomes of leukocytes predict prostate cancer clinical outcomes. *PloS one*, 10(8):e0135982.
20. SungHwan Kim, **Zhiguang Huo**, YongSeok Park and George Tseng. (2015) MetaOmics: transcriptomic meta-analysis methods for biomarker detection, pathway analysis and other exploratory purposes. Book chapter in Integrating omics data: statistical and computational methods. Edited by George C. Tseng, Debashis Ghosh, Xianghong Jasmine Zhou. *Cambridge University Press*. Page 39-67.
21. Xingbin Wang, Dongwan Kang, Kui Shen, Chi Song, Shuya Lu, Lunching Chang, Serena G. Liao, **Zhiguang Huo**, Naftali Kaminski, Etienne Sibille, Yan Lin, Jia Li and George C. Tseng. (2012) A Suite of R Packages for Quality Control, Differentially Expressed Gene and Enriched Pathway Detection in Microarray Meta-analysis. *Bioinformatics*, 28:2534-2536.

AWARD

Student Awards

- Delta Omega Membership April 2017
- American Statistics Association (ASA) Pittsburgh chapter March 2016
 - Student of the year
- Department of Physics, Harbin Institute of Technology May 2009
 - National Scholarship of P.R. China.
 - (Awarded to the top 2 students in my Bachelors degree.)

Travel Awards

- 2018 ASA Biometrics Section JSM Travel Award, Vancouver, BC, Canada. Aug 2018
- Objective Bayes meeting 2017 travel award, Austin, TX. Dec 2017
- SAMSI, Research Triangle Park, NC.
 - Interface of Statistics and Optimization Feb 2017
 - Optimization Summer School Aug 2016
 - Epigenetics Workshop Mar 2015
 - Beyond Bioinformatics Workshop June 2014

TEACHING EXPERIENCE

Lecturer, University of Florida

- PHC6937 - Frontiers in Biostatistics Feb 2018
- PHC6068 - Biostatistical computing Fall 2017

Lecturer, University of Pittsburgh

- BIOST2094 - Advanced R Computing – (with Tianzhou Ma) Spring 2017
- BIOST2025 - Special Studies in Bayesian Data Analysis Fall 2016
 - (with George Tseng, Tianzhou Ma and Li Zhu)

Guest Lecturer, University of Pittsburgh

- BIOST2055 - Introductory high-throughput genomic data analysis I: data mining and applications Mar 2016
 - Differential and isoform analysis of RNA-seq data
- BIOST2078 - Introductory high-throughput genomic data analysis II: theories and algorithms Dec 2015
 - Reproducible research and parallel computing in R

- BIOST2078 - Introductory high-throughput genomic data analysis II:
theories and algorithms Dec 2014
- Reproducible research

Teaching Assistant, University of Pittsburgh

- BIOST 2078 - Introductory high-throughput genomic data analysis II:
theories and algorithms Fall 2014
- PHYS 0212 - Introduction to Laboratory Physics Spring 2012
- PHYS 0212 - Introduction to Laboratory Physics Fall 2011

PRESENTATIONS

Invited Oral Presentation

- Joint Statistical Meetings, Vancouver, BC, Canada August 2018
- Bayesian meta-analysis for biomarkers of meta-patterns.
- International Chinese Statistical Association conference, New Brunswick, NJ June 2018
- Two-way Horizontal and Vertical Omics Integration for Disease Subtype Discovery.
- Rush Alzheimer's Disease Center ROSMAP Investigator's Meeting, Chicago, IL May 2018
- Identifying variably methylated regions (VMRs) associated with AD.
- International Indian Statistical Association conference, Gainesville, FL May 2018
- Two-way Horizontal and Vertical Omics Integration for Disease Subtype Discovery.
- Department of Biostatistics, University of Florida, Gainesville, FL Feb 2017
- Meta-analytic and integrative framework for sparse K -means to identify disease subtypes.

Contributed Poster and Oral Presentation

- Poster, ENAR conference, Atlanta, GA Mar 2018
- p-value evaluation, variability index and biomarker categorization for adaptively weighted Fisher's meta-analysis method in omics applications
- Poster, 2018 UF Stats Winter Workshop, University of Florida, Gainesville, FL Jan 2018
- Bayesian latent hierarchical model for transcriptomic meta-analysis to detect biomarkers with clustered meta-patterns of differential expression signals
- Poster, Objective Bayes meeting 2017, University of Texas, Austin, TX Dec 2017
- Bayesian latent hierarchical model for transcriptomic meta-analysis to detect biomarkers with clustered meta-patterns of differential expression signals
- Poster, Dean's Day's competition, GSPH, University of Pittsburgh April 2017
- Circadian rhythms of gene expression in the human prefrontal cortex reveal distinct pattern between schizophrenia and control subjects
- Oral Presentation, ENAR, Washington, DC Mar 2017
- Bayesian latent hierarchical model for transcriptomic meta-analysis to detect biomarkers with clustered meta-patterns of differential expression signals.
- Poster, SAMSI optimization summer school, Research Triangle Park, NC Aug 2016
- Integrative Sparse K -means for disease subtype discovery using multi-level omics data.
- Poster, Pittsburgh ASA banquet, Pittsburgh, PA Mar 2016
- Integrative Sparse K -means for disease subtype discovery using multi-level omics data.
- Department of Biostatistics, University of Pittsburgh Nov 2015
- How to use Latex to make slides
- Oral Presentation, JSM, Seattle, WA Aug 2015
- Meta-analytic framework for sparse K -means to identify disease subtypes in multiple transcriptomic studies.

- Poster, Pittsburgh ASA banquet, Pittsburgh, PA Apr 2015
 - Meta-analytic framework for sparse K -means to identify disease subtypes in multiple transcriptomic studies.
- Oral Presentation, ENAR Conference, Miami, FL Mar 2015
 - Meta-analytic framework for sparse K -means to identify disease subtypes in multiple transcriptomic studies.
- Poster, Dean's Day's competition, GSPH, University of Pittsburgh Mar 2015
 - Discover and Characterize Invasive Lobular Breast Carcinoma Subtypes.
- Oral Presentation, ENAR Conference, Baltimore, MA Mar 2014
 - Meta-analytic framework for sparse K -means to identify disease subtypes in multiple transcriptomic studies.
- Poster, Dean's Day's competition, GSPH, University of Pittsburgh Mar 2014
 - Meta-analytic framework for sparse K -means to identify disease subtypes in multiple transcriptomic studies.

CONFERENCE SERVICE

- ICSA, New Brunswick, NJ June 2018
 - Chair for Session New developments in microbiome sequencing data modeling and analysis.
 - Chair for Session Modern Statistical Development for Biomedical Big data.

REVIEWER SERVICE

- Journal of the American Statistical Association (1)
- Journal of the Royal Statistical Society Series C (1)
- Bioinformatics (1)
- BMC Bioinformatics (1)
- PLOS ONE (2)
- Scientific Reports (2)

DEPARTMENT SERVICE

- Member of PhD Qualifying Exam committee Jan 2018 ~ Now
 - Department of Biostatistics, University of Florida
- Director of the Biostatistics Consulting Lab Sep 2017 ~ Now
 - Department of Biostatistics, University of Florida

MEMBERSHIP

- Member of International Chinese Statistical Association Mar 2015 ~ Now
- Member of Eastern North American Region International Biometric Society Oct 2013 ~ Now
- Member of American Statistical Association Nov 2013 ~ Now

HOBBIES

Running, skiing, other endurance activities.

Running Record

- Dick's Sporting Goods Pittsburgh half Marathon, Pittsburgh, PA. 05/06/2018
- Five Points of Life Race Marathon, Gainesville, FL. 02/18/2018
- Bank of America Chicago Marathon, Chicago, IL. 10/09/2016
- First National Bank Pittsburgh Triathlon (Sprint), Pittsburgh, PA 08/14/2016
- Dick's Sporting Goods Pittsburgh Marathon, Pittsburgh, PA. 05/01/2016
- First National Bank Pittsburgh Triathlon (Olympic standard), Pittsburgh, PA 08/09/2015
- Dick's Sporting Goods Pittsburgh Marathon, Pittsburgh, PA 05/03/2015

- Dick's Sporting Goods Pittsburgh Marathon, Pittsburgh, PA
- Dick's Sporting Goods Pittsburgh Marathon, Pittsburgh, PA

05/04/2014

05/05/2013