ZHIGUANG (CALEB) HUO

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https://caleb-huo.github.io

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

• Director of the Biostatistics Consulting Lab

Sep $2017 \sim Now$

- Department of Biostatistics, University of Florida
- Assistant Professor

July $2017 \sim Now$

- Department of Biostatistics, University of Florida

PUBLICATIONS

2018

- 1. 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)
- 2. 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. (Submitted) (†: co-first author, *: co-coresponding author).
- 3. 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)

⁰Last modified: April 4, 2018

- 4. **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 to *Bioinformatics* (Under revision) (*: co-corresponding author).
- 5. 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).
- 6. **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)
- 7. 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* (accepted)
- 8. **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. Submitted to *Annals of Applied Statistics* (under revision).

2017

- 9. SungHwan Kim, Dongwan Kang, **Zhiguang Huo**, Yongseok Park, George C. Tseng. (2017) Meta-analytic principal component analysis in integrative omics application. *Bioinformatics*, 1, 8.
- 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.
- 11. **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.
- 12. 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

- 13. **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.
- 14. 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

- 15. 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.
- 16. 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.
- 17. 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.
- 18. 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.
- 19. 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

AWARD	
Student Awards	
 Delta Omega Membership American Statistics Association (ASA) Pittsburgh chapter Student of the year Department of Physics, Harbin Institute of Technology 	April 2017 March 2016 May 2009
 National Scholarship of P.R. China. (Awarded to the top 2 students in my Bachelors degree.) 	
Travel Awards	
\bullet 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 Optimization Summer School Epigenetics Workshop Beyond Bioinformatics Workshop 	Feb 2017 Aug 2016 Mar 2015 June 2014
TEACHING EXPERIENCE	
Lecturer, University of Florida	
 PHC6937 - Frontiers in Biostatistics PHC6068 - Biostatistical computing 	Feb 2018 Fall 2017
Lecturer, University of Pittsburgh	
 BIOST2094 - Advanced R Computing – (with Tianzhou Ma) BIOST2025 - Special Studies in Bayesian Data Analysis – (with George Tseng, Tianzhou Ma and Li Zhu) 	Spring 2017 Fall 2016
Guest Lecturer, University of Pittsburgh	
 BIOST2055 - Introductory high-throughput genomic data analysis I: data mining and applications Differential and isoform analysis of RNA-seq data 	Mar 2016
 BIOST2078 - Introductory high-throughput genomic data analysis II: theories and algorithms Reproducible research and parallel computing in R 	Dec 2015
 BIOST2078 - Introductory high-throughput genomic data analysis II: theories and algorithms Reproducible research 	Dec 2014

Teaching Assistant, University of Pittsburgh

theories and algorithms

• BIOST 2078 - Introductory high-throughput genomic data analysis II:

 PHYS 0212 - Introduction to Laboratory Physics PHYS 0212 - Introduction to Laboratory Physics 	Spring 2012 Fall 2011
PRESENTATIONS	
Poster and Oral Presentation	
 Poster, 2018 UF Stats Winter Workshop, University of Florida, Gainesville, FL Bayesian latent hierarchical model for transcriptomic meta-analysis to detect biomarkers with clustered meta-patterns of differential expression signals 	Jan 2018
 Poster, Objective Bayes meeting 2017, University of Texas, Austin, TX Bayesian latent hierarchical model for transcriptomic meta-analysis to detect biomarkers with clustered meta-patterns of differential expression signals 	Dec 2017
 Poster, Dean's Day's competition, GSPH, University of Pittsburgh Circadian rhythms of gene expression in the human prefrontal cortex reveal distinct pattern between schizophrenia and control subjects 	April 2017
 Invited talk, University of Florida, Gainesville, FL Meta-analytic and integrative framework for sparse K-means to identify disease subtypes. 	Feb 2017
 Poster, SAMSI optimization summer school, Research Triangle Park, NC Integrative Sparse K-means for disease subtype discovery using multi-level omics data. 	Aug 2016
 Poster, Pittsburgh ASA banquet, Pittsburgh, PA Integrative Sparse K-means for disease subtype discovery using multi-level omics data. 	Mar 2016
 Department of Biostatistics, University of Pittsburgh How to use Latex to make slides 	Nov 2015
 Oral Presentation, JSM, Seattle, WA Meta-analytic framework for sparse K-means to identify disease subtypes in multiple transcriptomic studies. 	Aug 2015
 Poster, Pittsburgh ASA banquet, Pittsburgh, PA Meta-analytic framework for sparse K-means to identify disease subtypes in multiple transcriptomic studies. 	Apr 2015
 Oral Presentation, ENAR Conference, Miami, FL Meta-analytic framework for sparse K-means to identify disease subtypes in multiple transcriptomic studies. 	Mar 2015
 Poster, Dean's Day's competition, GSPH, University of Pittsburgh Discover and Characterize Invasive Lobular Breast Carcinoma Subtypes. 	Mar 2015
 Oral Presentation, ENAR Conference, Baltimore, MA Meta-analytic framework for sparse K-means to identify disease subtypes in multiple transcriptomic studies. 	Mar 2014
 Poster, Dean's Day's competition, GSPH, University of Pittsburgh Meta-analytic framework for sparse K-means to identify disease 	Mar 2014

Fall 2014

REVIEWER SERVICE

• Journal of the Royal Statistical Society Series C (1)

subtypes in multiple transcriptomic studies.

- Bioinformatics (1)
- BMC Bioinformatics (1)

- PLOS ONE (2)
- Scientific Reports (2)

MEMBERSHIP

• Member of International Chinese Statistical Association	$Mar~2015 \sim Now$
• Member of Eastern North American Region International Biometric Society	$Oct\ 2013 \sim Now$
• Member of American Statistical Association	$Nov \ 2013 \sim Now$

HOBBIES

Running, skiing, other endurance activities.

Running Record

• Dick's Sporting Goods Pittsburgh 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	05/04/2014
• Dick's Sporting Goods Pittsburgh Marathon, Pittsburgh, PA	05/05/2013