ZHIGUANG (CALEB) HUO

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http://www.pitt.edu/~zhh18/dev/

EDUCATION

University of Pittsburgh,

Pittsburgh, PA, US

• Ph.D. in Biostatistics, Expected:

Summer 2017

- Dissertation: Statistical integrative omics methods for disease subtype discovery and methods for single cell methylation
- 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.

PUBLICATIONS

Methodology

- 1. **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.
- 2. **Zhiguang Huo**, Chi Song, George C. Tseng. (2016) 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 second round of review).
- 3. **Zhiguang Huo**, George C. Tseng. (2016) Integrative Sparse K-means with overlapping group lasso in genomic applications for disease subtype discovery. Submitted to *Annals of Applied Statistics* (under second round of review).
- 4. 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.
- 5. SungHwan Kim, Dongwan Kang, **Zhiguang Huo**, Yongseok Park, George C. Tseng. (2016) Meta-analytic principal component analysis in integrative omics application. (Submitted).
- 6. 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.

 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.

Application

- 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. Submitted
- 9. 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. Submitted to *Biological Psychiatry*, (under second round of review).
- 10. 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.
- 11. 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.

Manuscript in Preparation

• Methodology

- 12. **Zhiguang Huo**, Shaowu Tang, YongSeok Park and George Tseng. (2017) Biomarker categorization and fast computing of adaptively weighted Fisher's method for meta-analysis in omics applications.
- 13. YongSeok Park, **Zhiguang Huo**, Shaowu Tang and George Tseng. (2017) Asymptotic properties of adaptive weighted Fisher's method.
- 14. Li Zhu, **Zhiguang Huo**, Tianzhou Ma, George Tseng. (2017) Bayesian indicator variable selection model with multi-layer overlapping groups.
- 15. Tianzhou Ma*, **Zhiguang Huo***, Anche Kuo*, Xiangrui Zeng, Li Zhu, Ark Fang, Lin Wang, Chien-Wei Lin, Tanbin Rahman, Shuchang Liu, YongSeok Park, Sunghwan Kim, Jia Li, Lun-Ching Chang, Chi Song, George Tseng. (2017) MetaOmics a Comprehensive Software Suite with Interactive Visualization for Transcriptomic Meta-Analysis. (*: co-first author).

• Application

- 16. Logan, R.W., Ozburn, A.R., **Huo, Z.**, Zhu, X., Fitzgerald, E., Arey, R.N., Jarpe, M., Tseng, G. and McClung, C.A. (2017) Valproic acid targets HDAC2 to normalize mania-like behaviors in mice. In preparation.
- 17. Rachel Puralewski, **Zhiguang Huo**, George Tseng, Ryan Logan, Marianne Seney. (2017) Sex differences in basolateral amygdala transcriptome associated with effects of chronic stress. In preparation.
- 18. **Zhiguang Huo**, Rachel Puralewski, George Tseng, Ryan Logan, Marianne Seney. (2017) Circuitwide transcriptional profiling reveals sex differences in coherence patterns across brain regions. In preparation.

Book

19. George C. Tseng, **Zhiguang Huo** and Tianzhou Ma. (2017) Foundations for High-Throughput Omics Data Analysis: Methods, Theories and Applications. *Chapman & Hall/CRC*. (Under preparation).

Book Chapter

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.

AWARD

Student Awards

• 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

• 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 (UNIVERSITY OF PITTSBURGH)

Main Lecturer (teaching fellow)

• 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

• 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

 $\mathrm{Dec}\ 2014$

- Reproducible research

Teaching Assistant

PRESENTATIONS

Poster and Oral Presentation

• 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.	
• 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.	M 0015
• Poster, Dean's Day's competition, GSPH, University of Pittsburgh	Mar 2015
- Discover and Characterize Invasive Lobular Breast Carcinoma Subtypes.	Man 2014
 Oral Presentation, ENAR Conference, Baltimore, MA Meta-analytic framework for sparse K-means to identify disease 	Mar 2014
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	Wiai 2014
subtypes in multiple transcriptomic studies.	
Seminar Talk	
• Department of Biostatistics, University of Pittsburgh	Nov 2015
- How to use Latex to make slides	
OBBIES	
Running, skiing, other endurance activities.	
Running Record	

HOB

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• 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