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,

- GPA: 3.86/4.00

Harbin Institute of Technology,

Harbin, Heilongjiang, China

• B.S. in Physics,

June 2011

Apr 2012

- GPA: 90.43/100

RESEARCH INTEREST

My research interest lies in both statistical methodology and application on genomics and bioinformatics. I am particularly interested in genomic data integration, modeling and variable selection in high-dimensional data, graphical model, Bayesian methods, optimization and statistical computing. I have collaborated with biologists in the fields of cancer and psychiatry to analysis a broad range of genomic data, which motivates me to develop practical methodology and user-friendly software.

PUBLICATIONS

Methydology

- 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 for disease subtype discovery using multi-level omics data. Submitted to Annals of Applied Statistics (under second round of review).
- 4. Li Zhu, Ying Ding, Cho-Yi Chen, Lin Wang, **Zhiguang Huo**, SungHwan Kim, Christos Sotiriou, Steffi Oesterreich and George C. Tseng. (2016) MetaDCN: meta-analysis framework for differential coexpression network detection with an application in breast cancer. *Bioinformatics* (accepted).
- 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. Dominique Arion, **Zhiguang Huo**, John F. Enwright, John P. Corradi, George Tseng and David A. Lewis. (2016) Transcriptome alterations in prefrontal pyramidal neurons distinguish schizophrenia from bipolar and major depressive disorders. Submitted to *Biological Psychiatry*, (under second round of review).
- 9. 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.
- 10. 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

Methydology

- 11. **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.
- 12. Li Zhu, **Zhiguang Huo**, Tianzhou Ma, George Tseng. (2017) Bayesian indicator variable selection model with multi-layer overlapping groups.
- 13. Tianzhou Ma, **Zhiguang Huo**, ..., George Tseng. MetaOmics a Comprehensive Software Suite with Interactive Visualization for Transcriptomic Meta-Analysis.
- 14. AW theory

• Application

- 15. Enwright, John, Dominique Arion, John Corradi, Aiqing He, **Zhiguang Huo**, George Tseng, and David Lewis. Transcriptome Profiling of Layer 3 Parvalbumin Neurons from the Dorsolateral Prefrontal Cortex of Schizophrenia Subjects.
- 16. RNAseq96 from Marianne.
- 17. iPSC Ryan.

Book

18. 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

19. 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	March 2010
• 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.	
- Optimization Summer School	Aug 2016
- Epigenetics Workshop	Mar 2015 June 2014
- 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 – (with George Tseng, Tianzhou Ma and Li Zhu) 	Fall 2016
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	Dec 2019
\bullet BIOST2078 - Introductory high-throughput genomic data analysis II:	
theories and algorithms — Reproducible research	Dec 2014
Teaching assistant	
• BIOST 2078 - Introductory high-throughput genomic data analysis II: theories and algorithms	Sep 2014 - Dec 2014
• PHYS 0212 - Introduction to Laboratory Physics	Jan 2012 - Apr 2012
• PHYS 0212 - Introduction to Laboratory Physics	Aug 2011 - Dec 2011
PRESENTATIONS	
Poster and oral presentation	
\bullet 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
 Oral Presentation, JSM, Seattle, WA Meta-analytic framework for sparse K-means to identify disease 	Aug 2015
subtypes in multiple transcriptomic studies.	
Poster, Pittsburgh ASA banquet, Pittsburgh, PA Mote applytic framework for approx K manns to identify disease.	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.

Seminar talk

• Department of Biostatistics, University of Pittsburgh

Nov 2015

- How to use Latex to make slides

REFERENCES

George C. Tseng

Professor Phone: 412-624-5318

Department of Biostatistics (primary appointment)

Department of Human Genetics

Department of Computational & Systems Biology E-mail: ctseng@pitt.edu

University of Pittsburgh

Yong Seok Park

Assistant Professor Phone: 412-624-3028
Department of Biostatistics E-mail: yongpark@pitt.edu

University of Pittsburgh

David A. Lewis, MD

Distinguished Professor of Psychiatry and Neuroscience,

Thomas Detre Professor of Academic Psychiatry, Chair Phone: 412-246-6010

Department of Psychiatry E-mail: lewisda@upmc.edu

University of Pittsburgh

HOBBIES

Running, skiing, endurance activities.

Running record

TIME 4:48:49

• Bank of America Chicago Marathon, Chicago, IL. TIME 04:08:27	10/09/2016
• First National Bank Pittsburgh Triathlon (Sprint), Pittsburgh, PA	08/14/2016
TIME 1:10:30 (only biking + running)	
• Dick's Sporting Goods Pittsburgh Marathon, Pittsburgh, PA. TIME 3:58:46	05/01/2016
• First National Bank Pittsburgh Triathlon (Olympic standard), Pittsburgh, PA	08/09/2015
Time 3:29:24	
• Dick's Sporting Goods Pittsburgh Marathon, Pittsburgh, PA	05/03/2015
TIME 3:49:38	
• Dick's Sporting Goods Pittsburgh Marathon, Pittsburgh, PA	05/04/2014
TIME 4:07:44	
• Dick's Sporting Goods Pittsburgh Marathon, Pittsburgh, PA	05/05/2013