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

PUBLICATIONS

2018

1. 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)
2. **Zhiguang Huo***, Li Zhu, Tianzhou Ma, Song Han, Daiqing Liao, Jinying Zhao and George Tseng* (2018). Two-way Horizontal and Vertical Omics Integration for Disease Subtype Discovery. (Submitted) (*: co-corresponding author).
3. 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).
4. **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)

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5. 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)
6. **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

7. SungHwan Kim, Dongwan Kang, **Zhiguang Huo**, Yongseok Park, George C. Tseng. (2017) Meta-analytic principal component analysis in integrative omics application. *Bioinformatics*, 1, 8.
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.*
9. **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.
10. 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

11. **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.
12. 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

13. 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.
14. 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.
15. 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.
16. 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.
17. 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

Poster and Oral Presentation

- 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
- Invited talk, University of Florida, Gainesville, FL — Feb 2017
  - – Meta-analytic and integrative framework for sparse K-means to identify disease subtypes.
- 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.

REVIEWER SERVICE

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

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 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