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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. 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.

7. 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

- **Methodology**

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***, Anche Kuo*, Xiangrui Zeng, Li Zhu, Ark Fang, Lin Wang, Chien-Wei Lin, Tanbin Rahman, Shuchang Liu, YongSeok Park, Sunghwan Kim, George Tseng. (2017) MetaOmics - a Comprehensive Software Suite with Interactive Visualization for Transcriptomic Meta-Analysis. (*: co-first author).

- **Application**

14. Enwright, John, Dominique Arion, John Corradi, Aiqing He, **Zhiguang Huo**, George Tseng, and David Lewis. (2017) Transcriptome Profiling of Layer 3 Parvalbumin Neurons from the Dorsolateral Prefrontal Cortex of Schizophrenia Subjects.
15. 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.
16. 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.
17. **Zhiguang Huo**, Rachel Puralewski, George Tseng, Ryan Logan, Marianne Seney. (2017) Circuit-wide transcriptional profiling reveals sex differences in coherence patterns across brain regions. In preparation.

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.