

August 2017

# Weiqiang Zhou, Ph.D.

Department of Biostatistics  
Johns Hopkins Bloomberg School of Public Health  
615 N. Wolfe Street, Rm E3011  
Baltimore, MD, 21205, USA  
Phone: +1 410-736-8377  
Email: [kenandzhou@hotmail.com](mailto:kenandzhou@hotmail.com)  
Website: <http://weiqiangzhou.com/aboutme>

## EDUCATION

---

- Ph.D.** Electronic Engineering (focus on bioinformatics and computational biology), 2013  
City University of Hong Kong, Hong Kong  
Advisor: Prof. Hong Yan  
Thesis: Alpha shape based methods for analysis and prediction of biomolecular interactions.
- B.E.** Information Engineering (Talented student program), 2008  
South China University of Technology, China

## PROFESSIONAL EXPERIENCE

---

- Postdoctoral Fellow** Department of Biostatistics  
(11/2013-present) Johns Hopkins Bloomberg School of Public Health  
Advisor: Prof. Hongkai Ji

## RESEARCH INTERESTS

---

Bioinformatics; Genomics; Single-cell genomics; High-dimensional data;  
Computational biology; Linear models.

My primary research interest is developing statistical and computational methods for integrative analysis of various types of large-scale genomic data.

## PUBLICATIONS

---

### Paper in progress

1. **Zhou, W.**, Ji, Z. & Ji, H. Global Prediction of Chromatin Accessibility Using RNA-seq from Small Number of Cells. bioRxiv, 035816. Manuscript in submission.
2. Stephens, K., **Zhou, W.**, Ji, Z., He, S., Ji, H., Guan, Y. & Taverna, S. Sex differences in gene regulation in the dorsal root ganglion after nerve injury. bioRxiv, 152652. Manuscript in submission. [contribution: analyze RNA-seq data]
3. Zhu, J.\*, Xu, J.\*, Yin, X.\*, **Zhou, W.**, Andrabi, S., Fan, J., Chen, R., Chen, L., Guan, I., Ji, H., Liu, X., Dawson, T. & Dawson, V. Botch improves neuronal maturation of human stem cell-derived transplants into cortex and functional recovery following stroke. Manuscript in submission. (\*equal contribution) [contribution: analyze RNA-seq data and perform functional annotation analysis]
4. **Zhou, W.**, Sherwood, B., Ji, Z. & Ji, H. PDDB: Predicted DNase I Hypersensitivity Database. Manuscript in preparation.
5. Sherwood, B., **Zhou, W.** & Ji, H. Clustering Covariates in High-dimensional Multivariate Linear Regression. Manuscript in preparation.
6. Du, F., Sherwood, B., **Zhou, W.** & Ji, H. Big Data K-means clustering. Manuscript in preparation.

### Refereed Journal Articles

1. **Zhou, W.** et al. Genome-wide Prediction of DNase I Hypersensitivity Using Gene Expression. *Nature communications* (2017). (accepted)
2. Ji, Z.\*, **Zhou, W.\*** & Ji, H. Single-cell regulome data analysis by SCRAT. *Bioinformatics* btx315. (2017). (\*joint first authors)
3. **Zhou, W.**, Sherwood, B. & Ji, H. Computational Prediction of the Global Functional Genomic Landscape: Applications, Methods and Challenges. *Human Heredity* **81**, 88-105 (2016).
4. Jin, K. et al. (including **Zhou, W.**) HOXB7 Is an ER $\alpha$  Cofactor in the Activation of HER2 and Multiple ER Target Genes Leading to Endocrine Resistance. *Cancer. Discov.* **5**, 944-959 (2015). [contribution: perform statistical and computational analysis of genomic data]
5. Wang, D., **Zhou, W.** & Yan, H. Mining of protein-protein interfacial residues from massive protein sequential and spatial data. *Fuzzy Sets Syst.* **258**, 101-116 (2015).
6. Fan, T. et al. (including **Zhou, W.**) Antagonistic effects of MYC and hypoxia in channeling glucose and glutamine into de novo nucleotide biosynthesis. *Cancer & Metabolism* **2** (Suppl 1), O10 (2014). [contribution: perform statistical and computational analysis of genomic data]

7. Wang, D. D., **Zhou, W.**, Yan, H., Wong, M. & Lee, V. Personalized prediction of EGFR mutation-induced drug resistance in lung cancer. *Scientific Reports* **3**, 2855 (2013).
8. Yang, X., **Zhou, W.**, Wang, D. D., Wu, Q. & Yan, H. A Survey on Structural Analysis of Nucleosome Core Particles. *Current Bioinformatics* **8**, 112-132 (2013).
9. **Zhou, W.**, Yan, H., Fan, X. & Hao, Q. Prediction of Protein-Protein Interactions Based on Molecular Interface Features and the Support Vector Machine. *Current Bioinformatics* **8**, 3-8 (2013).
10. Zhu, Y., **Zhou, W.**, Dai, D. & Yan, H. Identification of DNA-Binding and Protein-Binding Proteins Using Enhanced Graph Wavelet Features. *IEEE/ACM Transactions on Computational Biology and Bioinformatics (TCBB)* **10**, 1017-1031 (2013).
11. Guan, P. P., **Zhou, W.** & Yan, H. The relationship between geometric patterns of hydrogen bonds and periodic dinucleotides in nucleosome structures. *J. Theor. Biol.* **313**, 136-141 (2012).
12. **Zhou, W.** & Yan, H. Alpha shape and Delaunay triangulation in studies of protein-related interactions. *Briefings in Bioinformatics* **15**(1), 54-64 (2012).
13. **Zhou, W.**, Yan, H. & Hao, Q. Analysis of surface structures of hydrogen bonding in protein-ligand interactions using the alpha shape model. *Chemical Physics Letters* **545**, 125-131 (2012).
14. Wu, Q., **Zhou, W.**, Wang, J. & Yan, H. Correlation between the flexibility and periodic dinucleotide patterns in yeast nucleosomal DNA sequences. *J. Theor. Biol.* **284**, 92-98 (2011).
15. **Zhou, W.** & Yan, H. Prediction of DNA-binding protein based on statistical and geometric features and support vector machines. *Proteome science* **9**, 1-6 (2011).
16. **Zhou, W.** & Yan, H. Relationship between periodic dinucleotides and the nucleosome structure revealed by alpha shape modeling. *Chemical Physics Letters* **489**, 225-228 (2010).
17. **Zhou, W.** & Yan, H. A discriminatory function for prediction of protein-DNA interactions based on alpha shape modeling. *Bioinformatics* **26**, 2541-2548 (2010).

### Refereed Conference Papers

1. **Zhou, W.**, Wang, D. & Yan, H. Prediction of anti-EGFR drug resistance base on binding free energy and hydrogen bond analysis. *2013 IEEE Symposium on Computational Intelligence in Bioinformatics and Computational Biology*, Singapore, April 2013.
2. **Zhou, W.** & Yan, H. Analysis of Ligand Binding Sites Using Alpha Shapes. *2012 IEEE International Conference on System, Man, and Cybernetics*, Seoul, Korea, October 2012.
3. **Zhou, W.**, Yan, H., Fan, X. & Hao, Q. Prediction of protein-protein interactions using alpha

shape modeling. *2011 International Symposium on Computational Models for Life Sciences*, Toyama City, Japan, October 2011, pp 244-252.

4. **Zhou, W.** & Yan, H. Prediction of DNA-binding protein based on alpha shape modeling. *2010 IEEE International Conference on Bioinformatics and Biomedicine (BIBM)*, Hong Kong, December 2010, pp 23-28.
5. **Zhou, W.**, Xu, X. & Huang, W. Shape and Boundary Analysis for Classification of Breast Masses. *2008 International Symposium on Computational Intelligence and Design*, Wuhan, China, October 2008, Vol. 2, pp 42-46.
6. Tang, X., Xu, X., **Zhou, W.** & Mao, Y. A Novel Semantic based CAD System for Mammography. *2008 International Conference on Computer Science and Information Technology*, Singapore, August 2008, pp 97-101.

### **Posters**

1. **Zhou, W.**, Du, F., Bai, J., Ying M., Laterra J. & Ji, H. Computational prediction of cistrome with application to stem cells. *The 7<sup>th</sup> Annual Maryland Stem Cell Research Symposium*, Silver Spring, MD, USA, December 2014.

### **Conference presentations**

1. **Zhou, W.** & Ji, H. Big Data Regression and Prediction in Functional Genomics. *The 2015 INFORMS Annual Meeting*, Philadelphia, PA, USA, November 2015.
2. **Zhou, W.** et al. Big data regression and prediction for high-throughput genomic data. *Joint Statistical Meetings*, Chicago, IL, July 2016.
3. **Zhou, W.**, Ji, Z. & Ji, H. Global Prediction of Chromatin Accessibility Using RNA-seq from Single Cell and Small Number of Cell. *2017 ICSA Applied Statistics Symposium*, Chicago, IL, June 2017.
4. **Zhou, W.**, Ji, Z. & Ji, H. Next Generation Analysis Tools for Single-Cell Functional Genomic Data. *Joint Statistical Meetings*, Baltimore, MD, August 2017.

### **Patent Applications**

1. **Zhou, W.**, & Yan, H. METHODS FOR MODELING AND ANALYSIS OF INTERFACE BETWEEN POINT PATTERNS. US Patent Application 20130024175, publication date: January 24, 2013.

### **SOFTWARE AND DATABASE**

---

1. BIRD: Big data Regression for predicting DNase I hypersensitivity.  
<https://github.com/WeiqiangZhou/BIRD>

2. PDDB: Predicted DNase I Hypersensitivity Database.  
<http://jilab.biostat.jhsph.edu/~bsherwo2/bird/index.php>
3. SCRAT: Single-cell regulome analysis toolbox.  
<https://zhiji.shinyapps.io/scrat/>

## PROFESSIONAL ACTIVITIES

---

<b>Reviewer</b>	Nature Methods, Nature Communications, Nucleic Acid Research, Biostatistics, BMC Bioinformatics, Proteome Science, IEEE Transactions on NanoBioscience, The Eleventh Asia Pacific Bioinformatics Conference 2013, The Tenth Asia Pacific Bioinformatics Conference 2012.
<b>Session chair</b>	Joint Statistical Meetings, 2016 Joint Statistical Meetings, 2017
<b>Thesis examiner</b>	Hamidreza Khataee Gavgani. 2016. Theoretical Investigation of Intracellular Transport by Molecular Motors. Ph.D. Thesis, Griffith University, Brisbane.

## TEACHING ACTIVITIES

---

2012	<b>Teaching assistant</b> in EE5806: Topics in Image Processing City University of Hong Kong
2010-2011	<b>Teaching assistant</b> in EE2000: Logic Circuit Design City University of Hong Kong
2010	<b>Teaching assistant</b> in EE3206: Java Programming & Applications City University of Hong Kong

## ACADEMIC HONORS & AWARDS

---

**Research Tuition Scholarships** (2009-2010, 2010-2011, 2011-2012), Chow Yei Ching School of Graduate Studies, City University of Hong Kong, Hong Kong.

**Outstanding Academic Performance Award for Research Degree Students** (2009-2010, 2010-2011, 2011-2012), Chow Yei Ching School of Graduate Studies, City University of Hong Kong, Hong Kong.

**Postgraduate Studentship** (2009-2013), University Grants Committee, Hong Kong.