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# Weiqliang Zhou, Ph.D.

Department of Biostatistics  
Johns Hopkins Bloomberg School of Public Health  
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## EDUCATION

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- 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

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

## RESEARCH INTERESTS

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Genomics; Data science; Single-cell genomics; Big data; Bioinformatics;  
Computational biology.

My primary research interest is developing statistical and computational methods for integrative analysis of big data with focus on data science and genomics.

## PUBLICATIONS

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### 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. PDDDB: 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. Qiu, X. et al. (including **Zhou, W.**) Sequential Enhancer Sequestration Dysregulates Recombination Center Formation at the *IgH* Locus. *Molecular Cell*, In Press (2018). [contribution: perform statistical and computational analysis of genomic data]
2. **Zhou, W.** et al. Genome-wide Prediction of DNase I Hypersensitivity Using Gene Expression. *Nature Communications* **8**, 1038 (2017).
3. Ji, Z.\* , **Zhou, W.\*** & Ji, H. Single-cell regulome data analysis by SCRAT. *Bioinformatics* **33**, 2930-2932 (2017). (\*joint first authors)
4. **Zhou, W.**, Sherwood, B. & Ji, H. Computational Prediction of the Global Functional Genomic Landscape: Applications, Methods and Challenges. *Human Heredity* **81**, 88-105 (2016).
5. 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]
6. 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).

7. 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]
8. 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).
9. 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).
10. **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).
11. 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).
12. 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).
13. **Zhou, W.** & Yan, H. Alpha shape and Delaunay triangulation in studies of protein-related interactions. *Briefings in Bioinformatics* **15**(1), 54-64 (2012).
14. **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).
15. 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).
16. **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).
17. **Zhou, W.** & Yan, H. Relationship between periodic dinucleotides and the nucleosome structure revealed by alpha shape modeling. *Chemical Physics Letters* **489**, 225-228 (2010).
18. **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.
2. **Zhou, W.**, Ji, Z. & Ji, H., Analysis and prediction of single-cell functional genomic data. *CSHL Single Cell Analyses meeting*, Cold Spring Harbor, NY, USA, November 2017.

#### **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.

#### **Invited Talks**

1. Prediction and Analysis of High Dimensional Functional Genomics Data, Institute for Basic Biomedical Sciences at Johns Hopkins School of Medicine, Baltimore, MD, December 2016.

2. Genome-wide prediction of DNase I Hypersensitivity Using Gene Expression, *11th Annual Symposium and Poster Session on Genomics and Bioinformatics*, Center for Computational Genomics at Johns Hopkins, Baltimore, MD, October 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**

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1. BIRD: Big data Regression for predicting DNase I hypersensitivity.  
<https://github.com/WeiqiangZhou/BIRD>
2. PDDDB: 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/>
4. SCDV: Single-cell differential variance analysis.  
<https://github.com/WeiqiangZhou/SCDV>

### **PROFESSIONAL ACTIVITIES**

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<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**

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

## **MENTORING EXPERIENCE**

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- 2017      Runzhe Li, summer intern (Johns Hopkins)  
Predicting chromatin accessibility using gene expression across different  
platforms.
- 2015      Steffen Cornwell, summer intern (Johns Hopkins)  
Predicting tissue-specific locations of cis-regulatory elements using chromatin  
immunoprecipitation sequencing data.

## **ACADEMIC HONORS & AWARDS**

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- 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.