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

RESEARCH INTERESTS

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

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

PUBLICATIONS

Paper in progress

1. **Zhou, W.** et al. Genome-wide Prediction of DNase I Hypersensitivity Using Gene Expression. bioRxiv, 035808. Under revision in *Nature communications*. (2016).

2. **Zhou, W.**, Sherwood, B. & Ji, H. Methods and Challenges in Global Prediction of the Functional Genomic Landscape. Under revision in *Human Heredity*. (2016).

3. **Zhou, W.**, Ji, Z. & Ji, H. Global Prediction of Chromatin Accessibility Using RNA-seq from Small Number of Cells. bioRxiv, 035816. Submitted to *Nucleic Acids Research*. (2016).

4. Ji, Z.*, **Zhou, W.*** & Ji, H. SCRAT: a toolbox for analyzing single-cell regulome data. Manuscript ready for submission. (2016). (***joint first authors**)

5. 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 ready for submission. (*equal contribution)

6. **Zhou, W.**, Sherwood, B., Ji, Z. & Ji, H. PDDB: Predicted DNase I Hypersensitivity Database. Manuscript in preparation. (rough draft exist)

7. Sherwood, B., **Zhou, W.** & Ji, H. Clustering Covariates in High-dimensional Multivariate Linear Regression. Manuscript in preparation. (rough draft exist)

8. Du, F., Sherwood, B., **Zhou, W.** & Ji, H. Big Data K-means clustering. Manuscript in preparation. (rough draft exist)

Refereed Journal Articles

1. Jin, K. et al. (including **Zhou, W**.) HOXB7 Is an ERα 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]

2. Wang, D., **Zhou, W.** & Yan, H. Mining of protein-protein interfacial residues from massive protein sequential and spatial data. *Fuzzy Sets Syst.* (2015).

3. 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** (2013).

4. 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).

5. **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).

6. 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).

7. 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).

8. **Zhou, W.** & Yan, H. Alpha shape and Delaunay triangulation in studies of protein-related interactions. *Briefings in Bioinformatics* (2012).

9. **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).

10. 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).

11. **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).

12. **Zhou, W.** & Yan, H. Relationship between periodic dinucleotides and the nucleosome structure revealed by alpha shape modeling. *Chemical Physics Letters* **489**, 225-228 (2010).

13. **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 7th Annual Maryland Stem Cell Research Symposium*, Silver Spring, MD, USA, December 2014.

Conference presentation

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.

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.
2. PDDB: Predicted DNase I Hypersensitivity Database.
3. SCRAT: a toolbox for analyzing single-cell regulome data.

PROFESSIONAL ACTIVITIES

Reviewer	Proteome Science, Nucleic Acid Research, Nature Methods, Nature Communications, BMC Bioinformatics, IEEE Transactions on NanoBioscience. The Eleventh Asia Pacific Bioinformatics Conference, 2013 The Tenth Asia Pacific Bioinformatics Conference, 2012
Session chair	Joint Statistical Meetings, 2016

TEACHING ACTIVITIES

2012	**Teaching assistant** in EE5806: Topics in Image Processing City University of Hong Kong
2010-2011	**Teaching assistant** in EE2000: Logic Circuit Design City University of Hong Kong
2010	**Teaching assistant** 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.