

# Zhizhuo Zhang

## Research Interests

Machine learning, High throughput data analysis, Regulatory genomics and Complex human disease traits.

## Academic Summary

- 2014–present **Postdoctoral Associate**, *Computational Biology Group, Computer Science and Artificial Intelligence Lab, MIT, USA*, Advisor: Prof. Manolis Kellis.
- 2008–2013 **Ph.D.**, *School of Computing, National University of Singapore(NUS)*, Singapore, Advisor: Dr. Ken Wing-Kin Sung .
- 2004–2008 **Bachelor**, *Computer Science and Engineering, South China University of Technology(SCUT)*, China, Advisor: Dr. Qiong Chen .

## Publications

- [1] Anshul Kundaje, Wouter Meuleman, Jason Ernst, Misha Bilenky, Angela Yen, Alireza Heravi-Moussavi, Pouya Kheradpour, **Zhang, Zhizhuo**, et.al., and Manolis Kellis. Integrative analysis of 111 reference human epigenomes. *Nature*, 518(7539):317–330, 2015. (co-integrative analysis lead).
- [2] Yumei Luo, Detu Zhu, **Zhang, Zhizhuo**, Yaoyong Chen, and Xiaofang Sun. Integrative analysis of crispr/cas9 target sites in the human hbb gene. *BioMed research international*, 2015, 2015.
- [3] Chwee Tat Koe, Song Li, Fabrizio Rossi, Jack Jing Lin Wong, Yan Wang, **Zhizhuo Zhang** , Keng Chen, Sherry Shiyong Aw, Helena E Richardson, Paul Robson, et al. The brm-hdac3-erm repressor complex suppresses dedifferentiation in drosophila type ii neuroblast lineages. *eLife*, 3, 2014.
- [4] **Zhizhuo Zhang** . *Study of protein-DNA interaction using new generation data*. PhD thesis, 2013.
- [5] **Zhang, ZhiZhuo**, Guoliang Li, Kim-Chuan Toh, and Wing-Kin Sung. 3d chromosome modeling with semi-definite programming and hi-c data. *Journal of computational biology*, 20(11):831–846, 2013.
- [6] **Zhizhuo Zhang**, Guoliang Li, Kim-Chuan Toh, and Wing-Kin Sung. Inference of spatial organizations of chromosomes using semi-definite embedding approach and Hi-C data. In *Research in Computational Molecular Biology*, pages 317–332. Springer, 2013.
- [7] Matthew T Weirauch, Atina Cote, Raquel Norel, Matti Annala, Yue Zhao, Todd R Riley, Julio Saez-Rodriguez, Thomas Cokelaer, Anastasia Vedenko, Shaheynoor Talukder, Matthew T Weirauch, Atina Cote, Raquel Norel, Matti Annala, Yue Zhao, Todd R Riley, Julio Saez-Rodriguez, Thomas Cokelaer, Anastasia Vedenko, Shaheynoor Talukder, DREAM5 Consortium(**Zhizhuo Zhang**), et.al., Gustavo Stolovitzky, and Timothy R Hughes. Evaluation of methods for modeling transcription factor sequence specificity. *Nature biotechnology*, 31(2):126–134, 2013.

- [8] Arkasubhra Ghosh, Gaye Saginc, Shi Chi Leow, Ekta Khattar, Eun Myong Shin, Ting Dong Yan, Marc Wong, **Zhizhuo Zhang**, Guoliang Li, Wing-Kin Sung, et al. Telomerase directly regulates NF- $\kappa$ B-dependent transcription. *Nature cell biology*, 14(12):1270–1281, 2012.
- [9] **Zhang, ZhiZhuo**, Cheng Wei Chang, Willy Hugo, Edwin Cheung, and Wing-Kin Sung. Simultaneously learning dna motif along with its position and sequence rank preferences through expectation maximization algorithm. *Journal of Computational Biology*, 20(3):237–248, 2013.
- [10] **Zhizhuo Zhang**, Cheng Wei Chang, Willy Hugo, Edwin Cheung, and Wing-Kin Sung. Simultaneously learning dna motif along with its position and sequence rank preferences through EM algorithm. In *Research in Computational Molecular Biology*, pages 355–370. Springer, 2012.
- [11] Guoliang Li, Xiaoan Ruan, Raymond K Auerbach, Kuljeet Singh Sandhu, Meizhen Zheng, Ping Wang, Huay Mei Poh, Yufen Goh, Joanne Lim, Jingyao Zhang, Hui Shan Sim, Su Qin Peh, Fabianus Hendriyan Mulawadi, Chin Thing Ong, Yuriy L. Orlov, Shuzhen Hong, **Zhizhuo Zhang**, et.al, Michael Snyder, and Yijun Ruan. Extensive promoter-centered chromatin interactions provide a topological basis for transcription regulation. *Cell*, 148(1):84–98, 2012.
- [12] **Zhizhuo Zhang\***, Cheng Wei\* Chang, Wan Ling Goh, Wing-Kin Sung, and Edwin Cheung. Centdist: discovery of co-associated factors by motif distribution. *Nucleic acids research*, 39(suppl 2):W391–W399, 2011.
- [13] Haifeng Wan, **Zhizhuo Zhang**, and Ruijie Liu. A parallel dynamic convex hull algorithm based on the macro to micro model. In *Image and Signal Processing, 2009. CISP'09. 2nd International Congress on*, pages 1–5. IEEE, 2009.
- [14] **Zhizhuo Zhang**, Qiong Chen, Shang-Fu Ke, Yi-Jun Wu, Fei Qi, and Ying-Peng Zhang. Ranking potential customers based on group-ensemble. *International Journal of Data Warehousing and Mining (IJDWM)*, 4(2):79–89, 2008.

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## Skills

- o Eight year experiences for high-throughput sequencing data analysis.
- o In-depth analysis on large scale population data of human complex trait
- o Machine Learning: Bayseian graphical model, Deep learning, Convex Optimization.
- o Programming language: Java, Python, C-Sharp, Matlab, R , PHP, Ajax.

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## Awards & Fellowship

- 2016 **Broadnext10 Trainee Award** , *Broad Institute*, \$40,000.
- 2016 **Microsoft Azure Research Award**, *Microsoft Research*, \$20,000.
- 2016 **MIT IMPACT Program Fellow**, *MIT, USA*.
- 2014 **Dean's Graduate Research Excellence Award**, *NUS, Singapore*.
- 2013 **RECOMB 2013-TNLIST Travel Fellowship**, *TNLIST, China*.
- 2008–2012 **Graduate Research Scholarship**, *NUS, Singapore*.
- 2007 **Honorable Mention of Interdisciplinary Contest in Modeling**, *COMAP, Inc. USA*.
- 2007 **Second prize of National Challenge Cup**, *China*.
- 2007 **Computer World Magazine Scholarship**, *China*.
- 2007 **IBM Excellent Student scholarship**, *China*.
- 2007 **HP Excellent Student scholarship**, *China*.
- 2005 **EPSON foundation scholarship**, *China*.

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## Invited Talks & Posters

- 2016 **Insight of Gene Regulation and Disease Mechanism from Epigenomics Roadmap**, *UESTC/SYSU/HZAU, China*, Talk.
- 2016 **Comprehensive Allele Imbalance Analysis on 419 Human Post-Mortem Brains**, *Feb 2016 GTEx imprint conference call*, Talk.
- 2015 **Comprehensive Allele Imbalance Analysis on 419 Human Post-Mortem Brains**, *October 2015 Boston eQTL Meeting*, Talk.
- 2015 **Using Motif Enrichment for Antibody Validation**, *August 2015 ENCODE BINDING CALL*, Talk.
- 2015 **Decipher Regulatory Grammar from DNA Sequence**, *July 2015 The 4th EITA Young Investigator Conference*, Talk.
- 2015 **The regulatory genetic mechanisms underlying Alzheimer Disease**, *May 2015 ROSMAP Investigators Meeting*, Talk.
- 2015 **Dissecting Alzheimer disease GWAS using multiple sources of functional data**, *April 2015 Boston eQTL Meeting*, Talk.
- 2015 **Modeling complex DNA sequence grammar with recurrent neural network**, *2015 ENCODE Consortium Meeting*, Poster.
- 2014 **Modeling complex DNA sequence grammar with recurrent neural network**, *ISMB 2014 Conference*, Poster.
- 2013 **3D Chromosome Modeling with Semi-Definite Programming and Hi-C Data**, *RECOMB 2013 Conference*, Talk.
- 2013 **Inference of Spatial Organizations of Chromosomes Using Semi-definite Embedding Approach and Hi-C Data**, *Korea-Singapore Workshop on Bioinformatics and NLP*, Talk.
- 2012 **Simultaneously Learning DNA Motif along with Its Position and Sequence Rank Preferences through EM Algorithm**, *RECOMB 2012 Conference*, Talk.
- 2010 **Peak Oriented Motif Discovery Algorithm**, *RECOMB 2010 Conference*, Poster.

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## Professional Service

- 2014 Present **Member, NIH Genotype-Tissue Expression (GTEx) Consortium.**
- 2014 Present **Member, The ENCODE (Encyclopedia of DNA Elements) Consortium.**
- 2014 Present **Member, NIH Epigenome-roadmap Consortium.**
- 2015 Present **Member, The Religious Orders Study and the Rush Memory and Aging Project.**
- 2015 Present **Reviewer, BMC Bioinformatics.**
- 2015 Present **Reviewer, Biomedical Engineering and Computational Biology.**
- 2015 Present **Reviewer, Computers in Biology and Medicine.**
- 2015 **Program chair, Symposium of Health Informatics in Latin America and the Caribbean.**
- 2014 **Program chair, The 2nd Workshop on Big Data in Bioinformatics and Health Care Informatics.**

- 2014 Present **Reviewer,IEEE Transactions on Computational Biology and Bioinformatics(Journal) .**
- 2012 Present **Reviewer,Nucleic Acids Research(Journal) .**
- 2010 Present **Reviewer,Bioinformatics(Journal) .**