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### **Research Interests**

- 1) Systems biology of development and aging
- 2) Evolution of regulatory networks
- 3) Computational algorithm development for data integration and network analysis

### **Biography**

Prof. Jing-Dong Jackie Han obtained Ph.D. degree from Albert Einstein College of Medicine. She had her postdoctoral training at The Rockefeller University and Dana-Farber Cancer Institute. In 2004, she became an investigator/professor at the Institute of Genetics and Developmental Biology, Chinese Academy of Sciences. She is currently a director of the CAS-Max Planck Partner Institute for Computational Biology. Her research focuses on the structure and dynamic inference of molecular networks, using a combination of large-scale experiments and computational analysis to probe the networks and to integrate functional interaction data in order to explore the design principles of the networks and to find how the complex phenotypes, such as aging, cancer and stem cell development are regulated through molecular networks. She was awarded the Chinese Academy Sciences Hundred Talent Plan and NSFC Outstanding Young Scientist Award in 2006, and the Hundred Talent Plan Outstanding Achievement Award in 2009, selected as a Max Planck Follow in 2011 and a MaxNetAging Fellow in 2014.

### **Talk abstract**

#### **Integrative Analysis of Biological Big Data**

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New high-throughput technologies, such as microarrays and deep sequencing technologies, have provided unprecedented opportunities for mapping mutations, transcripts, transcription factor binding and histone modifications at high resolution and at genome-wide level. This has revolutionized the way regulations of diseases and other biological processes are studied and generated a large amount of heterogeneous data, which is begging to be unbiasedly and efficiently integrated. How to integrate these data still remains a big challenge. We have explored to *ab initio* predict or reconstruct regulatory networks based on heterogeneous data on gene expression, histone modification and genomic changes. We find that innovative integrations of these data can lead to not only global pictures of the complex biological processes, such as aging and early development, but also key regulatory events of these processes. We have also

developed new computational algorithms to facilitate mapping of epigenetic features from the deep sequencing data. I will highlight our new methods and results for the integrative analyses of large datasets to infer regulatory events, in particular in light of incorporating the epigenome and imaging data recently generated by international consortiums.

### **Selected Publications**

1. Lei Hou<sup>^</sup>, Dan Wang<sup>^</sup>, Di Chen<sup>^</sup>, Yi Liu, Yue Zhang, Hao Cheng, Chi Xu, Na Sun, Joseph McDermott, and William B. Mair and **Jing-Dong J. Han<sup>\*</sup>**. A Systems Approach to Reverse Engineer Lifespan Extension by Dietary Restriction. *Cell Metabolism*, 2016, 8;23(3):529-40.
2. Weiyang Chen<sup>1</sup>, Wei Qian<sup>1</sup>, Gang Wu<sup>1</sup>, Weizhong Chen<sup>1</sup>, Bo Xian<sup>1</sup>, Xingwei Chen<sup>1</sup>, Yaqiang Cao<sup>1</sup>, Christopher D Green<sup>1</sup>, Fanghong Zhao<sup>2</sup>, Kun Tang<sup>1</sup> and **Jing-Dong J. Han<sup>1,\*</sup>**, Three-dimensional human facial morphologies as robust aging markers, *Cell Research*, 2015, 25:574-587 (highlighted by Nature Press Release, Science News, New Scientists, The Guardian, Daily Mail, and NewsWeek, etc).
3. Weizhong Chen<sup>1,2†</sup>, Yi Liu<sup>1,3†</sup>, Shanshan Zhu<sup>1</sup>, Christopher D. Green<sup>1</sup>, Gang Wei<sup>1</sup>, **Jing-Dong J. Han<sup>1,\*</sup>**, Improved Nucleosome Positioning Algorithm iNPS for Accurate Nucleosome Positioning from Sequencing Data, *Nature Communications* 2014, doi:10.1038/ncomms5909.
4. Ming Su<sup>^</sup>, Dali Han<sup>^</sup>, Jerome D Boyd-Kirkup, Xiaoming Yu and **Jing-Dong J Han<sup>\*</sup>**, Evolution of Alu towards enhancers, *Cell Reports*, 2014, 7(2): 376-385
5. Jin'e Li<sup>^</sup>, Yi Liu<sup>^</sup>, Min Liu and **Jing-Dong J Han<sup>\*</sup>**, Functional dissection of regulatory models using gene expression data of deletion mutants, *PLoS Genetics*, 2013, 9(9): e1003757.
6. Wei Zhang<sup>^</sup>, Yi Liu<sup>^</sup>, Na Sun, Dan Wang, Jerome Boyd-Kirkup, Xiaoyang Dou, **Jing-Dong J Han<sup>\*</sup>**, Integrating Genomic, Epigenomic and Transcriptomic Features Reveals Modular Signatures Underlying Poor Prognosis in Ovarian Cancer, *Cell Reports*, 2013, 4(3):542–553
7. Zhou, B., Yang, L., Li, S.F., Huang, J.L., Chen, H.Y., Hou, L., Wang, J.B., Green, C.D., Yan, Z., Huang, X., Zhu L., Xiao H.S., Liu Y. \*, and **Han J.D.J. \*** (2012). Midlife Gene Expressions Identify Modulators of Aging through Dietary Interventions, *Proc Natl Acad Sci U S A.* 8;109(19):E1201-9.
8. Jin, C., Li, J., Green, C.D., Yu, X. , Tang, X, Han, D., Xian, Bo., Wang, D, Huang, X., Cao, X., Yan. Z., Hou, L., Liu, J., Shukeir, N., Khaitovich, P., Chen, C.D., Zhang, H., Jenuwein, T. and **Han, J.-D.J \***, Histone Demethylase UTX-1 Regulates *C. elegans*

Lifespan by Targeting Insulin/IGF-1 Signaling Pathway, ***Cell Metabolism***, 2011, 14:  
161-172.