

XIN HE

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RESEARCH INTERESTS

Bioinformatics of gene regulation, evolution of gene regulatory networks, comparative genomics, statistical and systems genetics

EDUCATION

- Oct 2009 **University of Illinois at Urbana-Champaign**
Ph.D. in Computer Science (Advisor: Prof. Saurabh Sinha)
Thesis: Computational models of function and evolution of *cis*-regulatory sequences
- 2003-2004 **University of North Carolina at Chapel Hill**
Ph.D. student in Program of Bioinformatics and Computational Biology
- Dec 2002 **Loyola University Chicago**
M.S. in Computer Science
- 1999-2001 **Northwestern University, School of Medicine**
Ph.D. student in Integrated Graduate Program in Life Sciences
- Jul 1999 **University of Science and Technology of China**
B.S. in Biochemistry (Special Class for Gifted Young)

PROFESSIONAL POSITIONS

Postdoctoral Researcher Dept. of Biochemistry and Biophysics, University of California at San Francisco, (2009-present)

Work with Prof. Hao Li on evolution of gene regulatory networks and statistic genetics

Research Assistant Dept. of Computer Science and Institute of Genomic Biology, University of Illinois at Urbana Champaign, (2005-2009)

Work with Prof. Bruce Schatz and Prof. Chengxiang Zhai on the Beespace project: the literature-mining system for insect biologists

Teaching Assistant Dept. of Biology, University of North Carolina at Chapel Hill, (2004)

Grading and discussion sessions for the course "Cellular and Developmental Biology".

AWARDS AND HONORARIES

- 2003-2004 University of North Carolina at Chapel Hill
Bioinformatics and Computational Biology Fellowship
- 1999-2001 Northwestern University, School of Medicine
Graduate Fellowship
- 1995 University of Science and Technology of China
Cheng Yaolin Scholarship (5-th place in College Entrance Exam in Anhui Province)

PUBLICATIONS

- [1] Dan Xie*, Chieh-Chun Chen*, **Xin He**, Xiaoyi Cao and Sheng Zhong, An evolutionary model of transcription networks: application in mammalian pre-implantation development (submitted)
- [2] **Xin He**, Md. Abul Hassan Samee, Charles Blatti and Saurabh Sinha, Thermodynamics-based models of transcriptional regulation by enhancers: the roles of synergistic activation, cooperative Binding and short-range repression. *PLoS Comput Biol*, 2010, 6(9)
- [3] **Xin He**, Yanen Li, Radhika Khetani, Barry Sanders, Yue Lu, Xu Ling, ChengXiang Zhai and Bruce Schatz, BSQA: integrated text mining using entity relation semantics extracted from biological literature of insects. *Nucleic Acids Res*, 2010, 38, W175-81
- [4] **Xin He**, Moushumi Sen Sarma, Xu Ling, Brant Chee, Chengxiang Zhai and Bruce Schatz, Identifying overrepresented concepts in gene lists from literature: a statistical approach based on Poisson mixture model. *BMC Bioinformatics* 2010, 11:272
- [5] **Xin He** and Saurabh Sinha, ChIPs and Regulatory Bits. *Nature Biotechnology*, 2010, 28, 142-143 (invited News and Views article)
- [6] **Xin He** and Saurabh Sinha, Evolution of cis-regulatory sequences in Drosophila. Computational Biology of Transcription Factor Binding: Methods Mol Biol. Ed: Istvan Ladunga. Humana Press, 2010 (invited book chapter)
- [7] **Xin He**, Chieh-Chun Chen, Feng Hong, Fang Fang, Saurabh Sinha, Huck-Hui Ng and Sheng Zhong, A biophysical model for analysis of transcription factor interaction and binding site arrangement from genome-wide binding data. *PLoS ONE* 2009 4(12): e8155 (accepted by RECOMB Regulatory Genomics)
- [8] Xu Ling, **Xin He** and Dong Xin, Detecting gene clusters under evolutionary constraint in a large number of genomes. *Bioinformatics*, 2009, 25(5):571-577
- [9] **Xin He**, Xu Ling and Saurabh Sinha, Alignment and prediction of regulatory sequences based on a probabilistic model of evolution. *PLoS Comput Biol*, 2009, 5(3):e1000299
- [10] Jaebum Kim*, **Xin He*** and Saurabh Sinha, Evolution of regulatory sequences in 12 Drosophila species. *PLoS Genetics* 2009 Jan;5(1):e1000330. (joint first author)
- [11] Xu Ling, **Xin He**, Dong Xin and Jiawei Han, Efficiently identifying max-gap clusters in pairwise genome comparison. *J Comput Biol* 2008 Jul-Aug;15(6):593-609.

- [12] Saurabh Sinha and **Xin He**, MORPH: probabilistic alignment combined with hidden Markov models of cis-regulatory modules. *PLoS Comput Biol* 2007 Nov;3(11):e216
- [13] Long Li, Qianqian Zhu, **Xin He**, Saurabh Sinha and Marc S Halfon, Large-scale analysis of transcriptional cis-regulatory modules reveals both common features and distinct subclasses. *Genome Biol*, 2007;8(6):R101
- [14] Yue Lu, **Xin He** and Sheng Zhong, Cross-species microarray analysis with the OSCAR system suggests an INSR-Pax6-NQO1 neuro-protective pathway in aging and Alzheimer's disease. *Nucleic Acid Research* 2007 Jul;35:W105-14
- [15] Xu Ling, Jing Jiang, **Xin He**, Qiaozhu Mei, Chengxiang Zhai and Bruce Schatz, Generating gene summaries from biomedical literature: a study of semi-structured summarization. *Information Processing and Management*, 43, 2007, 1777-1791 (an earlier version was accepted by Pacific Symposium on Biocomputing)
- [16] **Xin He** and Michael Goldwasser, Identifying conserved gene clusters in the presence of homology families. *J Comput Biol*, 2005 Jul-Aug;12(6):638-56 (an earlier version was accepted by RECOMB)

REFERENCES

- Prof. Saurabh Sinha (Ph.D. Advisor)
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