

Chieh-Chun Chen

Curriculum Vitae

Contact

Department of Bioengineering
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Research Interests

Computational inference of gene regulatory networks, quantitative modeling of gene expression, evolution of cis-regulatory sequences.

Education

Ph.D., Bioengineering, in progress (expected Summer 2011)
University of Illinois at Urbana-Champaign
Urbana, IL
Adviser: Prof. Sheng Zhong
GPA: 3.90/4.0

M.S., Bioengineering, in progress (expected December 2009)
University of Illinois at Urbana-Champaign
Urbana, IL
Thesis: *Analysis of combinatorial gene regulation with thermodynamic models*
Adviser: Prof. Sheng Zhong
GPA: 3.90/4.0

M.B.A., Information Management, May 2006
National Taiwan University
Taiwan, R.O.C.
Thesis: *Mining Regulation Relationships between Gene Clusters by Using Time-Series Gene Expression Data*
Adviser: Prof. Anthony J. T. Lee
GPA: 4.0/4.0

B.B.A., Information Management, May 2001
National Taiwan University
Taiwan, R.O.C.
GPA: 3.79/4.0

Employment

- 1/2007–present Research Assistant
Dept. Bioengineering, University of Illinois at Urbana-Champaign
Urbana, IL
- 1/2007–8/2009 Webmaster
Molecular Science Student Workbench, National Center for Supercomputing Applications
Urbana, IL
- 8/2006–1/2007 Teaching Assistant
Dept. Computer Science, University of Illinois at Urbana-Champaign
Urbana, IL
- 8/2004–5/2006 Webmaster Assistant
Dept. Information Management, National Taiwan University
Taiwan, R.O.C.
- 8/2004–5/2006 Teaching Assistant
Undergraduate Project on Bioinformatics, National Taiwan University
Taiwan, R.O.C.

Publications

Dan Xie*, **Chieh-Chun Chen***, Leon Ptaszek*, Shu Xiao, Xiaoyi Cao, Yanen Li, Douglas A. Melton, Harris A Lewin, Chad Cowan, Sheng Zhong, Rewirable gene regulatory networks in the preimplantation development of three mammalian species. (Ready to be submitted to PNAS, *These authors contributed equally.)

Xin He, Feng Hong*, **Chieh-Chun Chen***, Fang Fang, Saurabh Sinha, Huck-Hui Ng, Sheng Zhong, Predicting combinatorial protein-DNA interactions from sequences and ChIP-seq data using biophysical modeling. (Accepted by RECOMB Regulatory Genomics 2009, *These authors contributed equally.)

Gloria Rendon, **Chieh-Chun Chen**, Jay Mashl, Alex Yahja, Edee Wiziecki, Eric Jakobsson, MyCyber-Bench, a NCSA Cyberinfrastructure for Education and Research in Information-based Disciplines, Tera-Grid09.

Chieh-Chun Chen, Sheng Zhong, Inferring gene regulatory networks by thermodynamic modeling, 2008, BMC Genomics, vol. 9, suppl 2.

Chieh-Chun Chen, Xinguang Zhu, Sheng Zhong, Selection of thermodynamic models for combinatorial control of multiple transcription factors in early differentiation of embryonic stem cells, 2008, BMC Genomics, vol.9, suppl 1.

Anthony J.T. Lee, Chao-Wen Lin, Wen-Hsing Lo, **Chieh-Chun Chen**, Jia-Xin Chen, A novel filtration method in biological sequence databases, 2007, Pattern Recognition, vol. 28, pp 447-458.

Chieh-Chun Chen, Mining Regulation Relationships between Gene Clusters by Using Time-Series Gene Expression Data, 2006, Masters thesis, National Taiwan Univeristy.

Research Experience

Identifying the cis-regulatory relationship by modeling the evolutionary constrains and expression patterns across multiple species

Joint work with Dan Xie from Spring 2009. Incorporate genomic sequences, gene expressions and a phylogenetic tree across multiple species to identifying the cis-regulatory relationships during evolutions.

Rewiring gene analysis in preimplementation data

Joint work with Dan Xie, Xiaoyi Cao, Shu Xiao in Fall 2008. Identify rewiring genes in Embryonic stem cells with multiple species preimplementation data and further generate the dynamics of transcriptional network across times in each species with MATTISE. (Ready to be submitted to PNAS.)

Predicting transcription factor binding intensities from sequence

Joint work with Xin He and Feng Hong in Fall 2008. Develop a thermodynamic model to depict TF-DNA interactions and TF-TF interactions to further predict TF binding intensities. (Accepted by RECOMB Regulatory Genomics.)

Inferring Transcription Networks in Embryonic Stem Cells

Combine microarray data, sequence data and kinetic models to predict mouse embryonic stem cell gene regulatory networks. (Published in BMC genomics 2008.)

Selection of thermodynamic models for combinatorial control of multiple transcription factors in early differentiation of embryonic stem cells

Identify possible TF-TF interaction forms of target genes by thermodynamic modeling. (Published in BMC genomics 2008.)

Technical Skills

Java, C++, Perl, LaTeX, Matlab, Javascript, ASP, JSP, PHP, Html, SQL

September 10, 2009