

The Center for Genome Sciences, Department of Genetics,
Washington University School of Medicine,
Campus Box 8232, 4566 Scott Ave., St. Louis, MO 63110
Tel.636-733-0670, Fax: 314-362-7855
e-mail: jjliu@ural.wustl.edu

RESEARCH EXPERIENCE

May, 2001-present. Post-doctoral research associate in Computational Biology. Department of Genetics, Washington University School of Medicine in St Louis, MO. Post-doctoral advisor: Dr. Gary Stormo.

- I. Identifying the DNA-binding recognition code for Cys₂His₂ zinc-finger transcription factors in eukaryotic model organisms.
 1. Quantitatively assessing the validity of the additivity model assuming independence of the contributions to binding between the positions in DNA-protein interactions.
 2. Development of the novel computational method based on the sequence data and structural information to predict the DNA recognition code for C₂H₂ zinc-finger proteins.
 3. Development of a systematically experimental and computational method to rapidly build improved models of DNA-protein interactions
 4. Genome-wide identification of DNA-binding sites and target genes for C₂H₂ zinc-finger transcription factors in *Saccharomyces cerevisiae* and other eukaryotic model organisms.

- II. Development of computational methods for genome-wide association of transcription factor binding sites with their cognate transcription factors in bacterial genomes.
 1. Computational identification of bacterial regulon in *Bacillus subtilis* using microarray gene expression profiles and comparative genomics approaches.
 2. Identify the genetic network controlling various biological activities in *Shewanella oneidensis*, a model organism for environmental bioremediation.
 - a) Identification of all transcription factors and a complete set of evolutionarily conserved regulated motifs in the genome of *S. oneidensis*.
 - b) Combining expression correlation, phylogenetic correlation and genomic location to develop new computational methods to make genome-wide connections between transcription factors with their cognate binding sites in *S. oneidensis*.

August, 1995-November, 2000. Graduate research assistant. Department of Biochemistry and Molecular Biology, Louisiana State University Health Sciences Center, Shreveport, LA.

- Identifying novel regulatory mechanisms controlling cellular differentiation and development in *B. subtilis*.

1991-1993. Research assistant professor, Division of Microbiology, Chinese Academy of Forestry, China.

- Characterization of cellulase-complex systems in *Trichoderma sp.*

1988-1991. Research Scientist, Division of Microbiology, Chinese Academy of Forestry, China.

- Characterization of cellulase complex systems in fungi. Ethanol fermentation from cellulosic materials.

EDUCATION

Ph. D. 2001, Department of Biochemistry and Molecular Biology, Louisiana State University Health Sciences Center, Shreveport, LA. Graduate advisor: Dr. Peter Zuber (Professor at Oregon Health & Sciences University, Portland, OR since July, 1998).

- Dissertation: Control of RNA polymerase sigma subunits that are required for developmentally regulated transcription in *Bacillus subtilis*.

Jan., 1999-April, 2001, part-time graduate, Department of Computer Science and Engineering, Oregon Graduate Institute of Science and Technology, Portland, OR.

M. Sci. 1988, Department of Microbiology, Shandong University, Jinan, P. R. China.

- Thesis: Genetical and physiological characterization of respiratory defect mutant (*petite*) in *Saccharomyces cerevisiae*.

B. S. 1985, Department of Microbiology, Shandong University, Jinan, P. R. China.

PROFESSIONAL SOCIETIES

The International Society for Computational Biology
American Society for Microbiology
American Society for Genetics

AWARD

Excellent paper in Microbiology awarded by Shandong Society of Science and Technology, P. R. China in 1991.

PUBLICATIONS

1. **Liu J.**, and G.D. Stormo. 2005. Computationally identifying the DNA recognition code for Cys₂His₂ zinc-finger transcription factors. *Submitted to Nature Biotechnology*
2. **Liu J.**, and G.D. Stormo. 2005. Quantitative analysis of EGR proteins binding to DNA: assessing additivity in both the binding site and the protein. *BMC Bioinformatics*, **6**: 176.
3. **Liu J.**, and G.D. Stormo. 2005. Combining SELEX with quantitative assays to rapidly obtain accurate models of protein-DNA interactions. *Nucleic Acids Res.* **33**. e141.
4. **Liu J.**, K. Tan and G.D. Stormo. 2003 Computational identification of the Spo0A-phosphate regulon that is essential for the cellular differentiation and development in Gram-positive spore-forming bacteria. *Nucleic Acids Res.*, **31**: 6891-6903.

5. **Liu, J.**, and P. Zuber. 2000 ClpX of *Bacillus subtilis* is required for σ^A displacement from core RNA polymerase and stimulates σ^H -dependent transcription in vitro. *Molecular Microbiology*, **37**: 885-987.
6. Nakano M.M., Y. Zhu, **J. Liu**, and P. Zuber. 2000 Mutations conferring amino acid residue substitutions in the carboxyl-terminal domain of RNA polymerase α - subunit can suppress *clpX* and *clpP* with respect to developmentally regulated transcription in *Bacillus subtilis*. *Molecular Microbiology*, **37**: 869-884.
7. **Liu, J.**, W. M. Cosby, and P. Zuber. 1999 Role of Lon and ClpX in the post-translational regulation of a sigma subunit of RNA polymerase required for cellular differentiation of *Bacillus subtilis*. *Molecular Microbiology*, **33**: 415-428.
8. **Liu, J.**, and P. Zuber. 1998. A molecular switch controlling motility and competence: Competence regulatory factors, ComS, MecA, and ComK control the σ^D -dependent gene expression. *J. Bacteriology*. **180**: 4243-4251.
9. **Liu, J.**, and J.J. Morrell. 1997. Effect of bio-control inoculum growth conditions on subsequent chitinase and protease levels in wood exposed to bio-controls and fungi. *Material & Organism*. **30**: 265-279.
10. **Liu, J.**, and Y. Lu. 1995. Effect of pretreatment of cellulosic material on the efficiency of cellulase hydrolysis activities. *J. Chem. Forest Products*. **15(3)**: 67-71.
11. **Liu, J.**, and Y. Lu. 1995. Minireview: Components of cellulase complex and their functions. *Forest Chem. Rev.* **15(1)**: 6-10.
12. **Liu, J.**, J. Jin and D. Gao., 1989. Mechanism of mutation and mtDNA repair of respiratory defect mutant (*petite*) in *Saccharomyces cerevisiae*. *Genetica Sinica*, **6**: 28-34.

CONFERENCE PRESENTATIONS

1. **Liu J.**, and GD Stormo. Computationally exploring DNA recognition codes of Cys₂His₂ zinc-finger transcription factors. 13th Intelligent systems for Molecular Biology, Detroit, June. 2005
2. **Liu J.**, and GD Stormo. Computational identification of phosphorylated Spo0A regulon in Gram-positive bacteria. 10th Intelligent systems for Molecular Biology, Edmonton, Canada, August, 2002.
3. Nakano S., Leelakriangsak M., Nakano M., **Liu J.**, and Zuber P. The *Bacillus subtilis* *spx* gene encodes a stress-induced, ClpXP-controlled negative regulator of early competence and sporulation gene transcription. Gordon Research Conference of Microbial Stress Reponse, Newport, Rhode Island. July, 2002.

4. **Liu, J.**, and P. Zuber. 1998. Genetic Competence and motility, Competence regulatory factors, ComS, MecA, and ComK control the σ^D -dependent gene expression. East Park, Co., Wind River Conference of Prokaryotic Biology. Jun, 1998.
5. Zuber, P., **J. Liu**, M. Ogura, L. Liu and M. Nakano. 1998. A molecular switch controlling genetic competence and motility in *Bacillus subtilis*. 8th international symposium on the genetics of industrial microorganisms. Jerusalem, Israel. July, 1998.
6. **Liu, J.**, and P. Zuber. 1997. The function of *mecA* in the regulation of genetic competence and cell motility in *Bacillus subtilis*. Molecular Genetics of Bacteria and Phage Meeting, Madison, Wisconsin. August, 1997.

INVITED SEMINAR

Department of Biological Sciences, University of Texas at Arlington, Dec., 2004. Toward understanding DNA-protein recognition codes and gene expression. Host: Dr. James V. Robinson.

Department of Computational Bioscience, Pacific Northwest National Laboratory, Department of Energy of USA, Richland, Nov. 2005. Computational and experimental approaches to identify DNA-protein recognition code. Host: Dr. T. P. Straatsma

SOFTWARE

zifcodeNet package for identifying the DNA recognition code of zinc finger proteins developed with C programming. The package includes five components: 1) sequence data management, 2) the delta rule based perceptron learning, 3) back-propagation algorithm based the non-linear work model learning, 4) statistical analysis for predictions, and 5) prediction of the DNA-binding profiles for the given zinc-finger proteins.

RELATED SKILLS IN COMPUTATIONAL SCIENCES

Computer Science

- Proficiency in programming with C, Perl, C++. Experiences in development of relational database. Proficiency with both UNIX (LINUX) and Window operating systems.
- Relevant Courses:
 - 1) Undergraduate level: C Programming, C++ Programming, Data structure and Discrete Math.
 - 2) Graduate level: Analysis and Design of Algorithms, Introduction to Computer Architecture, Introduction of Database Systems, Principle of Compiler Design, Statistical computing, Machine Learning (Classes offered by Oregon Graduate Institute of Science and Technology).

Statistics

- Strong background in statistical theory. Proficiency in programming with S-plus. Familiar with Matlab.
- Related Courses (graduate level): Methods of Data Analysis I, Methods of Data Analysis II, Methods of Data Analysis III, Statistical Computing (with S-Plus) (Classes offered by Oregon State University and Oregon Graduate Institute of Science and Technology, respectively).

Computational Biology, Genomics and Bioinformatics

- Strong background in theory and algorithm designs for Computational Biology and Genomics.
- Related Courses: Computational Molecular Biology, Introduction to Genomics. Mathematics in Biochemistry and Biophysics (Classes offered by Washington University in St. Louis).