

Curriculum Vitae

Henry (Xiufeng) Wan

CONTACT INFORMATION

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EDUCATION

- Training** Prokaryotic Annotation and Analysis Training, The Institute of Genome Research
Rockville, MD, 11/2002
- Workshop** Campus Writing Program Faculty Workshop, University of Missouri-Columbia, 08/2004.
- Ph.D.** Veterinary Medicine, minor in Biochemistry and Molecular Biology,
Mississippi State University, Mississippi State, MS, 08/2002
- M. Sc.** Computer Science, Mississippi State University, Mississippi State, MS, 08/2002
- M. Sc.** Avian Medicine, South China Agricultural University, Guangzhou,
Guangdong Province, P. R. China, 06/1998
- B.S. (D.V.M.)** Jiangxi Agricultural University, Nanchang, Jiangxi Province, P. R. China, 07/1995

PROFESSIONAL EXPERIENCE

- 11/2003—present Postdoctoral Fellow, Digital Biology Laboratory, Department of Computer Science,
University of Missouri-Columbia, Columbia, MO, 65211. Computational modeling of
emerging viral diseases (avian influenza virus, SARS-Cov, HIV), RNA local secondary
structure prediction, intrinsic termination prediction and its application in *Synechococcus*,
regulatory motif prediction, regulatory network construction using microarray data,
proteomics data analysis (MS/MS) (*Mycoplasma gallinarum*), statistical assessment for
proteomics data (MS finger printing), anti-sense gene prediction using EST and tiling array
in *Arabidopsis*, membrane protein structure prediction, codon usage analysis in avian
influenza virus, and phylogenetic construction using whole genomic sequences.
- 08/2002—11/2003 Postdoctoral Research Associate, Environmental Sciences Division, Oak Ridge National
Laboratory, Oak Ridge, TN, 37831. Microarray hybridization and data analysis for null
mutants (*etrA*⁻, *fur*⁻, *crp*⁻, *arcA*⁻, *etrA*⁻*fur*⁻, and *etrA*⁻*crp*⁻) in *Shewanella*, phenotype
characterization for these five mutations, microarray database construction, microarray
data analysis for PH stress and respiratory stimulations, oligo design for microbial
community study, primer design for phage display for *Shewanella*, regulatory network
construction using microarray data, and codon usage analysis.
- 08/1998—08/2002 Research associate, College of Veterinary Medicine, Mississippi State University,
Mississippi State, MS, 39762. Host adaptation of *Mycoplasma gallinarum*, research
focusing on the leucine aminopeptidase (identification by screen library, genetic and
biomedical characterization, and gene expression), P30 gene identification in *M.*
gallinarum, identification and characterization of pMGA gene in *M. gallisepticum*.
Laboratory technologies involved (PCR, RT-PCR, library construction and screening,
Southern/Northern/Western blotting, cloning, expression, protein folding, site-directed
mutagenesis, DNA sequencing, antibody preparation in chicken, monoclonal antibody

preparation). Research in Computer Science included development of an interactive clustering algorithm and its application in the analyses of translation and transcription initiation patterns in *Archaea*.

- 07/1995—07/1998 Research associate, College of Veterinary Medicine, South China Agricultural University, Guangzhou, P. R. China, 510642. Isolation and characterization of H5N1 Avian Influenza Virus in Southern China, anti-AI drug screening, vaccine preparation and clinical assessment, clinical diagnoses, prevention and treatment of avian diseases (infectious diseases, nutritional diseases, metabolic and developmental disorders, poisons and toxins). Laboratory technologies include viral isolation and identification using embryo and cell culture, gene cloning, PCR and RT-PCR, transmission electronic microscopy, cell culture, immunoassay, and AIV sub-typing.
- 01/1995—05/1998 Intern, South China Agricultural University. Development of diagnosis technologies for influenza A virus, including both clinical and laboratory technologies.

AWARDS AND HONORS

- 2003 The Best Paper Award Nomination for the International Conference of Artificial Neural Networks In Engineering (ANNIE) 2003.
- 2001 Outstanding Student Poster Presentation Award at the American Society for Microbiology, South Central Branch Meeting.
- 2001 Outstanding Progress in Scientific Technology Award (II) from Guangdong Province, P. R. China.
- 1998 ADM Award, Archer Daniels Midland Animal Health and Nutrition Division.
- 1996—1997 Excellent Graduate Awards, South China Agricultural University.
- 1996 Roche Award, Roche Inc.
- 1991—1995 Excellent Undergraduate Awards, Jiangxi Agricultural University.

PROFESSIONAL ACTIVITIES AND SERVICE

- **Member:** Member of American society for Microbiology (Since 2001), Member of International Society of Computational Biology (Since 2004), Member of Chinese Society for Veterinary Medicine (1995-1998).
- **Invited Reviewer:** *The 2nd IEEE Computational Systems Bioinformatics conference* (2003), *The 3rd IEEE Computational Systems Bioinformatics Conference* (2004), *The 12th international conference on intelligent systems for molecular biology* (2004), *FEBS Letters* (2004), *Journal of Virology* (2004), *Protein and Peptide Letters* (2004), *International Journal of Bioinformatics Research and Applications* (2004).

GRANTS

Projects in preparation

1. “Development of informatics systems for detecting potential pathogenic genotypes for emerging/re-emerging viral diseases”, Wan, P.I., and two other co-P.I.s, plan to submit on Feb 1 as NIH R21 (PA-03-178).
2. “Understanding prokaryotic gene expression”, Kilbane, P.I., and Wan, co-P.I., plan to submit to DOD DARPA proposal (BAA04 -12).

Projects funded

1. DOE NABIR, Zhou, P.I., Wan, and three others, co-P.I.s, “Development and use of integrated microarray-based genomic technologies for assessing microbial community composition and dynamics (2003-2005)”, US\$1,400,000.
2. Mississippi State University, Research Initiation, Pharr, P.I., and Wan, co-P.I., “Cloning and sequencing of cytoadhesin genes in *M. gallinarum* (1998-1999)”, US\$4,417.
3. Chinese Minister of Agriculture, Xin, P.I., and Wan, co-P.I., “Prevention and control of Avian Influenza in China (1995-1998)”, RMB 150,000 (equivalent to about US\$18,000).

Projects not funded

1. NIH, Xu, P.I, Wan, co-P.I. and two others, “Computational modeling of SARS”, US\$1,250,000.
2. DOE GTL Leuze, P.I., Wan, co-P.I. and two others, “Development and validation of computational tools for theoretical modeling of gene regulatory networks in (metal-reducing) bacteria”, US\$3,000,000.
3. ORNL, Seed Proposal, Xiong, P.I., Wan, co-P.I and three others, “An entropy maximization approach to the recovery and analysis of gene regulatory networks using microarray data”, \$125,000.

TEACHING EXPERIENCE

Courses: I have been given the opportunities to co-teach three courses with Prof. D. Xu, Introduction to Bioinformatics (fall of 2003), Algorithm (spring of 2004), and Computational Methods in Bioinformatics (fall of 2004, <http://digbio.missouri.edu/~wanx/cs7010>) at Department of Computer Science, University of Missouri-Columbia.

Supervised students: Peter Dempsey (undergraduate), Sara Stewart (graduate student), Chris Topinka (graduate student), and Shafquat B. Bhuiyan (graduate student).

PUBLICATIONS

Manuscripts in preparation

- **Wan, X.-F.**, T. Li, D. Stanek, D. Xu, J. Zhou, and D. Thompson. Characterization of *ArcA* deletion mutant transcriptome data for *Shewanella oneidensis* MR-1: possible involvement in the regulation of oxidative stress. In preparation.
- **Wan, X.-F.**, D. Stanek, J. Zhou, and D. Thompson. Defining a small regulatory network of *Shewanella oneidensis* MR-1 using double mutant strategy. In preparation.
- **Wan, X.-F.**, G. Lin, and D. Xu. Approaching optimal RNA local secondary structure using thermodynamic parameters. In preparation.
- **Wan, X.-F.**, S. L. Branton, and G. T. Pharr. Proteomic inferring host adaptation of *Mycoplasma gallinarum*. In preparation.
- **Wan, X.-F.** and D. Xu. Remote homology detection. Invited review for *Current Protein and Peptide Science*.

- Chung, W. H., S. K. Rhee, **X.-F. Wan**, J.-W. Bae, Z.-X. Quan, S.-M. Kim, and Y.-H. Park. Design of long oligonucleotide probe for detection of functional gene in microbial community. In preparation.

Manuscripts submitted

- Wu, X., **X.-F. Wan**, G. Wu, D. Xu, and G. Lin. Whole genome phylogeny via complete composition vectors. Submitted.
- **Wan, X.-F.** and D. Xu. Rnall: a new tool for RNA local secondary structure prediction. Submitted.
- **Wan, X.-F.**, J. Zhou, and D. Xu. CodonO: a new informatics method measuring synonymous codon usage bias. *International Journal of General Systems*. Invited paper.

Referred Journal publications

1. **Wan, X.-F.**, T. Ren, K.-J. Luo, M. Liao, G.-H. Zhang, J.-D. Chen, W.-S. Cao, Y. Li, N.-Y. Jin, D. Xu, and C.A. Xin. Genetic Characterization of H5N1 Avian Influenza Viruses isolated in Southern China during the 2003-04 avian influenza pandemic. *Archives of Virology*, in press.
2. **Wan, X.-F.** and D. Xu. Intrinsic terminator prediction and its application in *Synechococcus sp.* WH8102. *Journal of Computer Science and Technology*, in press.
3. **Wan, X.-F.**, N.C. VerBerkmoes, L. A. McCue, D. Stanek, H. Connelly, L. Wu, X. Liu, T. Yan, A. Leaphart, R. L. Hettich, J. Zhou, and D. K. Thompson. 2004. Transcriptomic and proteomic characterization of the fur modulon in the metal-reducing bacterium *Shewanella oneidensis*. *Journal of Bacteriology*, **186**: 8385-8400.
4. Rhee, S. K., X. Liu, L. Wu, S. C. Chong, **X. Wan**, and J. Zhou. 2004. Detection of biodegradation and biotransformation genes in microbial communities using 50-mer oligonucleotide microarrays. *Applied and Environmental Microbiology*, **70**: 4303-4317.
5. **Wan, X.-F.**, S. M. Bridges, and J. A. Boyle. 2004. Revealing different transcription initiation and translation initiation patterns in archaea using an interactive clustering model. *Extremophiles*, **8**: 291-299.
6. **Wan, X.-F.**, D. Xu, A. Kleinhofs, and J. Zhou. 2004. Quantitative relationship between codon usage bias and GC composition across the unicellular genomes. *BMC Evolutionary Biology*, **4**: 19 (<http://www.biomedcentral.com/1471-2148/4/19/>).
7. **Wan, X.**, S. L. Branton, L. A. Hanson, and G. T. Pharr. 2004. Identification and initial characterization of an aminopeptidase gene in *M. gallinarum*. *Current Microbiology*, **48**: 32-38.
8. **Wan, X.**, S. L. Branton, M. B. Hughlett, L.A. Hanson, and G. T. Pharr. 2004. Expression and subcellular location of a leucine aminopeptidase of *Mycoplasma gallinarum*. *International Journal of Poultry Science* **3(1)**: 70-74.
9. Pharr, G. T., S. L. Branton, L. A. Hanson, F. C. Minion, M. B. Hughlett, and **X. Wan**. 2002. Characterization of pMGA genes from the F-strain (Vaccine strain) of *Mycoplasma gallisepticum*. *International Journal of Poultry Science*, **1 (4)**: 63-73.
10. Guo, Y., M. Wang, X. Xu, **X. Wan**, J. Guo, J. Dong, and Y. Zhang. 1999. Nucleotide sequence of A/Goose/Guangdong/2/96(H5N1) virus M and NS RNA. *Chinese Journal of Experimental and Clinical Virology*, **4 (13)**: 305-309.

11. Guo, Y., X. Xu, and **X. Wan**. 1998. Genetic characterization of an avian influenza A (H5N1) virus isolated from a sick goose in China. *Chinese Journal of Experimental and Clinical Virology*, **12(4)**: 322-325.
12. **Wan, X.** and C. Xin. 1998. Prevention and control of Avian Influenza. *Journal of Poultry Husbandry and Diseases Control*, **6**: 5-6.
13. Xin, C., M. Liao, G. Huang, and **X. Wan**. 1996. Avian Influenza. *Journal of Poultry Husbandry and Diseases Control*, **12**: 4-5.
14. Xin, C., M. Liao, G. Huang, and **X. Wan**. 1995. Fluoride and soft leg symptom in poultry. *Journal of Poultry Husbandry and Diseases Control*, **12**: 13-14.

Referred Conference Proceedings

1. Ganapathy, A., **X.-F. Wan**, B. D. Gue, J. Wan, J. Thelen, D. W. Emerich, G. Stacey and D. Xu. 2004. Statistical assessment for Mass-spec protein identification using peptide fingerprinting approach. In *Proceedings of the 26th Annual International Conference IEEE Engineering in Medicine and Biology Society (EMBS'04), Bioinformatics and Computational Biology*, San Francisco, CA, pp. 3051-3054.
2. **Wan, X.**, D. Xu, and J. Zhou. 2003. A new informatics method measuring synonymous codon usage bias. In *Intelligent engineering systems through artificial neural networks*, vol **13**, eds. Dagli et al., 1101-1018. New York, NY: ASME Press.
3. **Wan, X.**, S. M. Bridges, J. A. Boyle, and A. P. Boyle. 2002. Interactive clustering for exploration of genomic data. In *Intelligent engineering systems through artificial neural networks*, vol **12**, eds. Dagli et al., 753-758. New York, NY: ASME Press.

Book Chapters

1. **Wan, X.-F.**, D. Ataman, and D. Xu. 2004. Application of computational biology in understanding emerging infectious diseases: inferring the biological function for S-M complex of SARS-CoV. Invited book chapter for *Progress in Bioinformatics*, Nova Publisher, Inc., in press. (Protein structure prediction and protein sequence analysis)
2. Xu, D., O. Duzlevski, and **X.-F. Wan**. 2004. In search of remote homolog. In *Handbook of Computational Molecular Biology*, CRC Press, in press. (Sequence analysis)

Technical Reports

1. **Wan, X.** 2002. Interactive clustering for exploration of genomic data.
2. Pharr, G. T. and **X. Wan**. 1999. Cloning and characterization of P30 gene in *M. gallinarum*.

Software Developed

- [Interactive Clustering Model \(ICM\)](#): a software for discovering the gene regulation pattern. ICM performed sequence clustering analysis. Jointly developed with S. M. Bridges and J. A. Boyle.
- [CodonO](#): a software for calculating synonymous codon usage orderliness (SCUO). codonO performs codon usage bias analysis within and across genomes. Jointly developed with D. Xu, A. Kleinhofs, and J. Zhou.

- [Rnall](#): a software package for predicting local RNA secondary structure. Rnall performs local RNA secondary structure prediction in genome scale in a linear time complexity. The function of intrinsic terminator prediction has also been included. Jointly developed with D. Xu.
- [ContactMapper](#): a software for predicting protein-protein interaction using correlated mutation strategy.

Degree Theses

- An aminopeptidase acting as a potential factor in host adaptation of *Mycoplasma gallinarum*. 2002. Ph.D. thesis in Veterinary Medicine.
- Interactive clustering for exploration of genomic data. 2002. M.Sc. in Computer Science.
- Isolation and characterization of avian influenza viruses in China. 1998. M.Sc. in Avian Medicine.

POSTER PRESENTATIONS

1. **Wan, X.** and D. Xu. Rnall: a new tool for local RNA secondary structure prediction. The Pacific Symposium on Biocomputing (PSB), January 4-8, 2005, Big Island of Hawaii.
2. **Wan, X.**, and D. Xu. Diverse Genotypes of 2003-04 Avian Influenza H5N1 Pandemic in Asia. ASM Conference on Functional Genomics and Bioinformatics Approaches to Infectious Disease Research, October 6-9, 2004, in Portland, Oregon.
3. **Wan, X.**, and D. Xu. Application of computational biology in understanding emerging infectious diseases: inferring the biological function for S-M complex of SARS-CoV. ASM Conference on Functional Genomics and Bioinformatics Approaches to Infectious Disease Research, October 6-9, 2004, in Portland, Oregon.
4. **Wan, X.**, O. Duzlevski, and D. Xu. Rnall: a novel algorithm for predicting RNA local secondary structure and its application in Rho-independent terminator prediction. MU Live Life Science Week poster section, Apr 5-9, Columbia, MO.
5. **Wan, X.**, D. Xu, and J. Zhou. Quantitative relationship between codon usage bias and GC content, American Society of Microbiology 104th annual meeting, May 23-27, 2004, New Orleans, LA.
6. Su, Z. P. Dam, H. Peng, Y. Xu, X. Chen, T. Jiang, D. Xu, **X. Wan**, and B. Palenik. Computational Inference of Regulatory Networks in *Synechococcus sp* WH8102. Genome to Life Contractor-Grantee Workshop II, Feb 29-Mar 2, 2004, Washington, D.C.
7. Zhou, J., D. K. Thompson, M. W. Fields, T. Palzkill, J. M. Tiedje, K. H. Nealson, A. S. Beliaev, T. Li, **X. Wan**, *etc.* Integrated Analysis of Gene Functions and Regulatory Networks Involved in Anaerobic Energy Metabolism of *Shewanella oneidensis* MR-1. Genome to Life Contractor-Grantee Workshop II, Feb 29-Mar 2, 2004, Washington, D.C.
8. **Wan, X.**, N. VerBerkmoes, D. Stanek, L. A. McCue, A. Leaphart, T. Li, R. L. Hettich, C. E. Lawrence, D. K. Thompson, and J. Zhou. Transcription expression profiling of *etrA*, *fur* and *etrA/fur* deletion mutants of *Shewanella oneidensis* MR-1. The 11th International Conference on Microbial Genomes, Sep 28-Oct 2, 2003, in Durham, NC.
9. Romine, M., A. Beliaev, G. Newton, S. Reed, V. Crusselle, A. Alford, P. Lu, J. Fredrickson, M. Fields, **X. Wan**, *etc.* Progress in Development of Genetic Tools for *Shewanella oneidensis* MR-1. Genome to Life Contractor-Grantee Workshop I, Feb 9-12, 2003, Arlington, VA.

10. **Wan, X.**, D. K. Thompson, and J. Zhou. Transcriptome characterization of *etrA*, *fur*, and *etrA/fur* deletion mutants. *Shewanella* federation meeting, Aug 5-7, 2003, Pacific Northwest National Laboratory.
11. Leaphart, A., Stanek, D., **X. Wan**, and J. Zhou. Phage display development for *S. oneidensis* MR-1. *Shewanella* federation meeting, Aug 5-7, 2003, Pacific Northwest National Laboratory.
12. **Wan, X.**, Y. Liu, and J. Zhou. A simple informational index measuring synonymous codon usage order (SCUO). The 103rd ASM General Meeting, May 18-22, 2003, Washington, D.C.
13. Stanek, D., Thompson, D. K., **X. Wan**, M. Fields, and J. Zhou. Microarray expression profiles of different electron receptors from *Shewanella oneidensis* MR-1 revealing the possible metal reducing pathway. The 103rd ASM General Meeting, May 18-22, 2003, Washington, D.C.
14. Connelly, H., N. C. VerBerkmoes, **X. Wan**, D. Stanek, D. K. Thompson, L. Hauser, F. W. Larimer, J. Zhou, and R. L. Hettich. Proteome profiling of *Shewanella oneidensis* MR-1 *fur*, *etrA*, and *fur/etrA* mutants. The 52nd ASMS Conference on Mass Spectrometry, Jun 8 - 12, 2003, Montreal, Canada.
15. Rhee, S. K., **X. Wan**, J. Zhou. A microarray for monitoring bioremediation by detecting expression of biodegradation and metal resistance genes. The 103rd ASM General Meeting, May 18-22, 2003, Washington, D.C.
16. Rhee, S. K., **X. Wan**, J. Zhou. Biodegradation gene-based oligonucleotide microarray for assessing metabolic diversity and activity in bioremediation sites. The 7th international symposium: *in situ* and on-site bioremediation, Jun 2-5, 2003, Orlando, FL.
17. **Wan, X.**, S. Branton, L. Hanson, and G. T. Pharr. 2001. Identification of a putative aminopeptidase gene from *M. gallinarum*. The 2001 Meeting of the American Society for Microbiology South Central Branch, Oct 12-13, Baton Rouge, LA.

INVITED TALKS

1. Computational exploration of biological systems. Department of Microbiology, Miami University, Oxford, OH. January 2005.
2. Defining regulon in *Shewanella oneidensis* using transcriptomic data. Ellis Fischel State Cancer Center, University of Missouri-Columbia, Columbia, MO. January 2005.
3. Construction of regulatory network using Bayesian networks. Digital Biology Laboratory, Department of Computer Science, University of Missouri-Columbia, Columbia, MO. December 2004.
4. Application of computational biology in understanding emerging infectious diseases : inferring contact residues for S-M complex of SARS-CoV. Digital Biology Laboratory, Department of Computer Science, University of Missouri-Columbia, Columbia, MO. October 2004.
5. Rnall: a novel algorithm for locally stable RNA secondary structure prediction and its potential applications. Department of Computer Science, University of Missouri-Columbia, Columbia, MO. April 2004.
6. Rnall and SaRna: simple algorithm for RNA secondary structure prediction. Digital Biology Laboratory, Department of Computer Science, University of Missouri-Columbia. February 2004.

7. A new informatics method measuring synonymous codon usage bias. ANNIE 2003 conference, St. Louis, MO. November 2003.
8. Interactive clustering of genomic data. ANNIE 2002 conference, St. Louis, MO. November 2002.
9. Exploration of genomic data using a k -clustering model. Life Science Division, Oak Ridge National Laboratory. October 2002.

REFERENCES

1. *Current Postdoc Training Supervisor*

Dong Xu, Ph.D., James C. Dowell Associate Professor
Digital Biology Laboratory
Department of Computer Science
University of Missouri-Columbia
E-mail: xudong@missouri.edu
Tel: 573-882-7064

2. *Postdoc Training Supervisor at ORNL*

Dorothea K. Thompson, Ph.D., Group Leader, Research Scientist
Microbial Ecology and Functional Genomics Group
Environmental Sciences Division
Oak Ridge National Laboratory
E-mail: thompsondk@ornl.gov
Tel: 865-574-4815

3. *Graduate Mentor in Veterinary Medicine*

G. Todd Pharr, Ph.D., Associate Professor
College of Veterinary Medicine
Mississippi State University
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