

Erliang Zeng

CONTACT INFORMATION	Department of Computer Science and Engineering The University of Notre Dame 384 Fitzpatrick Hall Notre Dame, IN 46556 USA	<i>Phone:</i> (574) 631-1375 <i>E-mail:</i> ezeng@nd.edu <i>Web:</i> www.nd.edu/~ezeng
RESEARCH INTERESTS	Bioinformatics, computational biology, knowledge discovery and data mining, statistical modeling and data analysis, algorithm design, software development	
EDUCATION	Florida International University , Miami, FL USA Ph.D., Computer Science, 2008 <ul style="list-style-type: none">• Advisor: Professor Giri Narasimhan• Area of Study: Bioinformatics M.S., Computer Science, 2007 Shanghai Jiao Tong University , Shanghai, China M.S., Biochemistry and Molecular Biology, 2001 B.S., Biotechnology, 1998	
ACADEMIC APPOINTMENTS	Research Assistant Professor Department of Computer Science and Engineering, The University of Notre Dame Managing Director The Bioinformatics Core Facility (BCF), The University of Notre Dame Postdoctoral Researcher Department of Computer Science, The University of Miami <ul style="list-style-type: none">• Advisor: Professor Mitsunori Ogiwara• Area of Research: Bioinformatics and Data Mining	July 2009 to present July 2009 to present September 2008 to June 2009
AFFILIATIONS	Eck Institute for Global Health, The University of Notre Dame	2009 to present
RESEARCH GROUP	Wei Zhang (PhD candidate, coadvised with Scott Emrich) Rory Carmichael (Senior analyst, Bioinformatics Core)	
PUBLICATIONS	Papers in Preparation or Submitted J. J. Hellmann ¹ , J. D. K. Dzurisin, S. T. O'Neil, S. J. Emrich, N. F. Lobo, J. A. Keppel, J. M. Mueller, C. M. Williams, R. D. Carmichael, E. Zeng , Comparative genomics and whole-transcriptome responses of two insects to altered climate. D. Shin, E. Zeng , A. Mori, D. W. Severson, Expression profiling by genome wide microarray reveals differential gene expression in meiotic drive system of <i>Aedes aegypti</i> . P. McHenry, P. Sirisha, M. Hwang, J. Sears, K. Park, C. Mohar, E. Zeng , J. Rosen, T. Vargo-Gogola, Changes in mammary gland p190B RhoGAP levels alter mitosis leading to chromosomal instability, submitted.	

Book Chapters

E. Zeng, C. Ding, K. Mathee, L. Schneper, G. Narasimhan, Gene function prediction and functional network: the role of gene ontology. *DATA MINING: Foundations and Intelligent Paradigms*. D.E. Holmes and L.C. Jain (Eds), Springer, Accepted.

C. Yang*, **E. Zeng***, K. Mathee, G. Narasimhan, PlasmoTFBM: A Database of Predicted Transcription Factor Binding Motifs in Plasmodium falciparum. *Methods of Microarray Data Analysis V*. McConnell, Lin, Hurban (Eds.), Springer, p121-136, 2007. *Joint first authors.

Journals

W. Zhang, S. Emrich, **E. Zeng**, Comparative study of machine learning approaches for pathway analysis, accepted by the International Journal of Data Mining & Bioinformatics.

P. P. Singh, C. LeMaire, J. Tan, **E. Zeng**, J. S. Schorey, Exosomes released from M.tuberculosis infected cells can suppress IFN- γ mediated activation of nave macrophages, *PLoS ONE*. 2011; 6(4):e18564. doi:10.1371/journal.pone.0018564.

E. Zeng, C. Yang, T. Li, G. Narasimhan, Clustering genes using heterogeneous data sources, *International Journal of Knowledge Discovery in Bioinformatics*. 2010; 1(2):12-28.

M. Doud, **E. Zeng**, L. Schneper, G. Narasimhan, K. Mathee, Approaches to analyze dynamic microbial communities such as those seen in cystic fibrosis lung, *Human Genomics*. 2009; 3(3):246-256.

K. Mathee, G. Narasimhan, C. Valdes, X. Qiu, J. Matewish, M. Koehrsen, A. Rokas, C. Yandava, R. Engels, **E. Zeng**, R. Olavarietta, M. Doud, R. Smith, P. Montgomery, J. White, P. Godfrey, C. Kodira, B. Birren, J. Galagan, S. Lory, Dynamics of Pseudomonas aeruginosa genome evolution , *Proceedings of the National Academy of Sciences (PNAS)*. 2008; 105(8):3100-05.

J. Yue, W. Shi, J. Xie, Y. Li, **E. Zeng**, L. Liang, H. Wang, Detection of rifampin-resistant Mycobacterium tuberculosis strains by using a specialized oligonucleotide microarray, *Diagn Microbiol Infect Dis*. 2004 Jan;48(1):47-54.

X. Gao, X. Fu, T. Li, J. Zi, Y. Luo, Q. Wei, **E. Zeng**, Y. Xie, Y. Li, Y. Mao, Determining a detectable threshold of signal intensity in cDNA microarray based on accumulated distribution , *J Biochem Mol Biol*. 2003 Nov 30;36(6):558-64.

J. Yue, W. Shi, J. Xie, Y. Li, **E. Zeng**, H. Wang, Mutations in the rpoB gene of multidrug-resistant Mycobacterium tuberculosis isolates from China, *J Clin Microbiol*. 2003 May;41(5):2209-12.

J. Yue, **E. Zeng**, J. Xie, Y. Li, L. Liang, H. Wang, Reliable Detection of Rifampin-Resistance of Mycobacterium tuberculosis Strains by Using a Specialized Oligonucleotide Microarray (in Chinese), *Chinese Journal of Biochemistry and Molecular Biology*. 2004 ;20(2):264-9.

J. Yue, **E. Zeng**, J. Xie, Y. Li, L. Liu, H. Wang, Molecular mutations of rpoB gene of multidrug resistant Mycobacterium tuberculosis isolates from China (in Chinese), *Journal of Genetics and Genomics*. 2004 Dec;31(12):1332-6.

M. He, **E. Zeng**, Y. Zheng, Z. Tang, X. Lu, B. Sun, D. Xu, Z. Zhang, L. Yang, Identification of Mycobacterium tuberculosis and rifampin-resistant strains by gene-chips (in Chinese), *Chinese Journal of Epidemiology*. 2003 May; 24(5):385-8.

L. Li, Y. Lin, Y. Liu, **E. Zeng**, C. Li, The Use of Shareware for mtDNA Sequence Comparison (in Chinese), *Chinese Journal of Forensic Sciences*. 2003;(1):29-31.

E. Zeng, J. Liu, Z. Lin, The nucleic acid analysis by DNA chip technique based on nuclease S1 protection (in Chinese), *Acta Academiae Medicinae Sinicae*. 2001 Feb;23(1):89-92.

D. Wang, M. Li, **E. Zeng**, W. Zhang, X. Wu, Cloning of Secondary Lymphoid-tissue Chemokine (SLC) and Its Expression in Prokaryotic System (in Chinese), *Chinese Journal of Biotechnology*. 2001; 17(4):392-395.

Conference Proceedings

W. Zhang, S. Emrich, **E. Zeng**, A Two-Stage Machine Learning Approach for Pathway Analysis, to appear in the *Proceedings of BIBM'10: the IEEE International Conference on Bioinformatics and Biomedicine*, Hong Kong, December, 2010.

Y. Zhang, **E. Zeng**, T. Li, G. Narasimhan, Weighted Consensus Clustering for Identifying Functional Modules in Protein-Protein Interaction Networks, *Proceedings of ICMLA'09: the International Conference on Machine Learning and Applications*, Miami, December, 2009.

E. Zeng, M. Ogihara, Nonnegative Least Square - A New Look Into SAGE Data, *Proceedings of CSB'09: the LSS Computational Systems Bioinformatics Conference*, P151-161, Stanford, CA, August, 2009.

E. Zeng, K. Mathee, L. Schneper, G. Narasimhan, A Functional Network of Yeast Genes Using Gene Ontology Information, *Proceedings of BIBM'08: the IEEE International Conference on Bioinformatics and Biomedicine*, p343-346, Philadelphia, PA, November, 2008.

E. Zeng, C. Ding, G. Narasimhan, S. R. Holbrook, Estimating Support for Protein-Protein Interaction Data with Applications to Function Prediction, *Proceedings of CSB'08: the LSS Computational Systems Bioinformatics Conference*, p73-84, Stanford, CA, August, 2008.

E. Zeng, C. Yang, T. Li, G. Narasimhan, On the Effectiveness of Constraints Sets in Clustering Genes, *Proceedings of BIBE'07: the 7th IEEE International Symposium on Bioinformatics & Bioengineering*, p79-86, Boston, MA, October, 2007.

E. Zeng, K. Mathee, G. Narasimhan, IEM: An Algorithm for Iterative Enhancement of Motifs Using Comparative Genomics Data, *Proceedings of CSB'07: the LSS Computational Systems Bioinformatics Conference*, p227-235, UCSD, CA, August, 2007.

E. Zeng, G. Narasimhan, Enhancing Motif Refinement by Incorporating Comparative Genomics Data, *Proceedings of ISBRA'07: the International Symposium on Bioinformatics Research and Applications*, Lecture Notes in Computer Science, Vol. 4463, Springer Verlag, p329-337, 2007.

C. Yang, **E. Zeng**, T. Li, G. Narasimhan, Clustering Genes using Gene Expression and Text Literature Data, *Proceedings of CSB'05: the IEEE Computer Society Bioinformatics Conference*, p329-340, Stanford, CA, August 2005.

C. Yang, **E. Zeng**, T. Li, G. Narasimhan, A Knowledge-Driven Method to Evaluate Multi-Source Clustering, *Proceedings of BIOS'05: the International Workshop on Bioinformatics*, Lecture Notes in Computer Science, Vol. 3759, Springer Verlag, 2005.

C. Yang*, **E. Zeng***, K. Mathee, G. Narasimhan, Querying a Database of Regulatory Elements, *Proceedings of ICBA'04: the International Conference on Bioinformatics and its Applications*, Fort Lauderdale, Florida, December 2004. *contributed equally.

C. Yang*, **E. Zeng***, K. Mathee, G. Narasimhan, Mining Regulatory Elements in the Plasmodium falciparum Genome Using Gene Expression Data, *Proceedings of CAMDA'04: the Critical Assessment of Microarray Data Analysis*, Durham, NC, November 2004. *contributed equally.

Conference Posters

E. Zeng, S. Chatterjee, K. Mathee, G. Narasimhan, Iterative Enhancement of Motifs Using Comparative Genomics Data, *Fourth Annual RECOMB Satellite on Regulatory Genomics*, Boston, October 2007.

- G. Narasimhan, K. Mathee, C. Valdes, **E. Zeng**, R. Olavarietta, M. Doud, P. Godfrey, M. Koehrsen, A. Rokas, C. Yandava, R. Engels, C. Kodira, Bruce Birren, J. Galagan, S. Lory, Comparative Genomics of the Pathogen *Pseudomonas aeruginosa*, *Fifth Annual RECOMB Satellite on Comparative Genomics*, San Diego, September 2007.
- P. Godfrey, K. Mathee, G. Narasimhan, C. Valdes, **E. Zeng**, R. Olavarietta, M. Doud, C. Yandava, M. Koehrsen, R. Engels, P. Montgomery, J. White, C. Kodira, S. Lory, B. Birren, J. Galagan, Comparative genomics of *P. aeruginosa*, *CSHL workshop on Genome Informatics*, Cold Spring Harbor Laboratory, November 2007.
- C. Yang, **E. Zeng**, G. Narasimhan, A Knowledge-Driven Method to Evaluate Multi-Source Clustering, *The ISMB BioLINK Special Interest Group*, Detroit, June 2005.
- G. Zheng, **E. Zeng**, E.O. George, G. Narasimhan, Integrating Information from Different Microarray Data Sets, *In Silico Conference*, Atlanta, November 2003.

PATENTS

E. Zeng, J. Liu, Z. Lin, Number: 00119541.7 (Chinese), 2001.

RESEARCH
EXPERIENCE

Research Assistant Professor University of Notre Dame, July 2009 to present

Bioinformatics Algorithm Development

- Develop new algorithms for microarray data analysis, next-generation sequencing data analysis, and metagenomic data analysis.

Managing Director of BCF University of Notre Dame, July 2009 to present

Bioinformatics Core Facility (BCF) Management

- Daily management of bioinformatics core facility including overseeing core lab functions and technical staff.
- Build collaborative relationships with faculty members from other departments.

Postdoctoral Researcher University of Miami, September 2008 to June 2009

Study of Neurological Disorders

- Data mining on genomics data and gene expression data of neurological disorders such as Alzheimer's disease and Parkinson's disease.

Research Assistant Bioinformatics Research Group (BioRG), Florida International University, September 2003 to August 2008

Protein-Protein Interaction Mining

- Predicted protein function and networks using comparative genomics and multi-source data.

Gene Regulation Mining

- Revealed gene regulation mechanisms using comparative genomics and gene expression data.

Clustering Genes Using Heterogeneous Biological Data

- Investigated effectiveness of constraints sets in clustering genes.
- Developed a new algorithm called Multi-Source Clustering (MSC) to cluster genes by combining microarray data and text information.

Mining Regulatory Elements Using Gene Expression Data

- Predicted putative transcription factor binding motifs (TFBMs) in *P.falciparum* using two different computational approaches and building a relational database called PlasmotFBM with a user-friendly web interface.

Internship Lawrence Berkeley National Laboratory, June 2007 to August 2007
Research on Mining Protein-Protein Interaction Data

Internship Centocor (a subsidiary of Johnson&Johnson), May 2006 to August 2006
Implemented a Web-based Program for Target Explorer
Developed a Web Application of Codon Usage
Analyzed Flow Cytometry Data for Department of Experimental Pathology
Microarray Data Analysis and Promoter Sequence Data Analysis

Group Leader Research and Development Dept., Biostar Genechip Inc., Shanghai, China, May 2001 to June 2003

Developed Oligonucleotide Microarrays for SNP Detection

- Developed SNP chips for forensics testing.

Study of Expression Profiles of Hepatocellular Carcinoma Using cDNA Microarray

- Participated in using cDNA microarray to investigate gene expression profiles of Hepatocellular Carcinoma.

Developed Oligonucleotide Microarrays for M. tuberculosis Drug Resistance Detection

- Developed microarrays for detecting drug resistance in *M.tuberculosis*.

Basic Research on Oligonucleotide Microarrays

- Participated in establishing a oligonucleotide microarray technical platform for organization.

TEACHING
EXPERIENCE

- Workshop of microarray data analysis, Instructor, ND BCF, ND, IN Spring 2010
- Guest lectures for a genomics course (with a topic of Statistics in Biology), ND, IN Fall 2009
- CSC410, CSC411 and CSC412 Computer Science Project, CS, UM, Miami, FL Spring 2009
- COP 2250 Programming in Java, Instructor, SCIS, FIU, Miami, FL Spring 2008
- COP 2210 Programming I, Lectured and supervised lab, SCIS, FIU, Miami, FL Spring 2007
- CGS-2518 Computer Data Analysis, Lectured and supervised lab, SCIS, FIU, Miami, FL Spring 2006 to Fall 2006
- CGS-2100 Computer Applications for Business, Lectured and supervised lab, SCIS, FIU, Miami, FL Fall 2005

ACADEMIC
ACTIVITIES

Editor

- Central European Journal of Computer Science (CEJCS) 2011 to present

Editorial Review Board

- International Journal of Knowledge Discovery in Bioinformatics (IJKDB) 2009 to present

Program Committee Member

- International Conference on Bioinformatics Models, Methods and Algorithms (BIOINFORMATICS 2012)
- International Conference on Bioinformatics and Computational Biology (BiCoB), New Orleans, Louisiana, March 2011
- IEEE International Conference on Bioinformatics & Biomedicine (BIBM), Atlanta, November 2011

- International Workshop on Collaboration Technologies and Systems in Healthcare and Biomedical Fields (CoHeB 2011)
- International Conference on Bioinformatics Models, Methods and Algorithms (BIOINFORMATICS), Rome, Italy, January 2011
- IEEE International Conference on Bioinformatics & Biomedicine (BIBM), Hong Kong, December 2010
- International Conference on Bioinformatics & Computational Biology (BIOCOMP), Las Vegas, July 2010
- International Conference on Bioinformatics and Computational Biology (BiCoB), Honolulu, Hawaii, March 2010
- International Conference on Bioinformatics, Valencia, Spain, January 2010
- IEEE International Conference on Bioinformatics & Biomedicine (BIBM), Washington D.C., November 2009
- International Joint Conference on Bioinformatics, Systems Biology and Intelligent Computing (IJCBS), Shanghai, China, August 2009

Proposal Writing

- One pending NSF ABI proposal (Role: PI)
- One pending NIH R21 proposal (Role: PI)
- One pending NIH R21 proposal (Role: Co-PI)
- One pending NIH R21 proposal (Role: Paid Consultant)
- One funded NSF ABI proposal (Role: Unpaid Consultant)
- Assistant to write one NIH SC2 proposal, one NSF ABI proposal, and one NSF CCF proposal

AWARDS

- Dissertation Year Fellowship, Florida International University, 2008
- Outstanding Graduate Academic Achievement Award, School of Computing and Information Sciences, FIU, 2007
- Excellence Award, School of Computing and Information Sciences, FIU, 2007-2008
- Presidential Fellowship, Florida International University, 2003-2005
- Graduate Teaching Assistantship, Florida International University, 2006-2008
- Summer Internship, Lawrence Berkeley National Laboratory, Berkeley, CA, 2007
- Summer Internship, Centocor Inc., 2006
- Travel Awards, School of Computing and Information Sciences, FIU, 2008
- Travel Awards, School of Computing and Information Sciences, FIU, 2007
- Travel Awards, Graduate Student Association, FIU, 2005
- Travel Awards, College of Arts and Sciences, FIU, 2005