**Summary of CV**

Nan Wang, Ph.D. Associate Professor in Department of Computer Science, New Jersey City University

E-mail: [nwang1@njcu.edu](mailto:nwang1@njcu.edu); [nan.wang.ms@gmail.com](mailto:nan.wang.ms@gmail.com) Phone: 484-934-2628

**General**

* Research Assistant, 2002-2005, Department of Computer Science and Engineering, Mississippi State University, Starkville, MS
* Research Associate, 2005-2008, Department of Computer Science and Engineering, Mississippi State University, Starkville, MS
* Tenure Track Assistant Professor, 2008-2014, School of Computing, University of Southern Mississippi, Hattiesburg, MS
* Tenured Associate Professor, 2014-2017, School of Computing, University of Southern Mississippi, Hattiesburg, MS
* Tenure Track Associate Professor, 2017-Present, Department of Computer Science of New Jersey City University, Jersey City, NJ

**Faculty Annual Evaluations**

Faculty annual evaluations: consistently excellent in teaching, research and services since joined NJCU in 2017

**Teaching**

* Received Consistently excellent in Student teaching evaluations
* Developed **five** new courses since 2017, one General Ed tier I and II courses, three high level courses for Cyber Security Program
* Taught **eight** different Computer Science core, elective and GE courses with full/overload enrollment.
* Advised major student’s summer research
* Developed major, minor and transfer curriculums

**Research**

* Published **five** peer reviewed journal papers since 2017
* Submitted two peer reviewed papers
* Preparing three papers
* Presented four oral/poster at conference
* Advised three student summary research projects
* Submitted two NSF research grant proposals since 2017

**Service**

* Design and development new B.S. in Cyber Security Program (2017-2020)
* Revise Computer Science Major and Minor Curriculum (2017-2019)
* Revise the transfer student curriculum (2017-2019)
* Committee Chair for Faculty Search Committee for Computer Science (2018-2019)
* Committee Member for Faculty Search Committee for Chemistry Department (2018-2019)
* Serve as University Senator for Computer Science (2019-2020)
* Participate University Open house events (2018-2020)
* Serve as the advisor for international visiting scholar

**Honor and Award**

* **MCBIOS 2008, Second Place Talk Award**
* **Outstanding Doctoral-Level Research Award** in Institute for Neurocognitive Science and Technology Research Forum at Mississippi State University, 2006.
* **2007-2008 fellowship for Female Graduate Student** in Department of Computer Science and Engineering at Mississippi State University.

Nan Wang, Ph.D.

Associate Professor in Computer Science

Department of Computer Science

New Jersey City University

Jersey City, NJ 07305

E-mail: nwang1@njcu.edu

Phone: 484-934-2628

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| Education |

## Ph.D. in Computer Science

## Mississippi State University, 2009

**M.S. in Computer Engineering**

Mississippi State University, 2005

**B.S. in Computer Science**

Xidian University, China, 1997

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| Professional Experience |

**Tenure tracked Associate Professor,** 2017 – to present

Department of Computer Science, New Jersey City University, Jersey City, NJ 07305

**Tenured Associate Professor,** 2014 – to 2017

School of Computing, University of Southern Mississippi, Hattiesburg, MS 39406

**Assistant Professor,** 2008 – 2014

School of Computing, University of Southern Mississippi, Hattiesburg, MS 39406

**Research Associate I,** 2005- 2008

Department of Computer Science and Engineering, Mississippi State University, Starkville, MS

**Research Assistant**, 2002-2005

Department of Computer Science and Engineering, Mississippi State University, Starkville, MS

**Engineer**, 1997-2001

Wisdom Computer and Communication Company, Xi’an, China

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| Teaching |

**Courses taught**

**2017 – present: New Jersey City University**

CS209: Data Structures and Algorithms

CS306: Database Management and Design

CS355: Visual Program using Visual Basic

CS125: Game Programming

CS430: Internet Multimedia Programming

CS120: Computers and Information Technologies

CS232: Introduction to Database

CS214: Business Application Microsoft I

CS102: Computer Science II

**2008 – 2017: The University of Southern Mississippi**

Database Management (CSC 411 / CSC 511)

Data Structures (CSC 307)

Introduction to Java (CSS 346)

Advanced Java (CSS 446)

Internet Concepts (CSS 404)

Data Handling Techniques (COS 703)

Analytical Models for Computer Systems (CSC 623)

Special Topic in Computer Science (new course: CSC 591)

Introduction to Bioinformatics (COS 789)

Advanced Bioinformatics (COS 791)

Android Programing (CSC424)

Introduction to Programming in C++ I(CSC101)

Introduction to Programming in C++ II(CSC102)

**Advisor of independent study and Co-op projects**

In addition to regular courses taught per semester, advise students with their cop-op projects and summer research projects.

**Curriculum Development**

**Develop New Courses**

2017-Present

Game Programming (New Course Developed, GE Tie I)

Introduction to Python (New Course Developed, GE Tie II)

Introduction to Cryptograph (New Course Developed, High level elective)

Linux Operating System (New Course Developed, High level elective)

Introduction to Data Science (New Course Developed, High level elective)

2008-2017

## Data Mining

Introduction to Bioinformatics

Android Programming

**Revise Existing Courses**

Virtual Programming using VB

Internet Concept

Introduction to Programming in C++

**Other Curriculum Development Activities**

1. Computer Science Master Program Development, Cyber security and Data Science Tracks
2. Computer Science Major and Minor Curriculum Design for New Jersey City University.
3. B.S. of Cybersecurity Program Design for New Jersey City University
4. M.S. of Cybersecurity in Computer Science Program Design for New Jersey City University
5. Curriculum development for the new Computational Science PhD program for University of Southern Mississippi
6. Propose Mobile Device Programming Minor for School of Computing for University of Southern Mississippi

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| Research, Scholarly and Creative Activities |

**Peer Reviewed Journal Publications (2006-2020)**

**Published peer reviewed journal papers**

1. Idakwo, G., Thangapandian, S., Luttrell, J. **Nan Wang**, Chaoyang Zhang, Ping Gong. “Structure–activity relationship-based chemical classification of highly imbalanced Tox21 datasets”. *J Cheminform* **12,**66 (2020).

<https://doi.org/10.1186/s13321-020-00468-x>

1. Hao Zhu**, Nan Wang**, Jonathan Z. Sun, Ras B. Pandey, Zheng Wang, “Inferring the three-dimensional structures of the X-chromosome during X-inactivation”, *Mathematical Biosciences and Engineering,* 2019, 16(6). 7384-7404. Doi: [10.3934/mbe.2019369](http://dx.doi.org/10.3934/mbe.2019369).

<https://www.aimspress.com/article/10.3934/mbe.2019369>

1. Tong Liu, Jacob Porter; **Nan Wang**; Zheng Sun; Yin-yuan Mo; Zheng Wang, “TADKB: Family Classification and a knowledge base of topologically associating domain”, *BMC Genomics 20*, 2019. GICS-D-18-01449

<https://bmcgenomics.biomedcentral.com/articles/10.1186/s12864-019-5551-2>

1. Saish Bhende, Kutub Thakur, Jason Teseng, Md Liakat Ali, Nan Wang, “Character Recognition Using Hidden Markov Models”, International Journal of Recent Technology and Engineering (IJRTE) ISSN: 2277-3878, Volume-7, Issue-4S2, 2018.

<https://www.ijrte.org/wp-content/uploads/papers/v7i4s2/Es2046017519.pdf>

1. Zheng Wang, Chenguan Zhao, Yiheng Wang, Zheng Sun, **Nan Wang**. “PANDA: Protein function prediction using domain architecture and affinity propagation” *Scientific**Reports*, 2018. DOI:10.1038/s41598-018-21849-1.

<https://www.nature.com/articles/s41598-018-21849-1>

1. Isaac Akogwu, **Nan Wang**, Chaoyang Zhang, Ping Gong. “A comparative study of k-spectrum-based error correction methods for next-generation sequencing data analysis” Human Genomics 2016, 10(Suppl 2):20 DOI: 10.1186/s40246-016-0068-0

<https://www.ncbi.nlm.nih.gov/pubmed/27461106>

1. Yan Peng, Andrew S Maxwell, Natalie D Barker, Jennifer G Laird, Alan J Kennedy, **Nan Wang**, Chaoyang Zhang, Ping Gong. “SeqAssist: A novel toolkit for preliminary analysis of next-generation sequencing data” BMC Bioinformatics 2014, 15(suppl 11): S10

<http://www.biomedcentral.com/1471-2105/15/S11/S10>

<http://orca.st.usm.edu/cbbl/seqassist/index.html>

1. Peng Li, Ping Gong, Haoni Li, Edward J Perkins, **Nan Wang** and Chaoyang Zhang, “Gene regulatory network inference and validation using relative change ratio analysis and time-delayed dynamic Bayesian network”, EURASIP Journal on Bioinformatics and Systems Biology 2014, 2014:12.

<http://bsb.eurasipjournals.com/content/2014/1/12>

1. Yang Y., Maxwell A., Zhang X., **Wang N.**, Perkins E. J., Zhang C.-Y. AND Gong P. (2013): Differential reconstructed gene interaction networks for deriving toxicity threshold in chemical risk assessment.  BMC Bioinformatics 14 (Suppl 13), S3.

<http://www.biomedcentral.com/qc/1471-2105/14/S14/S3>

1. Yang Y., Li S., Maxwell A.S., Barker N.D., Peng Y., Li Y., Li H., Wu X., Li P., Huang T., Zhang C.-H., **Wang N.**, Perkins E.J., Zhang C.-Y., Gong P. (2013): “Deciphering chemically-induced reversible neurotoxicity by reconstructing perturbed pathways from time series microarray gene expression data”. Proceedings of GENSIPS 2013.

<http://ieeexplore.ieee.org/xpl/abstractAuthors.jsp?url=http%3A%2F%2Fieeexplore.ieee.org%2Fstamp%2Fstamp.jsp%3Ftp%3D%26arnumber%3D6735927%26userType%3Dinst&denyReason=-134&arnumber=6735927&productsMatched=null&userType=inst>

1. Wu X, Li P, **Wang N**, Gong P, Perkins EJ, Deng Y, Zhang C.”[State Space Model with hidden variables for reconstruction of gene regulatory networks”.](http://www.ncbi.nlm.nih.gov/pubmed/22784622)BMC Syst Biol. 2011 Dec 23;5 Suppl 3:S3. doi: 10.1186/1752-0509-5-S3-S3. Epub 2011 Dec 23.PMID:22784622

<http://www.ncbi.nlm.nih.gov/pubmed/22784622>

1. Xing J, Xing F, Zhang C, Zhang Y, **Wang N**, “Genome-wide gene expression profiles in lung tissues of pig breeds differing in resistance to porcine reproductive and respiratory syndrome virus” Plos One (2014)DOI:10.1371/journal.pone.0086101, PubMed PMID: 24465897; PubMed Central PMCID: PMC3900479.

<http://www.plosone.org/article/info%3Adoi%2F10.1371%2Fjournal.pone.0086101>

1. Li H, **Wang N**, Gong P, Perkins EJ, Zhang C. “[Learning the structure of gene regulatory networks from time series gene expression data.](http://www.ncbi.nlm.nih.gov/pubmed/22369588)”BMC Genomics. 2011 Dec 23;12 Suppl 5:S13. doi: 10.1186/1471-2164-12-S5-S13. Epub 2011 Dec 23. PMID: 22369588

<http://www.ncbi.nlm.nih.gov/pubmed/?term=22369588>

1. Li Y, Gong P, Perkins EJ, Zhang C, **Wang N** ”[RefNetBuilder: a platform for construction of integrated reference gene regulatory networks from expressed sequence tags.](http://www.ncbi.nlm.nih.gov/pubmed/22166047)” BMC Bioinformatics. 2011 Oct 18;12 Suppl 10:S20. doi: 10.1186/1471-2105-12-S10-S20.PMID:22166047

<http://www.ncbi.nlm.nih.gov/pubmed/?term=22166047>

1. Xiaofei Nan, **Nan Wang**, Ping Gong, Chaoyang Zhang, Yixin Chen,  
   Dawn Wilkins: “Biomarker Discovery Using 1-Norm Regularization for Multi-Class Earthworm Microarray Gene Expression Data”, Neurocomputing, 2010.

<http://www.sciencedirect.com/science/article/pii/S0925231212000811>

1. Gong P, Loh PR, Barker ND, Tucker G, Wang **N, Zhang** C, Escalon BL, Berger B, Perkins EJ. “[Building quantitative prediction models for tissue residue of two explosives compounds in earthworms from microarray gene expression data.](http://www.ncbi.nlm.nih.gov/pubmed/21776976)”Environ Sci Technol. 2012 Jan 3;46(1):19-26. doi: 10.1021/es201187u. Epub 2011 Aug 8.PMID:21776976

<http://www.ncbi.nlm.nih.gov/pubmed/?term=21776976>

1. Li Y, **Wang N**, Perkins EJ, Zhang C, Gong P. “[Identification and optimization of classifier genes from multi-class earthworm microarray dataset.](http://www.ncbi.nlm.nih.gov/pubmed/21060837)”PLoS One. 2010 Oct 28;5(10):e13715. doi: 10.1371/journal.pone.0013715.PMID:21060837

<http://www.ncbi.nlm.nih.gov/pubmed/?term=21060837>

1. Sanders WS, **Wang N**, Bridges SM, Malone BM, Dandass YS, McCarthy FM, Nanduri B, Lawrence ML, Burgess SC. “[The proteogenomic mapping tool.](http://www.ncbi.nlm.nih.gov/pubmed/21513508)”BMC Bioinformatics. 2011 Apr 22;12:115. doi: 10.1186/1471-2105-12-115. PMID:21513508

<http://www.ncbi.nlm.nih.gov/pubmed/?term=21513508>

1. Nanduri B, **Wang N**, Lawrence ML, Bridges SM, Burgess SC. “[Gene model detection using mass spectrometry.](http://www.ncbi.nlm.nih.gov/pubmed/20013369)” Methods Mol Biol. 2010;604:137-44. doi: 10.1007/978-1-60761-444-9\_10.PMID:20013369

<http://www.ncbi.nlm.nih.gov/pubmed/?term=20013369>

1. Buza TJ, McCarthy FM, **Wang N**, Bridges SM, Burgess SC. “[Gene Ontology annotation quality analysis in model eukaryotes.](http://www.ncbi.nlm.nih.gov/pubmed/18187504)” Nucleic Acids Res. 2008 Feb;36(2):e12. doi: 10.1093/nar/gkm1167. Epub 2008 Jan 10. PMID:18187504

<http://www.ncbi.nlm.nih.gov/pubmed/?term=18187504>

1. Bridges, SM; Magee. GB; **Wang, Nan**; Williams, WP; Burgess, SC; Nanduri, B: “**ProtQuant: A Tool for the Label-Free Quantification of MudPIT Proteomics Data”.** BMC Bioinformatics 2007, **8**(Suppl 7)**:**S24. PubMed PMID: 18047724

<http://www.ncbi.nlm.nih.gov/pubmed/18047724>

1. McCarthy, Fiona; Bridges, Susan; **Wang, Nan**; Magee, Bryce; Williams, W. Paul; Luthe, Dawn S; and Burgess, Shane: “AgBase:  A unified resource for functional analysis in agriculture”. Nucleic Acids Research. Research Jan; 35 (Database issue):D599-603. 2007 Jan. PubMed PMID: 17135208; PubMed Central PMCID: PMC1751552.

<http://www.ncbi.nlm.nih.gov/pubmed/17135208>

1. McCarthy, Fiona; Bridges, Susan; **Wang, Nan**; Magee, Bryce; Burgess, Shane: “AgBase: A Functional Genomics Resource for Agriculture”, BMC Genomics, 2006 Sep 8;7(1):229

PubMed PMID: 16961921; PubMed Central PMCID: PMC1618847.

<http://www.ncbi.nlm.nih.gov/pubmed/16961921>

1. McCarthy, F., A. Cooksey, **Wang, Nan**, S. Bridges, T. Pharr, and S. Burgess, “Modeling a Whole Organ Using Proteomics: The Avian Bursa of Fabricius,” Proteomics, May: 2006(9), pp. 2759-71. PubMed PMID: 16596704

<http://www.ncbi.nlm.nih.gov/pubmed/16596704>

1. Nanduri B., F. M. McCarthy, S.M. Bridges, A. Corzo, M. D. Koter, J.J. Buza, B. van Den Berg, **N. Wang**, & S. C. Burgess, "Proteomics applied to disease in poultry," World's Poultry Science Journal, 2006.
2. Liangyou Chen, Hasan M. Jamil and **Nan Wang**. “Automatic Composite Wrapper Generation for Semi-Structured Biological Data Based on Table Structure Identification”. ACM SIGMOD Record, Special Issue for June 2004, Volume 33.
3. Liangyou Chen, Hasan Jamil, and **Nan Wang**; “[Automatic Wrapper Generation for Semi-Structured Biological Data Based on Table Structure Identification](http://www.cse.msstate.edu/~cly/cgi-bin/clyproxy.cgi?__url=http://oishii.cse.msstate.edu/user/cly/download/chenl_wrapper.pdf)”. [1st International Workshop on Biological Data Management - BIDM 03](http://www.ntu.edu.sg/home/assourav/bidm.htm). Prague, Czech Republic. 2003. Proceedings of the 14th International Workshop on Database and Expert Systems Applications P55, 2003

**In preparation**

1. PENG Y., ZHANG C.-Y., KENNEDY A. GONG P, **WANG N.**. “SVDisc: A novel integrative pipeline for structural variants discovery from genome re-sequencing data”. (In preparation; To be submitted to Bioinformatics - software issue, or Nucleic Acids Res. - Web server issue)
2. YANG L., PENG Y., BARKER N.D., ZHANG C.-Y., PERKINS E.J., **WANG N.**, AND GONG P. “miRDisc: A novel computational program for microRNA discovery from short deep sequencing reads”. (In preparation; To be submitted to Bioinformatics)
3. **Wang N**, Yuan C, Bridges SM. “PepOut: a Distance-based Outlier Detection for Peptide Validation.” International Journal of data mining and bioinformatics (in preparation, to be submitted to BMC bioinformatics).

**Book Chapter**

1. **Wang N\***, Nanduri B\*, Lawrence ML, Bridges SM and Burgess SC. Gene Model Detection Using Mass Spectrometry. Method in Molecular Biology: Proteome Bioinformatics: Informatics for Mass-Spectrometry Based Protein Science. (2008)Vol. 604 ISBN: 978-1-60761-443-2

**Peer Reviewed Papers Published in Conference Proceedings**

**Published in conference publications**

1. Haoni Li, Peng Li, Chaoyang Zhang, **Nan Wang**, Ping Gong, Edward Perkins, “Performance Evaluation of the Time-Delayed Dynamic Bayesian Network Approach to Inferring Gene Regulatory Networks from Time Series Microarray Data,” ACM BCB 2010.

1. Ying Li, Ping Gong, Chaoyang Zhang, Edward J. Perkins, **Nan Wang**, “ETKB: a knowledgebase for earthworm toxicogenomics”MCBIOS’10
2. Ying Li, **Nan Wang**, Chaoyang Zhang, Edward J. Perkins, Ping Gong. “Discovery of Biomarker Genes from Earthworm Microarray Data by Discriminant Analysis and Clustering” MCBIOS’10
3. **Nan Wang**, Shane Burgess, Mark Lawrence, Susan Bridges, "Proteogenomic Mapping for Structural Annotation of Prokaryote Genomes," Bioinformatics, Systems Biology and Intelligent Computing, International Joint Conference on, pp. 103-106, 2009
4. Ying Li, **Nan Wang**, Edward J. Perkins, Ping Gong, "Discovery of Biomarker Genes from Earthworm Microarray Data by Discriminant Analysis and Clustering," Bioinformatics, Systems Biology and Intelligent Computing, International Joint Conference on, pp. 23-29, 2009 International Joint Conference on Bioinformatics, Systems Biology and Intelligent Computing, 2009
5. **Nan Wang**, Guangming Yao, Susan Bridges, Chaoyang Zhang, “Statistics Measurements for Increased Confidence in Target-Decoy Search Strategy”, MCBIOS2009, February 20-21, 2009, Starkville, MS.

#### Poster/Oral Presentation at Conference/Symposium

1. Yan Peng, Andrew Maxwell, Lijuan Yang, Natalie Barker, Chaoyang Zhang, **Nan Wang**, Ping Gong, “miRDisc: A Novel Computational Program for microRNA Discovery from Short Deep Sequencing Reads and Transcriptomic Assembly”, *MCBIOS 2018*, The 15th Annual MCBIOS conference March 29-31, 2018.
2. Issac Akogwu, **Nan Wang**, Zhaoxian Zhou, Ping Gong, Chaoyang Zhang, “CECOND: A Novel Cuckoo Filter-Based Error Correction Method for Next Generation Sequencing Data”, *MCBIOS 2018*, The 15th Annual MCBIOS conference March 29-31, 2018.
3. Sundar Thangapandian, Gabriel Idakwo, **Nan Wang**, Chaoyang Zhangand Ping Gong, “Quantitative Target-specific Toxicity Prediction Model (QTTPM): A Novel Computational Toxicology Approach Integrating Molecular Dynamics Simulation and Machine Learning”, *MCBIOS 2018*, The 15th Annual MCBIOS conference March 29-31, 2018.
4. Gabriel Idakwo, Ping Gong, Sundar Thangapandian, Yan Li, **Nan Wang**, Zhaoxian Zhou, Chaoyang Zhang, “SMOTEENNBagging: A novel ensemble resampling and learning approach to QSAR modeling with imbalanced data”, *MCBIOS 2018*, The 15th Annual MCBIOS conference March 29-31, 2018.
5. Xiaofei Nan, **Nan Wang**, Ping Gong, Chaoyang Zhang, Yixin Chen,  
   Dawn Wilkins, Gene Selection for Earthworm Microarray Data Classification Using 1-norm SVM feature selection and multiclass classification method, The 7th annual Biotechnology and Bioinformatics Symposium, Lafayette, October 14 and 15, 2010.
6. Haoni Li, Peng Li, Chaoyang Zhang, **Nan Wang**, Ping Gong, Edward Perkins, “Performance Evaluation of the Time-Delayed Dynamic Bayesian Network Approach to Inferring Gene Regulatory Networks from Time Series Microarray Data,” ACM BCB 2010.
7. Ying Li, Ping Gong, Chaoyang Zhang, Edward J. Perkins, **Nan Wang**, “ETKB: a knowledgebase for earthworm toxicogenomics”MCBIOS’10.
8. Ying Li, **Nan Wang**, Chaoyang Zhang, Edward J. Perkins, Ping Gong. “Discovery of Biomarker Genes from Earthworm Microarray Data by Discriminant Analysis and Clustering” MCBIOS’10
9. **Wang, Nan**; Yuan, Chuanghe; Burgess, Shane; Bridges, Susan: “Distance-based Outlier Detection Model for Improving MS/MS Peptide Identification Confidence”. MCBIOS’08 Feb 23&24 2008, Oklahoma City, OK.
10. Xiaofei Nana, **Nan Wang**, Ping Gong, Chaoyang Zhang, Yixin Chen,  
    Dawn Wilkins "Gene Selection Using 1-Norm Regularization for Multi-Class Microarray Data" BIBM 2010, Dec16-20 Hong Kong, China

**Invited Talks**

* 1. 2011, Shandong University, Jinan, Shandong, China, “Functional Genomics”
  2. 2011, Shandong Agriculture University, Taian, Shandong, China, “Computational Biology”
  3. 2010, Simon Fraser University, Burnaby, BC, Canada, “Proteogenomics Mapping”
  4. 2009, U.S. Army Engineer Research and Development Center, Vicksburg, MS, USA, “Structural and Functional Genomics”

**International conference committee member / chair**

Program chair

Program chair of the High Performance Computing Technology and Applications (HPCTA06) Symposium at the IMSCCS06 international conference, Hangzhou, China, 2006.

**Other Academic Services**

* Reviewer of International Journals: J. of Supercomputing; MBC Bioinformatics.
* Paper reviewer of conferences/workshops (reviewed about 60 articles)
* Chaired presentation sessions of BMBIOS 2010.

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| Economic Development |

**Proposal Submitted in 2018:**

1. NSF, (Co-PI), 2018. “Pick Up Students in Hispanic Community for Computer Science (PUSH4CS)”
2. NSF, (Co-PI), 2018. “Engage to EXCEL (Expanding Curricula and Evidence-based Learning): a unique, technology-enhanced program to improve student experience and success”

**Proposal Awarded:**

* 1. USDA, (P.I.), 2008. “Annotation of Bovine Respiratory Disease Pathogen Genomes,” $20,707. (**Funded**)
  2. NSF, (Senior Personnel), 2009-2014. “Modeling and Simulation of Complex Systems,” $20,000,000. (**Funded**)
  3. U.S. Army ERDC, (Co-PI), 2008-2010. “Bayesian Learning and Optimization Approaches to Microarray Data Analysis and Gene Regulatory Network Reconstruction,” $439,608 (**Funded**)
  4. NSF, (P.I.), 2010-2011. “Structural determinants for canine influenza infection,” $33,785. (**Funded**)
  5. United Soybean Board (Co-PI), 2010. “Management and Analysis of Soybean Microarray Data”, $10,658.87. (**Funded**)
  6. USAID, (Co-PI), 2010-2013. “Arthropod functional genomics initiative; building community resources for animal health,” $391,894. (**Funded**)
  7. NSF, (P.I.), 2011. “Combined Computational Chemistry and Computational Biology Modeling for Understanding Protein-Protein and Protein-Ligand Interactions”, $30,787 (**Funded**).
  8. NOAA, (Co-PI), 2011-2014, “The initiation and persistence of blooms of the toxic inofagellate Karenia brevis, along coastlines of the Gulf of Mexico results”, $718,268 (**Funded**).
  9. NSF (Co-PI), 2011-2015. “Modeling, Reconstruction and Validation of Gene Regulatory Networks,” $458,433 (**Funded**).
  10. NSF (PI), 2014-2015. “A Cyber-based Platform for Building Gene Regulatory Networks from Expressed Sequence Tags,” $36,000 (**Funded**)
  11. NSF (PI), 2015-2016. “A Cyber-based Platform for Building Gene Regulatory Networks from Expressed Sequence Tags,” $36,000 (**Funded with extended grant support**)

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| Research Interests |

### Computational Biology and Bioinformatics

### Functional genomics structural and functional annotation

### Transcriptomic regulation of gene expression

### Statistical analysis of microarray data

### Structural annotation pipeline for prokaryotic genomes

### Database and Data Mining

### Modeling, Machine Learning, Data Mining and Statistical analysis

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| Service |

**University-Level service**

* Design and Develop the foundational curriculum for the Cyber Security Program Proposal (2019-2020)
* Serve as an advisor for Visiting Scholar from Changchun University (2019-2020)
* Serve as University Senator for Computer Science (2019-2020)

**College-Level service**

* Serve as committee member for Computational Chemistry Faculty Search
* Serve as committee chair for Computer Science Faculty Search
* Participation in the 2018 Fall, 2019 Spring and 2019 Fall, 2020 Spring Open House Events

**Department-Level service**

* Revised the Computer Science major curriculum including retiring some courses, add new cutting-edge courses, and refine some courses with updated content.
* Revised the Computer Science minor curriculum, updated the required courses and electives for the minor.
* Revised the transfer student curriculum.
* Serve as Committee member for Computer Science Curriculum Committee