

Dongsheng Che

Curriculum Vitae

Department of Computer Science
East Stroudsburg University of Pennsylvania
330 Science & Technology Center
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East Stroudsburg, PA 18301

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Academic Positions

East Stroudsburg University of Pennsylvania

Assistant Professor, Department of Computer Science

August 2008-present

The University of Georgia

Graduate Research Assistant, Department of Computer Science

2003-2008

Graduate Teaching Assistant, Department of Computer Science

2000-2002

Graduate Research Assistant, Warnell School of Forest Resources

1997-2000

Education

The University of Georgia

Ph.D. Computer Science

2008

Thesis title: "Computational methods for deciphering microbial genomic structures"

Graduate Certificate Bioinformatics

2008

M.S. Computer Science

2002

Thesis title: "Application of efficient external memory algorithms to simulated web graphs"

M.S. Forest Biotechnology

2000

Thesis title: "Development of transgenic eastern cottonwood for mercury phytoremediation"

Zhejiang Forestry University

B.Agr. Forestry

1992

Book Chapters

1. **D. Che**, Q. Liu, K. Rasheed and X. Tao (2010). Decision tree and ensemble learning algorithms with their applications in bioinformatics, in *Software Tools and Algorithms for Biological Systems*, Springer Publisher, accepted.
2. **D. Che**, G. Li (2009). Computational methods in unravelling transcriptional regulatory networks in prokaryotes, in *Biological Data Mining*, Jake Chen and Stefano Lonardi, Eds., Chapman & Hall/CRC Press, 377-396.
3. P. Dam, F. Mao, **D. Che**, P. Wan, T. Tran, G. Li, Y. Xu (2008). Computational elucidation of operons and uber-operons, in *Computational Methods for Understanding Bacterial and Archaeal Genomes*, Y. Xu and J. P. Gogarten, Eds., World Scientific Publishing, 233-257.

Referred Journal Publications

4. Q. Liu, R. Zhu, **D. Che**, Y. Yang, and Z. Cao (2010). RNACompare: an efficient computational framework for RNA secondary structure comparison and classification based on grammar inference and indefinite kernel learning, submitted.
5. **D. Che**, C. Hockenbury, R. Marmelstein, and K. Rasheed (2010). Classification of genomic islands using decision trees and their ensemble algorithms, *BMC Genomics*, accepted.
6. G. Li*, **D. Che***, Y. Xu (2009). A universal operon predictor for prokaryotic genomes, *Journal of Bioinformatics and Computational Biology*. 7(1):19-38. (*co-first authors)
7. Y. Li, P. Bahti, N. Shaw, G. Song, S. Chen 1, X. Zhang, M. Zhang, C. Cheng, J. Yin, J. Zhu, H. Zhang, **D. Che**, H. Xu, A. Abbas, B. Wang, Z. Liu (2008). Crystal structure of a novel non-Pfam protein AF1514 from *Archeoglobus fulgidus* DSM 4304 solved by S-SAD using a Cr X-ray source. *Proteins: Structure, Function, and Bioinformatics*, 71(4):2109 - 2113.
8. P. Bahti, S. Chen, Y. Li, N. Shaw, X. Zhang, M. Zhang, C. Cheng, G. Song, J. Yin, H. Zhang, **D. Che**, A. Abbas, H. Xu, B. Wang and Z. Liu (2008). Purification, crystallization and preliminary crystallographic analysis of the non-Pfam protein AF1514 from *Archeoglobus fulgidus* DSM 4304. *Acta Cryst.*, F64, 91-93.
9. **D. Che**, J. Zhao, L. Cai, Y. Xu (2007). Decision tree modeling predicts operon structures of prokaryotic genomes, *International Journal of Information Technology and Intelligent Computing*, vol. 2(1).
10. **D. Che**, R. Meagher, C. Rugh, T. Kim, A. Heaton, S. Merkle (2006). Expression of organomercurial lyase in eastern cottonwood enhances organomercury resistance. *In Vitro Cellular and Developmental Biology*, 228-234.
11. **D. Che**, G. Li, F. Mao, H. Wu, Y. Xu (2006). Detecting uber-operons in prokaryotic genomes. *Nucleic Acids Research*, 34(8):2418-2427. (**Highlight: cited 16 times**)
12. **D. Che**, S. Jensen, L. Cai, J.S. Liu (2005). BEST: Binding-site estimation suite of tools. *Bioinformatics*, 21(12):2909-2911. (**Highlight: cited 24 times**)
13. **D. Che**, R. Meagher, A. Heaton, A. Lima, C. Rugh, S. Merkle (2003). Expression of mercuric ion reductase in Eastern cottonwood (*Populus deltoides*) confers mercuric ion reduction and resistance. *Plant Biotechnology Journal*, 1(4):311-9. (**Highlight: cited 41 times, made the cover of Plant Biotechnology Journal**)

Referred Conference Publications

14. Y. Wei, HK Brown, X. Tao, S. Moore, **D. Che** (2010). Brain MRI Image Segmentation Using Fuzzy C-Means Clustering. *The 2010 International Conference on Image Processing, Computer Vision, and Pattern Recognition (IPCV2010)*, accepted.
15. P. Lakshminarasimhan, Q. Liu, R. Marmelstein, M. Devito, and **D. Che** (2010). A Multi-Objective Evolutionary Approach for Haplotype Inference. *The 2010 International Conference on Bioinformatics & Computational Biology (BioComp2010)*, 202-208.
16. P. Lakshminarasimhan, Q. Liu, R. Marmelstein, M. Devito, and **D. Che** (2010). A Maximum Likelihood Based Genetic Algorithm for Inferring Haplotypes from Genotypes. *The 2010 International Conference on Educational Technology and Computers (ICETC 2010)*, V5,92-96.

17. **D. Che**, C. Hockenbury, R. Marmelsteinand, and K. Rasheed (2009). Classification of genomic islands using decision-tree based algorithms. *The 2009 International Conference on Bioinformatics & Computational Biology (BioComp2009)*, 252-258.
18. **D. Che**, H. Tang, Y. Song (2009). Haplotype inference using a genetic algorithm. *Proceedings of IEEE Symposium on Computational Intelligence in Bioinformatics and Computational Biology (CIBCB2009)*, 31-37.
19. **D. Che**, G. Li, S. Jensen, J.S. Liu, Y. Xu (2008). PFP: a computational framework for phylogenetic footprinting in prokaryotic genomes. *Proceedings of International Symposium on Bioinformatics Research and Applications (ISBRA2008)*, 110-121.
20. J. Zhao, **D. Che**, L. Cai (2007). Comparative pathway prediction via unified graph modeling of genomic structure. *Proceedings of International Symposium on Bioinformatics Research and Applications (ISBRA2007)*, 627-637.
21. **D. Che**, J. Zhao, L. Cai, Y. Xu (2007). Operon prediction in microbial genomes using decision tree approach. *Proceedings of IEEE Symposium on Computational Intelligence in Bioinformatics and Computational Biology (CIBCB2007)*, 135-142.
22. J. Zhao, **D. Che**, L. Cai (2007). Comparative pathway annotation with protein-DNA interaction and operon information via graph tree decomposition. *Pacific Symposium on Biocomputing*, 12:496-507.
23. **D. Che**, Y. Song, K. Rasheed (2005). MDGA: motif discovery using a genetic algorithm. *Genetic and Evolutionary Computation Conference (GECCO2005)*, 447-452. (**Highlight: cited 20 times**)
24. S. Sipani, K. Verma, S. Chandrasekaran, X. Zeng, J. Zhu, **D. Che**, K. Wang (2002). Designing an XML database engine: API and performance. *Proceedings of the 40th Annual ACM Southeast Conference (ACMSE2002)*, 239-245. (**Highlight: cited 11 times, won the runner-up paper award**)

Working Papers

25. B. Liu, G. Li, **D. Che**, J. Z. Sun, Y. Xu. Motif length could be computationally recognized, Working paper.
26. P. Wan, F. Mao, V. Olman, **D. Che**, H. Liu, Y. Xu. Operon structural diversity is a reflection of adaptive evolution. Working paper.
27. F. Pan, **D. Che**, M. Momany, L. Cai, R. Malmberg. Co-evolution analysis of protein complexes and its applications in predicting residue interactions. Working paper.
28. **D. Che**, H. Xu, H. Zhang, Z. Liu, J. Rose, B. Wang. Is it worthy to target non-Pfam proteins in structural genomics? Working paper.

Abstracts and Posters

1. A general framework for the whole-genome regulon prediction across prokaryotic genomes, **D. Che**, G. Li and Ying Xu. *The Third Computational & Systems Biology Symposium*, Athens, GA, March 21, 2008.
2. Co-evolution analysis of protein complexes and its applications in predicting residue interactions, F. Pan, **D. Che**, M. Momany, L. Cai and R. Malmberg. *Proceedings of International Symposium on Bioinformatics Research and Applications (ISBRA)*, Atlanta, GA, May 7-10, 2007.

3. Operon prediction in microbial genomes using decision tree approach, **D. Che**, J. Zhao, L. Cai and Ying Xu. *Proceedings of IEEE Symposium on Computational Intelligence in Bioinformatics and Computational Biology (CIBCB)*, Honolulu, HI, April 2, 2007.
4. A universal operon predictor for prokaryotic genomes, **D. Che**, G. Li and Ying Xu. *The Second Computational & Systems Biology Symposium*, Athens, GA, March 23, 2007.
5. High-resolution functional assignments of genes in bacterial genomes, P. Dam, F. Mao, H. Wu, V. Olman, Z. Liu, G. Li, **D. Che**, P. Wan, T. Tran, Z. Su, and Y. Xu. *DOE Genomics: GTL Awardee Workshop*, Bethesda, Maryland, February 11-14, 2007.
6. Detecting uber-operons in prokaryotic genomes, F. Mao, **D. Che**, G. Li, H. Wu, and Y. Xu. *International Conference on Computational Systems Bioinformatics*, Stanford, CA, August 14-18, 2006.
7. SGXPRO: A Software Suite with a Parallel Workflow Engine for the Automation on Structure Solving Process, Z.-Q. Fu, G. Wu, **D. Che**, J. Zhao, H. Yan, F. Sun, J. Rose and B.C. Wang. *International Conference on Structural Genomics*, Washington D.C., November 17-21, 2004.
8. SGXPRO: A Versatile Structure Solving Engine for Structural Biology/Genomics, BC Wang, Z. Fu, Y. Wu, **D. Che**, J. Zhao, H. Yan and J. Rose. *American Crystallographic Association Meeting*, Chicago, July 25-31, 2004.
9. Expression of mercuric ion reductase in Eastern cottonwood confers mercuric ion reduction and resistance, S. Merkle, **D. Che**, A. Lima, A. Heaton and R. Meagher. *International Symposium on Ecological and Societal Aspects of Transgenic Forest Plantations*, Stevenson, Washington, July 22-24, 2001.

Invited Presentations

1. "A Multi-Objective Evolutionary Approach for Haplotype Inference", The 2010 International Conference on Bioinformatics & Computational Biology (BioComp), Las Vegas, NV, July 15, 2010.
2. "A Maximum Likelihood Based Genetic Algorithm for Inferring Haplotypes from Genotypes", 2010 International Conference On Information and Electronics Engineering (ICIEE), Shanghai, China, June 23, 2010.
3. "Computational Methods for Deciphering Genomic Structures of Bacteria", Department of Computer Science, New Jersey Institute of Technology, Newark, NJ, March 8, 2010. (Host: Dr. Zhi Wei)
4. "Classification of genomic islands using decision-tree based algorithms", The 2009 International Conference on Bioinformatics & Computational Biology (BioComp), Las Vegas, NV, July 14, 2009.
5. "Haplotype inference using a genetic algorithm", Proceedings of IEEE Symposium on Computational Intelligence in Bioinformatics and Computational Biology (CIBCB), Nashville, TN, March 30, 2009.
6. "Dynamic programming and its applications", Department of Computer Science, East Stroudsburg University, East Stroudsburg, PA, June, 12, 2008.
7. "PFP: a computational framework for phylogenetic footprinting in prokaryotic genomes", Proceedings of International Symposium on Bioinformatics Research and Applications (ISBRA), Atlanta, GA, May 7, 2008.
8. "Graph-theoretic algorithms for deciphering microbial genomic structures", Lewis-Sigler Institute for Integrative Genomics, Princeton University, Princeton, NJ, April 25, 2008. (Host: Dr. John Storey)

9. "Graph-theoretic algorithms for deciphering microbial genomic structures", Department of Computer Science and Engineering, Mississippi State University, March 5, 2008.
10. "Comparative pathway prediction via unified graph modeling of genomic structure, Proceedings of International Symposium on Bioinformatics Research and Applications (ISBRA), Atlanta, GA, May 10, 2007.
11. "Genetic algorithms and their applications in bioinformatics", Computational Systems Biology Laboratory (CSBL), The University of Georgia, Athens, GA, February 27, 2007.
12. "Statistical analysis of Pfam and non-Pfam PDB sequences", Southeast Collaboratory for Structural Genomics (SECSG) Annual Meeting, Unicoi State Park, Helen, GA, June 14, 2006
13. "MDGA: motif discovery using a genetic algorithm", Genetic and Evolutionary Computation Conference (GECCO), Washington, D.C., June 28, 2005.

Software and Database

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|---|------|
| GIDetector: Genomic Islands Detector for Prokaryotic Genomes URL: http://www.esu.edu/~dche/GIDetector/ | 2010 |
| UNIPOP: Universal Predictors for Operons URL: http://www.esu.edu/~dche/UNIPOP/ | 2009 |
| OperonDT: Operon prediction using decision-tree approach URL: http://www.esu.edu/~dche/OperonDT/ | 2007 |
| Uber-OperonDB: Uber-operon database consisting of 91 bacterial genomes URL: http://csbl.bmb.uga.edu/uber/ | 2006 |
| BEST: Binding-site Estimation Suite of Tools URL: http://www.esu.edu/~dche/BEST/ | 2005 |

Grants

Co-Principal Investigator, 2010-2011, Shanghai White Magnolia Talent Fund, China (PI: Qi Liu)
Non-coding RNA Structure Comparison and Classification Algorithm Platform

Principal Investigator, 2010-2011, President Research Funding, ESU
Automated Genomic Island Detection for All Sequenced Microbial Genomes

Faculty Development & Research Mini Grant, 2009-2010, East Stroudsburg University

Faculty Development & Research Travel Grant, 2009-2010, East Stroudsburg University

Keystone Innovation Starter Kits, 2008-2009, Pennsylvania Department of Community and Economic Development

Awards and Honors

| | |
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| Selected for inclusion in Marquis 2009 Whos Who in America | 2009 |
| Graduate School Travel Award, The University of Georgia | 2008 |
| GECCO Travel Award, ACM SIGEVO | 2005 |
| University-Wide Graduate School Fellowship, The University of Georgia | 1997-1999 |
| The First Prize Undergraduate Scholarship, Zhejiang Forestry University, China | 1989-1992 |

Professional Membership

Member of the Science Advisory Board
 Member of the IEEE and the IEEE Computational Intelligence Society
 Member of the International Society of Computational Biology
 Member of Institute of Mathematical Statistics

Service

Conference Program Committee

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| International Conference on Data Mining (DMIN) | 2009, 2010 |
| International Workshop on Applications of Machine Learning in Bioinformatics | 2009 |
| International Conference on Bioinformatics and Computational Biology (BIOCOMP) | 2009 |
| International Conference on Genetic and Evolutionary Methods (GEM) | 2009 |
| International Conference on Artificial Intelligence (ICAI) | 2009 |

Book Chapter Reviewer

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|------------------------|------|
| Biological Data Mining | 2009 |
|------------------------|------|

Journal Reviewer

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|-----------------------------|------|
| BMC Genomics | 2010 |
| Briefings in Bioinformatics | 2008 |

Conference Reviewer

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| Computational Intelligence in Bioinformatics and Computational Biology (CIBCB) | 2010 |
| The First International Conference on Networked Digital Technologies (NDT) | 2009 |
| The 12th IEEE International Conference on Computational Science and Engineering (CSE) | 2009 |
| The 6th Annual Conference on Theory and Applications of Models of Computation (TAMC) | 2009 |
| International Conference on Intelligent Computing (ICIC) | 2007, 2009 |
| Asia-Pacific Bioinformatics Conference (APBC) | 2008 |
| Conference on Computational Systems Bioinformatics (CSB) | 2007, 2009 |
| The 18th International Conference on Genome Informatics (GIW) | 2007 |
| International Conference on Life System Modeling and Simulation (LSMS) | 2007 |
| IEEE International Conference on Granular Computing (GrC) | 2006 |
| The 44th ACM Southeast Conference (ACMSE) | 2006 |
| International Conference on Intelligent Systems for Molecular Biology (ISMB) | 2006 |

University and Departmental Service

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| Survey coordinator for graduating seniors and alumni in the Computer Science Dept. | 2010-present |
| Serving as a judge for Sigma Xi research forum | 2010 |
| Curriculum Committee for the Computer Science Dept. | 2010-present |
| Graduate Program Committee for the Computer Science Dept. | 2009-present |
| Initiating the first East Asian Study | 2009-present |
| ABET Committee for the Computer Science Dept. | 2008-present |
| Serving as CPSC faculty representative for 2008 ESU Fall Open House | 2008 |

Teaching Experience

Department of Computer Science, East Stroudsburg University, Assistant Professor

| | |
|---|-----------|
| CPSC100: Personal Computers and Their Uses | 2008-2010 |
| CPSC101: Personal Computers and Their Uses in the Sciences | 2009 |
| CPSC151: Linear Data Structures and Elementary Algorithm Analysis | 2009-2010 |
| CPSC528: Artificial Intelligence | 2008 |
| CPSC529: Machine Learning | 2010 |

Department of Computer Science, The University of Georgia, Teaching Assistant

| | |
|---|-----------|
| CSCI6300: Web Programming | 2002 |
| CSCI1302: Software Development | 2001 |
| CSCI1301: Introduction to Computing and Programming | 2000-2002 |

Student Mentored

Han Wang

MS student, Department of Computer Science, East Stroudsburg University 2010-

Mathew Booth

Undergraduate, Department of Computer Science, East Stroudsburg University 2010-

John Fazekas

Undergraduate, Department of Computer Science, East Stroudsburg University 2010-

Cory Hockenbury

Department of Computer Science, East Stroudsburg University 2008-

Priyadarshini Lakshminarasimhan

Department of Computer Science, East Stroudsburg University M.Sc. 2008-2010