

Chengpeng Bi, *Senior Member, IEEE*

EDUCATION Postdoctoral, **The University of California**, Davis, California USA August 2003
Ph.D., **The Pennsylvania State University**, University Park, Pennsylvania USA May 2002
Ph.D. minor in Operations Res., **The Pennsylvania State University**, USA May 2002
M.Eng. in Computer Science, **The Pennsylvania State University**, USA December 2000

ACADEMIC **Children's Mercy Hospitals and Clinics**, Kansas City, Missouri USA
EXPERIENCE Director of Bioinformatics & Intelligent Computing July 2007 – present
Research Scientist in Bioinformatics August 2003 – June 2007

University of Missouri - Kansas City, Kansas City, Missouri USA
Assistant Professor of Pediatrics, UMKC School of Medicine July 2007 – present
Adjunct Assistant Professor, School of Computing & Engineering July 2007 – present

The University of California, Davis, California USA
Postdoctoral Researcher, UC Davis Genome Center June 2002 – August 2003

The Pennsylvania State University, University Park, Pennsylvania USA
Research Associate, Department of Anthropology January 2002 – June 2002
Research/Teaching Assistant, Department of Entomology August 1997 – December 2001

RESEARCH AND PROFESSIONAL SERVICES

I). RESEARCH: Using machine learning, statistical modeling, and computational intelligence methods to design novel algorithms in the following areas: **(1)** biomedical data-mining from heterogeneous data sources (e.g. clinical data, microarray data, molecular markers, SNPs, biological pathways, RNA-Seq, ChIP-Seq etc.) for diagnosis and prognosis of pediatric diseases as well as prediction of drug responses, **(2)** *de novo* motif discovery algorithms for DNA and protein sequence analysis, **(3)** statistical mechanical modeling on DNA structural transition or DNA melting, **(4)** massively parallel sequencing data analysis, e.g. computing methods for ChIP-Seq, RNA-Seq and mutation detection, **(5)** hidden Markov models in sequence analysis, **(6)** MySQL database system for biomedical data mining and management.

II). PROFESSIONAL SERVICES: **(1)** Referee for international journals in bioinformatics including the following: *Bioinformatics*, *BMC Bioinformatics*, *IEEE / ACM Transactions on Computational Biology and Bioinformatics*, *IEEE Transactions on Evolutionary Computation*, *IEEE Computational Intelligence Magazine*, *Journal of Computational and Graphical Statistics*, *Intl. Journal of Data Mining and Bioinformatics*, *Journal of Bioinformatics and Computational Biology*, *Neurocomputing*, *Nucleic Acids Res.*, *Pattern Recognition Letters*, *PLoS One*, *The Open Bioinformatics Journal*. **(2)** Senior Member of the Institute of Electrical and Electronics Engineers (IEEE), IEEE Computational Intelligence Society (CIS), and CIS Bioinformatics and Bioengineering Technique Committee (BBTC). **(3)** Program Committee Member and Reviewer of numerous international conferences including: *i. IEEE Symposium on Computational Intelligence in Bioinformatics and Computational Biology (CIBCB)*, 2008 – 2012; *ii. IEEE Congress on Evolutionary Computation (CEC)*, 2008 – 2012; *iii. IEEE International Conference on Bioinformatics & Biomedicine (BIBM)*, 2009 – 2012; *iv. The 9th International Meeting on Computational Intelligence Methods for Bioinformatics and Biostatistics*, Houston, Texas USA, 2012; *v. The First IEEE Symposium on Biological Data Visualization*, 23-24 October 2011, Providence, RI USA; *vi. Annual BioTechnology and Bioinformatics Symposium*, 2009 – 2011; *vii. IEEE International Workshop on Machine Learning for Signal Processing*, 2008 – 2011; *viii. IEEE International Conference on Machine Learning and Applications*, 2008, 2009; *ix. IEEE International Conference on Bioinformatics & BioEngineering (BIBE)*, 2007, 2008. **(4)** External grants reviewer. **(5)** External examiner for faculty promotion. **(6)** Editor for the following journals: *Frontiers in Bioinformatics and Computational Biology*. **(7)** Reviewer for several book chapters.

- C. Bi** (2012) Memetic Algorithms for Biomedical Sequence Analysis (In Revision)
- C. Bi** and J.S. Leeder (2012) Large-scale computation of pediatric growth percentiles with fuzzy logic justification of parameter selection. In: *Proceedings of 2012 IEEE Symposium on Computational Intelligence in Bioinformatics and Computational Biology*. IEEE Press, Piscataway, NJ. (In Press).
- K Miller, M Silvey, D Logsdon, F Balch, N Nsumu, I Sokolovsky, M Gibson, **C Bi**, D Heruth, and RA White (2011) The Xla (X-linked anemia) mouse: A transient neonatal anemia caused by a Gata1 splicing mutation. *Blood*, 118, 1366-1367
- C. Bi**, M.L. Becker and J.S. Leeder (2011) Derivation of minimum best sample size from microarray data sets: A Monte Carlo approach. In: *Proceedings of 2011 IEEE Symposium on Computational Intelligence in Bioinformatics and Computational Biology*. IEEE Press, Piscataway, NJ. pp. 29-134 (2011).
- C. Bi** (2011) Tackling the challenging motif problem through hybrid particle swarm optimized alignment clustering. In: *Proceedings of 2011 IEEE Symposium on Computational Intelligence in Bioinformatics and Computational Biology*. IEEE Press, Piscataway, NJ. pp. 84-89 (2011)
*** **winner of Best Paper Award** received from *The 2011 IEEE Symposium Series on Computational Intelligence* (IEEE SSCI-2011, Paris, France)
- C. Bi** (2010) Deterministic local alignment methods improved by a simple genetic algorithm. *Neurocomputing*, 73, 2394-2406.
- C. Bi** (2010) Comparison of optimization techniques for sequence pattern discovery by maximum-likelihood. *Pattern Recognition Letters*, 31, 2147-2160.
- C. Bi**, C.A. Vyhldal and J.S. Leeder (2010) Supervised machine learning of maternal cigarette-smoking signatures from placental gene expression data: A case study. In: *Proceedings of 2010 IEEE Symposium on Computational Intelligence in Bioinformatics and Computational Biology*, pages 1-6. Montreal Canada. IEEE Press, Piscataway, NJ.
- C.J. Saunders, M. Friez, M. Patterson, M. Nasbi, W. Zhao and **C. Bi** (2010) Allele dropout in the MECP2 gene due to G-quadruplex and i-motif sequences when using PCR-based diagnosis for Rett syndrome. *Genetic Testing and Molecular Biomarkers*, 14 (2), 241-247.
- C. Bi** (2009) A Monte Carlo EM algorithm for motif discovery in biomolecular sequences. *IEEE/ACM Transactions on Computational Biology and Bioinformatics*, 6, 370-386.
- C. Bi** (2009) DNA motif alignment by evolving a population of Markov chains. *BMC Bioinformatics*, 10, S13
- J. Meng, **C. Bi**, C.G. McKnight, S.W. Handoyo and L.J. Rosenwasser (2009) Genome-wide screening SNPs with arginine vs tryptophan change associated with allergy. *Journal of Allergy and Clinical Immunology*, 123, S167.
- C. Bi** (2008) Data augmentation algorithms for detecting conserved domains in protein sequences. *Journal of Proteome Research*, 7, 192-201.
- C. Bi**, C.A. Vyhldal and J.S. Leeder (2008) A comparative study on structured motif detection: algorithms and applications. *Molecular Pharmaceutics*, 5, 3-16.
- C. Bi** (2008) Evolutionary Metropolis sampling in sequence alignment space. In: *Proceedings of 2008 IEEE Congress on Evolutionary Computation*, pp. 189-194. Hong Kong CHINA. IEEE Press,

Piscataway, NJ.

C. Bi, M.C. Saunders and B.A. McPheron (2008) Neuro-Fuzzy classification of the *Rhagoletis pomonella* species group using digitized wing structure. In: *Proceedings of 2008 IEEE Symposium on Computational Intelligence in Bioinformatics and Computational Biology*, pp. 159-165. Idaho USA. IEEE Press, Piscataway, NJ.

C. Bi (2007) Multiple sequence local alignment using Monte Carlo EM algorithm. In: I. Mandoiu and A. Zelikovsky (Eds.): ISBRA07, *Lecture Notes in Bioinformatics*, vol. 4463, pp. 465-476. Springer-Verlag Berlin Heidelberg.

C. Bi (2007) SEAM: A stochastic EM-type algorithm for motif-finding in biopolymer sequences. *Journal of Bioinformatics and Computational Biology*, 5, 47-77.

C. Bi (2007) A genetic-based EM motif-finding algorithm for biological sequence analysis. In: *Proceedings of 2007 IEEE Symposium on Computational Intelligence in Bioinformatics and Computational Biology*, pp. 275-282. Hawaii USA. IEEE Press, Piscataway, NJ.

*** **winner of Best Overall Paper Award** received from *IEEE SSCI'2007*

C. Bi, M.C. Saunders and B.A. McPheron (2007) Wing pattern-based classification of the *Rhagoletis pomonella* species complex using genetic neural networks. *Intl J. Computer Sci. & Appl.*, 4, 1-14.

C. Bi and P.K. Rogan (2006) BIPAD: A web server for modeling bipartite sequence elements. *BMC Bioinformatics*, 7, 76

J. Bode, S. Winkelman, S. Gotze, S. Spiker, K. Tsutui, **C. Bi**, P. AK and Craig Benham (2006) Correlation between scaffold/matrix attachment region (S/MAR) binding activity and DNA duplex Destabilization energy. *Journal of Molecular Biology*, 358, 597-613.

C.J. Benham and **C. Bi** (2004) The analysis of stress-induced duplex destabilization in long genomic DNA sequences. *Journal of Computational Biology*, 11, 519-543.

C. Bi and C.J. Benham (2004) WebSIDD: server for prediction of the stress-induced duplex destabilized (SIDD) sites in superhelical DNA. *Bioinformatics*, 20, 1477-1479.

C. Bi and P.K. Rogan (2004) Bipartite pattern discovery by entropy minimization-based multiple local alignment. *Nucleic Acids Research*, 32, 4979-4991.

C. Bi and C.J. Benham (2003) The approximate algorithm for analysis of the strand separation transition in superhelical DNA using nearest neighbor energetics. In: *Proceedings of IEEE Computer Society for Bioinformatics*, pp. 460-461. Stanford USA. IEEE Press, Piscataway, NJ.