

## BIOGRAPHICAL SKETCH

<b>Chengpeng Bi</b>		<b>Bioinformatics Scientist</b>
INSTITUTION	DEGREE	FIELD OF STUDY
Central China Ag. University, Wuhan, China	B.S.	Plant Pathology & Entomology
China (Beijing) Ag. University, Beijing, China	M.S.	Entomology
The Pennsylvania State University, University Park, Pennsylvania	M.Eng.	Computer Science
The Pennsylvania State University, University Park, Pennsylvania	Ph.D.	Entomology
The Pennsylvania State University, University Park, Pennsylvania	Ph.D. minor	Operations Research
The University of California, Davis, California	Postdoctoral	Bioinformatics

### **Area of Scholarly Interest:**

Bioinformatics  
Biomedical Informatics  
Systems Biology  
Gene Regulation & Protein-DNA Interactions  
Machine Learning and Medical Biomarker Discovery  
Novel Computer Algorithm Design for BioMedical Applications  
Web Database Design for Electronic Medical Healthcare System

### **Professional Experience:**

2007 - Present      Children's Mercy Hospital, Assistant Professor of Pediatrics, University of Missouri Kansas City, Kansas City, Missouri  
2005 - Present      Children's Mercy Hospital, Adjunct Assistant Professor of Computer Science, University of Missouri Kansas City, Kansas City, Missouri

### **Board Certification and Professional Organization Membership:**

Senior Member	<b>Institute of Electrical and Electronics Engineers</b>	2010 - Present
Member	<b>IEEE Computational Intelligence Society</b>	2008 - Present
Member	<b>International Society for Computational Biology</b>	2002 - Present
Member	<b>IEEE Computer Science Society</b>	2002 - Present

### Professional and Community Service (Previous 5 Years):

Associate Editor	<b>International Journal of Computational Mathematics</b>	2014 - Present
Editor	<b>Frontier in Bioinformatics and Computational Biology</b>	2010 - Present
Editor	<b>World Journal of Pharmacology</b>	2012 - Present
Proceedings Chair	<b>IEEE Symposium on Computational Intelligence in Bioinformatics and Computational Biology</b>	2010
PC Member	<b>Many International Bioinformatics Conferences</b>	2007 - Present
Journal Reviewer	<b>Artificial Intelligence in Medicine, Bioinformatics, BMC Bioinformatics, IEEE Trans. Computational Biology and Bioinformatics, IEEE Trans. Evolutional Computation, Pattern Recognition Letter, Neurocomputing, IEEE Computational Intelligence Magazine, Journal of Computational &amp; Graphical Statistics, PLoS One, Nucleic Acids Res., BioTechniques etc.</b>	2005 - Present

### Honors and Awards (Previous 5 Years):

**Invited Speaker, 2013 X-GEN Congress & Expo: Cambridge Healthtech Institute's Fourth Annual Genomic Data Analysis: Sequencing's Strategic Step, San Diego, CA USA** 2013

**Best Paper Award, Granted by The 2011 IEEE Symposium Series on Computational Intelligence (SSCI) Committee, Paris, France** 2011

### Publications (Previous 5 Years):

**Bi C**, Methylome-seq Data Analysis. IN: S.Q. Ye (Editor) Big Data Analyses for Bioinformatics and Biomedical Discoveries, CRC Press/Taylor & Francis Group (2015) [Book Chapter, IN PRESS]

**Bi C**, A maximum likelihood framework for multiple sequence local alignment. In: M Elloumi, CS Iliopoulos, JTL Wang and AY Zomaya (Editors) PATTERN RECOGNITION IN COMPUTATIONAL MOLECULAR BIOLOGY: TECHNIQUES AND APPROACHES, John Wiley & Sons Ltd. (2015) [Book Chapter, IN PRESS]

Carrie A. Vyhlidal, **Charlie Bi**, Roger Gaedigk, Dmitry Grigoryev, Shui Q. Ye, Stephen Kingsmore, J. Steven Leeder, Developmental changes in DNA methylation of CYP3A5 in human pediatric and prenatal liver 2015 ASPET at Experimental Biology (EB), March 28 - April 1, Boston, Massachusetts USA (Abstract)

Vyhlidal CA, **Bi C** and Leeder JS, Dynamics of DNA methylation of human CYP3A gene promoters in pediatric liver 2014 Annual Meeting of The American Society for Pharmacology and Experimental Therapeutics (ASPET), San Diego, California USA

Zhang X, Chen QH, Farmer P, Nasim M, Demopoulos A, Devoe C, Ranjan T, Eisenberg MB, Schulder M, **Bi C**, Li JY, Central nervous system lymphoma in immunocompetent patients: The North Shore-Long Island Jewish Health System experience. J Clin Neurosci. 2013 Jan;20(1):75-79

**Bi C** and Leeder JS, Large-scale computation of pediatric growth percentiles with fuzzy logic justification of parameter selection. Proceedings of The 2012 IEEE Computational Intelligence Symposium on Bioinformatics & Computational Biology (CIBCB). IEEE Press, Piscataway, NJ, pages 43-46 (2012).

**Bi C**, Memetic algorithms for de novo motif-finding in biomedical sequences. *Artificial Intelligence in Medicine* 56 (1), 1-17 (2012)

**Bi C**, Becker ML and J.S. Leeder. 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*. Paris France. IEEE Press, Piscataway, NJ. April 2011. pages 1-6 (DOI: 10.1109/CIBCB.2011.5948461)

**Bi C**, 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*. Paris France. IEEE Press, Piscataway, NJ. April 2011 pages 1-8 (DOI: 10.1109/CIBCB.2011.5948452)

\*\*\***Best Paper Award received from IEEE SSCI-2011**

**Bi C**, Deterministic local alignment methods improved by a simple genetic algorithm. *Neurocomputing*, 2010; 73, 2394-2406.

**Bi C**, Comparison of optimization techniques for sequence pattern discovery by maximum-likelihood. *Pattern Recognition Letters*, 2010; 31, 2147-2160.

**Bi C**, Vyhlidal CA and Leeder, JS, 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*, IEEE Press, Piscataway, NJ. 2010, pages 1-6.

Saunders CJ, Friez M, Patterson M, Nasbi M, Zhao W and **Bi C**. 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*, 2010; 14 (2), 241-247. PMID: 20384458

**Bi C**. A Monte Carlo EM algorithm for motif discovery in biomolecular sequences. *IEEE/ACM Transactions on Computational Biology and Bioinformatics*, 2009; 6, 370-386. PMID: 19644166

**Bi C**. DNA motif alignment by evolving a population of Markov chains. *BMC Bioinformatics*, 2009; 10, S13 PMID: 20456999

### **Grants and Contracts (Previous 5 Years):**

**1. Modeling on homodimer-DNA binding energy: A Case Study on NF- $\kappa$ B p50 Binding Sites Using a Novel QMH Assay**

**Grant:** Katharine B. Richardson Associates Endowment Fund. *Completed*  
**Investigators:** **Bi C**, Newkirk H.

**2. Genome-wide Screening SNPs with Arginine to Tryptophan Change in an Association with Allergy and Asthma**

**Grant:** Katharine B. Richardson Associates Endowment Fund. *Completed*  
**Investigators:** Meng J, **Bi C**