

Curriculum Vitae

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EDUCATION:

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| B.S. | Physics, 1992 - Peking University, Beijing, China |
| M.S. | Theoretical Physics, 1995 - Institute of Theoretical Physics, Chinese Academy of Sciences, Beijing, China |
| Ph.D. | Biophysics, 1998 - Institute of Biophysics, Chinese Academy of Sciences, Beijing, China |
| Postdoctoral | Bioinformatics and Computational Biology, 1999-2000 – Department of Statistics, University of California, Los Angeles (UCLA) |
| Postdoctoral | Bioinformatics and Computational Biology, 2000-2002 – Department of Biostatistics, Harvard University and Dana-Farber Cancer Institute |

UNIVERSITY APPOINTMENTS:

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| 2008-present | Associate Professor (with tenure), Department of Molecular Sciences, University of Tennessee Health Science Center |
| 2002-2008 | Assistant Professor, Department of Molecular Sciences, University of Tennessee Health Science Center |
| 2002-2008 | Director of Bioinformatics Core, Center of Genomics and Bioinformatics, University of Tennessee Health Science Center |

OTHER ACADEMIC APPOINTMENTS:

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| 2007-present | Affiliated Faculty Member, Bioinformatics Program, University of Memphis |
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OTHER PROFESSIONAL AFFILIATIONS:

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| 2002-present | Tennessee Mouse Genome Consortium |
| 2003-present | The International Society for Computational Biology |

2007-present The New York Academy of Sciences
2009-present Institute of Electrical and Electronics Engineers (IEEE)

TEACHING EXPERIENCE:

2004-Present Course Lecturer: Bioinformatics I (MSCI814) and Bioinformatics II (MSCI815) (Joint with colleagues)

BOOK CHAPTERS:

1. **Cui Y** (2006) Elucidating Gene Regulatory Networks Underlying Complex Phenotypes: Genetical Genomics and Bayesian Network. In Shannon, F. (ed), *Microarrays and Transcription Networks*. Landes Bioscience, Georgetown, Page 114-126.
2. **Cui Y** (2007) Bridging Genotype and Phenotype: Causal Pathways from DNA to Complex Traits. In Deng, H.W. (ed), *Current Topics in Human Genetics: Studies of Complex Diseases*. World Scientific, Singapore, Page 433-448.

PEER-REVIEWED JOURNAL ARTICLES:

1. **Cui Y**, Chen RS* and Wong WH* (1998) Protein folding simulation using genetic algorithm and supersecondary structure constraints. *Proteins: Structure, Function and Genetics* 31:247-257.
2. **Cui Y**, Chen RS* and Wong WH* (1998) Molecular dynamic simulation of chaperonin-mediated protein folding. *Journal of Protein Chemistry* 17:377-380.
3. Wong WH*, **Cui Y** and Chen RS (1998) Torsional Relaxation for Biopolymers. *Journal of Computational Biology* 5:655-665.
4. Sun ZR, **Cui Y**, Ling LJ, Guo Q and Chen RS* (1998) Molecular dynamics simulation of protein folding with supersecondary structure constraints. *Journal of Protein Chemistry* 17:765-769.
5. **Cui Y**, Ling LJ and Chen RS* (1998) A fast algorithm for computation of solvent accessible surface area of biomolecules. *Acta Biophysica Sinica* 14:799-801.
6. **Cui Y**, Ling LJ and Chen RS*, Bai LC, Yuan JG, Qiang BQ (1999) Molecular dynamics simulation of site-directed mutagenesis of HIV type 1 Tat trans-activator. *Chinese Science Bulletin* 44:708-711.
7. **Cui Y**, Chen RS and Wong WH* (2000) The coevolution of cell senescence and diploid sexual reproduction in unicellular organisms, *Proceedings of the National Academy of Sciences USA* 97:3330-3335.
8. **Cui Y** and Wong WH* (2000) Multiple sequence information provides protection against mis-specified potential energy function, *Physical Review Letters* 85:5242-5245.
9. **Cui Y**, Wong WH, Bornberg-Bauer E and Chan HS* (2002) Recombinatoric exploration of novel folded structures: a heteropolymer-based model of protein

evolutionary landscapes, *Proceedings of the National Academy of Sciences USA* 99:809-814.

10. Ling L*, Wang J, **Cui Y**, Li W and Chen RS* (2002) Proteome-wide analysis of protein function composition reveals the clustering and phylogenetic properties of organisms, *Molecular Phylogenetics and Evolution* 25: 101-111.
11. Qi Z, **Cui Y**, Fang W, Ling L* and Chen RS* (2004) Autosomal Similarity Revealed by Eukaryotic Genomic Comparison. *Journal of Biological Physics* 30: 305-312.
12. Zhou M and **Cui Y*** (2004) GeneInfoViz: constructing and visualizing gene relation networks. *In Silico Biology* 4:323-332.
13. **Cui Y***, Zhou M and Wong WH* (2004) Integrated analysis of microarray data and gene function Information. *OMICS: A Journal of Integrative Biology* 8: 106-117.
14. Li H, Zhou M and **Cui Y*** (2005) Ranking Gene Regulatory Network Models with Microarray Data and Bayesian Network. *Lecture Notes in Computer Science* 3327: 109 - 118.
15. Bao L and **Cui Y*** (2005) Prediction of the phenotypic effects of nonsynonymous single nucleotide polymorphisms. *Bioinformatics* 21:2185-2190.
16. Bao L, Zhou M and **Cui Y*** (2005) nsSNPAnalyzer: identifying disease-associated nonsynonymous single nucleotide polymorphisms. *Nucleic Acids Research* 33: W480-W482.
17. Li H, Lu L, Manly KF, Chesler EJ, Bao L, Wang J, Zhou M, Williams RW and **Cui Y*** (2005) Inferring Gene Transcriptional Modulatory Relations: A Genetical Genomics Approach. *Human Molecular Genetics* 14:1119-1125.
18. Deng W, Zhu X, Skogerbø G, Zhao Y, Fu Z, Wang Y, He H, Cai L, Sun H, Liu C, Li B, Bai B, Wang J, Jia D, Sun S, He H, **Cui Y**, Wang Y, Bu D and Chen R* (2006) Organisation of the *Caenorhabditis elegans* small non-coding transcriptome: genomic features, biogenesis and expression. *Genome Research* 16:20-29.
19. Bao L and **Cui Y*** (2006) Functional impacts of nonsynonymous single nucleotide polymorphisms: selective constraint and structural environments. *FEBS Letters* 580:1231-1234.
20. Bao L, Wei L, Peirce JL, Homayouni R, Li H, Zhou M, Chen H, Lu L, Williams RW, Pfeffer LM, Goldowitz D and **Cui Y*** (2006) Combining gene expression QTL mapping and phenotypic spectrum analysis to uncover gene regulatory relations. *Mammalian Genome* 17:575-583.
21. He H, Cai L, Skogerbo G, Deng W, Liu T, Zhu X, Wang Y, Jia D, Zhang Z, Tao Y, Zeng H, Aftab MN, **Cui Y**, Liu G and Chen R* (2006) Profiling *Caenorhabditis elegans* non-coding RNA expression with a combined microarray. *Nucleic Acids Research* 34:2976-2983.
22. Li H, Chen H, Bao L, Manly KF, Chesler EJ, Lu L, Wang J, Zhou M, Williams RW and **Cui Y*** (2006) Integrative Genetic Analysis of Transcription Modules: Towards Filling the Gap between Genetic Loci and Inherited Traits, *Human Molecular Genetics* 15:481-492.
23. Bao L, Zhou M, Wu L, Lu L, Goldowitz D, Williams RW and **Cui Y*** (2007) PolymiRTS Database: linking polymorphisms in microRNA target sites with complex traits. *Nucleic Acids Research* 35: D51-D54.

24. Bao L, Peirce JL, Zhou M, Li H, Goldowitz D, Williams RW, Lu L and **Cui Y*** (2007) An integrative genomics strategy for systematic characterization of genetic loci modulating phenotypes. *Human Molecular Genetics* 16:1381-1390.
25. Bao L, Zhou M and **Cui Y*** (2008) CTCFBSDB: a CTCF binding site database for characterization of vertebrate genomic insulators. *Nucleic Acids Research*. 36: D83-D87.

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PEER-REVIEWED CONFERENCE PAPERS:

1. Verma NK, Gupta P, Agrawal P, Hanmandlu M, Vasikarla S and **Cui Y** (2009) Medical Image Segmentation Using Improved Mountain Clustering Approach. The 6th IEEE International Conference on Information Technology (ITNG) - New Generation, Las Vegas.
2. Verma NK, Agrawal P and **Cui Y** (2009) Fuzzy Rule Based Unsupervised Approach for Gene Saliency. Applied Imagery Pattern Recognition (AIPR): Vision: Humans, Animals, and Machines. Washington DC, USA [October 14-16, 2009]
3. Verma NK, Gupta P, Agrawal P and **Cui Y** (2009) MRI Brain Image Segmentation for Spotting Tumors Using Improved Mountain Clustering Approach, Applied Imagery Pattern Recognition (AIPR): Vision: Humans, Animals, and Machines. Washington DC, USA [October 14-16, 2009]
4. Verma NK, Roy A, Gupta S and **Cui Y** (2009) Improved Mountain Clustering Technique for Microarray Data. Joint International Conference on Applied Systems Research (ASR) and XXXIII National Systems Conference (NSC 2009). Agra, India. [November 27-29, 2009]

PEER-REVIEWED ABSTRACTS:

1. Zhou M and **Cui Y**. GeneNetViz: Batch Retrieval of Gene Function Information and Visualization of Functional Relationships between Genes. *3rd Annual TMGC Retreat*, January 16-18, 2003, Carriage Lane Inn, Murfreesboro, Tennessee.
2. Zhou M and **Cui Y**. Determination and visualization of gene relation networks. *2nd UT-ORNL Bioinformatics Summit*, March 28-29, 2003, Fall Creek Falls State Resort Park, Pikeville, Tennessee.
3. Homyouni R, Heinrich K, Wei L, **Cui Y**, Zhou M and Berry M. SGO: Semantic Gene Organizer, *2nd UT-ORNL Bioinformatics Summit*, March 28-29, 2003, Fall Creek Falls State Resort Park, Pikeville, Tennessee.
4. Williams RW, Peirce J, Wang J, Manly KF, Chesler EJ, **Cui Y** and Lu L. Systems genetics of gene expression and the use of reference populations to integrate across biological scales. *Systems Biology: Global Regulation of Gene Expression*. March 23-26, 2006, Cold Spring Harbor, New York.
5. D. J. SWANSON, T. HA, R. GLENN, **Y. CUI**, R. HOMAYOUNI, M. BERRY, E. TJIOE, M. A. LANGSTON, C. PHILLIPS, J. SONG, E. J. CHESLER, S. DUVVURU, E. BRAUER, K. HAMRE, D. GOLDOWITZ. Gene regulation in time

& space (grits): molecular signatures of cerebellar development. Neuroscience 2008 (the 38th annual meeting of the Society for Neuroscience), November 15 - 19, 2008. Washington, DC.

6. Robert W. Williams, Xusheng Wang, Daniel Ciobanu, **Yan Cui**, David Li, Kyobenic Mozhui, Megan Mulligan, Stanley Nelson, William Taylor, Donald Thomason, Evan G. Williams, Lu Lu. Next-Generation Genomic Resources for the BXD Genetic Reference Panel. International Meeting on BXD Phenotyping. November 30 - December 1, 2009, Braunschweig, Germany

DATABASE, SOFTWARE AND WEB SERVERS:

1. **PolymiRTS Database (<http://compbio.utm.edu/miRSNP/>)** A database of naturally occurring DNA variations in putative microRNA target sites. This database characterizes Polymorphisms in microRNA Target Sites (PolymiRTS) as a new class of sequence variants underlying gene expression traits and/or higher order mammalian traits.
2. **CTCFBSDB (<http://insulatordb.utm.edu/>)** A CTCF binding site database for characterization of vertebrate genomic insulators. The database is a comprehensive collection of experimentally identified and computationally predicted CTCF binding sites. It is also a resource for studying insulators and their roles in demarcating functional genomic domains and regulating gene expression.
3. **Gifi Array Analyzer (<http://compbio.utm.edu/Gifi.php>)** A Java software for interpreting microarray data in the context of existing biological knowledge. It implements Homogeneity Analysis, a graphical multivariate statistical method for analyzing categorical data, to integrate the analysis of microarray data and gene functional classification data.
4. **QSB (<http://compbio.utm.edu/QSB/>)** A Java software developed for genetical genomics, an emerging field that combines quantitative genetics and genomics. QSB integrates QTL mapping, SNP analysis and Bayesian network to infer the genetic networks.
5. **nsSNP Analyzer (<http://snpanalyzer.utm.edu/>)** A web server for predicting phenotypic effects of nonsynonymous single nucleotide polymorphism (nsSNP). It extracts structural and evolutionary information from a query nsSNP and uses a machine learning method called Random Forest to predict the nsSNP's phenotypic effects.
6. **GeneInfoViz (<http://genenet2.utm.edu/geneinfoviz/>)** A Gene Ontology tool to construct and visualize gene relation networks using a dynamic graph layout of the networks. Directed acyclic graphs are also generated to show the hierarchical structure of the Gene Ontology tree. GeneInfoViz is featured by The Gene Ontology Consortium (<http://www.geneontology.org/GO.tools.browsers.shtml#geneinfoviz>).