

Qingpeng Zhang

CONTACT INFORMATION	Department of Computer Science and Engineering Michigan State University 428 S. Shaw Ln., RM 3115 East Lansing, MI 48824 USA	<i>Phone:</i> (678) 901-9911 <i>E-mail:</i> qingpeng@msu.edu <i>Web:</i> http://www.cse.msu.edu/~qingpeng/ <i>Twitter:</i> @qingpengzhang
RESEARCH INTERESTS	Broadly my research interest is developing and applying scalable computational tools to enable investigations of large, complex biological dataset. My dissertation developed approaches to investigate the diversity of various complex metagenomic samples based on k-mer counting algorithms.	
EDUCATION	Michigan State University , <i>Department of Computer Science and Engineering</i> , East Lansing, USA Ph.D. Candidate, Computer Science and Quantitative Biology (Dual Major) <ul style="list-style-type: none">• Dissertation Topic: “A Novel Computational Approach to Investigate Microbial Diversity using Whole-genome Shotgun Metagenomic Data”• Advisor: C. Titus Brown• Anticipated Graduation Spring 2015 Nanjing University , <i>Department of Physics</i> , Nanjing, China B.S., Physics (Biophysics), July, 2003	
RESEARCH EXPERIENCE	Michigan State University , Department of Computer Science and Engineering, East Lansing, USA <i>Graduate Research Assistant</i> in GED Lab (Advisor: C. Titus Brown), August, 2008 - present <ul style="list-style-type: none">• developed an efficient k-mer counting software package - khmer. [1] (collaboratively)• developed digital normalization approach for scaling shotgun seq analysis [2] (collaboratively)• investigated the genomic versatility and functional variation between two heterotrophic symbionts of deep-sea Osedax worms. [3] (collaboratively)• developed novel methods required for diversity measurement of extremely large metagenomics samples. [Manuscript in preparation] (independently) Chinese Academy of Sciences , Institute of Genetics and Developmental Biology, Beijing, China <i>Research Staff in Bioinformatics</i> in Han Lab (Advisor: Jing-Dong Jackie Han), May, 2005 - July, 2008 <ul style="list-style-type: none">• identified the proliferation/differentiation switch in the cellular network of multicellular organisms. [5] (collaboratively)• investigated the regulatory circuitry of aging. [4] (collaboratively)• identified microRNA/siRNA in human intron region using Bayesian classifier. (collaboratively) BGI-Beijing , Bioinformatics Department, Beijing, China <i>Research Staff in Bioinformatics</i> July, 2003 - May, 2005 <ul style="list-style-type: none">• silkworm genome sequencing project as core member of the genomic analysis group. [7] (collaboratively)• assembled and analyzed deer BAC clones. [6] (collaboratively)	

PUBLICATIONS

up-to-date publication list at: <http://scholar.google.com/citations?user=3TddZSQAAAAJ>

1. *These are not the k-mers you are looking for: efficient online k-mer counting using a probabilistic data structure.* **Qingpeng Zhang**, Jason Pell, Rosangela Canino-Koning, Adina Chuang Howe, C. Titus Brown. PLOS ONE, July 25, 2014, DOI: 10.1371/journal.pone.0101271
2. *A Reference-Free Algorithm for Computational Normalization of Shotgun Sequencing Data.* C. Titus Brown, Adina Howe, **Qingpeng Zhang**, Alexis B. Pyrkosz, Timothy H. Brom. submitted. <http://arxiv.org/abs/1203.4802>
3. *Genomic versatility and functional variation between two dominant heterotrophic symbionts of deep-sea Osedax worms.* Shana K Goffredi, Hana Yi, **Qingpeng Zhang**, Jane E Klann, Isabelle A Struve, Robert C Vrijenhoek and C Titus Brown. The ISME Journal , (14 November 2013) — doi:10.1038/ismej.2013.201
4. *A Modular Network Model of Aging.* Xue H, Xian B, Dong D, Xia K, Zhu S, Zhang Z, Hou L, **Zhang Q**, Zhang Y, Han J-D J. Molecular Systems Biology, 2007, 3: 147.
5. *Identification of the Proliferation/Differentiation Switch in the Cellular Network of Multicellular Organisms.* Kai Xia, Huiling Xue, Dong Dong, Shanshan Zhu, Jiamu Wang, **Qingpeng Zhang**, Lei Hou, Hua Chen, Ran Tao, Zheng Huang, Zheng Fu, Ye-Guang Chen, and Jing-Dong J Han PLoS Comput Biol. 2006 Nov 24;2(11):e145
6. *Comparative genomic analysis links karyotypic evolution with genomic evolution in the Indian Muntjac (Muntiacus muntjak vaginalis).* Qi Zhou, Ling Huang, Jianguo Zhang, Xiangyi Zhao, **Qingpeng Zhang**, Fei Song, Jianxiang Chi, Fengtang Yang and Wen Wang Chromosoma. 2006 Dec;115(6):427-436. Epub 2006 Jun 22.
7. *A Draft Sequence for the Genome of the Domesticated Silkworm (Bombyx mori)* Science. 2004 Dec 10;306(5703):1937-40 (list author)

CONFERENCE
PRESENTATIONS

- *A probabilistic approach to k-mer counting.* Annual Bioinformatics Open Source Conference (BOSC2012) July 2012, Long Beach, USA

TEACHING
EXPERIENCE

- Teaching Assistant of EDAMAME Workshop - Explorations in Data Analyses for Metagenomic Advances in Microbial Ecology, Kellogg Biological Station, Michigan State University, August 2014
- Teaching Assistant of MSU NGS Summer Course - Analyzing Next-Generation Sequencing Data, Kellogg Biological Station, Michigan State University, August 2014
- Instructor of Software Carpentry Workshop at Wuhan Institute of Virology, Chinese Academy of Sciences, China, July 2013
- Teaching Assistant of Software Carpentry Workshop at The Scripps Research Institute, La Jolla, CA, November 2012
- Teaching Assistant of MSU NGS Summer Course - Analyzing Next-Generation Sequencing Data, Kellogg Biological Station, Michigan State University, June 2012
- Teaching Assistant of CSE491 - Introduction to Database-Backed Web Development, Department of Computer Science and Engineering, Michigan State University, 2008 Fall, 2012 Spring
- Teaching Assistant of CSE231 - Introduction to Programming I -Python, Department of Computer Science and Engineering, Michigan State University, 2010 Spring, 2010 Fall, 2011 Spring, 2012 Fall, 2013 Spring

PROFESSIONAL
TRAINING

Selected Courses (at Michigan State University)

CSE 824 Advanced Computer Networks and Communications
 CSE 830 Design and Theory of Algorithms
 CSE 847 Machine Learning
 CSE 860 Foundations of Computing
 CSE 881 Data Mining

CSE 891 Probabilistic Models and Algorithms in Computational Biology
CSE 891 Open Problems in Bioinformatics
QB 826 Introduction to Quantitative Biology Techniques
QB 827 Problems in Quantitative Biology
QB 828 Biology for the Interdisciplinary Scientist
MMG 890 Environmental Metagenomics

Workshops and Conferences (as attendee or poster presenter)

2014.10 The 6th Annual Argonne Soil Metagenomics Meeting, Chicago, IL, USA
2014.04 Software Carpentry Instructor Training Workshop, Toronto, Canada
2014.04 PyCon2014, Montreal, Canada
2012.07 Annual Bioinformatics Open Source Conference (BOSC2012) Long Beach, CA, USA
2012.07 20th Annual International Conference on Intelligent Systems for Molecular Biology (ISMB2012) Long Beach, CA, USA
2012.05 Great Lakes Bioinformatics Conference 2012 (GLBIO2012) Ann Arbor, MI, USA
2012.05 Frontiers in Metagenomics Symposium, Columbia, MO, USA
2011.06 The First International Earth Microbiome Project Conference, Shenzhen, China
2010.05 Certification in College Teaching Institute, East Lansing, MI, USA
2009.05 Google Developer Days 2009, Beijing, China
2007.03 International Networking for Young Scientists (INYS) Workshop on computational biology, Beijing, China
2006.10 International Conference on Genomics, Hangzhou, China

HONORS AND
AWARDS

2009-2014 CSE Summer Research Fellowship, Michigan State University
2008 Quantitative Biology(QB) Recruiting Fellowship, Michigan State University
2003 Honored Graduate Award, Nanjing University (3% of all graduates)
1999-2001 Scholarship for Annually Excellent Student, Nanjing University (20% of all students)
1999 First Grade Scholarship for Freshman, Nanjing University (5% of all freshmen)

REFERENCES

(*Contact details available upon request.*)

Dr. C. Titus Brown, Associate Professor, University of California, Davis, ctbrown@ucdavis.edu

Dr. James Cole, Assistant Professor, Michigan State University, colej@msu.edu

Dr. Adina Chuang Howe, Assistant Professor, Iowa State University, achuang@engineering.uiowa.edu