
CUNCONG ZHONG Ph.D.

University of Kansas
1450 Jayhawk Blvd.
Lawrence, KS, USA 66045

Email: cczhong@ku.edu
Cell: (407) 421 3048
Work: (785) 864 7785

Research area

Bioinformatics and computational biology:

Algorithms and data structure, machine learning, and data mining

Biological big data and precision medicine:

Next-generation sequencing-based human metagenomics, genomics, genetics/epigenetics, transcriptomics, and oncology research

Functional non-coding RNA:

Structural biology and functional genomics

Education

2013: University of Central Florida, Ph.D., in Computer Science

2009: University of Central Florida, M.S., in Computer Science,

2007: Huazhong University of Science and Technology, B.S. in Computer Science and Biotechnology
(double major)

Experiences

2016-current: Department of EECS, University of Kansas, Assistant Professor

2013-2016: J. Craig Venter Institute, Post-doctoral fellow (Computational)

2013: Illumina Inc., Bioinformatics intern

Funding

Current: “Transforming Metagenomic Sequencing Data Analysis with Scalable Assembly and Comprehensive Annotation”

National Science Foundation EPSCoR First Award

Role: Principal Investigator

Project period: 05/01/2018-07/31/2019

Current: “TEEN Connections for Support from Multidisciplinary Professionals & Peers”

National Institute of Health (NR015743-02)

Role: Co-Investigator

Project period: 01/15/2018-06/30/2018

Current: “Identification of the molecular mechanism of miR-211 and its target genes in melanocytes and pigmented melanoma senescence and apoptosis”

National Institute of Health (5R21CA202197)

Role: Co-Investigator

Project period: 09/01/2016 – 08/31/2018

Completed: “A Novel Protein Fragment Assembler for Metagenomic Data Analysis”

National Science Foundation (DBI-1262295)

Role: Key Personnel

Project period: 05/15/2013 – 11/30/2016

Completed: “Identification, Discovery, and Public Archiving of RNA Structural Motifs”

National Institutes of Health (R01GM102515)

Role: Key Personnel

Project period: 09/01/2012 – 08/31/2017

Publications

1. Zhong, C. and Zhang, S. (In preparation) CLAN: the CrossLinked reads ANalysis tool (Corresponding author)
2. Zhong, C., Yang, Y., and Yooseph, S. (In revision) GRASP2: Fast and Memory-efficient Gene-centric Assembly and Homolog Search for Metagenomic Sequencing Data, *BMC Bioinformatics* (Corresponding author)
3. Zou A, Magee N, Deng F, Lehn S, Zhong C, Zhang Y. (2018) Hepatocyte nuclear receptor SHP suppresses inflammation and fibrosis in a mouse model of nonalcoholic steatohepatitis. *Journal of Biological Chemistry*. pii: jbc.RA117.001653.
4. Ge, P., Islam, S., Zhong, C., and Zhang, S. (2018) De novo discovery of structural motifs in RNA 3D structures through clustering, *Nucleic Acids Research*, gky139, doi: 10.1093/nar/gky139
5. Zhong, C., Yang, Y., and Yooseph, S. (2017) GRASP2: Fast and Memory-efficient Gene-centric Assembly and Homolog Search, In *IEEE 7th International Conference on Computational Advances in Bio and Medical Sciences (ICCBMS)*, Orlando, FL USA (Corresponding author)
6. Zhong, C., Edlund, A., Yang, Y., McLean, J., and Yooseph, S. (2016) Metagenome and metatranscriptome analyses using protein family profiles, *PLoS Computational Biology* 12(7): e1004991. doi:10.1371/journal.pcbi.1004991
7. Zhong, C., Yang, Y., and Yooseph, S. (2016) GRASPx: an efficient reference-guided short peptide assembler, *BMC Bioinformatics Suppl* 8:283. doi: 10.1186/s12859-016-1119-1.
8. Zhong, C., Yang, Y., and Yooseph, S. (2015) GRASPx: an efficient reference-guided short peptide assembler. In *11th International Symposium on Bioinformatics Research and Applications (ISBRA)*, Norfolk, VA, USA
9. Yang, Y., Zhong, C., and Yooseph, S. (2015) SFA-SPA: a suffix array based short peptide assembler

for metagenomic data. *Bioinformatics* doi: 10.1093/bioinformatics/btv052

10. Zhong, C. and Zhang, S. (2015) RNAMotifScanX: a graph alignment approach for RNA structural motif identification. *RNA* 10.1261/rna.044891.114
11. Zhong, C., Yang, Y., and Yooseph, S. (2014) GRASP: Guided Reference-based Assembly of Short Peptides. *Nucleic Acids Research* doi: 10.1093/nar/gku1210
12. Ge, P., Zhong, C., and Zhang, S. (2014) ProbeAlign: incorporating high-throughput sequencing based structure probing information into ncRNA homology search. *BMC Bioinformatics* 15 (Suppl 9):S15
13. Ge, P., Zhong, C., and Zhang, S. (2014) ProbeAlign: incorporating high-throughput sequencing based structure probing information into ncRNA homology search. In *4th Annual RECOMB Satellite Workshop on Massively Parallel Sequencing*, Pittsburgh, PA, USA
14. Li, Y., Zhong, C., and Zhang, S. (2014) Finding consensus stable local optimal structures for aligned RNA sequences and its application to discovering riboswitch elements. *International Journal of Bioinformatics Research and Applications* DOI: 10.1504/IJBRA.2014.062997
15. Zhong, C., Andrews, J., and Zhang, S. (2014) Discovering non-coding RNA elements in drosophila 3' untranslated regions. *International Journal of Bioinformatics Research and Applications* DOI: 10.1504/IJBRA.2014.062996
16. Zhong, C. and Zhang, S. (2014) Simultaneous folding of alternative RNA structures with mutual constraints: an application to next-generation sequencing-based RNA structure probing. *Journal of Computational Biology* DOI:10.1089/cmb.2013.0044
17. Li, J., Mazar, J.*, Zhong, C.*, Faulkner, G., Govindarajan, S., Zhang, Z., E.Dinger M., Meredith, G., Adams, C., Zhang, S., Mattick, J., Ray, A., and Perera, R. (2013) Genome-wide methylated CpG island profiles of melanoma cells reveal a melanoma coregulation network. *Scientific Reports* 2013, 3:2962 (*equal contribution)
18. Zhong, C. and Zhang, S. (2013) Efficient alignment of RNA secondary structures using sparse dynamic programming. *BMC Bioinformatics* 2013, 14:269
19. Zhong, C., Andrews, J., and Zhang, S. (2012) Discovering non-coding RNA elements in drosophila 3' untranslated regions. In *2nd IEEE International Conference on Computational Advances in Bio and Medical Sciences*, Las Vegas, NV, USA (**Best paper award**)
20. Zhong, C. and Zhang, S. (2012) Clustering RNA structural motifs in ribosomal RNAs using secondary structural alignment. *Nucleic Acids Research* 40, 1307-1317 (**Cover page story**)
21. Mazar, J., Khaitan, D., DeBlasio, D., Zhong, C., Govindarajan, S., Kopanathi, S., Zhang, S., Ray, A. and Perera, R. (2012) Epigenetic Regulation of MicroRNA Genes and the Role of miR-34b in Cell Invasion and Motility in Human Melanoma. *PLoS ONE* 6(9): e24922
22. Zhang, S and Zhong, C. (2010) Computational tools for RNA structural motif identification. *Biotech International*, Vol 22, page 6-9 (invited review)
23. Zhong, C., Tang, H. and Zhang, S. (2010) RNAMotifScan: automatic identification of RNA structural motifs using secondary structural alignment. *Nucleic Acids Research*, 38(18): e176

Awards and honors

- 2013: Award of Outstanding Dissertation: College of Engineering and Computer Science, University of Central Florida (**only one selected from the entire college**)
- 2012: Best Paper Award: *IEEE International Conference on Computational Advances in Bio and Medical Sciences (ICCABS)*, Las Vegas, NV, USA (**only one selected from all accepted papers of the conference**)

Invited talks/posters

- 2018: School of Engineering, SUNY Polytechnic Institute, Utica, NY, USA
- 2017: *IEEE 7th International Conference on Computational Advances in Bio and Medical Sciences (ICCABS)*, Orlando, FL, USA
- 2016: School of Medicine, University of Kansas, Kansas City, KS
- 2016: Department of Electrical Engineering and Computer Science, University of Kansas, Lawrence, KS
- 2016: School of Medicine, Indiana University, Indianapolis, IN
- 2015: Scripps Institute of Oceanography, University of California San Diego, La Jolla, CA
- 2015: Department of Electrical Engineering and Computer Science, University of Central Florida, Orlando, FL
- 2015: *International Symposium of Bioinformatics Research and Applications (ISBRA)*, Norfolk, VA, USA
- 2013: J. Craig Venter Institute, La Jolla, CA
- 2012: *IEEE International Conference on Computational Advances in Bio and Medical Sciences (ICCABS)*, Las Vegas, NV, USA
- 2009: *Research in Computational Molecular Biology (RECOMB)*, Tucson, AZ, USA

Teaching experience

- 2017: Fundamentals of Computer Algorithms
- 2016: Introduction to Bioinformatics
- 2012: Discrete mathematics
- 2011: System software
- 2011: Computer architecture concepts
- 2010: Programming in JavaScript
- 2009: Operating system concepts
- 2008: Introduction to computer information system
- 2008: Database concepts
- 2007: Introduction to programming language with C

Research projects

Assistant Professor, Department of EECS, University of Kansas

Current-2017: Developing efficient and memory frugal metagenomics *de novo* assembly framework

Current-2017: Reconstruction of genome-wide RNA-RNA interactome and RNA secondary structure

Current-2017: Improving effect prediction of non-coding RNA single-nucleotide variants
Current-2017: Improving protein and non-coding RNA discovery and annotation in metagenomic sequencing data
Current-2016: Developing crosslinked chimera reads analysis algorithm (CLAN)
Current-2016: Developing more efficient simultaneous alignment and assembly algorithm and software (GRASP2)
Current-2016: Elucidating the roles of mir-211 in melanoma onset and development

Postdoctoral fellow, Informatics Department, J. Craig Venter Institute

2016-2015: Analysis of metatranscriptomics data from human oral plaque microbiome
2016-2015: Developing profile-based protein homology search programs for metagenomics/metatranscriptomics analysis (program: HMM-GRASPx)
2015-2014: Improving computational efficiency of sequence-based homology search program for metagenomics analysis (program: GRASPx)
2014-2013: Developing fast *de novo* short-peptide assembler (program: SFA-SPA)
2014-2013: Developing sequence-based homology search program for metagenomics analysis (program: GRASP)

Research assistant, Department of EECS, University of Central Florida

2014-2013: Developing RNA secondary homology search program that considers sequencing-based chemical probing data (program: ProbeAlign)
2014-2013: Developing a faster and more accurate RNA 3D motif search program (program: RNAMotifScanX)
2014-2012: Developing a *de novo* folding algorithm for RNA alternative structure detection with chemical probing data (program: MutualFold)
2013-2012: Developing an efficient pairwise RNA secondary structure alignment algorithm (program: ERA)
2013-2011: Analysis the epigenome of human melanoma cancer
2012-2011: Developing a clustering pipeline for non-coding RNA element discovery in the *Drosophila* genome (program: CLCL)
2012-2011: Developing a clustering pipeline to discover novel RNA 3D motif families (program: RNAMSC)
2011-2009: Analysis of bisulfite sequencing and RNA-seq data of human melanoma cancer
2009-2008: Developing a novel algorithm for RNA 3D motif homology search (program: RNAMotifScan)

Academic services

Current: Review Editor, *Frontiers in Genetics (Bioinformatics and Computational Biology)*
2017: Program committee member: *IEEE 7th International Conference on Computational Advances in Bio and Medical Sciences (ICCABS)*, Orlando, FL, USA
2016: Guest Editor, *Bioinformatics and Biology Insights* (Issue: Current Developments in RNA Sequence Analysis)

- 2016: External reviewer, *6th IEEE International Conference on Computational Advances in Bio and Medical Sciences (ICCABS)*, Atlanta, GA, USA
- 2016: Program committee member, *15th International Workshop on Data Mining in Bioinformatics (BIOKDD'16)*, San Francisco, CA, USA
- 2016: Guest reviewer, *Nucleic Acids Research*
- 2015: Guest reviewer, *PLoS ONE*
- 2015: External reviewer, *IEEE International Conference on Bioinformatics and Biomedicine (BIBM)*, Washington D.C., USA
- 2014: Guest reviewer, *BMC Research Note*
- 2014: Guest reviewer, *BMC Bioinformatics*
- 2013: External reviewer, *IEEE International Conference on Computational Advances in Bio and Medical Sciences (ICCABS)*, New Orleans, LA USA
- 2013: External reviewer, *Research in Computational Molecular Biology Satellite Workshop on Massively Parallel Sequencing (RECOMB-seq)*, Beijing, China
- 2012: Organizing volunteer, *ACM conference on Bioinformatics, Computational Biology, and Health Informatics (ACM BCB)*, Orlando, FL, USA
- 2012: External reviewer, *ACM conference on Bioinformatics, Computational Biology, and Health Informatics (ACM BCB)*, Orlando, FL, USA
- 2012: External reviewer, *IEEE International Conference on Bioinformatics and Biomedicine (BIBM)*, Philadelphia, PA, USA
- 2012: External reviewer, *IEEE International Conference on Computational Advances in Bio and Medical Sciences (ICCABS)*, Las Vegas, NV, USA
- 2011: Organizing volunteer, *IEEE International Conference on Computational Advances in Bio and Medical Sciences (ICCABS)*, Orlando, FL, USA

Educational services

- Current: Ph.D. qualifying exam committee member, Department of EECS, University of Kansas
- 2016: Del Lago Academy intern mentor
- 2015: Del Lago Academy eMENTOR program