

## CUNCONG ZHONG Ph.D.

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### Research Areas

**Methods in Computational Biology:** Algorithm and Data Structures, Machine Learning, and Data Mining

**Genomics and Next-generation Sequencing:** Sequence Alignment and Read Mapping, Genome Assembly, Metagenomics, Genetics/Epigenetics, Transcriptomics, and Cancer Genomics

**Noncoding RNA:** RNA Structure Prediction, Noncoding RNA Functional Annotation and Regulatory Network, RNA-RNA Interaction, Noncoding RNA Biomarker Discovery, microRNA Target Prediction

### Education

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

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

2007: Huazhong University of Science and Technology, China, B.S. in Biotechnology

2006: Huazhong University of Science and Technology, China, B.S. in Computer Science

2006: Nanyang Technological University, Singapore, Exchange Program in Chemical Engineering

### 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

Active: "Targeting RNA-Binding Protein HuR as a Novel Therapy for Lethal Prostate Cancer", \$15,000

Department of Defense

Role: co-Investigator

Project period: 08/01/2021 – 07/30/2024

Active: "An autonomous insect Sense, Identify, and Manage PLatform (SIMPL) to advance crop protection strategies", \$300,000

USDA NRI: INT: COLLAB

Role: co-Investigator

Project period: 12/01/2018 – 11/30/2022

Active: "CAREER: A Novel Bioinformatic Infrastructure for Comprehensive and Scalable Metagenomic Sequencing Data Analysis", \$722,398

NSF CAREER Award

Role: Principal Investigator

Project period: 07/01/2020 – 06/30/2025

Active: "RNA-binding protein HuR in liver pathophysiology and carcinogenesis", \$55,607

NIH (R01DK119131)  
Role: co-Investigator  
Project period: 07/01/2019 – 06/30/2024

Active: “Automated identification and classification of laryngeal diseases using deep neural networks”, \$101,190  
NIH 1R03CA253212-01  
Role: co-Investigator  
Project period: 07/10/2020 – 06/30/2022

Completed: “Analysis of genetic variations in the next-generation sequencing data of specific language impairment (SLI) families”, \$2,000  
The University of Kansas Research Excellence Initiative  
Role: Co-Investigator  
Project Period: 01/01/2019 – 12/31/2019

Completed: “Transforming Metagenomic Sequencing Data Analysis with Scalable Assembly and Comprehensive Annotation”, \$150,000  
NSF EPSCoR First Award  
Role: Principal Investigator  
Project period: 05/01/2018-07/31/2019

Completed: “Large-scale *de novo* identification of noncoding RNA”, \$8,000  
The University of Kansas New Faculty General Research Fund  
Role: Principal Investigator  
Project period: 02/28/2017-02/28/2019

Completed: “TEEN Connections for Support from Multidisciplinary Professionals & Peers”, \$6,000  
NIH (NR015743-02)  
Role: Co-Investigator  
Project period: 01/15/2018-06/30/2018

Completed: “High-Precision Polyp Detection based on Convolutional Neural Network”, \$952  
NVIDIA Corp.  
Role: Principal Investigator  
Project period: 12/01/2017-12/01/2018

Completed: “Identification of the molecular mechanism of miR-211 and its target genes in melanocytes and pigmented melanoma senescence and apoptosis”, \$15,000  
NIH (5R21CA202197)  
Role: Co-Investigator  
Project period: 09/01/2016 – 08/31/2018

## **Publications**

1. Thippabhotla, S., Liu, B., Yooseph, S., Yang, Y., Zhang, J., and Zhong, C., (submitted) Integrated *de novo* gene prediction for metagenomic sequencing data (Corresponding author)

2. Zhong, C. and Liu, X., (in revision), The Versatile Alignment Tool (VAT): A High-Performance Multi-Purpose Short Sequence Mapping Toolkit, *BMC Bioinformatics* (Corresponding author)
3. Gajurel, K., Zhong, C., and Wang, G. (2021) A Fine-Grained Visual Attention Approach for Fingerspelling Recognition in the Wild, *2021 IEEE International Conference on Systems, Man, and Cybernetics (SMC)*
4. Li, K., Fathan, M., Patel, K., Zhang, T., Zhong, C., Bansal, A., Rastogi, A., Wang, J., and Wang, G. (2021) Colonoscopy Polyp Detection and Classification: Dataset Creation and Comparative Evaluations, *PLoS ONE* 16(8): e0255809. <https://doi.org/10.1371/journal.pone.0255809>
5. Chau, J., Yadav, M., Liu, B., Furqan, M., Dai, Q., Gupta, A., Mercer, K., Eastman, E., Abu-Hejleh, T., Chan, C., Weiner, G., Cherwin, C., Lee, S., Zhong, C., Mangalam, A., and Zhang, J. (2021) Analysis of patient microbiome and its correlation to the response and immune related adverse effects from immunotherapy in lung cancer, *BMC Cancer*, 21, Article number: 808, <https://doi.org/10.1186/s12885-021-08530-z>
6. Liu, B., Thippabhotla, S., Zhang, J., and Zhong, C., (2021) DRAGoM: Classification and Quantification of Noncoding RNA in Metagenomic Data, *Frontiers in Genetics*, <https://doi.org/10.3389/fgene.2021.669495> (Corresponding author)
7. Zhang, J., Huang, C., Li, M., Liu, B., Zhu, H., Dai, Q., Fan, X., Mehta, K., Huang, C., Neupane, P., Wang, F., Sun, W., Umar, S., and Zhong, C. (2021) Relating gut microbiome and its modulating factors to immunotherapy in solid tumors: a systematic review, *Frontiers in Oncology*, Volume 11, Article 642110
8. Katsushima, K., Lee, B., Kunhiraman, H., Zhong, C., Murath, R., Ying, J., Liu, B., Garancher, A., Gonzalez-Gomez, I., Monforte, H., Stapleton, S., Vibhakar, R., Bettegowda, C., Wechsler-Reya, R., Jallo, G., Raabe, E., Eberhart, C., and Perara, P., (2021) The long non-coding RNA lnc-HLX-2-7 is oncogenic in group 3 medulloblastomas, *Neuro-Oncology*, Volume 23, Issue 4, April 2021, Pages 572–585
9. McClannahan, B., Patel, K., Sajid, U., Zhong, C., and Wang, G. (2020) Classification of Noncoding RNA Elements Using Deep Convolutional Neural Networks, In *IEEE International Conference on Systems, Man, and Cybernetics (SMC2020)*, Toronto, Ontario, Canada
10. Wu, X., Gardashova, G., Lan, L., Han, S., Zhong, C., Marquez, R., Wei, L., Wood, S., Roy, S., Gowthaman, R., Karanicolas, J., Gao, F., Dixon, D., Welch, D., Li, L., Ji, M., Aubé, J., and Xu, L. (2020) Targeting the interaction between RNA-binding protein HuR and FOXQ1 suppresses breast cancer invasion and metastasis, *Communications Biology*, 3:193
11. Aleti, G., Baker, J., Tang, X., Alvarez, R., Dinis, M., Tran, N., Melnik, A., Zhong, C., Ernst, M., Dorrestein, P., & Edlund, A. (2019). Identification of the bacterial biosynthetic gene clusters of the oral microbiome illuminates the unexplored social language of bacteria during health and disease. *mBio* Volume 10 Issue 2 e00321-19
12. Thippabhotla, S., Wei, L., Zhu, Q., Zhong, C., and He, M. (2019) 3D cell culture stimulates the secretion of in vivo like exosomes, *Scientific Reports*, 9, 13012
13. Zhong, C. and Zhang, S. (2019) Accurate and Efficient Mapping of the Crosslinked microRNA-mRNA Hybrid Reads, *iScience*, 18, 11-19 (Corresponding author)
14. Zhong, C. and Zhang, S. (2019) Accurate and Efficient Mapping of the Crosslinked microRNA-mRNA Hybrid Reads, *RECOMB-Seq 2019*, Washington DC, USA (Corresponding author)
15. Zhong, C., Yang, Y., and Yooseph, S. (2019) GRASP2: Fast and Memory-efficient Gene-centric Assembly and Homolog Search for Metagenomic Sequencing Data, *BMC Bioinformatics*, 20(Suppl 11):276 (Corresponding author)
16. 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.
17. 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
18. Zhong, C., Yang, Y., and Yooseph, S. (2017) GRASP2: Fast and Memory-efficient Gene-centric Assembly and Homolog Search, In *IEEE 7<sup>th</sup> International Conference on Computational Advances in Bio and Medical Sciences (ICCBS 2017)*, Orlando, FL USA (Corresponding author)
19. 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
20. 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.
  21. Zhong, C., Yang, Y., and Yooseph, S. (2015) GRASPx: an efficient reference-guided short peptide assembler. In *11<sup>th</sup> International Symposium on Bioinformatics Research and Applications (ISBRA 2015)*, Norfolk, VA, USA
  22. 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
  23. Zhong, C. and Zhang, S. (2015) RNAMotifScanX: a graph alignment approach for RNA structural motif identification. *RNA* 10.1261/rna.044891.114
  24. Zhong, C., Yang, Y., and Yooseph, S. (2014) GRASP: Guided Reference-based Assembly of Short Peptides. *Nucleic Acids Research* doi: 10.1093/nar/gku1210
  25. 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
  26. Ge, P., Zhong, C., and Zhang, S. (2014) ProbeAlign: incorporating high-throughput sequencing based structure probing information into ncRNA homology search. In *4<sup>th</sup> Annual RECOMB Satellite Workshop on Massively Parallel Sequencing (RECOME-Seq 2014)*, Pittsburgh, PA, USA
  27. 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
  28. 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
  29. 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
  30. 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*, 3:2962 (\*equal contribution)
  31. Zhong, C. and Zhang, S. (2013) Efficient alignment of RNA secondary structures using sparse dynamic programming. *BMC Bioinformatics* 2013, 14:269
  32. Zhong, C., Andrews, J., and Zhang, S. (2012) Discovering non-coding RNA elements in drosophila 3' untranslated regions. In *2<sup>nd</sup> IEEE International Conference on Computational Advances in Bio and Medical Sciences (ICCABS 2012)*, Las Vegas, NV, USA (**Best paper award**)
  33. 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**)
  34. 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
  35. Zhang, S and Zhong, C. (2010) Computational tools for RNA structural motif identification. *Biotech International*, Vol 22, page 6-9 (invited review)
  36. 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

### Invited Talks / Posters

2021: *International Conference on Intelligent Biology and Medicine (ICIBM 2021)*, Virtual due to COVID-19  
2019: San Antonio Breast Cancer Symposium, San Antonio, Texas  
2018: Guangdong Institute of Microbiology, Guangzhou, Guangdong, China  
2018: College of Life Science and Technology, Huazhong University of Science and Technology, Wuhan, China  
2018: School of Engineering, SUNY Polytechnic Institute, Utica, NY  
2017: *IEEE 7<sup>th</sup> 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

### **Academic Services**

Current: Review Editor, *Frontiers in Genetics (Bioinformatics and Computational Biology)*  
Current: Lead guest editor: *Frontiers in Physiology Special issue: Non-coding RNAs: Insights and state-of-the-art in Gastrointestinal Sciences*  
2021: Program committee member: *The IEEE International Conference on Bioinformatics and Biomedicine (BIBM 2021)*, Virtual due to COVID-19  
2021: Program committee member: *the 20th International Workshop on Data Mining in Bioinformatics (BIOKDD 2021)*, Virtual due to COVID-19  
2021: Conference section chair: *the 12<sup>th</sup> ACM Conference on Bioinformatics, Computational Biology, and Health Informatics (ACM BCB 2021)*, Virtual due to COVID-19  
2021: Program committee member: *the 12<sup>th</sup> ACM Conference on Bioinformatics, Computational Biology, and Health Informatics (ACM BCB 2021)*, Virtual due to COVID-19  
2021: Program committee member: *International Conference on Intelligent Biology and Medicine (ICIBM 2021)*, Philadelphia, PA, USA  
2021: Guest reviewer: *PLoS ONE*  
2021: Guest reviewer: *Current Microbiology*  
2021: Guest reviewer: *Scientific Reports*  
2020: *ad hoc* reviewer: National Science Foundation, SBIR/STTR program  
2020: Guest reviewer: *Briefings in Bioinformatics*  
2019: Guest reviewer, *RNA Biology*  
2018: Program committee member: *IEEE 8<sup>th</sup> International Conference on Computational Advances in Bio and Medical Sciences (ICCABS)*, Las Vegas, NV, USA  
2017: Program committee member: *IEEE 7<sup>th</sup> 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, *6<sup>th</sup> IEEE International Conference on Computational Advances in Bio and Medical Sciences (ICCABS)*, Atlanta, GA, USA



2016: Program committee member, *15<sup>th</sup> 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: Graduate Admission Committee member, Department of EECS, The University of Kansas  
Current: Scholarship Committee member, Department of EECS, The University of Kansas  
Current: Ph.D. Qualifying Exam Committee member, Department of EECS, The University of Kansas  
2021: Lawrence Free State High School job shadowing experience host  
2016: San Diego Del Lago Academy intern mentor  
2015: San Diego Del Lago Academy eMENTOR program

### **Academic Advising**

#### **Doctoral**

Committee chair: Ben Liu, PhD in Computer Science, Fall 2017 – Present  
Committee chair: Sirisha Thippabhotla, PhD in Computer Science, Fall 2017 – Present  
Committee chair: Hao Xuan, PhD in Computer Science, Spring 2020 – Present  
Committee chair: Adam Podgorny, PhD in Computational Biology, Summer 2020 – Present  
Committee chair: Xi Mo, PhD in Computer Science, Spring 2021 – Present  
Committee chair: Kaidong Li, PhD in Computer Science, Spring 2021 – Present  
Committee chair: Xiangyu Chen, PhD in Computer Science, Spring 2021 – Present  
Committee chair: Tianxiao Zhang, PhD in Computer Science, Spring 2021 – Present  
Committee member: Krushi Patel, PhD in Electrical Engineering, Fall 2018 – Present  
Committee member: Michael Meises, PhD in Computer Science, Spring 2018 – Present  
Committee member: Lanjing Wei, PhD in Bioengineering, Spring 2018 – Present  
Committee member: Sohaib Kiani, PhD in Computer Science, Spring 2018 – Present  
Committee member: Hao Xue, PhD in Computer Science, Fall 2018 - Summer 2019  
Committee member: Erin Andres, PhD in Genetics, Fall 2019 – Present

## **Master**

Committee chair: Tevin Niang-Trost, MS in Computer Science, Summer 2021 – Present  
Committee chair: Kamala Gajurel, MS in Computer Science, Fall 2020 – Fall 2021  
Committee member: Xiaohan Zhang, MS in Computer Science, Spring 2019 – Present  
Committee member: Shashank Sambamoorthy, MS in Computer Science, Spring 2017 – Fall 2019  
Committee member: Rui Cao, MS in Computer Science, Fall 2017 – Summer 2019  
Committee member: Pushkar Negi, MS in Computer Science, Spring 2018 – Fall 2019  
Committee member: Logan Sidener, MS in Computer Science, Spring 2018 – Summer 2018  
Committee member: Pegah Nokhiz, MS in Computer Science, Spring 2018 – Summer 2018  
Committee member: Brian McClannahan, MS in Computer Science, Spring 2019 – Summer 2021  
Committee member: Yiju Yang, MS in Computer Science, Spring 2021 – Summer 2021

## **Teaching Experiences**

### **The University of Kansas**

Current: Data Structures  
Current: Analysis of Algorithms  
Current: Fundamentals of Computer Algorithms  
Current: Introduction to Bioinformatics

### **University of Central Florida**

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

## **Awards and Honors**

2018: Excellence of Service Award: *8<sup>th</sup> IEEE International Conference on Computational Advances in Bio and Medical Sciences (ICCABS)*, Las Vegas, NV, USA  
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: *2<sup>nd</sup> 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**)