Cong Ma
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EDUCATION	**Princeton University**	*2020 - Present*
	Postdoctoral Research Associate in Department of Computer Science	
	Advisor: Ben Raphael	
	Carnegie Mellon University	*2015 - 2020*
	Ph.D. in Computational Biology	
	Advisor: Carl Kingsford	
	Zhejiang University	*2011 - 2015*
	BS Mathematics and Applied Mathematics	
EMPLOYMENT	**Internship at Bristol Myers Squibb**	*Jun 2018 - Aug 2018*
	Translational Bioinformatics-Single Cell Sequencing Analyses Intern Program	
AWARDS	Damon Runyon Quantitative Biology Fellowship	*2022*
	Graduate Student Assembly/Provost Conference Funds (CMU)	*2019*
	ISMB travel fellowship	*2018*
	Outstanding Academic Achievement (CPCB Program)	*2016*

PUBLICATION

Journal publication

1. Cong Ma*, Uthsav Chitra*, Shirley Zhang, and Benjamin J. Raphael. Belayer: Modeling discrete and continuous spatial variation in gene expression from spatially resolved transcriptomics. *Cell Systems*, 13(10):786–797.e13, 2022

2. Cong Ma*, Hongyu Zheng*, and Carl Kingsford. Exact transcript quantification over splice graphs. *Algorithms for Molecular Biology*, 16(1):1–15, 2021

3. Cong Ma and Carl Kingsford. Estimating mutual information under measurement error. *BioRxiv*, page 852384, 2019

4. Cong Ma and Carl Kingsford. Detecting, categorizing, and correcting coverage anomalies of rna-seq quantification. *Cell Systems*, 9(6):589–599, 2019

5. Yutong Qiu*, Cong Ma*, Han Xie, and Carl Kingsford. Detecting transcriptomic structural variants in heterogeneous contexts via the Multiple Compatible Arrangements Problem. *Algorithms for Molecular Biology*, 15(1):1–15, 2020

6. Cong Ma, Mingfu Shao, and Carl Kingsford. SQUID: transcriptomic structural variation detection from RNA-seq. *Genome Biology*, 19(1):52, 2018

7. Fan Wu, Cong Ma, and Cheemeng Tan. Network motifs modulate druggability of cellular targets. *Scientific Reports*, 6, 2016

Conference publication

1. Cong Ma*, Uthsav Chitra*, Shirley Zhang, and Ben Raphael. Belayer: Modeling discrete and continuous spatial variation in gene expression from spatially resolved transcriptomics. In *26th International Conference on Research in Computational Molecular Biology (RECOMB)*, 2022

2. Hongyu Zheng*, Cong Ma*, and Carl Kingsford. Deriving ranges of optimal estimated transcript expression due to non-identifiability. In *25th International Conference on Research in Computational Molecular Biology (RECOMB)*. Cold Spring Harbor Laboratory, 2021

3. Cong Ma*, Hongyu Zheng*, and Carl Kingsford. Exact transcript quantification over splice graphs. In *20th International Workshop on Algorithms in Bioinformatics (WABI 2020)*. Schloss Dagstuhl-Leibniz-Zentrum für Informatik, 2020

4. Yutong Qiu*, Cong Ma*, Han Xie, and Carl Kingsford. Detecting Transcriptomic Structural Variants in Heterogeneous Contexts via the Multiple Compatible Arrangements Problem. In *19th International Workshop on Algorithms in Bioinformatics (WABI 2019)*, volume 143, pages 18:1–18:19, 2019

TALK &
POSTER

- Cong Ma, Uthsav Chitra, Shirley Zhang, and Ben Raphael. Belayer: Modeling discrete and continuous spatial variation in gene expression from spatially resolved transcriptomics. *Damon Runyon Fellows Retreat*, 2022
- Matt Myers, Maya Gupta, Cong Ma, Rebecca Elyanow, Ron Zeira, Max Land, Alexander Strzalkowski, and Ben Raphael. Copy number and tumor clone inference in bulk, single-cell and spatial sequencing data. *NCI Informatics Technology for Cancer Research (ITCR)*, 2022
- Cong Ma. Exact Transcript Quantification Over Splice Graphs. *WABI*, 2020
- Cong Ma and Carl Kingsford. Detecting anomalies in RNA-seq quantification. *RECOMB*, 2019
- Cong Ma. SQUID: Transcriptomic structural variation detection from RNA- seq. *ISMB*, 2018
- Cong Ma. SQUID: Transcriptomic structural variation detection from RNA- seq. *Genome Informatics*, 2017

TEACHING

Guest lecture for Princeton COS 597D Advanced Topics in Computer Science: Computational Methods for Single-cell and Spatial Biology   *Fall 2022*

TA for CMU 02710 Computational Genomics   *Spring 2017*
TA for CMU 02712 Computational Methods for Biological Modeling and Simulation
Fall 2016

ACADEMIC
SERVICE

conference reviewer: RECOMB'15, RECOMB'16, WABI'16, RECOMB'17, RECOMB-CCB'17, ISMB'17, RECOMB'18, ISMB'18, RECOMB'19, ISMB'19, RECOMB'20, RECOMB'21, RECOMB'22, ESA'22, RECOMB'23
journal reviewer: Plos Compbio, Cell Systems, Genome Biology
CPCBGSA: senate for 2017 - 2019