

Yao Tong

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Education	University of Pittsburgh , Graduate School of Public Health Biostatistics Ph.D. Program	2020-Present
	Cornell University , College of Agriculture and Life Sciences Magna Cum Laude, GPA: 3.93 B.S. in Biological Sciences (Concentration: Computational Biology) B.S. in Biometry & Statistics (Concentration: General Statistics) Minor in Computer Science 2 + 2 Program with China Agricultural University	2017-2019
	CHILDREN'S HOSPITAL OF PHILADELPHIA UNIVERSITY OF PENNSYLVANIA <i>Research Tech, Department of Pathology</i> Supervisor: Kai Wang	2019-2020
	<ul style="list-style-type: none">• Develop bioinformatic tools to detect genome-wide short tandem repeat.• Detect DNA modification on the Oxford Nanopore long-read sequencing data by deep learning approaches.• Software development: DeepMod, NanoMod, and RepeatHMM.• Analyze RNA-seq data on Moesin knockout mice.	
	CORNELL UNIVERSITY <i>Research Assistant, Department of Molecular Biology and Genetics</i> Supervisor: Amnon Koren	2017-2019
Research Experience	<ul style="list-style-type: none">• Analyze DNA replication timing (rt) profiles.• Identify rtQTLs in <i>trans</i> and characterize the rtQTLs using computational and statistical methods.	
	GUANGDONG GASTROINTESTINAL HOSPITAL <i>Research Assistant</i> Supervisor: Feng Gao	2018-2019
	<ul style="list-style-type: none">• Use public high-throughput datasets to identify novel gene signature for cancer prognosis.	
Research Experience	CHINESE ACADEMY OF SCIENCES <i>Research Assistant, State Key Laboratory of Stem Cell and Reproductive Biology</i> Supervisor: Zhaoqian Teng	2015-2017
	<ul style="list-style-type: none">• Explore roles of inhibiting the proliferation of microglia in regulating gliosis and neurodegeneration after traumatic brain injury.	

Publications	<ul style="list-style-type: none"> • Liu, Q.#, Tong, Y.#, Wang, K. (2020). Genome-wide detection of short tandem repeat expansions by long-read sequencing. BMC bioinformatics, 21(21), 1-15. • Zhang, L., Zhu, P., Tong, Y. <i>et al.</i> (2019). An immune-related gene pairs signature predicts overall survival in serous ovarian carcinoma. OncoTargets and therapy, 12, 7005. • Shu, P., Wu, J., Tong, Y. <i>et al.</i> (2018). Gene pair based prognostic signature for colorectal colon cancer. Medicine, 97(42). • Ding, Q., Edwards, M.M., Hulke, M.L., Bracci, A.N., Hu, Y., Tong, Y. <i>et al.</i> The Genetic Architecture of DNA Replication Timing in Human Embryonic Stem Cells. (Under review by <i>Nature</i>) • Lai, W., Wang, Y., Tong, Y. <i>et al.</i> Functional evaluation of behavioral phenotypes in a Moesin knockout mouse model. (In preparation)
Softwares	<ul style="list-style-type: none"> • DeepMod A deep-learning tool for genomic-scale, strand-sensitive and single-nucleotide based detection of DNA modifications. • RepeatHMM A novel computational tool to detect any microsatellites from given long reads for a subject of interests.
Teaching Experience	<p>Graduate Teaching Assistant, University of Pittsburgh</p> <p>BIOST 2063: Bayesian Data Science, Spring 2021</p> <p>BIOST 2036: Introduction to Health Data Science, Fall 2020</p>
Technical Skills	<p>Programming Language: R (Advanced), python (Advanced), MATLAB (Intermediate), C (Intermediate), SAS (Basic), SPSS (Basic), Java (Basic)</p> <p>Computer: Linux bash shell, LaTeX, Markdown, Github, MS office suite</p>
Relevant Courses	<p>Statistics: Theory of Statistics ▪ Statistical Methods ▪ Applied Time Series Analysis ▪ Linear Models with Matrices ▪ Statistical Computing ▪ Quantitative Genomics and Genetics ▪ Survival Analysis ▪ Applied Regression Analysis</p> <p>Computer Science: Numerical Analysis ▪ Algorithm Design ▪ Computer System Organization ▪ Machine Learning ▪ Discrete Structures ▪ Object-oriented Programming & Data Structure</p> <p>Biology: Molecular Biology ▪ Bioinformatics ▪ Immunology ▪ Cell Biology ▪ Biochemistry ▪ Genetics ▪ Evolutionary Biology ▪ Cancer Genetics</p>