

CURRICULUM VITAE

Anqi Wang

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PERSONAL INFORMATION

Name: Anqi Wang
Gender: Male
Date of Birth: Feb. 21, 1989
Birth Place: Beijing
Nationality: People's Republic of China
Institution: Department of Systems Biology, Columbia University Irving Medical Center
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EDUCATION

Ph.D. Statistics, Academy of Mathematics and Systems Science, Chinese Academy of Sciences, 2016
Advisor, Prof. Lei M. Li
B.S. Mathematics and Applied Mathematics, School of Mathematical Sciences, Peking University, 2011

POSTDOCTORAL TRAINING

2019.11-Current Department of Systems Biology, Columbia University Irving Medical Center
2019.04-2019.11 Department of Biomedical Informatics, College of Medicine, The Ohio State University (Transferred with lab from Iowa)
2016.06-2019.04 Department of Internal Medicine, Carver College of Medicine, The University of Iowa

RESEARCH EXPERIENCES

2016.06-Current – Epigenetics analysis based on Oxford Nanopore Technologies (ONT): exogenous 5mC detection and nucleosome positioning on single DNA molecule, m6A and pseudouridine detection for direct RNA-seq data.
– Study on mouse sperm mRNA integrity based on RNA-seq (PacBio long reads and Illumina short reads), CAGE and poly(A) signals data.
– Error correction algorithms and related mathematical models for long reads.
2014.01-2016.06 Improving genome assembly that were highly fragmented, highly repetitive or far from complete.
2011.09-2013.12 Short read alignment algorithm and associated statistical evaluation.

PROGRAM PARTICIPATIONS

2014.06-2016.06 *Evolutionary Genotype-Phenotype Systems Biology*, a Strategic Priority Research Program of the Chinese Academy of Sciences

HONORS AND AWARDS

2015.09 2015 (13th) Dean Scholarship, Academy of Mathematics and System Sciences, Chinese Academy of Sciences

COMPUTER SKILLS

Skillful in writing C++ codes, combining C++ with OPENMP to achieve parallel computation. Capable of using Perl, MATLAB, R.

TEACHINGS

1. Autumn 2019, BMI8130, College of Medicine, The Ohio State University.
Course name: *Analysis and Applications of Genome-Scale Data (Tutorial 3: RNA-seq data analysis)*
2. 2019 BMI Bioinformatics Pipeline Training Workshops, College of Medicine, The Ohio State University.
Topic: *ONT long read data analysis*

CONFERENCE TALKS

1. Annual Conference on Intelligent Systems for Molecular Biology (ISMB), July 6-10th, Chicago, 2018.
Topic: *Theoretical analysis of graph-based and alignment-based hybrid error correction methods for error-prone long reads*

INVENTION PATENTS

1. Name: A Method and System of Mapping Sequencing Reads
Applicant: Academy of Mathematics and Systems Science, Chinese Academy of Sciences
Inventors: Lei Li, Anqi Wang, Shijian Chen
Application Date: Jul. 5, 2013
Patent No. 201310282312.1
Note: Application of registry in Hong Kong was submitted on Jan. 7, 2014, with an application No. 14100134.
2. Name: A Method and System of Genome Assembly
Applicant: Academy of Mathematics and Systems Science, Chinese Academy of Sciences
Inventors: Lei Li, Anqi Wang, Zheng Li, Zhanyu Wang
Application Date: Feb. 26, 2016
Application No. 201610109249.5

PUBLICATIONS

Published (* joint-first authors)

1. **Anqi Wang**, Kin Fai Au. Performance difference of graph-based and alignment-based hybrid error correction methods for error-prone long reads. *Genome Biology*, 2019. (Accepted)
2. Yunhao Wang*, **Anqi Wang***, Zujun Liu, Andrew L. Thurman, Linda S. Powers, Meng Zou, Yue Zhao, Adam Hefel, Yunyi Li, Joseph Zabner, Kin Fai Au. Single-molecule long-read sequencing reveals the chromatin basis of gene expression. *Genome Research*, 2019, DOI: 10.1101/gr.251116.119. Cover photo of issue August, 2019.
3. **Anqi Wang***, Zhanyu Wang*, Zheng Li, Lei M. Li. BAUM: improving genome assembly by adaptive unique mapping and local overlap-layout-consensus approach. *Bioinformatics*, 2018, DOI: 10.1093/bioinformatics/bty020. Reported by *Genomics Proteomics & Bioinformatics* as one of the top ten progress in bioinformatics, China, 2018.
4. Shijian Chen*, **Anqi Wang***, Lei M. Li. SEME: A fast mapper of Illumina sequencing reads with statistical evaluation. *Journal of Computational Biology*, 2013, 847-860, DOI: 10.1089/cmb.2013.0111. Proceedings of RECOMB 2013.
5. Shuhua Fu, **Anqi Wang**, Kin Fai Au. A comparative evaluation of hybrid error correction methods for error-prone long reads. *Genome Biology*, 2019, DOI: 10.1186/s13059-018-1605-z.
6. Bo Wang, Lin Wan, **Anqi Wang**, Lei M. Li. An adaptive decorrelation method removes Illumina DNA base-calling errors caused by crosstalk between adjacent clusters. *Scientific Reports*, 2017, DOI: 10.1038/srep41348.

Being processed (* joint-first authors)

1. Yu Huining Sun*, **Anqi Wang***, Chi Song, Rajesh K. Srivastava, Kin Fai Au, Xin Zhiguo Li. Single-molecule long-read sequencing reveals a selection mechanism retaining intact mRNAs enriched in protein synthesis functions in mouse and human sperm. (Under review in *Nature Communications*).