

# Curriculum Vitae

## Xian F. Mallory

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### RESEARCH INTERESTS

I am a computer scientist interested in developing novel computational tools for analyzing large biological data sets to understand biological phenomena and processes, with particular emphasis on cancer. My work draws upon methodologies from combinatorial optimization, statistical inference, and machine learning.

### PROFESSIONAL EXPERIENCE

<b>Florida State University</b> Assistant Professor	Tallahassee, FL Aug. 2020 –
<b>Rice University</b> Postdoctoral Research Associate	Houston, TX 2018 – Jul. 2020
<b>Institute for Genome Sciences University of Maryland in Baltimore</b> Software Engineer	Baltimore, MD 2011 - 2012
<b>The Genome Institute at Washington University</b> Statistical Analyst	St. Louis, MO 2010 - 2011
<b>Siemens Corporate Research</b> Intern	Malvern, PA May. 2008 – Aug. 2008

### EDUCATION

<b>Rice University</b> Ph.D. in Computer Science	Houston, TX 2012 - 2018
<b>Johns Hopkins University</b> M.S. in Electrical and Computer Engineering	Baltimore, MD 2006 - 2008
<b>Shanghai Jiao Tong University</b> M.S. in Pattern Recognition and Intelligent Systems	Shanghai, China 2004 - 2006
<b>Shanghai Jiao Tong University</b> B.S. in Information Engineering	Shanghai, China 2000 - 2004

## HONORS and AWARDS

- Gulf Coast Consortia CCBTP Post-doctoral Fellowship, 2018-2020.
- Travel fellowship to MBI Workshop on Evolutionary Dynamics in Cancer, OSU, 2019.
- Rising Star of EECS, UIUC, 2019.
- Fellowship in Computer Science Department, Rice University, 2012-2013.
- Travel fellowship to HiTSeq/ISMB, Orlando, 2016.

## INVITED TALKS

- Computer Science Department Colloquium @ FSU, Cancer phylogenetics: where computer science attacks cancer, Tallahassee, Florida, Nov. 2020
- Biomedical Sciences Seminar Series @ FSU, Using single-cell sequencing technologies to understand heterogeneity in cancer, Tallahassee, Florida, Aug. 2020
- Human Genome Structural Variation Consortium f2f meeting, May 2016 (CSHL), Oct 2016 (Vancouver) and Oct 2017 (CSHL)
- HiTSeq/ISMB, Orlando, 2016 (<20% oral)
- ASHG, Vancouver, 2016 (<3% oral)
- Southeast Texas Evolutionary Genetics and Genomics (STEGG), Houston, 2016 and 2017
- IEEE Computer Society Workshop on MMBIA, Anchorage, 2008.

## PEER-REVIEWED PUBLICATIONS

1. *Xian F. Mallory*, Mohammadamin Edrisi, Nicholas Navin and Luay Nakhleh, Methods for copy number aberration detection from single-cell DNA-sequencing data, **Genome Biology**, 21(208), (2020).
2. *Xian F. Mallory*, Mohammadamin Edrisi, Nicholas Navin and Luay Nakhleh, Assessing the performance of methods for copy number aberration detection from single-cell DNA sequencing data, **PLoS Computational Biology**, 16(7): e1008012, (2020).
3. Justin Zook ... *Xian Fan* ... Marc Salit, A robust benchmark for detection of germline large deletions and insertions, **Nature Biotechnology**, 1-9, (2020).
4. Mark Chaisson ... *Xian Fan* ... Charles Lee, Multi-platform discovery of haplotype-resolved structural variation in human genomes, **Nature communications**, 10 (2019).
5. *Xian Fan*, Jie Xu, Luay Nakhleh, Detecting Large Indels Using Optical Maps Data, **RECOMB-International Conference on Comparative Genomics** (2018).
6. *Xian Fan*, Mark Chaisson, Luay Nakhleh and Ken Chen, HySA: A Hybrid Structural variant Assembly approach using next generation and single-molecule sequencing technologies, **Genome Research**, 27(5), 793 (2017).
7. Zechen Chong ... *Xian Fan* ... Ken Chen, novoBreak: local assembly for breakpoint detection in cancer genomes, **Nature Methods**, 14(1), 65 (2017).
8. Matthew Wyczalkowski ... *Xian Fan* ... Li Ding, BreakPoint Surveyor: a pipeline for structural variant visualization, **Bioinformatics**, 33(19), 3121 (2017).
9. 1000 Genomes Project Consortium, A global reference for human genetic variation, **Nature**, 526(7571), 68 (2015).
10. Peter Sudmant ... *Xian Fan* ... 1000 Genomes Project Consortium, An integrated map of structural variation in 2,504 human genomes, **Nature**, 526(7571), 75 (2015).

11. Malachi Griffith ... *Xian Fan* ... Richard Wilson, Genome modeling system: a knowledge management platform for genomics, **PLOS Computational Biology**, 11(7), e1004274 (2015).
12. *Xian Fan*, Wanding Zhou, Zechen Chong, Luay Nakhleh and Ken Chen, Towards accurate characterization of clonal heterogeneity based on structural variation, **BMC Bioinformatics**, 15(1), 299 (2014).
13. *Xian Fan*, Travis E. Abbott, David Larson and Ken Chen, BreakDancer: Identification of Genomic Structural Variation from Paired-End Read Mapping, **Current Protocols in Bioinformatics**, 45(1), 15-6 (2014).
14. Ken Chen, Lei Chen, *Xian Fan*, John Wallis, Li Ding and George Weinstock, TIGRA: A targeted iterative graph routing assembler for breakpoint assembly, **Genome Research**, 24(2), 310 (2014) (**co-first author**).
15. *Xian Fan*, Luay Nakhleh, Ken Chen, Integrated genotyping of structural variation, 1<sup>st</sup> IEEE Global Conference on Signal and Image Processing (2013).
16. Ken Chen ... *Xian Fan* ... Li Ding, BreakTrans: uncovering the genomic architecture of gene fusions, **Genome Biology**, 14(8), R87 (2013).
17. Margaret Young ... *Xian Fan* ... Timothy Ley, Background mutations in parental cells contribute to the genetic heterogeneity of Induced Pluripotent, **Cell Stem Cells**, 10(5), 570 (2012).
18. Matthew Walter ... *Xian Fan* ... Timothy Graubert, Clonal architecture of secondary acute myeloid leukemia, **New England Journal of Medicine**, 366(12), 1090 (2012).
19. Jianmin Wang ... *Xian Fan* ... Jinghui Zhang, CREST maps somatic structural variation in cancer genomes with base-pair resolution, **Nature Methods**, 8(8), 652 (2011).
20. Lucas Wartman ... *Xian Fan* ... Timothy Ley, Sequencing a mouse acute promyelocytic leukemia genome reveals genetic events relevant for disease progression, **Journal of Clinical Investigation**, 121(4), 1445 (2011).

## ACADEMIC SERVICES

- **Reviewer for journals** (2015-2020): BMC Bioinformatics, Bioinformatics, Nucleic Acids Research
- **Reviewer for conferences** (2015-2017): RECOMB'17, RECOMB-CBB'17, ICBE'15, ACM-TCBB'17, AICoB'16, AICoB'17
- **Research mentor for an undergraduate student** (June 2019 – Aug. 2019): Rufino Oregon (Texas A&M University)
- **Teaching assistant at Rice University** (2012-2015): COMP582 (Design and Analysis of Algorithms) and COMP571 (Bioinformatics: Sequence Analysis)
- **Coach for an undergraduate project presentation** (Spring, 2017)
- **Coach for exchange students' poster presentations** (Summer, 2017)