

# XIN LI

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## EDUCATION

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**University of Connecticut, Storrs**

2014 - 2019

Ph.D. in Computer Science

**Beihang University, Beijing**

2006 - 2009

M.S. in Computer Software Engineering

## TECHNICAL SKILLS

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- Proficient in C++ (10 years); skillful in Linux shell, Python, C#
- Proficient in high-performance computing (HPC), Slurm
- Proficient in DNA sequence (NGS) analysis and STR fragment analysis
- Skillful in software design, machine learning, bioinformatics and statistics

## RESEARCH PROJECTS

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### **Detecting genomic deletions from NGS data with unsupervised learning**

Develop a new method called EigenDel. EigenDel first uses discordant & clipped reads to get initial deletion candidates, and then it clusters similar candidates by using PCA and hierarchical clustering. Finally, EigenDel uses a carefully designed approach for calling true deletions from each cluster.

### **Detecting circular RNA from high-throughput sequence data with de Bruijn graph**

Develop a new method named CircDBG. It creates a de Bruijn graph based on k-mers from the boundary parts of exons in annotated genome. Then, CircDBG takes advantage of this graph to find the relationship between k-mer of reads and the potential donor/acceptor exon by tracking the path in the graph for circRNA detection. A special case of circRNA, chimeric circRNA, is reported by CircDBG.

### **CircMarker: a fast and accurate algorithm for circular RNA detection**

Develop a new computational approach named CircMarker. CircMarker is based on k-mers rather than reads mapping and takes advantage of annotation files to create the k-mer table for circRNA detection.

## WORK EXPERIENCE

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### **HPC Administrator**

2016 - present

*University of Connecticut, Storrs, CT*

- Provide assistance to the users of HPC cluster in resolving issues and managing support tickets
- System performance analysis and tuning; monitor, analyze, and correct system issues
- Build, install and support user requested software
- Deploy the new hardware, such as computing node and clustered file system

### **R&D Director**

2011 - 2014

### **Software Engineer**

2009 - 2014

*Todaysoft Ltd, Beijing, China (Business Partner of SoftGenetics LLC, State College, PA)*

- Lead the research and development of DNA fragment analysis software (C++)
- Software design, algorithm research, and core code implementation

- Requirements analysis and prototype development for the market in both China and US
- Major Products: ChimerMarker (automated chimerism analysis), GeneMarker HID (STR Human Identity), GeneMarker (genotype analysis), GeneMarker MTP (multi-template processor), GeneMarker DxTerity (nuclear radiation exposure testing), GeneMarker Melting Curve (thalassemia and tuberculosis resistance testing), GeneMarker Maize (corn breeding testing)
- These products have been used by more than 2,000 top-notch labs worldwide

## Research Intern

2007 - 2008

*Siemens Corporate Technology, Beijing, China*

- Software design, algorithm research and implementation in computer graphics
- Develop a product: 3D simulation system of steel refrigeration conveyor line

## AWARDS AND PATENT

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Doctoral Dissertation Fellowship	2019
Predoctoral Fellowship	2019
Predoctoral Honorable Mention	2017, 2018
Travel fellowship, ICCABS	2017
Travel fellowship, ISBRA	2017
Jin Hui Prize, Science and Technology Department of Jiangsu Province, China	2013
PATENT: Wavelet Method to Process the Melting Curve	2013

## ACADEMIC ACTIVITIES

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Poster in 17 <sup>th</sup> APBC	2019
Paper presentation in 13 <sup>th</sup> and 14 <sup>th</sup> ISBRA	2017, 2018
Poster in RECOMB	2017, 2018
Paper presentation in 7 <sup>th</sup> ICCABS	2017
Exhibitor in ASHG	2010

## ACADEMIC SERVICE

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Reviewer of Asia Pacific Bioinformatics Conference (APBC)  
 Reviewer of International Symposium on Bioinformatics Research and Applications (ISBRA)  
 Reviewer of Intl Conference on Computational Advances in Bio and medical Sciences (ICCABS)  
 Reviewer of International Conference on Bioinformatics and Computational Biology (BICoB)

## PUBLICATIONS

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1. Detecting genomic deletions from high-throughput sequence data with unsupervised learning. Xin Li, Yufeng Wu, *Scientific Report*, Revise and Resubmit, 2019
  2. Detecting circular RNA from high-throughput sequence data with de Bruijn graph. Xin Li, Yufeng Wu, *BMC Genomics*, Accepted, 2019
  3. CircMarker: a fast and accurate algorithm for circular RNA detection. Xin Li, Chong Chu, Jingwen Pei, Ion Mandoiu, Yufeng Wu, *BMC Genomics*, 2018
  4. CLADES: A classification-based machine learning method for species delimitation from population genetic data. JW Pei, Chong Chu, Xin Li, Bin Lu, YF Wu, *Molecular Ecology Resources*, 2018
  5. GAPPadder: a sensitive approach for closing gaps on draft genomes with short sequence reads. Chong Chu, Xin Li and Yufeng Wu, *BMC Genomics*, 2017
  6. SpliceJumper: a classification-based approach for calling splicing junctions from RNA-seq data. Chong Chu, Xin Li and Yufeng Wu, *BMC Bioinformatics*, 2017