

XIN LI

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EDUCATION

University of Connecticut, Storrs

2014 - 2019

Ph.D. in Computer Science

Beihang University, Beijing

2006-2009

M.S. in Software Engineering

TECHNICAL SKILLS

- Proficient in C++ (10 years). Skillful in Linux Shell, Python, C#
- Proficient in High Performance Computing, Slurm
- Proficient in DNA Sequence (NGS) analysis and STR fragment analysis
- Skillful in Software Design, Machine Learning, Bioinformatics and Statistics

RESEARCH PROJECTS

Detecting genomic deletions from NGS data with unsupervised learning

Developed 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

Presented a new method named CircDBG, which creates a de Bruijn graph based on k-mers from the boundary parts of exons in annotated genome. Then, we take 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. Reported a special case of circRNA: chimeric circRNA.

CircMarker: a fast and accurate algorithm for circular RNA detection

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

WORK EXPERIENCE

HPC Administrator

2016 - present

University of Connecticut, Storrs, CT

- Providing 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.
- Building, installing and supporting user requested software.
- Deploy the new hardwares, such as computing nodes and storage file system.

R&D Director

2011 - 2014

Software Engineer

2009 - 2011

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

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

- User 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.
- Developed a product: 3D Simulation System of Steel Refrigeration Conveyor Line.

AWARDS AND PATENT

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

Poster in 17 th APBC	2019
Present paper in 13 th and 14 th ISBRA	2017, 2018
Poster in RECOMB	2017, 2018
Present paper in 7 th ICCABS	2017
Exhibitor in ASHG	2010

ACADEMIC SERVICE

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 WuEmail, BMC Bioinformatics, 2017