WEIHUA PAN

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EDUCATION

University of California, Riverside Ph.D. in Computer Science M.S. in Statistics	2019 (expected) 2018
University of Science and Technology of China M.E. in Computer Software and Theory	2014
Nanjing Normal University B.E. in Computer Science and Technology	2011

PUBLICATIONS

1. W. Pan, T. Jiang, S. Lonardi. "OMGS: Optical Map-based Genome Scaffolding." *Proceedings of Conference on Research in Computational Molecular Biology (RECOMB)*, to appear, Washington, DC, 2019.

2. W. Pan, S. Lonardi. "Accurate detection of chimeric contigs via Bionano optical maps." *Bioinformatics*, vol. 34, to appear.

3. W. Pan, S. Wanamaker, A. Ah-Fong, H. Judelson, S. Lonardi. "Novo&Stitch: Accurate Reconciliation of Genome Assemblies via Optical Maps." *Proceedings of Conference on Intelligent Systems for Molecular Biology (ISMB)*, Chicago, IL, 2018. *Bioinformatics*, vol. 34, no. 13, pp. i43-i51, 2018.

4. A. Polishko, M. A. Hasan, **W. Pan**, E. Bunnik, K. L. Roch, S. Lonardi. "ThIEF: Finding Genomewide Trajectories of Epigenetics Marks." *Proceedings of the Workshop on Algorithms in Bioinformatics* (WABI), 19:1-19:16, Boston, MA, 2017.

5. W. Pan, B. Chen, Y. Xu. "MetaObtainer: A Tool for Obtaining Specified Species from Metagenomic Reads of Next-generation Sequencing." *Interdisciplinary Sciences: Computational Life Sciences*, vol. 7, no. 4, pp. 405-413, 2015.

6. W. Pan, Y. Zhao, Y. Xu, F. Zhou. "WinHAP2: an extremely fast haplotype phasing program for long genotype sequences." *BMC bioinformatics* vol. 15, no. 1, pp. 164, 2014.

7. X. Su^{*}, **W. Pan**^{*}, B. Song, J. Xu, K. Ning. "Parallel-META 2.0: enhanced metagenomic data analysis with functional annotation, high performance computing and advanced visualization." *PloS one*, vol. 9, no. 3, pp. e89323, 2014. (* indicates authors that contributed equally)

EXPERIENCE

Graduate Student Researcher / Teaching Assistant University of California, Riverside

2014 -Advisor: Dr. Stefano Lonardi

- \cdot Developed three algorithms *Novo&Stitch*, *OMGS* and *Chimericognizer* to solve assembly reconciliation, scaffolding and chimeric removal problems in *de novo* genome assembly with Bionano optical maps.
- \cdot Developed two deep learning models for CRISPR guide RNA activity prediction and differential chromatin interactions detection.

Data Scientist Intern Tempus, Inc. Supervisor: Dr. Mathew Barber

· Developed statistics models and methods for deconvolution of mixed cancer transcriptomes and recognition of frequent cancer treatment regimens.

	Graduate Student Researcher / Teaching Assistant	2011 - 2014	
	University of Science and Technology of China	Advisor: Dr. Yun Xu	
•	Improved a haplotype inference algorithm $WinHAP$ to version 2 in time efficiency and memory efficiency		
	by divide-and-conquer strategy and parallelization.		
•	Developed a novel supervised metagenome short reads binning algorithm <i>Met</i> both similarity-based and composite-based binning methods.	<i>aObtainer</i> by combining	

Bioinformatics Intern

Chinese Academy of Sciences

• Improved a metagenomics functional analysis tool *Parallel-MATA* to version 2.

SOFTWARE

1. **OMGS**: Optical Map based *de novo* Genome Scaffolding Tool https://github.com/ucrbioinfo/OMGS

2. Chimericognizer: Optical Map based Chimeric Contigs Correction Tool https://github.com/ucrbioinfo/Chimericognizer

3. Novo&Stitch: Optical Map based de novo Genome Assemblies Reconciliation Tool https://github.com/ucrbioinfo/Novo_Stitch

4. WinHAP2: Large-scale Haplotype Inference Tool http://staff.ustc.edu.cn/~xuyun/winhap

5. **Parallel-META**: Metagenomics Functional Analysis Pipeline http://bioinfo.single-cell.cn/parallel-meta.html

6. MetaObtainer: Supervised Metagenome NGS Reads Binning Tool http://www.cs.ucr.edu/~wpan005/metaobtainer

REVIEWING ACTIVITIES

Reviewer for Journals

· Scientific Reports

Subreviewer for Conferences

- · Research in Computational Biology (RECOMB) 2015
- · International Conference on Intelligent Systems for Molecular Biology (ISMB) 2018, 2019
- · ACM Conference on Bioinformatics, Computational Biology, and Health Informatics (ACM-BCB) 2015, 2016, 2018
- · RECOMB Satellite Workshop on Massively Parallel Sequencing (RECOMB-Seq) 2015
- · Workshop on Algorithms in Bioinformatics (WABI) 2015, 2017

2018

2012

Advisor: Dr. Kang Ning