

YANG LU

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EMPLOYMENT

University of Washington, Department of Genome Sciences
Postdoctoral Fellow
Advisor: Prof. William Stafford Noble

Seattle, WA
2018/01 - present

EDUCATION

University of Southern California
Ph.D. in Computational Biology and Bioinformatics
Advisor: Prof. Fengzhu Sun

Los Angeles, CA
2017/08

Shanghai Jiao Tong University
M.S. in Computer Science

Shanghai, China
2013/03

Shanghai Jiao Tong University
B.S. in Computer and Software Engineering

Shanghai, China
2010/06

WORK EXPERIENCE

- **Microsoft Research Asia**, Beijing, 2011/06 - 2011/11
Research Intern: worked on spike detection and abnormal activity association in Office365 backend.
- **Microsoft Bing**, Shanghai, 2010/11 - 2011/05
Software Engineer Intern: worked on developing data analysis and deployment tools for Commerce Transaction Platform.
- **Tencent**, Shanghai, 2010/04 - 2010/08
Software Engineer Intern: worked on developing the user interface of Tencent Mobile Manager.
- **Ericsson**, Shanghai, 2009/08 - 2009/11
Software Engineer Intern: worked developing a rich-client SNS tool based on Flex.

TEACHING EXPERIENCE

- **Teaching Assistant.** Statistics for the Biological Sciences, Fall 2015
Department of Biological Science, University of Southern California
- **Teaching Assistant.** Introduction to Artificial Intelligence, Spring 2012
Department of Computer Science and Engineering, Shanghai Jiao Tong University
- **Teaching Assistant.** Introduction to Bioinformatics, Fall 2011
Department of Computer Science and Engineering, Shanghai Jiao Tong University

ACADEMIC HONORS

- Provost's Fellowship, University of Southern California, 2013-2015.
- Graduate Fellowship, Shanghai Jiao Tong University, 2010-2013.

PUBLICATIONS

* indicates equal contribution.

PAPERS AS LEADING AUTHOR

1. **Y.Y. Lu***, W. Guo*, X. Xing, and W.S. Noble. “DANCE: Enhancing saliency maps using decoys”. **International Conference on Machine Learning (ICML)**, 2021.
2. **Y.Y. Lu**, T. Yu, G. Bonora, and W.S. Noble. “ACE: Explaining cluster from an adversarial perspective”. **International Conference on Machine Learning (ICML)**, 2021.
3. **Y.Y. Lu**, J. Bilmes, R.A. Rodriguez-Mias, J. Villen, and W.S. Noble. “DIAMeter: Matching peptides to data-independent acquisition mass spectrometry data”. **International Conference on Intelligent Systems for Molecular Biology (ISMB)**, 2021
4. **Y.Y. Lu***, J. Bai*, Y. Wang, Y. Wang, and F. Sun. “CRAFT: Compact genome Representation towards large-scale Alignment-Free daTabase”. **Bioinformatics**, 37(2):155-161, 2020.
5. J. Schreiber*, **Y.Y. Lu ***, and W.S. Noble. “Ledidi: Designing genomic edits that induce functional activity”. **ICML Workshop on Computational Biology**, 2020.
6. **Y.Y. Lu***, Y. Fan*, J. Lv, and W.S. Noble. “DeepPINK: reproducible feature selection in deep neural networks”. **Advances in Neural Information Processing Systems (NeurIPS)**, 8676-8686, 2018
7. **Y.Y. Lu**, J. Lv, J.A. Fuhrman, and F. Sun. “Towards enhanced and interpretable clustering/classification in integrative genomics”. **Nucleic Acids Research**, 45(20):e169, 2017.
8. **Y.Y. Lu**, K. Tang, J. Ren, J.A. Fuhrman, M.S. Waterman and F. Sun. “CAFE: aCcelerated Alignment-FrEe sequence analysis”. **Nucleic Acids Research**, 45(W1):W554-W559, 2017.
9. **Y.Y. Lu**, T. Chen, J.A. Fuhrman, and F. Sun. “COCACOLA: binning metagenomic contigs using sequence COMposition, read CoverAge, CO-alignment and paired-end read LinkAge”. **Bioinformatics**, 33(6):791-798, 2017.

PAPERS AS SUPPORTING AUTHOR

10. Z. Wang, Z. Wang, **Y.Y. Lu**, F. Sun, and S. Zhu. “SolidBin: Improving Metagenome Binning with Semi-supervised Normalized Cut”. **Bioinformatics**, 35(21):4229-4238, 2019.
11. D.F. Read, K. Cook, **Y.Y. Lu**, K.G. Le Roch, and W.S. Noble. “Predicting gene expression in the human malaria parasite Plasmodium falciparum using histone modification, nucleosome positioning, and 3D localization features”. **PLoS Computational Biology**, 15(9):e1007329, 2019.
12. A. Hu, **Y.Y. Lu**, J. Bilmes, and W.S. Noble. “Joint precursor elution profile inference via regression for peptide detection in data-independent acquisition mass spectra”. **Journal of Proteome Research**, 18(1):86-94, 2018.
13. J. Ren, X. Bai, **Y.Y. Lu**, K. Tang, Y. Wang, G. Reinert, and F. Sun. “Alignment-free sequence analysis and applications”. **Annual Review of Biomedical Data Science**, 1:93-114, 2018.
14. K. Tang, **Y.Y. Lu**, and F. Sun. “Background Adjusted Alignment-free Dissimilarity Measures Improve the Detection of Horizontal Gene Transfer”. **Frontiers in Microbiology**, 9:711, 2018.
15. Y. Wang, K. Wang, **Y.Y. Lu**, and F. Sun. “Improving contig binning of metagenomic data using d_2^S oligonucleotide frequency dissimilarity”. **BMC Bioinformatics**, 18(1):425, 2018.
16. J. Ren, N.A. Ahlgren, **Y.Y. Lu**, J.A. Fuhrman, and F. Sun. “VirFinder: a novel k-mer based tool for identifying viral sequences from assembled metagenomic data”. **Microbiome**, 5(1):69, 2017.
17. N.A. Ahlgren, Jie Ren, **Y.Y. Lu**, J.A. Fuhrman, and F. Sun. “Alignment-free d_2^* oligonucleotide frequency dissimilarity measure improves prediction of hosts from metagenomically-derived viral sequences”. **Nucleic Acids Research**, 45(1):39-53, 2017.

INVITED TALKS

1. “Binning metagenomic contigs using sequence composition, read coverage, co-alignment and paired-end read linkage”
 - The Joint Statistical Meetings (JSM), Chicago, 2016/08
 - RECOMB-Seq, Santa Monica, 2015/04
 - USC MCB Retreat, Los Angeles, 2014/11
2. “DIASibling: Learning to detect sibling peptide pairs in data independent acquisition mass spectrometry data”

- Cascadia Proteomics Symposium, Seattle, 2019/07
 - ASMS Conference on Mass Spectrometry and Allied Topics, Atlanta, 2019/06
3. “DIAMeter: Matching peptides to data independent acquisition mass spectrometry data”
 - ASMS Conference on Mass Spectrometry and Allied Topics, 2020/06
 - International Conference on Intelligent Systems for Molecular Biology (ISMB), 2021/07
 4. “ACE: Explaining cluster from an adversarial perspective”
 - International Conference on Machine Learning (ICML), 2021/07
 - International Conference on Intelligent Systems for Molecular Biology (ISMB), 2021/07
 5. “DANCE: Enhancing saliency maps using decoys”
 - International Conference on Machine Learning (ICML), 2021/07

SERVICE

- Reviewer (Journals) - *Nature Methods*, *Nature Communications*, *Genome Biology*, *Nucleic Acids Research*, *Bioinformatics*, *Briefings in Bioinformatics*, *BMC Bioinformatics*, and *Frontiers in Genetics*.
- Reviewer (Conferences) - *NeurIPS*, *ICML*, *ICLR*, *AISTATS*, *AAAI*, *RECOMB*, *ISMB*, and *APBC*

REFERENCES

FROM ACADEMIA

Prof. William Stafford Noble
 Professor
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 Computer Science and Engineering
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Prof. Michael Waterman
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 Dept. of Biological Sciences, Mathematics,
 and Computer Science
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FROM INDUSTRY

Dr. Qingwei Lin
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