

CURRICULUM VITAE

Yu Lin

CONTACT INFORMATION	Research School of Computer Science College of Engineering & Computer Science Australian National University Acton, ACT 2601, Australia	<i>Office:</i> (+61)261254509 <i>Mobile:</i> (+61)420811129 <i>E-mail:</i> yu.lin@anu.edu.au <i>Website:</i> users.cecs.anu.edu.au/u1024708/
WORKING AND EDUCATION	Australian National University, 2016– Lecturer in the Research School of Computer Science University of California, San Diego (UCSD), 2013–2016 Postdoctoral Scholar in the Department of Computer Science and Engineering <ul style="list-style-type: none">• Advisor: Prof. Pavel Pevzner Ecole Polytechnique Fédérale de Lausanne (EPFL), 2007–2013 PhD., Computer Science in 2012 <ul style="list-style-type: none">• Advisor: Prof. Bernard Moret• Thesis: Models and algorithms for whole-genome evolution and their use in phylogenetic inference (nominated for the EPFL Thesis Award) Chinese Academy of Sciences, China, 2004–2007 M.S., Computer Science and Engineering in 2007 <ul style="list-style-type: none">• Advisor: Prof. Dongbo Bu University of Science and Technology of China (USTC), 2000–2004 B.S., Computer Science and Engineering in 2004	
PROFESSIONAL ACTIVITIES:	<i>Program Committee</i> ISMB'14, ISMB/ECCB'15, APBC'16, XRCI Open'16, ISMB'16, ECCB'16, APBC'17, WABI'17 <i>Journal Referee</i> IEEE/ACM Transactions on Computational Biology and Bioinformatics, PLoS One, Journal of Discrete Algorithms, BMC Research Notes, Information Processing Letters, Algorithms for Molecular Biology, Journal of Combinatorial Optimization, Discrete Applied Mathematics, Bioinformatics, Journal of ACM <i>Conference Referee</i> RECOMB'10, WABI'11, WABI'12, ALLENEX'12, ECCB'14, WABI'14 RECOMB-CG'14, APBC'15, BIBM'15, RECOMB'16, SODA'16	
AWARDS	Swiss National Science Foundation, Award P300P2_154563 (Nov 2014 – Apr 2016) PI (providing salary and support for postdoctoral research) Swiss National Science Foundation, Award PBELP2_146708 (May 2013 – Oct 2014) PI (providing salary and support for postdoctoral research) Best Paper Award, the 14th Asia Pacific Bioinformatics Conference (2016) Chinese Government Award for Outstanding Self-Financed Students Abroad (2012) K.C. Wong Scholarship, Oxford University (2007) Full scholarship and stipend for DPhil study (declined) Director's Award, Institute of Computing Technology, Chinese Academy of Sciences (2007) Guo Moruo Award (President's Award), University of Science and Technology of China (2004)	
RESEARCH INTERESTS	Computational Biology and Bioinformatics: <i>Genome Assembly:</i> sequence assembly and error correction in DNA sequencing	

PUBLICATIONS

1. **Lin, Y.**, Yuan, J., Shen, M.W., Kolmogorova, M., Chaisson, M. and Pevzner, P.A., "Assembly of long error-prone reads using de Bruijn graphs," *Proc Natl Acad Sci* (2016).
2. Zhou, L., **Lin, Y.**, Feng, B., Zhao, J., and Tang, J., "Phylogeny reconstruction from whole-genome data using variable length binary encoding", *Proc. 12th Int'l Symp. Bioinformatics Research & Appls. ISBRA16*, 345-346, (2016)
3. Zhou, J., **Lin, Y.**, Rajan, V., Hoskins, W., Feng, B., and Tang, J., "Analysis of gene copy number changes in tumor phylogenetics", *Algorithms for Molecular Biology* 11(1) 26, (2016)
4. **Lin, Y.**, Shen, M.W., Yuan, J., and Pevzner, P.A., "Assembly of long error-prone reads using de Bruijn graphs", in *Proc. 20th Int'l Conf. on Research in Comput. Molecular Bio. (RECOMB'16)* .
5. Nair, N.U., Hunter, L., Shao, M., Grnarova, P., **Lin, Y.**, Bucher, P. and Moret, B.M.E., "A maximum-likelihood approach for building cell-type trees by lifting", *BMC Genomics*, 17, 1, 14 (2016).
6. Zhou, J., **Lin, Y.**, Rajan, V., Hoskins, W., and Tang, J., "Maximum parsimony analysis of gene copy number changes in tumor phylogenetics," *Proc. 15th Workshop on Algorithms in Bioinformatics (WABI'15)*, 108-120, Springer Berlin Heidelberg, (2015).
7. Zhou, J., **Lin, Y.**, Hoskins, W., and Tang, J., "An iterative approach for phylogenetic analysis of tumor progression using FISH copy number," *Int'l Symp. Bioinformatics Research & Appls. (ISBRA'15)*, 402-412. Springer International Publishing (2015).
8. Shao, M., **Lin, Y.**, and Moret, B.M.E., "An exact algorithm to compute the DCJ distance for genomes with duplicate genes," *J. Computational Biology* 22, 5, 425-435 (2015).
9. **Lin, Y.** and Pevzner, P.A., "Manifold de Bruijn Graphs," *Proc. 14th Workshop on Algorithms in Bioinformatics (WABI'14)*, 296-310, Springer Berlin Heidelberg, (2014).
10. **Lin, Y.**, Nurk, S., and Pevzner, P.A., "What is the difference between the breakpoint graph and the de Bruijn graph?" *BMC Genomics*, 15(Suppl 6), S6, (2014).
11. Hu, F. **Lin, Y.**, and Tang, J., "MLGO: phylogeny reconstruction and ancestral inference from gene-order data" *BMC Bioinformatics* 15:354, (2014).
12. Shao, M., **Lin, Y.**, and Moret, B.M.E., "An exact algorithm to compute the DCJ distance for genomes with duplicate genes," *Proc. 18th Int'l Conf. on Research in Comput. Molecular Bio. (RECOMB'14)*, in Lecture Notes in Computer Science 8394, 280-292, Springer Verlag (2014).
13. Nair, N.U., **Lin, Y.**, Manasovska, A., Antic, J., Grnarova, P., Sahu, A.D., Bucher, P., and Moret, B.M.E., "Study of cell differentiation by phylogenetic analysis using histone modification data," *BMC Bioinformatics*, 15:269 (2014)
14. **Lin, Y.**, Hu, F., Tang, J., and Moret, B.M.E., "Maximum likelihood phylogenetic reconstruction from high-resolution whole-genome data and a tree of 68 eukaryotes," *Proc. 18th Pacific Symp. on Biocomputing (PSB'13)*, 285-296, (2013).
15. Shao, M., **Lin, Y.**, and Moret, B.M.E., "Sorting genomes with rearrangements and segmental duplications through trajectory graphs," *Proc. 11th RECOMB Workshop on Comparative Genomics (RECOMB-CG'13)*, published in *BMC Bioinformatics* 14 (Suppl. 15):S9 (2013).
16. Nair, N.U., **Lin, Y.**, Bcher, P., and Moret, B.M.E., "Phylogenetic Analysis of Cell Types using Histone Modifications," *Proc. 13th Workshop on Algorithms in Bioinformatics (WABI'13)*, in Lecture Notes in Computer Science 8126, 326-337, Springer Verlag (2013).
17. Moret, B.M.E., **Lin, Y.**, and Tang, J., "Rearrangements in phylogenetic inference: Compare, model, or encode?" *Proc. Conf. on Models and Algorithms in Genome Evolution (MAGE) 2013*, vol. 19 of Computational Biology series, Chauve, C., et al., eds, 147-172, Springer Verlag (2013).
18. **Lin, Y.**, Rajan, V., and Moret, B.M.E., "TIBA: A tool for phylogeny inference from rearrangement data with bootstrap analysis," *Bioinformatics* 28(24), 3324-3325 (2012).

19. Shao, M., **Lin, Y.**, “Approximating the edit distance for genomes under DCJ, insertion and deletion,” *Proc. 10th RECOMB Workshop on Comparative Genomics (RECOMB-CG’12)*, published in *BMC Bioinformatics* 13 (Suppl 19):S13 (2012).
20. **Lin, Y.**, Rajan, V., and Moret, B.M.E., “Bootstrapping phylogenies inferred from rearrangement data,” *BMC Algorithms for Molecular Biology* 7, 21 (2012).
21. **Lin, Y.**, Rajan, V., and Moret, B.M.E., “A metric for phylogenetic trees based on matching,” *IEEE/ACM Trans. on Computational Biology and Bioinformatics* 9, 4, 1014-1022 (2012).
22. **Lin, Y.**, Rajan, V., and Moret, B.M.E., “Bootstrapping phylogenies inferred from rearrangement data,” *Proc. 11th Workshop on Algorithms in Bioinformatics (WABI’11)*, Lecture Notes in Computer Science 6833, 175-187, Springer Verlag (2011).
23. **Lin, Y.**, and Moret, B.M.E., “A new genomic evolutionary model for rearrangements, duplications, and losses that applies across eukaryotes and prokaryotes,” *J. Computational Biology* 18, 9, 1055-1064 (2011).
24. **Lin, Y.**, Rajan, V., and Moret, B.M.E., “Fast and accurate phylogenetic reconstruction from high-resolution whole-genome data and a novel robustness estimator,” *J. Computational Biology* 18, 9, 1131-1139 (2011).
25. **Lin, Y.**, Rajan, V., and Moret, B.M.E., “A metric for phylogenetic trees based on matching,” *Proc. 7th Int’l Symp. Bioinformatics Research & Appls. (ISBRA’11)*, Lecture Notes in Computer Science 6674, 197-208, Springer Verlag (2011).
26. **Lin, Y.**, and Moret, B.M.E., “A new genomic evolutionary model for rearrangements, duplications, and losses that applies across eukaryotes and prokaryotes,” *Proc. 8th RECOMB Workshop on Comparative Genomics (RECOMB-CG’10)*, in Lecture Notes in Computer Science 6398, 228-239, Springer Verlag (2010).
27. **Lin, Y.**, Rajan, V., and Moret, B.M.E., “Fast and accurate phylogenetic reconstruction from high-resolution whole-genome data and a novel robustness estimator,” *Proc. 8th RECOMB Workshop on Comparative Genomics (RECOMB-CG’10)*, in Lecture Notes in Computer Science 6398, 137-148, Springer Verlag (2010).
28. **Lin, Y.**, Rajan, V., Swenson, K.M., and Moret, B.M.E., “Estimating true evolutionary distances under rearrangements, duplications, and losses,” *Proc. 8th Asia-Pacific Bioinformatics Conf. (APBC’10)*, published in *BMC Bioinformatics* 2010, 11 (Suppl. 1):S54.
29. Rajan, V., Xu, A.W., **Lin, Y.**, Swenson, K.M., and Moret, B.M.E., “Heuristics for the inversion median problem,” *Proc. 8th Asia-Pacific Bioinformatics Conf. (APBC’10)*, published in *BMC Bioinformatics* (Suppl. 1):S30 (2010).
30. Swenson, K.M., Rajan, V., **Lin, Y.**, and Moret, B.M.E., “Sorting signed permutations by inversions in $O(n \log n)$ time,” *J. Computational Biology*, 17, 3 (2010), 489-501.
31. Swenson, K.M., **Lin, Y.**, Rajan, V., and Moret, B.M.E., “Hurdles and sorting by inversions: Combinatorial, statistical, and experimental results,” *J. Computational Biology*, 16(10):1339-1351 (2009).
32. Swenson, K.M., Rajan, V., **Lin, Y.**, and Moret, B.M.E., “Sorting signed permutations by inversions in $O(n \log n)$ time,” *Proc. 13th Int’l Conf. on Research in Comput. Molecular Biol. (RECOMB’09)*, in Lecture Notes in Computer Science 5541, 386-399, Springer Verlag (2009).
33. Swenson, K.M., **Lin, Y.**, Rajan, V., and Moret, B.M.E., “Hurdles hardly have to be heeded,” *Proc. 6th RECOMB Workshop on Comparative Genomics (RECOMB-CG’08)*, in Lecture Notes in Computer Science 5267, 239-249, Springer Verlag (2008).
34. **Lin, Y.**, and Moret, B.M.E., “Estimating true evolutionary distances under the DCJ model”, *Proc. 16th Conf. on Intelligent Systems for Molecular Biol. (ISMB’08)*, published in *Bioinformatics* 24(13):i114-i122 (2008).
35. Wang, L., **Lin, Y.**, and Liu, X., “Approximation algorithms for biclustering problems”, *SIAM J. Computing* 38(4): 1504-1518 (2008).

36. **Lin, Y.**, Qiao, Y., Sun, S., Yu, C, Dong G., and Bu, D. "A fragmentation event model for peptide identification by mass spectrometry," *Proc. 12th Int'l Conf. on Research in Comput. Molecular Biol. (RECOMB'08)*, in Lecture Notes in Computer Science 4955, 154-166, Springer Verlag (2008).
37. Sun, S., Yu, C., Qiao, Y., **Lin, Y.**, Dong, G., Liu, C., Zhang, J., Zhang, Z., Cai, J., Zhang, H., and Bu, D., "Deriving the probabilities of water loss and ammonia loss for amino acids from tandem mass spectra", *J. Proteome Research*, 7 (01): 202-208 (2008).
38. Yu, C., **Lin, Y.**, Sun, S., Cai, J., Zhang, J., Bu, D., Zhang, Z., and Chen, R., "An iterative algorithm to quantify factors influencing peptide fragmentation during tandem mass spectrometry", *J. Bioinformatics and Computational Biology*, 5(2a):297-311 (2007).
39. Wang, L., **Lin, Y.**, and Liu, X., "Approximation algorithms for bi-clustering problems," *Proc. 6th Workshop on Algorithms in Bioinformatics (WABI'06)*, Lecture Notes in Computer Science 4175, 310-320, Springer Verlag (2006).
40. Yu, C., **Lin, Y.**, Sun, S., Cai, J., Zhang, J., Bu, D., Zhang, Z., and Chen, R., "An iterative algorithm to quantify the factors influencing peptide fragmentation for MS/MS spectrum", *Proc. 5th Comput. Systems Bioinformatics Conf. (CSB'06)*, 353-360, Imperial College Press (2006)