CURRICULUM VITAE

Yu Lin

CONTACT INFORMATION	R4.25, Building 145

CONTACT
INFORMATION

R4.25, Building 145
School of Computing
College of Engineering and Computer Science
Australian National University
Canberra, Australia

Phone: (+61) 2 6125 4509
E-mail: yu.lin@anu.edu.au
Personal website: users.cecs.anu.edu.au/u1024708/
Group website: cgg-anu.github.io
Google Scholar: Link

CURRENT
EMPLOYMENT

Australian National University, Australia, 2016-
    Lecturer (2016-2020), Senior Lecturer (2021-) at the School of Computing,
    the College of Engineering and Computer Science

EDUCATION AND
TRAINING

University of California, San Diego (UCSD), USA, 2013-2016
    Postdoctoral Scholar in Department of Computer Science and Engineering
    • Advisor: Prof. Pavel Pevzner

Ecole Polytechnique Fédérale de Lausanne (EPFL), Switzerland, 2007-2013
    Ph.D., Computer Science in 2012
    • Advisor: Prof. Bernard Moret
    • Thesis: Models and Algorithms for Whole-Genome Evolution and Their Use in Phylogenetic
      Inference

Chinese Academy of Sciences, China, 2004-2007
    M.S., Computer Science
    • Advisor: Prof. Dongbo Bu

University of Science and Technology of China (USTC), China, 2000-2004
    B.S., Computer Science

AWARDS

Early Career Researcher (ECR) Outstanding Contribution Award, the Australian Bioinformatics and
Computational Biology Society (2020)

Best Paper Award, the 14th Asia Pacific Bioinformatics Conference (2016)

Nominated for EPFL Thesis Award (2012)

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 (University Medal), University of Science and Technology of China (2004)

RESEARCH
INTEREST

Models and Algorithms in:
    Genome Assembly
    Metagenomics Analysis
    Comparative Genomics
    Phylogenomics
    Functional Genomics and Epigenetics
    Cancer Genomics
    Computational Proteomics
    Network Analysis and Data Management

GRANTS	Australian Research Council, Discovery Projects DP220101352 (Jan 2022 – Dec 2024)

GRANTS

Australian Research Council, Discovery Projects DP220101352 (Jan 2022 – Dec 2024)
How novel ribosomal RNA gene repeat variants drive cellular function
- Chief Investigator, led by Prof Eduardo Eyras at JCSMR, ANU (AUD 637,955)

PacBio HiFi for All SMRT Grant
Unraveling the Mechanisms of Sex Determination in Reptiles (2021)
- Awarded to Ira Deveson (lead, Garvan Institute, Australia), Yu Lin and other colleagues
- 10 SMRT Cells 8M for sequencing (AUD 100,000, estimated)

ANU Vice-Chancellor's Teaching Enhancement Grant (2017 - 2018)
DataAnalytics-Bench: Personalised Learning in Large Classes
- Awarded to Qing Wang (lead), Yu Lin and other colleagues (AUD 10,000)

NVIDIA GPU Grant (2018)
Integration of GPU Accelerated Computations in Bioinformatics
- Awarded one Titan Xp ($\approx$ AUD 2,000) via the GPU Grant Program

ANU ECR Travel Grant (2018)
Travel support for RECOMB'18 conference (AUD 3,000)

Hong Kong Research Grants Council, Grant 11203115 (Nov 2015 – Oct 2018)
Chromosome structure inference, alignment and application
- co-Investor with PI Shuaicheng Li (HKD 500,000 $\approx$ AUD 90,000, providing 24-month salary and support for a postdoc)

Swiss National Science Foundation, Grant P300P2_154563 (Nov 2014 – Apr 2016)
Study of mosaic structures of segmental duplications from de Bruijn graphs
- sole PI (USD 74,000 $\approx$ AUD 100,000, providing 18-month salary and support for a postdoc)

Swiss National Science Foundation, Grant PBELP2_146708 (May 2013 – Oct 2014)
Comparative and phylogenetic analyses of multiple whole genomes using graph models
- sole PI (USD 63,000 $\approx$ AUD 90,000, providing 18-month salary and support for a postdoc)

COMPUTING
SUPPORT

National Computational Infrastructure (NCI), Australia (2020)
The Amphibian and Reptile Genome Assembly and Annotations
- sole PI, 3,000,000 CPU hours in 2021 (ANUMAS Scheme)

National Computational Infrastructure (NCI), Australia (2019-)
Metagenome Sequence Assembly and Analysis
- sole PI, 100,000 CPU hours per year (ANU-Startup Scheme)

National Computational Infrastructure (NCI), Australia (2019-)
Large Graph Models and Analysis in Genome Assembly
- sole PI, 100,000 CPU hours per year (ANU-Biodev Scheme)

National Computational Infrastructure (NCI), Australia (2017)
Large-Scale Genome Assembly and Analysis
- sole PI, 100,000 CPU hours (ANU-Startup Scheme)

LIST OF
PUBLICATIONS

Book Chapters

1. B. Moret, **Y. Lin**, and J. Tang., "Rearrangements in Phylogenetic Inference: Compare, Model, or Encode?", *Models and Algorithms in Genome Evolution*, 147-172, Springer (2013).

Journal Publications

2. M. Farhan, Q. Wang, **Y. Lin** and B. Mckay, "Fast fully dynamic labelling for distance queries", in press, *The VLDB Journal*, (2022).

3. H. Liany, **Y. Lin**, A. Jeyasekharan, V. Rajan, "An Algorithm to Mine Therapeutic Motifs for

Cancer from Networks of Genetic Interactions", in press, *IEEE Journal of Biomedical and Health Informatics* (2022).

4. J. Zhao, H. Feng, D. Zhu and **Y. Lin**, "MultiTrans: a novel algorithm for transcriptome assembly through mixed integer linear programming", *IEEE/ACM Trans. on Computational Biology and Bioinformatics*, 19(1), 48-56, Special Issue for *19th Asia Pacific Bioinformatics Conference (APBC'21)* (2022)

5. A. Wickramarachchi and **Y. Lin**, "GraphPlas: Refined Classification of Plasmid Sequences using Assembly Graphs", *IEEE/ACM Trans. on Computational Biology and Bioinformatics*, 19(1), 57-67, Special Issue for *19th Asia Pacific Bioinformatics Conference (APBC'21)* (2022)

6. V. Mallawaarachchi, A. Wickramarachchi and **Y. Lin**, "Improving Metagenomic Binning Results with Overlapped Bins Using Assembly Graphs", *Algorithms for Molecular Biology*, 16, No, 3, (2021)

7. P. Bongaerts, ..., **Y. Lin**, ..., O. Hoegh-Guldberg, "Morphological stasis masks ecologically divergent coral species on tropical reefs", *Current Biology*, 31(11), 2286-2298.e8 (2021).

8. M. Chen, P. Huang, **Y. Lin** and S. Cai, "SSNE: Effective Node Representation for Link Prediction in Sparse Networks," in *IEEE Access*, vol. 9, pp. 57874-57885, (2021)

9. V. Mallawaarachchi, A. Wickramarachchi and **Y. Lin**, "GraphBin: Refined Binning of Metagenomic Contigs Using Assembly Graphs", *Bioinformatics*, 36(11):3307-3313 (2020)

10. A. Wickramarachchi, V. Mallawaarachchi, V. Rajan and **Y. Lin**, "MetaBCC-LR: Metagenomics Binning by Coverage and Composition for Long Reads", *Bioinformatics*, 36(S1), i3-i11, Special Issue for *Proc. 26th Conf. on Intelligent Systems for Molecular Biology (ISMB'20)*, (2020)

11. Y. Li and **Y. Lin**, "DCHap: A Divide-and-Conquer Haplotype Phasing Algorithm for Third-Generation Sequences", *IEEE/ACM Trans. on Computational Biology and Bioinformatics*, Special Issue for *the 18th Asia Pacific Bioinformatics Conference (APBC'20)* (2020).

12. Y. Yang, X. Liu, C. Shen, **Y. Lin**, P. Yang and L. Qiao, "In Silico Spectral Libraries by Deep Learning Facilitate Data-Independent Acquisition Proteomics", *Nature Communications* 11 (1), 1-11 (2020).

13. M. Kolmogorov, J. Yuan, **Y. Lin**, P. Pevzner, "Assembly of Long Error-Prone Reads Using Repeat Graphs", *Nature Biotechnology*, 540–546 (2019).

14. J. Shao, Q. Wang and **Y. Lin**, "Skyblocking for Entity Resolution", *Information Systems*, Volume 85, 30-43 (2019)

15. Y. Zhang, W. Liu, **Y. Lin**, Y. Ng, and S. Li, "Large-scale 3D Chromatin Reconstruction from Chromosomal Contacts", *BMC Genomics*, 20 (Suppl 2) :186 (2019)

16. T. Wong, L. Ranjard, **Y. Lin**, A. Rodrigo, "HaploJuice: Accurate Haplotype Assembly from a Pool of Sequences with Known Relative Concentrations", *BMC Bioinformatics*, 22;19(1):389 (2018)

17. Y. Yang, **Y. Lin**, and L. Qiao, "Direct MALDI-TOF MS Identification of Bacterial Mixtures", *Analytical Chemistry*, 90 (17), pp 10400–0408 (2018)

18. L. Pu, **Y. Lin**, and P. Pevzner, "Detection and Analysis of Ancient Segmental Duplications in Mammalian Genomes", *Genome Research*, 28: 901-909 (2018).

19. R. Xia, **Y. Lin**, J Zhou, B. Feng and J. Tang, "Phylogenetic Reconstruction for Copy-Number Evolution Problems", *IEEE/ACM Trans. on Computational Biology and Bioinformatics*, 16(2): 694-699 (2018).

20. L. Pu, **Y. Lin**, D. Zhu and H. Jiang, "Can a Breakpoint Graph Be Decomposed Into None Other Than 2-cycles?", *Theoretical Computer Science* (2018), 743: 38-45.

21. R. Xia, **Y. Lin**, J. Zhou, B. Feng, and J. Tang, "A Median Solver and Phylogenetic Inference Based on Double-Cut-and-Join Sorting," *J. Computational Biology*, 5(3):302-312. (2018)

22. B. Feng, **Y. Lin**, L. Zhou, Y. Guo, R. Friedman, R. Xia, F. Hu, C. Liu and J. Tang, "Reconstructing Yeasts Phylogenies and Ancestors from Whole Genome Data", *Scientific Reports* 7 (1), 15209 (2017)

23. L. Zhou, **Y. Lin**, B. Feng, J. Zhao and J. Tang, "Phylogeny Analysis from Gene-Order Data with Massive Duplications," *BMC Genomics* 18 (7), 13 (2017)

24. Y. Yang, **Y. Lin**, Z. Chen, T. Gong, P. Yang, H. Girault, B. Liu, B and L. Qiao, "Bacterial Whole Cell Typing by Mass Spectra Pattern Matching with Bootstrapping Assessment," *Analytical Chemistry* 89 (22), 12556-12561 (2017).

25. **Y. Lin**, J. Yuan, M Shen, M. Kolmogorov, M Chaisson and P. Pevzner, "Assembly of Long Error-Prone Reads Using de Bruijn Graphs," *Proceedings of the National Academy of Sciences USA*, vol. 113, no. 52, E8396-E8405 (2016).

26. J. Zhou, **Y. Lin**, V. Rajan, W. Hoskins and J. Tang, "Analysis of Gene Copy Number Changes in Tumor Phylogenetics", *BMC Algorithms for Molecular Biology* 11(1) 26, (2016)

27. N. Nair, L. Hunter, M. Shao, P. Grnarova, **Y. Lin**, P. Bucher and B. Moret. "A Maximum-Likelihood Approach for Building Cell-Type Trees by Lifting", *BMC Genomics*, 17, 1, 14, Best Paper Award in *Asia Pacific Bioinformatics Conference (APBC'16)* (2016).

28. M. Shao, **Y. Lin**, and B. Moret, "An Exact Algorithm to Compute the DCJ Distance for Genomes with Duplicate Genes," *J. Computational Biology* 22, 5, 425-435 (2015).

29. **Y. Lin**, S. Nurk and P. Pevzner, "What is the Difference between the Breakpoint Graph and the de Bruijn Graph?" *BMC Genomics*, 15(Suppl 6), S6, (2014).

30. F. Hu, **Y. Lin** and J. Tang., "MLGO: Phylogeny Reconstruction and Ancestral Inference from Gene-Order Data" *BMC Bioinformatics* 15:354, (2014).

31. N. Nair, **Y. Lin**, A. Manasovska, J. Antic, P. Grnarova, A. Sahu, P. Bucher and B. Moret, "Study of Cell Differentiation by Phylogenetic Analysis Using Histone Modification Data," *BMC Bioinformatics*, 15:269 (2014)

32. M. Shao, **Y. Lin** and B. Moret, "Sorting Genomes with Rearrangements and Segmental Duplications through Trajectory Graphs," *BMC Bioinformatics* 14 (Suppl. 15):S9 (2013).

33. M. Shao, **Y. Lin**, "Approximating the Edit Distance for Genomes under DCJ, Insertion and Deletion," *BMC Bioinformatics* 13 (Suppl 19):S13 (2012).

34. **Y. Lin**, V. Rajan, and B. Moret, "TIBA: A Tool for Phylogeny Inference from Rearrangement Data with Bootstrap Analysis," *Bioinformatics* 28(24), 3324-3325 (2012).

35. **Y. Lin**, V. Rajan, and B. Moret, "Bootstrapping Phylogenies Inferred from Rearrangement Data," *BMC Algorithms for Molecular Biology* 7, 21 (2012).

36. **Y. Lin**, V. Rajan, and B. Moret, "A Metric for Phylogenetic Trees Based on Matching," *IEEE/ACM Trans. on Computational Biology and Bioinformatics* 9, 4, 1014-1022 (2012).

37. **Y. Lin**, and B. Moret, "A New Genomic Evolutionary Model for Rearrangements, Duplications, and Losses that Applies across Eukaryotes and Prokaryotes," *J. Computational Biology* 18, 9, 1055-1064 (2011).

38. **Y. Lin**, V. Rajan, and B. Moret, "Fast and Accurate Phylogenetic Reconstruction from High-Resolution Whole-Genome Data and A Novel Robustness Estimator," *J. Computational Biology* 18, 9, 1131-1139 (2011).

39. **Y. Lin**, V. Rajan, K. Swenson and B. Moret, "Estimating True Evolutionary Distances under Rearrangements, Duplications, and Losses," *BMC Bioinformatics 2010*, 11 (Suppl. 1):S54.

40. V. Rajan, A. Xu, **Y. Lin**, K. Swenson and B. Moret, "Heuristics for the Inversion Median Problem," *BMC Bioinformatics* (Suppl. 1):S30 (2010).

41. K. Swenson, V. Rajan, **Y. Lin** and B. Moret, "Sorting Signed Permutations by Inversions in O(nlogn) Time," *J. Computational Biology*, 17, 3 (2010), 489-501.

42. K. Swenson, **Y. Lin**, V. Rajan and B. Moret, "Hurdles and Sorting by Inversions: Combinatorial, Statistical, and Experimental Results," *J. Computational Biology*, 16(10):1339-1351 (2009).

43. **Y. Lin** and B. Moret, "Estimating True Evolutionary Distances under the DCJ model", *Bioinformatics* 24(13):i114-i122, Special Issue for *Proc. 16th Conf. on Intelligent Systems for Molecular Biology (ISMB'08)*, (2008).

44. L. Wang, **Y. Lin** and X. Liu, "Approximation Algorithms for Biclustering Problems", *SIAM J. Computing* 38(4): 1504-1518 (2008).

45. S. Sun, C. Yu, Y. Qiao, **Y. Lin**, G. Dong, C. Liu, J. Zhang, Z. Zhang, J. Cai, H. Zhang and D. Bu, "Deriving the Probabilities of Water Loss and Ammonia Loss for Amino Acids from Tandem Mass Spectra", *J. Proteome Research,* 7 (01): 202-208 (2008).

46. C. Yu, **Y. Lin**, S. Sun, J. Cai, J. Zhang, D. Bu, Z Zhang and R. Chen, "An Iterative Algorithm to Quantify Factors Influencing Peptide Fragmentation during Tandem Mass Spectrometry", *J. Bioinformatics and Computational Biology,* 5(2a):297-311 (2007).

Conference Publications

47. A. Wickramarachchi, **Y. Lin**, "Metagenomics Binning of Long Reads Using Read-Overlap Graphs" *Proc. 19th RECOMB Satellite Conference on Comparative Genomics (RECOMB-CG'22)*, (2022).

48. V. Mallawaarachchi and **Y. Lin**, "MetaCoAG: Binning Metagenomic Contigs via Composition, Coverage and Assembly Graphs", accepted, *the 26th International Conference on Research in Computational Molecular Biology (RECOMB'22)*, (2022).

49. H. Xue, V. Mallawaarachchi, Y. Zhang, V. Rajan, and **Y. Lin**, "RepBin: Constraint-based Graph Representation Learning for Metagenomic Binning", accepted, *the 36th AAAI Conference on Artificial Intelligence (AAAI'22)* (2022).

50. H. Xue, L. Yang, V. Rajan, W. Jiang, Y. Wei, and **Y. Lin**, "Multiplex Bipartite Network Embedding using Dual Hypergraph Convolutional Networks", *the 30th International World Wide Web Conference (WebConf'21)*, 1649–1660, (2021).

51. Y. Wang, Q. Wang, H. Koehler, and **Y. Lin**, "Query-by-Sketch: Scaling Shortest Path Graph Queries on Very Large Networks", *the ACM Special Interest Group on Management of Data (SIGMOD'21)*, 1946–1958, (2021).

52. A. Wickramarachchi and **Y. Lin**, "LRBinner: Binning Long Reads in Metagenomics Datasets", *Proc. 21st Workshop on Algorithms in Bioinformatics (WABI'21)*, 8:1-18, Springer Berlin Heidelberg, (2021).

53. A. Wickramarachchi, V. Mallawaarachchi, L. Pu and **Y. Lin**, "PlasLR Enables Adaptation of Plasmid Prediction for Error-Prone Long Reads ", *the 14th Great Lakes Bioinformatics (GLBIO) conference (GLBIO'21)* (2021).

54. Y. Li, H. Patel and **Y. Lin**, "Kmer2SNP: reference-free SNP calling from raw reads based on matching", *IEEE International Conference on Bioinformatics and Biomedicine (BIBM'20)*, 208-212, (2020).

55. V. Mallawaarachchi, A. Wickramarachchi and **Y. Lin**, "GraphBin2: Refined and Overlapped Binning of Metagenomic Contigs Using Assembly Graphs", *Proc. 20th Workshop on Algorithms in Bioinformatics (WABI'20)*, 8:1-21, Springer Berlin Heidelberg, (2020).

56. H. Xue, L. Yang, W. Jiang, Y. Wei, Y. Hu and **Y. Lin**, "Modeling Dynamic Heterogeneous Network for Link Prediction using Hierarchical Attention with Temporal RNN", accepted, *European Conference on Machine Learning and Principles and Practice of Knowledge Discovery in Databases (ECML-PKDD'20*, in Lecture Notes in Computer Science 12457, 282-298, Springer Verlag (2020).

57. H. Liany, **Y. Lin**, A. Jeyasekharan, V. Rajan, "Mining Pathway Associations from Networks of Mutual Exclusivity Interactions", accepted, *RECOMB Satellite Conference on Computational Cancer Biology (RECOMB-CCB'20)* (2020).

58. M. Iftikhar, Q. Wang and **Y. Lin**, "dK-Microaggregation: Anonymizing Graphs with Differential Privacy Guarantees", *Pacific-Asia Conference on Knowledge Discovery and Data Mining (PAKDD'20)*, 191-203 (2020).

59. M. Iftikhar, Q. Wang and **Y. Lin**, "Publishing Differentially Private Datasets via Stable Microaggregation " (short paper), *Proc. 22nd Int'l Conference on Extending Database Technology (EDBT'19),* 662-665 (2019).

60. M. Farhan, Q. Wang, **Y. Lin** and B. Mckay, "A Highly Scalable Labelling Approach for Exact Distance Queries in Complex Networks", *Proc. 22nd Int'l Conference on Extending Database Technology (EDBT'19),* 13-24 (2019).

61. M. Kolmogorov, J. Yuan, **Y. Lin** and P. Pevzner, "Assembly of Long Error-Prone Reads and Repeat Classification," *Proc. 22nd Int'l Conf. on Research in Comput. Molecular Bio. (RECOMB'18)*, in Lecture Notes in Computer Science 10812, 261-262, Springer Verlag (2018).

62. **Y. Lin**, M. Shen, J. Yuan and P. Pevzner, "Assembly of Long Error-Prone Reads using de Bruijn Graphs", in*Proc. 20th Int'l Conf. on Research in Comput. Molecular Bio. (RECOMB'16)*, in Lecture Notes in Computer Science 9649, 265, Springer Verlag (2016).

63. L. Zhou, **Y. Lin**, B. Feng, J. Zhao and J. Tang, "Phylogeny Reconstruction from Whole-Genome Data Using Variable Length Binary Encoding", *Proc. 12th Int'l Symp.Bioinformatics Research & Appls. (ISBRA'16)*, in Lecture Notes in Computer Science 9683, 345-346, Springer Verlag (2016)

64. J. Zhou, **Y. Lin**, V. Rajan, W. Hoskins and J. Tang, "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).

65. J. Zhou, **Y. Lin**, W. Hoskins and J. Tang, "An iterative Approach for Phylogenetic Analysis of Tumor Progression using FISH Copy Number," *Proc. 11th Int'l Symp. Bioinformatics Research & Appls. (ISBRA'15)*, 402-412. Springer International Publishing (2015).

66. **Y. Lin** and P. Pevzner, "Manifold de Bruijn Graphs," *Proc. 14th Workshop on Algorithms in Bioinformatics (WABI'14)*, 296-310, Springer Berlin Heidelberg, (2014).

67. M. Shao, **Y. Lin** and B. Moret, "An Exact Algorithm to Compute the DCJ Distance for Genomes with Duplicate Genes," *Proc. 18th Int'l Conf. on Research in Comput. Molecular Bio. (RE-COMB'14)*, in Lecture Notes in Computer Science 8394, 280-292, Springer Verlag (2014).

68. **Y. Lin**, F. Hu, J. Tang and B. Moret, "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).

69. N. Nair, **Y. Lin**, P. Bücher and B. Moret, "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).

70. **Y. Lin**, V. Rajan and B. Moret, "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).

71. **Y. Lin**, V. Rajan and B. Moret, "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).

72. **Y. Lin** and B. Moret, "A New Genomic Evolutionary Model for Rearrangements, Duplications, and Losses that Applies across Eukaryotes and Prokaryotes," *Proc. 8th RECOMB Satellite Conference on Comparative Genomics (RECOMB-CG'10)*, in Lecture Notes in Computer Science 6398, 228-239, Springer Verlag (2010).

73. **Y. Lin**, V. Rajan and B. Moret, "Fast and Accurate Phylogenetic Reconstruction from High-Resolution Whole-Genome Data and a Novel Robustness Estimator," *Proc. 8th RECOMB Satellite Conference on Comparative Genomics (RECOMB-CG'10)*, in Lecture Notes in Computer Science 6398, 137-148, Springer Verlag (2010).

74. K. Swenson, V. Rajan, **Y. Lin** and B. Moret, "Sorting Signed Permutations by Inversions in O(nlogn) 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).

75. K. Swenson, **Y. Lin**, V. Rajan and B. Moret, "Hurdles Hardly Have to be Heeded," *Proc. 6th RECOMB Satellite Conference on Comparative Genomics (RECOMB-CG'08)*, in Lecture Notes in Computer Science 5267, 239-249, Springer Verlag (2008).

76. **Y. Lin**, Y. Qiao, S. Sun, C. Yu, G. Dong and D. Bu. "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).

77. L. Wang, **Y. Lin** and X. Liu, "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).

78. C. Yu, **Y. Lin**, S. Sun, J. Cai, J. Zhang, D. Bu, Z. Zhang and R. Chen, "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)

STUDENT SUPERVISION AT ANU

Primary Supervisor and Panel Chair for PhD students
Yanbo Li, ANU School of Computing (08/2017-), Thesis submitted in 02/2022
Anuradha Wickramarachchi, ANU School of Computing (08/2018-), Thesis submitted in 02/2022
Vijini Mallawaarachchi, ANU School of Computing (08/2018-), Thesis submitted in 02/2022
Hansheng Xue, ANU School of Computing (09/2019-)
Yujia Zhang, ANU School of Computing (07/2021-)

Associate Supervisor and Panel Chair for PhD students
Yuchen Li, ANU School of Computing (08/2021-)
Jing Li, ANU School of Computing (08/2021-)

Associate Supervisor for PhD students
Wei Wang, ANU Research School of Biology (07/2018- 05/2020)
Muhammad Farhan, ANU School of Computing (02/2018-)
Dehai Zhao, ANU School of Computing (06/2018-)
Masooma Iftikhar, ANU School of Computing (08/2018-)
Emiliana Weiss, ANU John Curtin School of Medical Research (07/2020-)
Nhan Trong Ly, ANU School of Computing (02/2021-)

Supervisor for Undergraduate, Honours and Postgraduate Students
Runpeng Luo, ANU School of Computing (02/2022-)
Kishor J, ANU School of Computing (02/2022-)
Xingjian Leng, ANU School of Computing (02/2022-)
Wei Zhou, ANU School of Computing (02/2022-)
Kirat Alreja, ANU School of Computing (02/2022-)
Robert McArthur, ANU School of Computing (02/2022-)
Fenghua Chen, ANU School of Computing (02/2022-)
Ruikang Zhou, ANU School of Computing (02/2022-)
Wenhuan Song, ANU School of Computing (02/2021-06/2021)
Muxing Li, ANU School of Computing (02/2021-11/2021)
Jiajia Xu, ANU School of Computing (07/2019-11/2019)
Beilei Wang, ANU School of Computing (07/2018-06/2019)
Xinglu Dong, ANU School of Computing (07/2018-06/2019)
Yuting Zou, ANU School of Computing (07/2018-06/2019)
Qiuyue Wang, ANU School of Computing (07/2018-06/2019)
Yu Zhang, ANU School of Computing (07/2018-06/2019)
Boyu Zhang, ANU School of Computing (07/2017-06/2018)
Muduo Lei, ANU School of Computing (02/2018-06/2018)
Hao Zhang, ANU School of Computing (02/2017-06/2017)

INVITED TALKS	National Keynote Speaker

INVITED TALKS

National Keynote Speaker
- Australian Bioinformatics & Computational Biology Society Annual Conference, 2020

Invited Tutorials
- BioInfoSummer, the Australian Mathematical Sciences Institute, 2021
- STEM Guest Lecture Series, the Australian National University, 2021
- Workshop on Computational Methods for String and Graph and Their Applications in Bioinformatics, the National University of Singapore, 2020.
- 'Cai Xitao' Forum, the Chinese Academy of Sciences, 2018

Invited Research Talks (selected)
- Institute for Mathematical Sciences, the National University of Singapore, 2022
- Symposium on Host-Microbiome Interactions, the Australian National University, 2019
- Tongji Medical College, Huazhong University of Science and Technology, 2019
- Computational Biology Fest, the Australian National University, 2018
- ITN-ICBU Technology Department-Algorithm, the Alibaba Hangzhou Headquarters, 2017
- 'Bernard Moret Festschrift', Department of Electrical Engineering & Computer Sciences, the University of California, Berkeley, 2017
- School of Biological and Health Systems Engineering, the Arizona State University, 2016
- School of Computer and Communication Sciences, EPFL, 2016
- Computer Science Department, the State University of New York at Binghamton, 2016
- School of Informatics and Computing, Indiana University-Purdue University Indianapolis, 2016
- Department of Computer Science and Engineering, Lehigh University. 2016

TEACHING EXPERIENCES

Australian National University, Australia (2016 -)
Convener and Lecturer
2021: COMP2400/6240 (Relational Databases) 632 students
2020: COMP2400/6240 (Relational Databases) 609 students
2019: COMP2400/6240 (Relational Databases) 585 students
2018: COMP2400/6240 (Relational Databases) 584 students
2017: COMP2400/6240 (Relational Databases) 423 students

Lecturer
2020, COMP7240 Introduction to Database Concepts (Graduate Certificate of Data Engineering)
    (in charge of tutor interview and recruitment and 2-week online classrooms)
2019-2021, BIOL8002 Advanced Topics in Quantitative Biology and Bioinformatics
    (in charge of a 3-week module on "Computational Genomics")
2017, COMP7240 Introduction to Database Concepts (Master of Applied Data Analytics)
    (in charge of 3-week online lectures and 2-day on campus lectures in the blended mode)

University of California, San Diego (UCSD), USA (2013 - 2016)
Contributor
Bioinformatics Algorithms, MOOC on Coursera
Guest Lecturer
CSE282 Biological Sequence and Structure, CSE181 Bioinformatics Algorithms

Ecole Polytechnique Fédérale de Lausanne (EPFL), Switzerland (2008-2012)
Guest Lecturer
Advanced Algorithms, Computational Molecular Biology, Advanced Theoretical Computer Science

University of Geneva, Switzerland (2012)
Guest Lecturer
Phylogeny and Molecular Evolution

PROFESSIONAL SERVICE AND ACTIVITIES	**Australian National University, Australia**

Australian National University, Australia
- Associate Director (Educational Partnerships), School of Computing (2021-)
- HDR Scholarship Committee, School of Computing (2021-)
- HDR Convener for Computational Science and Data Science & Analytics (2021-)
- Student Experience Committee at College of Engineering and Computer Science (2018-2020)
- Disciplinary Committee of Master of Science in Quantitative Biology and Bioinformatics (2017-2018)
- Contributor, Summer School at College of Engineering and Computer Science, 2019
- Contributor, Winter School at College of Engineering and Computer Science, (2017-2019)

Professional Membership and Engagement within Australia
- Member, Australian Bioinformatics and Computational Biology Society (2016-)
- Contributor, Reef Future Genomics 2020 Consortium (2017-)
- Contributor, Reference Genome Project at National Centre for Indigenous Genomics (2018-)
- Member, Bioinformatics Working Group of Australian Amphibian and Reptile Genomics Initiative (2020-)

University of California, San Diego (UCSD), USA
- Graduate Admission Committee, the Department of Computer Science and Engineering (2014-2015)

Program Committee of International Conferences
- The Annual International Conference on Intelligent Systems for Molecular Biology (ISMB), 2014-2016
- The European Conference on Computational Biology (ECCB), 2015-2016
- The Workshop on Algorithms in Bioinformatics (WABI), 2017-2019, 2021-2022
- The annual RECOMB Satellite Conference on Comparative Genomics (RECOMB-CG), 2019-2022
- The Asia-Pacific Bioinformatics Conference (APBC), 2017-2020 (Session Chair in 2019)
- The ACM Conference on Bioinformatics, Computational Biology and Health Informatics (ACM-BCB), 2018

Editorial Board
- Associate Editor in Molecular Evolution, *Frontiers in Molecular Biosciences*
- Editorial Board in Statistical Genetics and Methodology, *Frontiers in Genetics*

Journal Referee
- Journal of ACM, Algorithmica, Systematic Biology, Proceedings of the National Academy of Sciences USA, Bioinformatics, BMC Genomics, Information Processing Letters, Algorithms, Journal of Combinatorial Optimization, Journal of Discrete Algorithms, IEEE/ACM Transactions on Computational Biology and Bioinformatics, PLoS One, Current Genomics, PeerJ, BMC Research Notes

Conference Referee
- The Annual International Conference on Research in Computational Molecular Biology (RECOMB)
- ACM-SIAM Symposium on Discrete Algorithms (SODA)
- The International Conference on Genome Informatics (GIW)
- The IEEE International Conference on Bioinformatics and Biomedicine (BIBM)
- The SIAM Meeting on Algorithm Engineering and Experiments (ALENEX)